



High throughput study of biofilm and virulence in *Listeria monocytogenes* using innovative approaches

Bo-Hyung Lee

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High throughput study of biofilm and virulence in
Listeria monocytogenes using innovative approaches

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General introduction

Listeria monocytogenes is ubiquitous in nature. The bacteria reveal high plasticity in the lifestyle from an extracellular free-living saprophyte or sessile bacteria embedded in a biofilm to an intracellular parasite causing listeriosis (Freitag et al., 2009). Soil is believed to be the natural reservoir, however, the bacteria is repeatedly discovered from a broad range of environments (Sauders et al., 2012). Despite the lack of sporulation, it is widely distributed as a result of its high adaptability and ability to survive adverse environments. The bacterium exhibits high tolerance and resistance to stressful physicochemical conditions. Even though it has mesophilic characteristic having an optimal growth temperature around 37°C (Jones and D’Orazio, 2013), it has a psychrotrophic nature demonstrated by a slow growth at refrigerating temperatures (Junttila et al., 2008; Lee et al., 2017), which leads to qualifying this species as psychrotolerant. It effectively resists osmotic stress (Shabala et al., 2008) as well as low water activity (Nolan et al., 1992). The bacteria also withstand acidic and alkali environments (Liu et al., 2005). Importantly, exposure to a stress factor provides cross-adaptation to subsequent exposure to other stresses which may function as a protective mechanism of the bacteria in fluctuating environmental conditions (Begley et al., 2002; Bergholz et al., 2012).

L. monocytogenes is the etiologic agent of listeriosis. As a foodborne pathogen, biofilm formation by *L. monocytogenes* in food premises is a growing concern (Colagiorgi et al., 2017). Bacterial cells growing in biofilms exert higher resistance to stress factors that the bacteria may encounter during food processing such as sanitizing compounds (Fagerlund et al., 2017), cold temperature, and desiccation stresses (Zoz et al., 2017). Therefore, they have higher chances of transferring to the final food products. With modern diet habits relying greatly on ready-to-eat foods and the increasing proportion of elderly population, the risk of listeriosis is increasing (Ricci et al., 2018).

Despite the wide distribution of *L. monocytogenes* in environments, incidence of listeriosis is considerably lower than other foodborne pathogens (EFSA and ECDC, 2017, 2018). The host risk factors play an important role in the development of the infection (Buchanan et al., 2017). Listeriosis can lead to severe consequences in pregnant women resulting in high rate of abortion or stillbirth caused by vertical transmission from the maternal circulation (Lamont et al., 2011). In non-pregnant adult, listeriosis is realized in two forms. Invasive listeriosis in immunocompromised individuals manifests by severe gastroenteritis and subsequent infection in bloodstream and the central nervous system causing meningitis. It results in high

fatality rate of more than 20% (EFSA and ECDC, 2017; Mylonakis et al., 1998). Non-invasive listeriosis often occurs in healthy individuals with symptoms of mild gastroenteritis, diarrhea and fever and most infection pass by unrecognized. However, certain listeriosis cases involve serious infections in immunocompetent individuals caused by *L. monocytogenes* strains of high virulence. Virulence potential varies between strains and serotype 4b in lineage I strains, compared to lineage II strains which show higher occurrence in environmental isolates, have been associated with the major outbreaks (Buchrieser et al., 1993; Farber and Peterkin, 1991; Jacquet et al., 2004). In the last decade, population genomics disclosed a clonal structure of the bacteria (Ragon et al., 2008). Analysing the epidemic data in the clonal frame revealed that hypervirulent genotypes were mainly composed of serotype 4b (Maury et al., 2016; Yin et al., 2015).

Heterogeneity in phenotypes and genetic composition prevails in the *L. monocytogenes* population. Advances in sequencing technologies and subsequent accumulation of genomic data allowed interspecies as well as intraspecies comparative genomic analyses which led to discoveries of genetic determinants for certain phenotypes, such as virulence (den Bakker et al., 2010a; Fox et al., 2016; Glaser et al., 2001; Hilliard et al., 2018; Rychli et al., 2017). Moreover, transcriptomic studies empowered by increased sequencing depth further unveiled the intricate transcriptional regulatory network (Soni et al., 2011; Vivant et al., 2017; Wurtzel et al., 2012). As a saprophyte that transforms to an intracellular parasite by opportunistic infections, cross-talk among numerous transcription factors such as PrfA and σ B (Guldimann et al., 2017; Ollinger et al., 2009b) as well as various non-coding RNAs (Izar et al., 2011; Mellin and Cossart, 2012; Peng et al., 2016) plays important roles in *L. monocytogenes* physiology. Therefore, the variations in genetic contents and transcriptional remodelling largely determine the phenotypic response to environmental signals. Since the first discovery of *L. monocytogenes* in 1924 (Murray et al., 1926), a large amount of studies contributed to deciphering its biology through implication of infection biology (Cossart and Toledo-Arana, 2008; Rolhion and Cossart, 2017). Furthermore, with the fundamental progress in molecular biology techniques and related data processing tools in genomics, transcriptomics and proteomics, we anticipate to unveil the complete picture of *L. monocytogenes* pathogenesis and physiology.

Chapter I

Objectives of the thesis

The current doctoral study was designed as a part of a European research project “List_MAPS” funded by Union Horizon2020 program under the Marie-Skłodowska Curie actions. The project engaged 11 early stage researchers in nine beneficiaries and two partners from both private and public domains in five European countries (France, Germany, Ireland, The Netherlands and Denmark). With divergent expertise of the participants, List_MAPS focused on exploring the dynamics of *L. monocytogenes* from different aspects including soil as natural habitat, biofilm formation in food processing environments, and *in vivo* infection model. Also, as a multidisciplinary team, List_MAPS aimed to integrate results obtained from high throughput epigenetics, transcriptome profiling, proteomics, microbiology and mathematics.

Under this scope, the research work for this thesis was carried out in two private companies, BioFilm Control in France and GenXPro in Germany. BioFilm Control is the inventor of a biofilm detection technique called Biofilm Ring Test (BRT) which discriminates microorganisms by comparing efficiency in the first step of biofilm formation, adhesion. GenXPro has expertise in sequencing library preparation for challenging samples such as host/pathogen mixed samples or microorganisms in the rhizosphere. Accordingly, the thesis was designed to take advantage of the innovative tools, BRT and RNA sequencing (RNA-seq). The current PhD thesis investigated the two most prominent phenotypes, virulence and biofilm formation, using large sets of *L. monocytogenes* strains to represent interspecies heterogeneity, and further explored their associations at genomic and transcriptomic levels.

The objectives of the present doctoral thesis are as follows:

- The first study investigated the phenotype change of *L. monocytogenes* under cold-shock (4°C), one of the most prominent stress factors for the bacteria in food chains. A set of 22 strains of different origins and serogroups were compared for adhesion level, using BRT, and total biomass between cold-stressed and cold-adapted cells. Cell surface physicochemical property was assessed searching for its association with bacterial phenotypes (Chapter III).

- In the second study, we evaluated the intraspecific diversity in biofilm formation and its association with genetic profiles (genes presence/absence properties) among food-related isolates. To achieve a comprehensive view of adhesion and biofilm production in food processing environment, different combinations of growth conditions were applied as follows: optimal (37°C) *versus* cold (10°C) temperatures; nutrient rich (BHI broth) *versus* nutrient poor (10-fold diluted BHI broth) conditions; and without *versus* with supplementary NaCl at 0.85%. Data were analyzed in multiple aspects as follows: lineages, serogroups, genotypes defined by MLST, and frequency of the genotypes described as persistent, prevalent and rare groups. The genetic compositions in relation to the observed phenotypes were analyzed using pan-genome wide association study (Chapter IV).

- The last study focused on disclosing the heterogeneity in transcriptome profiles of *L. monocytogenes* strains and exploring it with respect to phylogenetic divergence encompassing virulence-associated genotypes as well as *in vivo* virulence. In order to effectively compare the virulence potential, *G. mellonella* survival assay was performed on 91 isolates. A set of 33 strains represented by lineages I *versus* II, hyper- *versus* hypovirulent genotypes, as well as varying degree of *in vivo* virulence potential was subjected to high-throughput RNA-seq analysis (Chapter V).

Chapter II

Bibliography

I *Listeria monocytogenes*

I.1 General characteristics

The genus *Listeria* belongs to Firmicutes and consists of Gram-positive bacteria with low G+C content closely related to *Bacillus* and *Staphylococcus* (den Bakker et al., 2010a). *Listeria* spp. are facultative anaerobic, non-spore forming, catalase positive, and oxidase negative bacteria (Orsi and Wiedmann, 2016). The bacteria are rod shaped, 0.4 μm in width and 0.5-2 μm in length. *Listeria* species are ubiquitous in nature and the bacteria demonstrate a plant saprophyte lifestyle (Vivant et al., 2013). As an opportunistic pathogen, it demonstrates an intracellular lifestyle in host cells which results in fatal infection in susceptible individuals (Freitag et al., 2009). Heterogeneity in the virulence of *L. monocytogenes* has been demonstrated by epidemiological data and confirmed by *in vivo* and *in vitro* studies (Brosch et al., 1993; Werbrouck et al., 2008).

One of the most eminent features of the *L. monocytogenes* is the temperature-dependent motility. The bacteria express peritrichous flagella which confer motility at ambient temperatures, 20-25°C. However, the flagellar motility genes, including *flaA* encoding the structural protein flagellin, are transcriptionally down-regulated at around 37°C, a temperature that *L. monocytogenes* is exposed to inside animal hosts, including humans (Gründling et al., 2004; Peel et al., 1988). Thus, this temperature-dependent expression of flagella is proposed as an adaptive mechanism to avoid from recognition by host and prevent mobilization of host innate immune responses (Dons et al., 2004).

L. monocytogenes can tolerate extreme growth conditions. It revealed growth at 13% NaCl and survival at 40% NaCl (Liu et al., 2005; Shabala et al., 2008). It also resists highly acidic and alkali environment. A report showed that this species recovered after exposure to pH 12 or pH 3 (Liu et al., 2005). *L. monocytogenes* can easily grow between 3 and 45°C and as a psychrotolerant it adapts to grow at low temperatures with minimal temperature around -2°C (Augustin et al., 2005; Junttila et al., 2008). It can survive in dry conditions and has been reported to survive well in peanut butter spread at a_w 0.33 during a 24-week period at 20°C

(Kenney and Beuchat, 2004). *L. monocytogenes* is facultative anaerobes and it survives oxygen restriction for extended period (Buchanan and Klawitter, 1990).

To control bacterial growth in foods, temperature, pH, NaCl, and oxygen level are often adjusted. However, the physiological properties of *L. monocytogenes* such as growth at low temperatures and tolerance to low oxygen content and high NaCl concentration make the control of this pathogen difficult to food industries. Overall, *Listeria* is a highly adaptable species that survives under extreme conditions such as freezing, high salinity, and dehydration, however, it can easily be killed by cooking at temperatures higher than 65°C (Bunning et al., 1988; Ceylan et al., 2017; Huang, 2004).

I.2 Distribution

Genus *Listeria* is wide spread in nature. A study performed in Austria documented a high occurrence of the bacteria genus in ecosystems (Linke et al., 2014). They reported that *Listeria* was present in 30% of 467 soil samples and 26% of 68 water samples from distinct geological and ecological sites. Furthermore, they found that the most dominant species in soil and water samples were *L. seeligeri*, *L. innocua*, and *L. Ivanovii*. Similar study was conducted on 1,805 soil, water, and other environmental samples from New York state, United states (Sauders et al., 2012). The result revealed similar prevalence of *Listeria spp.* between natural (23.4%) and urban (22.3%) environmental samples. Interestingly, *L. innocua* and *L. monocytogenes* were significantly associated with urban environments.

During 1970's, soil has been believed to natural reservoir for *L. monocytogenes* (Welshimer and Donker-Voet, 1971). Soil is demonstrated to be the environmental niche for the transmission of this bacterium to plants and animals (Vivant et al., 2013). However, studies revealed that other sources such as animal manure, sewage, silage (fermented plant material) and vegetation (Garrec et al., 2003; Welshimer, 1968) as well as water sources such as rivers and ponds also harbour *L. monocytogenes* (Linke et al., 2014). Recent report from European Food Safety Authority (EFSA) showed that the highest level of non-compliance of RTE foods with the *L. monocytogenes* microbiological criteria was observed in the food category 'fish and fishery products' at both the processing and retail stages suggesting that sea water and fish could be one of the main reservoirs for *L. monocytogenes* (EFSA and ECDC, 2018). *L. monocytogenes* has also been isolated from a wide range of animal hosts. It covers a broad animal species from wild and domestic mammals specifically ruminants and avian species, including domestic and game fowl (Rothrock et al., 2017) to sea animals including crustaceans, fish, and oysters (Motes, 1991), as well as arthropods such as fruit flies (Mansfield et al., 2004). In addition, studies suggest that *L. monocytogenes* may be carried in the intestinal tracts of asymptomatic human population (Grif et al., 2003).

I.3 Taxonomy

Taxonomically, the genus *Listeria* contains 20 species: *L. aquatica*, *L. booriae*, *L. cornellensis*, *L. costaricensis*, *L. fleischmannii*, *L. floridensis*, *L. goaensis*, *L. grandensis*, *L. grayi*, *L. innocua*, *L. ivanovii*, *L. marthii*, *L. monocytogenes*, *L. newyorkensis*, *L. riparia*, *L. rocourtiae*, *L. seeligeri*, *L. thailandensis*, *L. weihenstephanensis*, and *L. welshimeri* (Leclercq et al., 2019; Orsi and Wiedmann, 2016; Weller et al., 2015). Among them, 2 species, *L. monocytogenes* and *L. ivanovii* are known to be intracellular bacterial pathogens. *L. monocytogenes* was first discovered in 1924 as the etiological agent for septicaemia disease in rabbits and guinea pigs (Murray et al., 1926). *L. monocytogenes* can cause severe infections in humans called listeriosis, especially in immunocompromised host, and a variety of other vertebrates, including birds and mammals. *L. ivanovii* is predominantly an animal pathogen which exclusively infects ruminants, especially sheep (Vázquez-Boland et al., 2001b), however, *L. ivanovii* have occasionally been associated with human illness (Guillet et al., 2010; Snapir et al., 2006). Although considered avirulent, occasional human infections caused by *L. welshimeri*, *L. seeligeri*, and *L. innocua* have been reported (Andre and Genicot, 1987; Perrin et al., 2003; Rocourt et al., 1986).

Because of the epidemiological importance of human listeriosis, numerous methods have been developed and employed to discriminate between isolates (Jadhav et al., 2012; Wiedmann, 2002). Bacterial subtyping methods serve 2 major tasks: to improve detection and tracking of human listeriosis outbreaks and to track sources of *L. monocytogenes* contamination. Moreover, the use of subtyping methods allows us better understanding of the epidemiology, population genetics, and ecology of *L. monocytogenes*.

Conventionally, subtyping methods were based on phenotypic characteristics such as serotyping and phage typing. However, new subtyping technologies has been constantly introduced and tested to increase the resolution (discriminatory power) and reproducibility and to reduce processing time and preferably, cost as well. The techniques can be grouped as follows: (i) methods based on biochemical constituents of isolates such as multilocus enzyme electrophoresis and spectroscopy; (ii) molecular subtyping techniques such as restriction fragment length polymorphisms, ribotyping, pulsed-field gel electrophoresis (PFGE), polymerase chain reaction (PCR), and random amplified polymorphic DNA; (iii) methods based on polymorphisms that exist in specific DNA nucleotide sequences of isolates such as multilocus sequence typing (MLST), multilocus variable-number tandem-repeat analysis and whole genome sequencing (WGS) (Nyarko and Donnelly, 2015).

The subtyping techniques are advancing to be faster, more standardisable, reproducible, and cost effective with more discriminatory power. We will discuss about serotyping as the most generally accepted method, PFGE and MLST as standardized methods used worldwide

and Whole genome sequencing (WGS) as a prospective solution in subtyping *L. monocytogenes* isolates in the following chapters.

I.3.1 Serotyping

The most widely applied conventional subtyping method is serotyping. The method utilizes 15 subtypes of somatic (O) and 4 subtypes of flagellar (H) antigens that are present as surface proteins on *L. monocytogenes* (Liu, 2006). By using corresponding monoclonal and polyclonal antibodies for serological detection, it can distinguish isolates into 13 distinct serovars: 1/2a, 1/2b, 1/2c, 3a, 3b, 3c, 4a, 4ab, 4b, 4c, 4d, 4e, and 7 (Allerberger, 2003) (Table 1).

Table 1. Compositions of somatic (O) and flagellar (H) antigens in *Listeria* serotypes (Based on Liu, 2006; Seeliger and Jones, 1986).

Serotype	O antigens	H antigens
1/2a	I, II	A, B
1/2b	I, II	A, B, C
1/2c	I, II	B, D
3a	II, IV	A, B
3b	II, IV	A, B, C
3c	II, IV	B, D
4a	(V), VII, IX	A, B, C
4b	V, VI	A, B, C
4c	V, VII	A, B, C
4d	(V), VI, VIII	A, B, C
4e	V, VI, (VIII), (IX)	A, B, C
7	XII, XIII	A, B, C
5	(V), VI, (VIII), X	A, B, C
6a	V, (VI), (VII), (IX), XV	A, B, C
6b	(V), (VI), (VII), IX, X, XI	A, B, C

Although all 13 serovars are presumed to be able to cause listeriosis in human, there are dominant serovars, 1/2a, 1/2b, 1/2c and 4b, that account for at least 95% of the cases (Farber and Peterkin, 1991; Swaminathan and Gerner-Smidt, 2007; Vázquez-Boland et al., 2001b). Serovars causing human listeriosis revealed a distribution bias as serovar 4b was found in 64% of listeriosis cases, serovar 1/2a in 15%, serovar 1/2b in 10%, and serovar 1/2c in 4% (McLauchlin, 1990). Moreover, while most *L. monocytogenes* strains from environment are composed of serotype 1/2a, 1/2b and 1/2c, isolates from human infection are mainly of serotype 4b (Gray et al., 2004; McLauchlin, 1990; Orsi et al., 2011).

Identification of the serotype of a strain allows an upfront differentiation between important food-borne strains (1/2a, 1/2b, and 4b). Serotyping can provide biological context for phylogenetic relationships and also it enables the comparisons of results from different studies. However, there are certain disadvantages of the method such as comparatively high cost, difficulty in standardization of reagents, as well as the needs of technical expertise. To reduce the difficulties of conventional serotyping, PCR serotyping methods have been developed to separate the major serovars (1/2a, 1/2b, 1/2c, and 4b) into distinct groups (Borucki and Call, 2003; Doumith et al., 2004). Identification of PCR primers for serotyping increased the accessibility and standardization across the different labs and decreased cost and time of laboratory process. PCR primers were designed from variable regions of the *L. monocytogenes* genome that can distinguish different divisions (lineages) as well as serogroups. The most widely applied multiplex PCR serotyping developed by Michel Doumith et al. (2004) targets 5 genes (*lmo0737*, *lmo1118*, *ORF2819*, *ORF2110*, and *prs*) and it can divide isolates into five phylogenetic groups, each correlated with serovars: I.1 (1/2a-3a), I.2 (1/2c-3c), II.1 (4b-4d-4e), II.2 (1/2b-3b-7), and III (4a-4c). Even though the method cannot distinguish the serovar 1/2a from 3a, 1/2c from 3c, 1/2b from 3b and 7, 4a from 4c or 4b from 4d and 4e, the method became widely applied because only 4 major serovars (1/2a, 1/2b, 1/2c and 4b) account for most cases.

Even though serotyping has served as one of the principal classification systems, unfortunately this approach lacks discrimination power and is unreliable compared to other methods such as PFGE or MLST.

I.3.2 Lineages

The first multilocus electrophoresis (MLEE) grouping study of *L. monocytogenes* isolates was conducted in 1989 (Piffaretti et al., 1989). In the study, *L. monocytogenes* strains were grouped into distinct phylogenetic divisions; division I (lineage I) were represented by strains of serovars 4b, 1/2b and 4a while division II (lineage II) contained strains of serovars 1/2a and 1/2c. In addition to those 2 major lineages, lineage III and IV were subsequently identified. Table 2 summarizes the 4 distinct lineages and their characteristics.

Table 2. The history of *L. monocytogenes* lineages: overview of different designations that have been used (Orsi et al., 2011).

Lineage	Initial identification	Serotypes	Genetic characteristics	Distribution
I	First described in an MLEE study by Piffaretti et al., 1989	1/2b, 3b, 3c, 4b	Lowest diversity among the lineages; lowest levels of recombination among the lineages	Commonly isolated from various sources; overrepresented among human isolates
II	First described in an MLEE study by Piffaretti et al., 1989	1/2a, 1/2c, 3a	Most diverse, highest recombination levels	Commonly isolated from various sources; overrepresented among food and food-related as well as natural environments
III	First described using partial sequence data analyses by Rasmussen et al., 1995	4a, 4b, 4c	Very diverse; recombination levels between those for lineage I and lineage II	Most isolates obtained from ruminants
IV	First described as IIIB using partial sequence data analyses by Roberts et al., 2006; first reported as lineage IV by Ward et al., 2008	4a, 4b, 4c	Few isolates analysed to date	Most isolates obtained from ruminants

Polygenetic analysis of 1,696 *L. monocytogenes* strains from diverse sources and geographical locations revealed that major phylogenetic lineages were clearly separated (Figure 1).

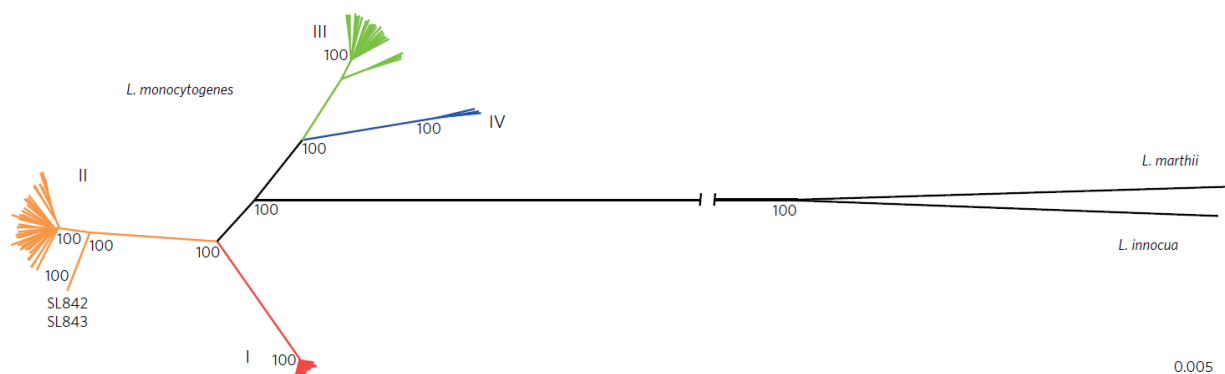


Figure 1. Phylogeny of the four phylogenetic lineages (I, red; II, orange; III, green; IV, blue). Representative isolates of the four lineages were used to determine the location of the root, using *L. innocua* and *L. marthii* as outgroups (The tree was obtained using FastME on the p-distance of the 1,748 concatenated alignments; Moura et al., 2016).

I.3.3 PFGE

Pulse field gel electrophoresis (PFGE) is applied as a routine subtyping method for several bacteria species such as *Escherichia coli* O157:H7, non-typhoidal *Salmonella* spp., and *Shigella* spp. (Hunter et al., 2005). It had been also served as the international gold standard for *L. monocytogenes* epidemiological investigations (Graves and Swaminathan, 2001). In USA, the Centers for Disease Control and Prevention (CDC) succeeded in implementing the harmonized system for nationwide database. From 1996 to 2016, PulseNet (the National Molecular Subtyping Network for Foodborne Disease Surveillance) has implemented PFGE analysis as a tool to identify pathogens causing foodborne illnesses. It fastened the whole process of detection of infectious bacteria and epidemiological follow-up of an outbreak.

For PFGE analysis, firstly DNA of *L. monocytogenes* isolate is extracted and digested using restriction enzymes such as *Ascl* and *Apal* to cut genomic DNA infrequently. This yields 8-25 large fragments ranging in size from 20kb to over 20Mb. The fragmented DNA is slowly separated on an agarose gel (for 30-50 h) during which alternating currents are applied to move the DNA back and forth, resulting in higher resolution (Nightingale, 2010). The pattern image is captured for computer-based analysis using specific software which allows rapid result acquisition and comparison with other strains by sharing the data via the internet (<https://www.cdc.gov/pulsenet/>). The exchange of PFGE patterns through PulseNet and food

regulatory agency laboratories is coordinated by the USA CDC. In Europe, European Union Reference Laboratory for *L. monocytogenes* collaborates with National Reference Laboratories to standardize the PFGE protocol, exchange the data within the network and integrate into the European surveillance system of *L. monocytogenes* strains (Félix et al., 2014). PFGE analysis was regarded considerably successful in differentiating strains which are implicated in outbreaks by clustering isolates into four lineages and discriminating isolates belonging to the same serotype. However, some drawbacks were noted, for example: (i) long time for completion since it requires at least 2 days to obtain a final result; (ii) expertise requirement in performing the technique; (iii) non-comparable results across laboratories due to different restriction enzymes used (Liu, 2006).

1.3.4 MLST and MVLST

Multilocus sequence typing (MLST) was first proposed in 1998 by Maiden and colleagues for typing bacterial isolates (Maiden et al., 1998). The method relies on variation in nucleic acids sequence at several chromosomal loci depending on bacteria species. In *L. monocytogenes*, the method is based on the sequences of gene fragments from several housekeeping loci, initially six then later extended to seven. The seven housekeeping genes used for MLST in *L. monocytogenes* are *abcZ* (ABC transporter), *bglA* (6-phospho-beta-glucosidase), *cat* (catalase), *dapE* (succinyl diaminopimelate desuccinylase), *dat* (D-amino acid aminotransferase), *ldh* (L-lactate dehydrogenase), and *lhcA* (histidine kinase) (Salcedo et al., 2003). The length of nucleotide sequences amplified for each locus is generally in the range of 400-600 bp. The internal fragments of each gene are accurately sequenced on both strands using an automated DNA sequencer. To analyse the sequences, the different sequences within a bacterial species are assigned as distinct alleles for each house-keeping gene. The combination of alleles at each of the seven loci defines the allelic profile termed sequence type (ST) for an isolate. Therefore, each isolate of a species is unambiguously characterized. Then from sequence types, clonal complexes (CCs) are defined as groups of allelic profiles sharing 6 out of 7 genes. Reports revealed that certain CCs represented by epidemic clones are responsible for numerous outbreaks (Cantinelli et al., 2013; den Bakker et al., 2010b).

The MLST data is publicly accessible on network-based database software at <http://bigsddb.pasteur.fr/listeria/>. Total 1,433 STs, part of which are comprising 107 CCs, have been identified by the time of 2019 May. The panel of MLST output can be further expanded if a different genome of an isolate is sequenced.

It appears that MLST is so far the best technique for population genetic study, however, it is costly. Moreover, it shows limitations for its use in epidemiological investigation due to the low discriminatory power originating from the high sequence conservation in housekeeping genes. To solve this problem, a multi-virulence-locus sequence typing (MVLST) method has

been developed in *L. monocytogenes* (Zhang et al., 2004). MVLST method targets virulence genes, which may be more polymorphic than housekeeping genes. Virulence factors are important in pathogenesis such as intracellular survival, cell-to-cell spread, and virulence. The six virulence and virulence-associated genes used for MVLST in *L. monocytogenes* are as follows: *prfA* (master virulence regulator), *inlB* (Internalin B), *inlC* (Internalin C), *dal* (alanine racemase), *lisR* (LisR), and *clpP* (ATP-dependent Clp protease proteolytic subunit). This method showed greater discriminatory power for subtyping *L. monocytogenes* isolates. Moreover, the virulence-associated genes are often highly mobile and recombining between strains therefore, MVLST method demonstrated high epidemiological relevance and efficiency in detection of epidemic clones (Chen et al., 2005). Moreover, the MLST can be assigned from whole-genome sequence information which can be obtained at relatively modest cost and effort by advent of second-generation sequencing technologies.

Genotypic analyses such as PFGE (Neves et al., 2008) and MLST (den Bakker et al., 2008) have been further applied to cluster *L. monocytogenes* isolates which revealed a structured population composed of divergent lineages (Orsi et al., 2011).

I.3.5 WGS related methods

Whole genome sequencing (WGS) has emerged today as an ultimate typing tool for identifying microbial source of food contamination and comparing bacterial isolates in outbreak investigation thanks to its decreasing cost and dominant competitiveness in resolution (Jackson et al., 2016; Lüth et al., 2018). EFSA and Food and Drug Administration of US are increasingly using WGS as a mean to better understand foodborne pathogens (Jackson et al., 2016; Moura et al., 2017). Bacterial sequence data can provide accurate phylogenetic characterization including lineage assignment. However, data analysis and comparability of WGS data across laboratories hampered WGS-based subtyping approach. To solve this problem, core genome MLST (cgMLST) was developed which interpret WGS data in standardized nomenclatures of alleles and types (Hyden et al., 2016; Lüth et al., 2018; Ruppitsch et al., 2015). The target core gene set was determined by genome-wide gene-by-gene comparison using SeqSphere+ software which resulted in 1,701 genes out of 2,867 genes of reference strain EGDe (accession number: NC_003210.1) (Ruppitsch et al., 2015; Schmid et al., 2014). The data is available on Internet at <https://www.cgmlst.org/ncs/schema/690488/>. By cgMLST, isolates that share very closely related genomes are grouped in a Complex Type or Cluster Type.

Using classic MLST approach, it is difficult to differentiate isolates in an outbreak from epidemiologically unrelated isolates which belong to the same clonal group. The cgMLST scheme demonstrated higher discriminatory power and thereby more suitable for outbreak

investigations by clearly differentiating outbreak isolates from non-outbreak isolates (Ruppitsch et al., 2015).

Along with the development of cgMLST, other methods based on WGS data were emerged such as whole genome MLST (wgMLST) or Single Nucleotide Polymorphism (SNP) analysis (Moura et al., 2016). Compared to cgMLST, wgMLST utilizes a set of genes from both core and accessory genome. For SNP approach, genomes of isolates are aligned to reference genomes such as EGDe and EGD (accession number: NC_022568.1) to find SNP. High concordance between wgMLST, cgMLST, and SNP approaches were found allowing all typing methods suitable for investigation of *L. monocytogenes* (Henri et al., 2017). Certainly, WGS genotyping will be the standard method due to its accurate outcome and high discriminatory power.

I.4 Genetic heterogeneity

Recent studies on population structure on a global scale revealed that *L. monocytogenes* is a genetically heterogeneous species (Bakker et al., 2010; Ragon et al., 2008). *L. monocytogenes* strains are composed of the distinction of phylogenetic lineages, each of which is genetically heterogeneous containing multiple CCs (Haase et al., 2014). The differences between the evolutionary lineages arise from the contributions of homologous recombination and genetic diversification. However, analyses of multilocus sequence data indicate that *L. monocytogenes* is one of the bacterial species with the lowest rate of homologous recombination (Ragon et al., 2008). Interestingly, unequal rates of recombination were noticed among the main lineages I and II, with recombination more prevalent in lineage II (Bakker et al., 2013). To date, total 178 complete genome sequences have been available on NCBI (<https://www.ncbi.nlm.nih.gov/genome/genomes/159?>) whose sizes vary from 2,776,520 to 3,243,300 base pairs containing 2858-3337 genes. In 2015, a pan-genome analysis using 44 complete genomes revealed that *L. monocytogenes* strains consists in $\approx 43\%$ (2360) of core genes and the remaining $\approx 57\%$ (3109) of accessory genes (Tan et al., 2015). Another study performed mapping of the distribution of accessory genes of 8 *L. monocytogenes* strains and found a distinct division in chromosome regions: an accessory gene rich region distributed in the first 65° adjacent to the origin of replication and comparatively, a more stable region enriched for core genes in the last 295° (Bakker et al., 2013).

Accessory loci that distinguish the two major lineages, I and II, exhibited large variations. For instance, transcriptional regulators and internalins were differently distributed and, furthermore, each lineage showed specific antimicrobial resistance-related genes (Bakker et al., 2013). Some evidences indicate the divergence of pathogenic and non-pathogenic *Listeria* species arose from a pathogenic ancestor containing the key virulence genes about 47 million years ago (den Bakker et al., 2010a). Supporting this, serogroup 4 was found to be ancestral and gene clusters associated with serogroup 1/2 were believed to be introduced through horizontal gene transfer in the ancestral population (Tan et al., 2015). Gene loss also plays an important role in diversification of *Listeria*, a well-known example is the loss of the *prfa* cluster, which accelerates transition of *Listeria* species from a facultative pathogen to a saprotroph, even though some non-pathogenic species still carry some virulence-associated genes (den Bakker et al., 2010a).

I.4.1 Phenotype-genotype heterogeneity

The apparent bias in the distribution between lineage I and II, or serotypes 4b and 1/2 strains among clinical and food isolates led to investigations on the related phenotypes. A

population diversity study using 1,696 isolates revealed distinct genetic features that account for heterogeneity in virulence and stress resistance among clinical and food isolates (Moura et al., 2016). The major pathogenicity island LIPI-1 (*Listeria* pathogenicity island-1, *prfA*, *plcA*, *hly*, *mpl*, *actA*, and *plcB*) was highly conserved in the bacteria, however complete LIPI-3 (*lIsA*, *lIsG*, *lIsH*, *lIsX*, *lIsB*, *lIsY*, *lIsD*, and *lIsP*) was almost exclusively present within lineage I. Moreover, the study found that certain genetic contents that were associated with sublineages were highly related with the origin of a strain. For example, *inlA* alleles encoding truncated internalin A variants which are related with virulence attenuation were significantly associated with food and food-related origins. Similarly, the presence of genes (*qac*, *bcrABC*, and *ermE*) that confer resistance to benzalkonium chloride (BC), a quaternary ammonium compound that is most commonly used disinfectant in food industry, were significantly associated with lineage II.

There also exist correlations between clonal groups and infection or source of isolates. The aforementioned subtyping methods such as MLST and MLVST enabled evaluation of phenotypes at clonal level in *L. monocytogenes*. It has long been suggested that the clonal genetic structure is related to the virulence potential of *L. monocytogenes* population (Bergholz et al., 2018; Piffaretti et al., 1989). Studies attempted to delineate *L. monocytogenes* clones in order to determine those that contribute the most to human or animal infections (Chen et al., 2007; Ducey et al., 2007; Kathariou, 2008). A study in 2016 made use of a large set of isolates comprising 4,049 food isolates and 2,584 clinical isolates (Maury et al., 2016). Using MLST approach, the collected strains were distinguished into 63 different genotypes. The result showed that the frequency distribution of the clones was markedly uneven; moreover, there was a significant difference in clonal distribution between food and clinical origin. While the most prevalent infection-associated clones were CC1, CC2, CC4 and CC6, food-associated clones were CC9 and CC121. Murine infection further confirmed that the clinical clones were hypervirulent in comparison to the food isolates. Moreover, LIPI-4, a cluster of 6 genes encoding a cellobiose-family phosphotransferase system, was found exclusively in certain subtypes such as CC4 strains that were specifically associated with neuroinvasiveness and maternal-neonatal infection.

In 2008, a listeriosis outbreak associated with ready-to-eat (RTE) meat products resulted in 22 deaths and at least 57 patients. The causative isolate belonged to CC8 and a novel 50 kbp (coding sequences LM5578_1850 to LM5578_1903) *Listeria* genomic island (LGI-1) was discovered that is specific to CC8 (Gilmour et al., 2010).

Similarly, a study from Hingston et al. (2017b) found certain connections between genotypes and bacterial growth under unfavorable conditions including low temperature, salt and acid stresses. For example, integrity of *inlA* was significantly associated with cold

tolerance and a plasmid with acid tolerance. However, they also revealed that a minor genetic variation could influence the stress tolerance traits.

Taken together, accumulating data demonstrated heterogeneity in genomic features with regard to bacterial virulence and stress resistance. As a matter of fact, it is difficult to make direct associations between specific genetic elements and phenotypes such as virulence due to high complexity in the pathogenesis in *L. monocytogenes*. Likewise, stress resistance in association with food contamination in food processing environments (FPE) is difficult to presume because of the uncertainty in the process of food contamination.

I.5 pathogenicity

I.5.1 Listeriosis

Infection caused by bacteria genus *Listeria* is called listeriosis in animals including humans. There are 20 *Listeria* species among which only few are known to be pathogenic responsible for listeriosis. *L. ivanovii* is predominantly an animal pathogen responsible for infections in ruminants, especially sheep (Vázquez-Boland et al., 2001b), though, few human cases have been reported (Guillet et al., 2010; Snapir et al., 2006). Listeriosis in human is predominantly a foodborne disease caused by ingestion of contaminated food products with *L. monocytogenes* except for foetal infection caused by congenital infection in pregnant women. Listeriosis manifests serious localized and generalized infections resulting in up to 90% hospitalization rate and a high fatality rate (Farber and Peterkin, 1991; Scallan et al., 2011). It is particularly deadly in senior group and immunocompromised population. In European Union, the annual number of deaths recorded since 2008 increased steadily and the overall fatality was reported as 16.2% in 2016 and 13.8% in 2017 (EFSA and ECDC, 2017, 2018).

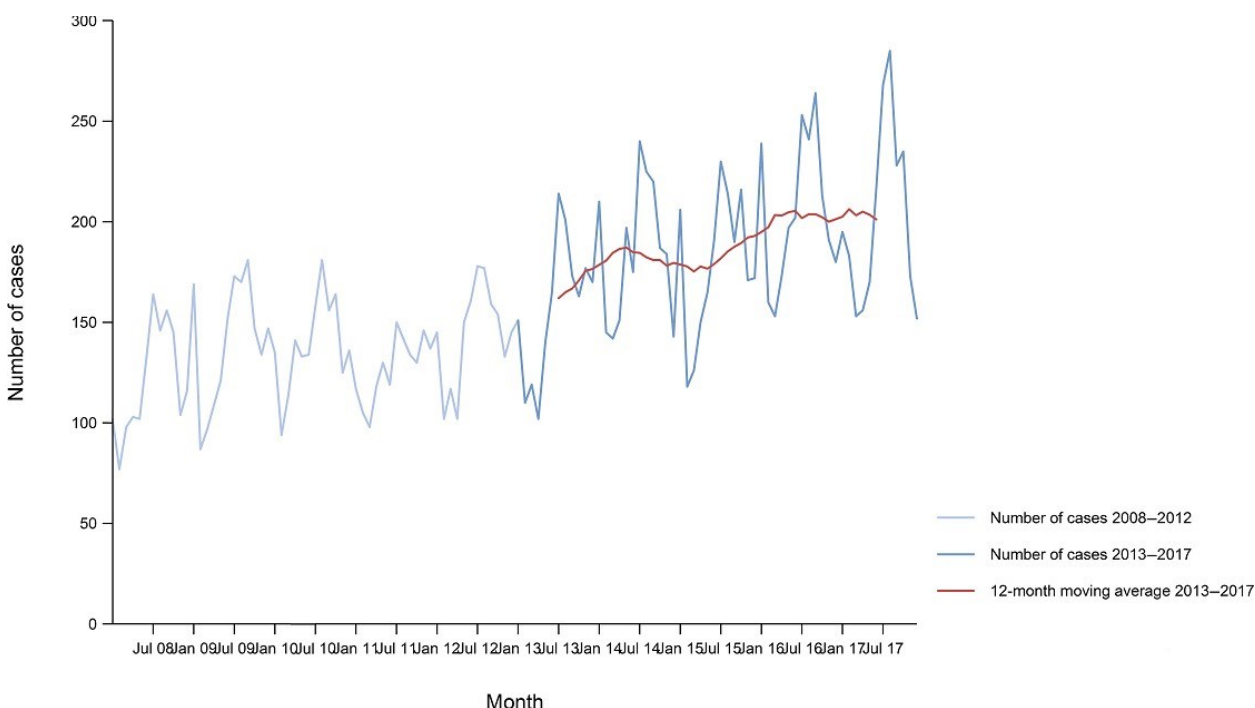
I.5.1.1 Phylogenetic distribution

As discussed earlier (Chapter I.3.1 Serotyping), accumulated epidemic data clearly show that serotype 4b strains are associated with high virulence potential. While serovar 4b strains were shown to be responsible for the most of listeriosis, it is the serogroup 1/2 (serotype 1/2a, 1/2b and 1/2c) which mainly compose food and environmental isolates (McLauchlin, 1990; Wiedmann, 2002; Wiedmann et al., 1997). This indicates that the association between 4b strains and clinical result is not due to the higher exposure to serotype 4b strains, but rather the hyper virulence of epidemic clones in serotype 4b strains (Barbosa et al., 2015; Evans et al., 2004; Ochiai et al., 2014).

As previously mentioned, Maury et al. (2016) reported the significant distribution bias among strains between food and clinical origins and further identified virulence-associated genotypes. When compared to the phylogenetic position, the genotype CC121 and CC9 representing a food origin were mostly composed of serotype 1/2a and 1/2c strains (Ragon et al., 2008). Meanwhile hypervirulent genotypes CC1, CC2, CC4, and CC6 mostly consisted of serotype 4b strains supporting the distinct phylogenetic distribution of the epidemic clones. Recent study further disclosed a distribution bias with regard to source of isolation among those high-virulent genotypes in a limited region. A total of 347 serotype 4b isolates primarily from North America revealed that while CC4 clone were significantly overrepresented among human isolates, CC2 exhibited significant propensity for food (Lee et al., 2018).

I.5.1.2 Incidence and outbreaks

EFSA reported that the incidence of listeriosis is continually increasing (Figure 2) with high fatality rate of 13.8% among the 1,633 confirmed cases with known outcome in EU in 2017 (EFSA and ECDC, 2018). Notably, European countries are experiencing an increased incidence of listeriosis among senior groups with > 60 years of age (Goulet et al., 2008). Recent report in 2017 showed that the senior population are most commonly affected by the infection by showing the fatality of 15.5% and 24.2% in the age group over 64 years and over 84 years, respectively (EFSA and ECDC, 2018).



Source: Austria, Belgium, Cyprus, Czech Republic, Denmark, Estonia, Finland, France, Germany, Greece, Hungary, Iceland, Ireland, Italy, Latvia, Lithuania, Malta, Netherlands, Norway, Poland, Romania, Slovakia, Slovenia, Spain, Sweden and United Kingdom.

Bulgaria, Croatia, Luxembourg and Portugal did not report data to the level of detail required for the analysis.

Figure 2. Trend in reported confirmed human cases of listeriosis in the EU/EEA, by month, 2008–2017 (EFSA and ECDC, 2018).

Similarly, in USA, annual predictions estimated that listeriosis causes approximately 1,600 invasive infections, 1,500 hospitalizations and 250 deaths. Confirmed cases of listeriosis infection showed 94% hospitalization rate and 15.9% death rate (Scallan et al., 2011).

Although the incidence of *L. monocytogenes* infection is comparatively low compared to *Salmonella* or *Campylobacter* infections, listeriosis outbreaks remain a serious public health

Table 3. The major outbreaks with more than 50 reported cases.

Year	Location	Invasive/Non-invasive	Number of cases (deaths)	Foods	References
1983-1987	Switzerland	Invasive	122 (31)	Soft cheese	Büla et al., 1995; Farber and Peterkin, 1991
1985	U.S.A.	Invasive	142 (48)	Mexican-style fresh cheese	Centers for Disease Control (CDC), 1985; Linnan et al., 1988
1987-1989	United Kingdom and Ireland	Invasive	355 (94)	Pâté	McLauchlin et al., 1991
1992	France	Invasive	279 (85)	Jellied pork tongue	Jacquet et al., 1995; McLauchlin et al., 1991; Salvat et al., 1995
1997	Italy	Non-invasive	1566	Corn and tuna salad	Aureli et al., 2000
1998-1999	U.S.A.	Invasive	108 (14)	Meat frankfurters	CDC, 1998, 1999; Mead et al., 2006
2001	Sweden	Non-invasive	> 120	Fresh cheese made from raw milk in a summer farm	Carrique-Mas et al., 2003; Danielsson-Tham et al., 2004
2002	Canada (BC)	Non-invasive	86	Cheese made from pasteurized milk	Pagotto et al., 2006
2008	Canada	Invasive	57 (22)	RTE meat products	Currie et al., 2015
2011	U.S.A.	Invasive	147 (33)	cantaloupe	CDC, 2011; McCollum et al., 2013
2014	Denmark	Invasive	41 (17)	RTE delicatessen meat	Kvistholm Jensen et al., 2016
2017-2018	South Africa	Invasive	1060 (216)	RTE processed meat products	Smith et al., 2019
2014-ongoing	Denmark, Estonia, Finland, France, and Sweden	Invasive	22 (5), number can increase	Cold-smoked trout and salmon	Multi-country outbreak, 2019

concern. By definition, an outbreak has the same meaning as an epidemic, but often outbreaks refer to geographically more limited epidemics. A listeriosis outbreak is a cluster of listeriosis cases caused by the same source of *Listeria* strain in excess during a specified period of time (Table 3).

1.5.1.3 Clinical features and host immune response

Listeriosis has a long incubation period (3 to 60 days) and host immune system status determines the development of clinical signs and disease. Listeriosis is often associated with patients with underlying debilitating diseases such as malignancies (leukemia, lymphoma, or sarcoma), anticancer chemotherapy or immunosuppressive therapy (organ transplantation or corticosteroid use), diseases in liver, kidney, and diabetes as well as immunocompromised groups such as HIV patients, pregnant women, and elderly persons (Drevets and Bronze, 2008; Goulet et al., 2012). This suggests that altered or deficient immune responses predispose to listeriosis. Listeriosis can be distinguished in 2 main forms: perinatal listeriosis and listeriosis in the adults. In both cases, the predominant clinical forms are manifested by disseminated infection or local infection in the central nervous system (Doganay, 2003; Vázquez-Boland et al., 2001b).

The severe forms of listeriosis infection include encephalitis, meningitis, and bacteremia in compromised groups as discussed above. In perinatal listeriosis *L. monocytogenes* infects the placenta and fetus. Listeriosis in pregnant women show flu-like symptoms, but the infection can severely infect the fetus resulting in spontaneous abortion, still birth, premature birth to either an infected or a healthy child (Frederiksen and Samuelsson, 1992; Mylonakis et al., 2002). A noninvasive form of listeriosis occurs in immunocompetent individuals, and it is characterized by febrile gastroenteritis including diarrheal illness and flu-like symptoms (Drevets and Bronze, 2008). Moreover, asymptomatic carriers shedding *L. monocytogenes* in their stools were detected (Grif et al., 2003). However, a few sporadic listeriosis cases with invasive form of infection have been reported in healthy adult individuals (Jamal et al., 2005; Kelly et al., 1999; Vrbi et al., 2013; Zhang et al., 2012). This may be ascribed to the differential bacterial load in the contaminated food involved in the infection or high virulence of the corresponding *L. monocytogenes* strains.

L. monocytogenes seldom results cutaneous form of infection but it occurs mainly in farmers and veterinarians. The cutaneous listeriosis is characterized by localized, nonpruritic, self-limited, nonpainful, papulopustular or vesiculopustular eruptions in healthy individuals (Godshall et al., 2013). The infection is largely owing to direct contact with infected animals or vegetations.

Most studies have investigated the host immune responses in *Listeria* infection using mice model (Bou Ghanem et al., 2013). In the murine model, the innate immunity is responsible for

detecting and restraining the pathogen while adaptive immunity is responsible for clearance of *L. monocytogenes* and enhanced protection against future infections. Once *L. monocytogenes* are ingested, innate immune responses rapidly activate involving macrophages that plays an essential role in the early control of the infection. After entering bloodstream, *L. monocytogenes* are engulfed by various myeloid cells such as macrophages and dendritic cells, mainly in the spleen and liver and other tissues (Waite et al., 2011). The bacteria are rapidly internalized by resident macrophages in which the bacterial replication occurs and at the same time which mediate clearance of the bacteria. This innate immune response, as the first line of defence against bacteria, combat the infection until specific CD4+ and CD8+ T-cells are recruited (Zenewicz and Shen, 2007). In relatively low number, the bacteria in circulation also phagocytosed by patrolling neutrophils that are very efficient in killing the bacteria. The role of neutrophils was shown to play a critical role in early resistance to *L. monocytogenes* infection and in central nervous system infection (Conlan, 1997; López et al., 2000).

1.5.2 Host barrier

First, virulence potential of *L. monocytogenes* strain is associated with its capacity to circumvent innate host barrier such as gut microbiota and bile acids exposure (Gahan and Hill, 2014). The varying adaptability of the bacterial cells to the host barriers plays selective force for infection. Several studies demonstrated that various stress factors related to food matrix induced virulence related genes and enhances subsequent infectivity of *L. monocytogenes* (Bo Andersen et al., 2007; Neuhaus et al., 2013). For instance, pre-exposure to 0.3 M NaCl for 1 h significantly increased the ability of *L. monocytogenes* to survive in the lethal concentrations of bile (Sleator et al., 2007). Moreover, prior adaptation to sublethal levels of bile acids (0.08%), acid (pH 5.5 with 3 M lactic acid), heat (42°C), salt (5% NaCl), or sodium dodecyl sulfate (0.01%) significantly enhanced bile resistance of exponential phase growing *L. monocytogenes* (Begley et al., 2002). Acid has been widely investigated in relation to virulence potential since stomach is the first barrier that the bacteria encounter upon ingestion. A study showed that acid shock at low environmental temperatures induced PrfA related genes and increased the invasiveness for epithelial cells and *in vivo* (*Caenorhabditis elegans*) virulence (Neuhaus et al., 2013).

1.5.3 Intracellular lifecycle

Furthermore, the pathogenicity of the bacterium is highly associated with its intracellular lifecycle concerning adherence, invasion, immune evasion and modulation, intracellular growth and cell-to-cell spread (Vázquez-Boland et al., 2001b). Figure 3 depicts the general scheme of *L. monocytogenes* infection of non-phagocytic cells. Briefly, the bacteria enter host

non-phagocytic cells, such as epithelial cells, through receptor-mediated endocytosis. Listeriolysin O (LLO), phospholipase A (PlcA) and PlcB mediate escape of the bacteria from the vacuole. Bacteria can transcytose across the cell within a vacuole in goblet cells in intestinal epithelium (Nikitas et al., 2011) and replicate in spacious *Listeria*-containing phagosomes (SLAPs) in some macrophages. In host cell cytosol, *L. monocytogenes* subsequently polymerizes actin to promote cell-to-cell spread. Activity of virulence factors provokes a cascade of effects on the infected host cells. For example, the pore-forming activity of extracellular LLO leads to changes in histone modification, endoplasmic reticulum (ER) stress and lysosomal permeabilization, desumoylation, and mitochondrial fission (Birmingham et al., 2008; Carrero et al., 2004; Gedde et al., 2000; Hamon et al., 2012; Kayal and Charbit, 2006; Schnupf et al., 2007; Wallecha et al., 2013). To derepress host interferon-stimulated genes (ISGs), nuclear targeted protein A (LntA) of *L. monocytogenes* interacts with the host Bromo adjacent homology domain-containing 1 protein (BAHD1) complex (Lebreton et al., 2011). *L. monocytogenes* provokes translocation of NAD-dependent protein deacetylase sirtuin 2 (SIRT2) to the host nucleus to deacetylate histone 3 at lysine 18. This leads to changes in chromatin packing repressing downstream gene expression (Eskandarian et al., 2013). *Listeria* infection also leads to the host cell DNA damage, and the host cell counteracts the infection by upregulating a number of antibacterial effectors such as ISG15, ubiquitin-like protein, that is induced in an early stage of infection. Expression of ISG15 and the process of modification by ISG15 called ISGylation modulates cytokine secretion by covalent modification of ER and Golgi proteins (Radoshevich et al., 2015).

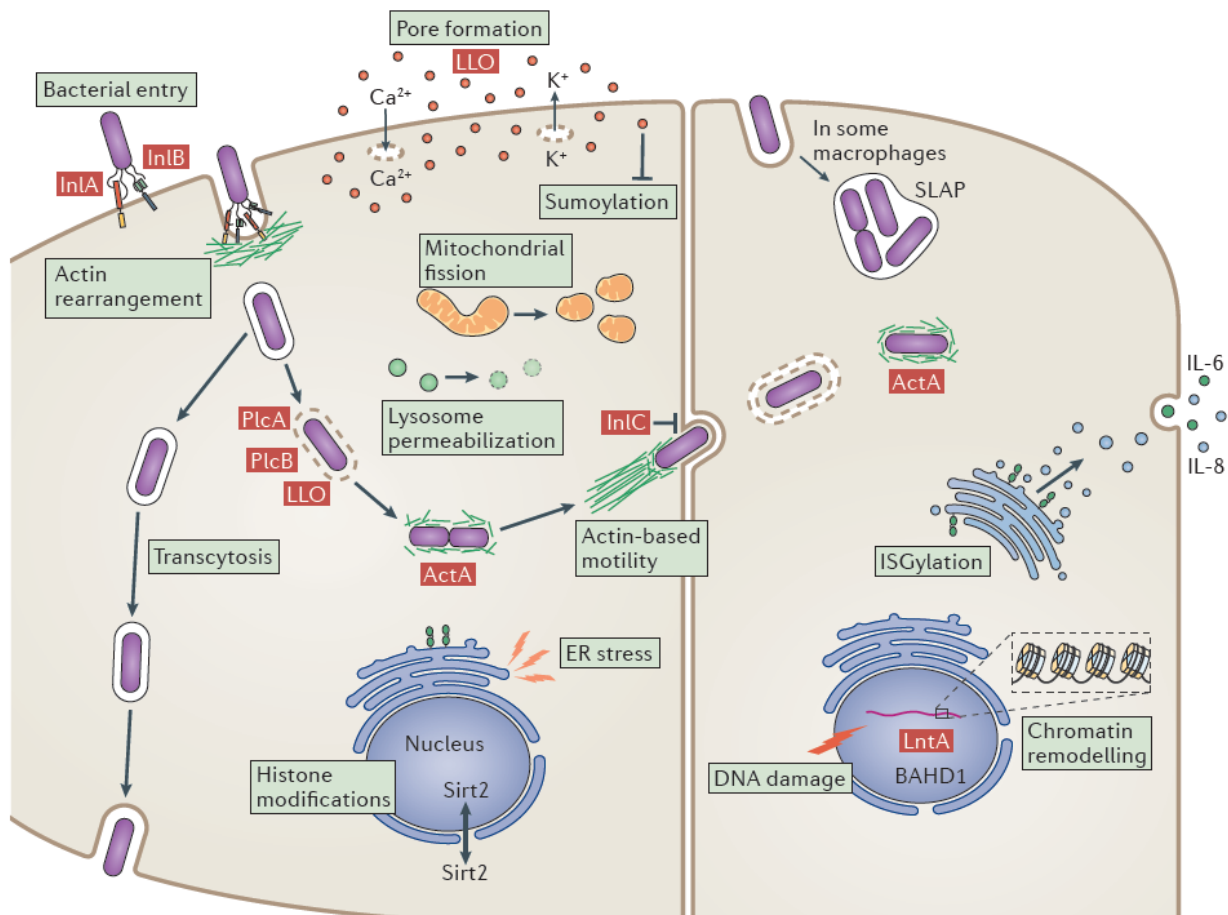


Figure 3. Overview of *Listeria monocytogenes* infection at cellular level. ActA, actin assembly-inducing protein; LLO, listeriolysin O; PlcA and PlcB, phospholipase A and B; Inl, Internalin; IL, interleukin; ER, endoplasmic reticulum; ISGs, interferon-stimulated genes; SLAPs, spacious *Listeria*-containing phagosomes; BAHD1, Bromo adjacent homology domain-containing 1 protein; SIRT2, sirtuin 2 (Radosheвич and Cossart, 2018).

I.5.4 Virulence factors and their regulation

To cause illness the bacteria first penetrate host cells of the epithelial lining in gastrointestinal track. Once internalized in host cells, *L. monocytogenes* proliferate in host cytosol, spread by cell-to-cell invasion to neighboring cells and cross brain-blood barrier and/or placental barrier. For this pathogenesis process, the status of host immune system plays an important role.

I.5.4.1 PrfA, master regulator of virulence

Positive regulatory factor A (PrfA) is a major transcription activator mediating the expression of the virulence factors in *L. monocytogenes*. The regulatory protein integrates environmental cues that signal the transition of a bacteria from saprotrophic to intracellular lifestyle (de las Heras et al., 2011). PrfA belongs to a member of the Crp/Fnr (Cyclic AMP (cAMP) receptor protein/fumarate nitrate reductase) family global transcriptional regulators mediating various metabolic pathways in bacteria (Freitag et al., 2009). Unlike other Crp/Fnr family regulators that requires a cofactor for DNA binding, PrfA is capable of binding to its consensus DNA sequence with low affinity without the presence of a cofactor. However, recent studies found that cofactors are required to exert its full activity. For instance, an allosteric mode of activation of PrfA mediated by a glutathione was suggested in the cytosol of the host cell (Hall et al., 2016).

PrfA was shown to induce the expression of virulence factors required for intracellular lifestyle when they are grown in blood (Toledo-Arana et al., 2009). The core PrfA virulon are clustered in a 9-kb chromosomal island LIPI-1, which is exclusively present in *L. monocytogenes* and *L. ivanovii* among *Listeria* spp. (Vázquez-Boland et al., 2001a). The cluster includes *prfA*, *plcA*, *hly*, *mpl*, *actA*, and *plcB*. *plcA* and *plcB* encode phospholipases (PlcA and PlcB) and *hly* encodes listeriolysin O (LLO); they mediate the lysis of the acidic phagosomes allowing the bacterial escape into the cytosol where they replicate intracellularly and they are also responsible for cell-to-cell spread (Dramsi and Cossart, 2002). As discussed earlier, the LLO toxin has a plethora of effects on the infected cell including histone modifications inducing host immune suppression (Hamon et al., 2007). The surface protein ActA encoded by *actA* mediates intracellular motility (Pistor et al., 1994) and metalloprotease encoded by *mpl* is responsible for the activation of PlcA and PlcB (Bitar et al., 2008; Poyart et al., 1993). PrfA coordinately activates the expression of genes in other loci than LIPI-1 that harbour a PrfA box in their promoter region such as: *bsh*, encoding a bile salt hydrolase which promotes survival within the gut (Dussurget et al., 2002); *inlC*, encoding a short, secreted internalin-like protein important for cell-to-cell spread and dampening of host innate response (Engelbrecht et al., 1996; Gouin et al., 2010); *hpt* (also known as *uhpT*), encoding an hexose phosphate transporter for intracytosolic proliferation (Chico-Calero et al., 2002); *inlAB* encoding InlA and B responsible for invasion of non-phagocytic cells (Parida et al., 2002; Schubert et al., 2002).

The regulation of PrfA is thermo-dependent. A thermosensor is located at the 5'-untranslated region (UTR) of the *prfA* transcript which serves conformational changes at different temperatures (Johansson et al., 2002). At low temperatures (< 30°C), it forms a secondary hairpin loop structure which masks the Shine-Dalgarno (SD) ribosome binding site and further prevents translation of PrfA. The secondary structure is disrupted at higher

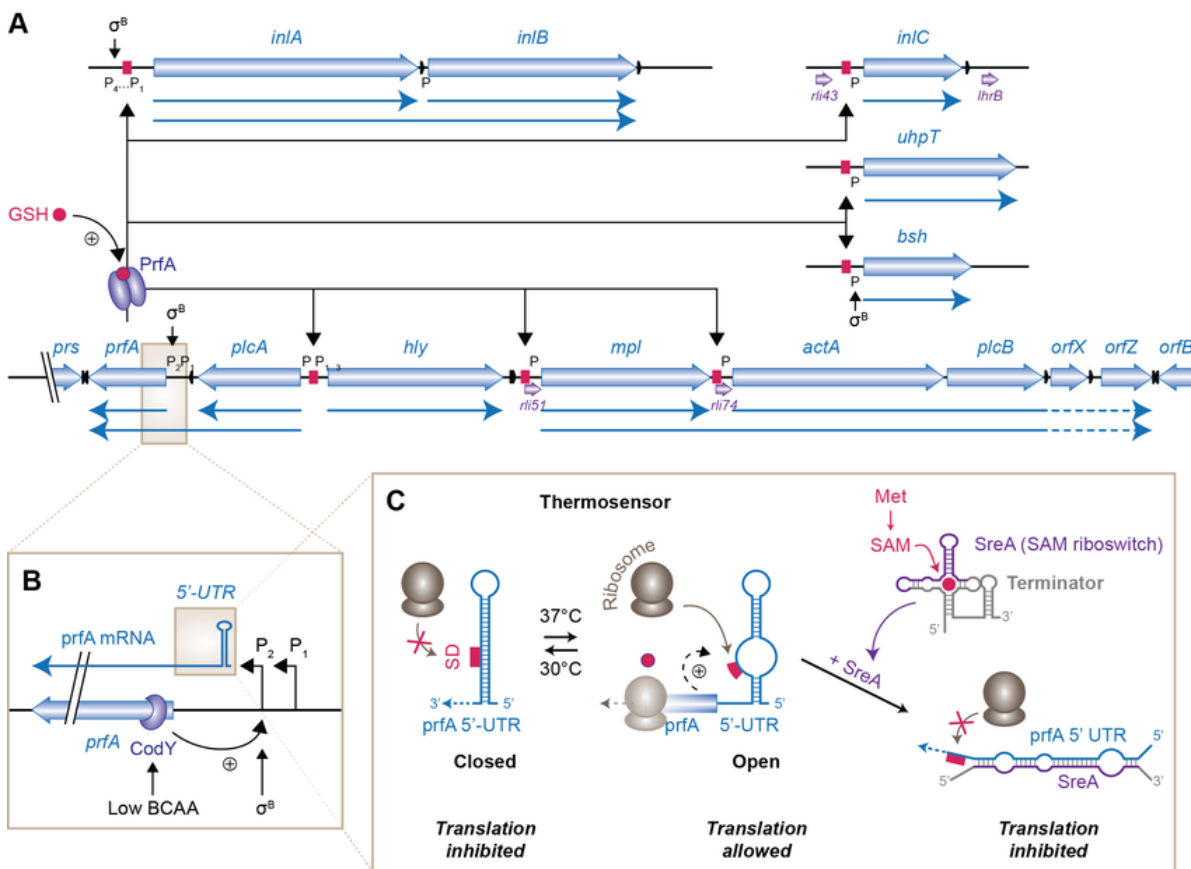


Figure 4. The PrfA regulon and its multiple control mechanisms. (A) Diagram of the main virulence cluster in *L. monocytogenes* and other PrfA-dependent genes, inspired from Kreft and Vázquez-Boland (2001) and de las Heras et al. (2011). Open reading frames (ORF) are highlighted in thick blue arrows, small RNAs in purple, terminators in black. The main transcriptional units are displayed with plain blue arrows. PrfA binding sites are boxed in magenta. Positive or negative regulators are shown. P, promoter; GSH, glutathione. (B) Transcriptional control of *prfA*. In addition to σ^B -dependent regulation, transcription is enhanced by binding of CodY in the coding sequence, in response to low availability of branched-chain amino-acids (BCAA). UTR, untranslated region. (C) Control of *prfA* translation initiation, adapted from Cossart and Lebreton (2014). At 30°C, the Shine-Dalgarno (SD) sequence of *prfA* mRNA is masked from ribosomes by a closed stem-loop structure. At 37°C, a change in the conformation of the 5'-UTR liberates the SD and allows translation initiation. Binding of ribosomes to the SD is further stabilised by the 20 first codons of the ORF. The SreA small RNA, which is the product of a S-adenosylmethionine (SAM) riboswitch, can also base-pair with *prfA* 5'-UTR and block access of ribosomes to the SD sequence (Lebreton and Cossart, 2016).

temperatures (37°C) allowing the binding of the ribosome and translation initiates. Followed by this discovery, several S-adenosylmethionine (SAM)-responsive riboswitches, regulatory segments of a mRNA molecule, which control the expression of virulence genes including PrfA were found in *L. monocytogenes* genomes (Loh et al., 2009; Xayarath and Freitag, 2009) (Figure 4). The RNA-mediated regulation will be discussed more in 'Chapter I.5.2.6 RNA-mediated regulators'.

A fine-tuned regulation of those virulence factors is critical for the successful infection of the bacteria. ActA is one of the most abundant proteins produced during intracellular infection. Transcription of *actA* is induced more than 200-fold during infection of host cells (Shetron-Rama et al., 2003). A small decrease in ActA level induced a dramatic decrease in the efficiency of cell-to-cell spread (Brundage et al., 1993; Smith et al., 1996; Wong et al., 2004); in contrast, overexpression of ActA also hampered cell-to-cell spread (Lauer et al., 2002). Similarly, mutants lacking LLO is avirulent; however, overexpression of LLO is also detrimental for the bacteria since it causes the early rupture of host cells which render the higher chance of immune clearance of the bacteria (Decatur and Portnoy, 2000). In sum, the stringent regulation of virulence factors by PrfA as well as its cross-talk with other virulence regulators are crucial for successful *L. monocytogenes* infection.

I.5.4.2 σ B regulation

In prokaryotes, sigma factors control the global switch of the genes expression (Mauri and Klumpp, 2014). Several types of sigma factors are conserved across diverse Gram-positive bacteria and some phages carry genes encoding sigma factors that control transcription of phage genes (Kolesky et al., 1999). Sigma factors are dissociable subunits of RNA polymerase in prokaryotic cells which enable the rapid modulation of transcription of regulons in response to environmental signals. In *L. monocytogenes* as well as in other Gram-positive bacteria, an alternative sigma factor σ B regulates genes important for adaptation and survival against adverse conditions, such as low pH, oxidative stress and carbon starvation (Ferreira et al., 2001, 2003). Therefore, a σ B deletion mutant have a deficient stress response rendering it more sensitive to environmental stresses. In addition to stress response, σ B is another major transcription regulator for virulence factors next to PrfA for the survival in host intestinal environment and intracellular growth (Chaturongakul et al., 2008). Importantly, σ B regulates expression of PrfA as seen above in Figure 4A (Nadon et al., 2002). It is not surprising that numerous PrfA regulons overlap with σ B regulons since the host barriers often mirror environmental stress (Ollinger et al., 2009a). For example, σ B regulates expression of some virulence genes required for survival and multiplication under acidic pH in the gastric environment or oxidative stress in the phagosome (Chaturongakul et al., 2008; Gahan and Hill, 2014). σ B also contributes to the transcriptional regulation of genes responsible for bile

tolerance such as *bsh*, which encodes a bile-salt hydrolase (Hain et al., 2008). A study revealed that 168 σ B regulon were comprised of 26 operons in *L. monocytogenes* including 10 genes that do not have homologues in *L. innocua* including *inlA*, *inlB*, *inlD*, *sepA*, *lmo2085*, *bsh*, *lmo0445*, *lmo2671*, *lmo2290*, and *lmo2387* (Raengpradub et al., 2008). A study using a σ B inhibitor, fluoro-phenyl-styrene-sulfonamidein, has newly identified σ B-dependent expressions in *lmo0937* and *lmo0915* (Palmer et al., 2011).

1.5.4.3 Other protein regulators

Comparative genomics and transcriptomics further identified various virulence regulators other than the major transcription factors, PrfA and σ B. Those regulators that contribute to the virulence regulatory network to a lesser extent are as follows: VirR/S (Mandin et al., 2005), CodY (Lobel et al., 2015), MogR (Shen and Higgins, 2006), RNA-binding protein Hfq (Christiansen et al., 2004), orphan response regulator DegU (Williams et al., 2005b), transcriptional antirepressor GmaR (Kamp and Higgins, 2009), transcriptional regulator MouR (Pinheiro et al., 2018) and accessory gene regulator Agr (Riedel et al., 2009). A complex cross-talk of those regulators plays a role in fine-tuned regulation of the virulence genes expression. In this chapter, we will scrutinize the details of the three regulators, VirR/S, CodY and MogR.

1.5.4.3.1 VirR/S

A study involving signature-tagged mutagenesis identified a novel virulence gene encoding a response regulator of a two-component system named VirR, for Virulence Regulator (Mandin et al., 2005). Together with VirS encoding histidine kinase, the 2-component system VirR/S controls the expression of 17 genes, including its own operon (Figure 5).

The *vir* operon :

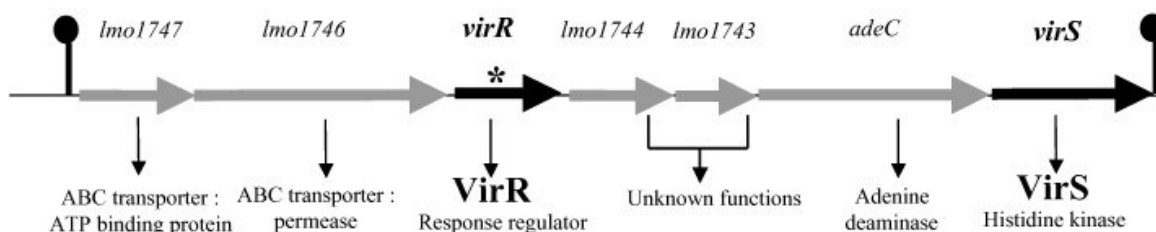


Figure 5. Genetic organization of the *virR/virS* locus. Hairpins indicate putative rho-independent terminators (Mandin et al., 2005).

The 17 genes of VirR/S regulon are as follows; *lmo2114*, *lmo2115*, *dltA/B/C/D*, *mprF* (*lmo1695*), *lmo1696*, *lmo2177*, *lmo0604*, *lmo2349*, *lmo2156*, *virR*, *lmo1744*, *lmo1743*, *adeC*, and *virC*. The *In vivo* test showed that the expressions of 13 out of 17 VirR/S regulon genes

were upregulated in the spleen of infected mice (Camejo et al., 2009). The *dlt* operon (*dltA/B/C/D*) encoding proteins involved in the incorporation of D-alanine residues into the cell wall-associated lipoteichoic acids are required for virulence. Mutant lacking DltA revealed impaired virulence in a mouse infection model and decreased adhesion in various cell lines (Abachin et al., 2002). Moreover, majority of the characterized VirR/S regulon genes contributes to the modification of bacterial surface components which confer resistance to antimicrobial peptides (Kang et al., 2015). *Lmo1695* encoding MprF confers resistance to cationic antimicrobial peptides (Thedieck et al., 2006). Similarly, *Lmo1696* encodes a putative glycopeptide antibiotic resistance protein of the VanZ family (Arthur and Courvalin, 1993). The ABC transporter encoded by *anrAB* (*lmo2114* and *lmo2115*) is involved in resistance to the bacteriocin nisin, and to other β -Lactam antibiotics (Collins et al., 2010).

1.5.4.3.2 CodY

CodY is a nutrient responsive regulator that modulates the expression of both metabolic and virulence genes in Gram-positive bacteria. CodY was shown to activate indirectly the expression of certain virulence genes in *Clostridium perfringens* (Li et al., 2013), *Bacillus anthracis* (Château et al., 2013; van Schaik et al., 2009) and *Streptococcus pyogenes* (Kreth et al., 2011). Recent study using RNA-Seq and ChIP-Seq techniques revealed that CodY serves as a repressor and activator of different genes of wide functional spectrum under nutrient rich and poor conditions (Lobel and Herskovits, 2016). A study conducted in macrophages found that 12 metabolic pathways were differentially active during the bacterial growth in macrophage cells (Lobel et al., 2012). Intracellular replication required *de novo* synthesis of histidine, arginine, purine, and branch chain amino acids (BCAAs) as well as catabolism of glycerol and L-rhamnose. Therefore, it is reasonable to assume that sensing of metabolite availability within the host cell may alert the bacteria of their intracellular location and the need to activate the virulence state. The BCCAAs serve as a ligand for CodY activation. Classically, CodY was presumed to bind DNA in its isoleucine-bound state, and function primarily as a repressor under rich growth conditions. A study demonstrated that limiting concentrations of BCAAs, primarily of isoleucine, resulted in a dramatic increase in virulence genes (Lobel et al., 2015). Most important role of CodY is its involvement in the regulation of the major virulence regulator *prfA*. When the bacteria are limited with BCAAs, it upregulates the expression of *prfA* by directly binding in its coding sequence, 15 nucleotides downstream of the start codon as shown in Figure 4B. Also, CodY binding region was found in the upstream to the *actA* gene, responsible for intracellular actin-based motility (Lobel and Herskovits, 2016). Interestingly, CodY induced a repression of σB expression in nutrient rich medium. This suggests that *prfA* transcription may be induced by CodY by two mechanisms when BCAAs are

limited: first, via a direct binding of CodY to the *prfA* promoter, or second, via an indirect mode by relieving σ^B repression.

The multifaceted CodY regulation of versatile genes in both directions (activation or repression) under different conditions establishes CodY as one of the main factors regulating *L. monocytogenes* physiology.

1.5.4.3.3 MogR/GmaR

Transition from an extracellular to an intracellular lifestyle provokes transcriptome reshaping involving the up-regulation of virulence factors and the reciprocal down regulation of other genes, such as genes related to flagellar motility in *L. monocytogenes*. Motility gene repressor (MogR) encoded by *Imo0674* was shown for its regulation in motility related genes (Gründling et al., 2004). Flagellum-mediated motility was shown to enhance *L. monocytogenes* invasion of human epithelial cells and the early colonization of the intestinal tract in mice soon after bacterial ingestion (O'Neil and Marquis, 2006). *In vitro* plaquing assays revealed that deletion of *mogR* resulted in a significant decrease in the efficiency of cell-to-cell spread and, furthermore, a dramatic attenuation (250-fold decrease) in virulence was observed in mice infection model.

Expression of flagellar motility genes, including *flaA* which encodes flagellin, are thermo-regulated. MogR acts as a repressor on the transcription of both flagella genes and *gmaR* which encodes bifunctional flagellar anti-repressor/glycosyltransferase GmaR. At 37°C, transcription of flagellar motility genes is repressed due to the binding activity of the MogR and GmaR. *gmaR* is co-transcribed within an operon harbouring *fliN* which encodes flagellar motor switch protein FliN. At lower temperatures, MogR is released from the *fliN-gmaR* promoter (*pfliN-gmaR*) by the anti-repressor GmaR which is transcriptionally activated by DegU, thereby positively regulating its own expression and allowing the transcription of flagellar motility regulon. Additionally, the regulation requires the DegU response regulator which constitutively activates transcription of *gmaR* in a temperature-independent manner (Kamp and Higgins, 2009) (Figure 6).

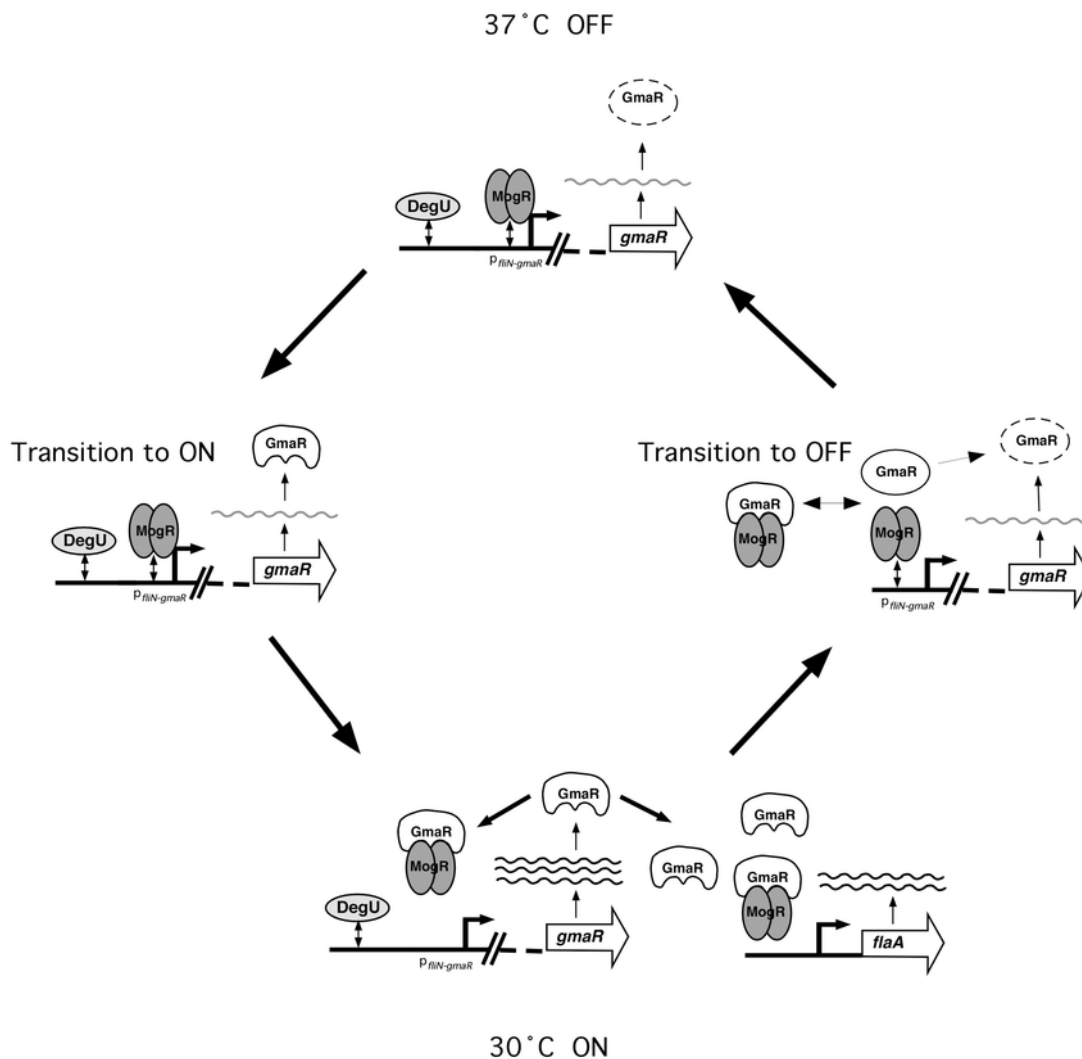


Figure 6. Model for the temperature-dependent regulation of GmaR expression and flagellar motility gene transcription in *L. monocytogenes*. 37°C OFF: At 37°C, when flagellar motility is OFF, the opposing activities of the MogR repressor and the DegU activator at *pflin-gmaR* result in minimal *fliN-gmaR* transcripts. Any GmaR produced at 37°C is rapidly degraded and cannot interact with MogR. Transition to ON: as the temperature decreases below 37°C, newly synthesized GmaR produced from *fliN-gmaR* transcripts is no longer degraded and is able to interact with MogR. 30°C ON: Once GmaR is initially translated at lower temperatures, GmaR removes MogR from the *fliN-gmaR* promoter increasing transcription of *gmaR*. Elevated levels of GmaR result in anti-repression of all flagellar motility gene promoters, allowing flagellar motility gene transcription to occur. Transition to OFF: as the temperature increases, the MogR:GmaR complex is destabilized due to a temperature-dependent conformational change in GmaR. Released GmaR is degraded, while released MogR binds flagellar promoter region DNA to reinstate repression of *gmaR* and all flagellar motility genes (Kamp and Higgins, 2011).

I.5.4.4 RNA-mediated regulators

Apart from the protein-based regulatory networks discussed above, some RNA can also regulate gene expression, both at the level of transcription and translation. Belonging to noncoding RNA, those RNA molecules are called small RNAs (sRNAs) that range from 50-500 nucleotides long and wide distributed both in prokaryotes and eukaryotes (Mandin et al., 2007). In addition, RNA carries out roles that once thought to be restricted to proteins. One of them is to bind low-molecular weight metabolites that doesn't require complementary base pairing which is the distinguished mode of action for sRNAs. The binding is mediated by the folding of the RNAs into 3-dimensional structure that recognizes the specific target molecule which induces allosteric structure changes of the RNA element. Those cis-regulatory RNA elements, which resemble repressors or activators regulating gene expressions, are called riboswitches (Mellin et al., 2013; Winkler and Breaker, 2005). The critical role of these regulatory RNAs including sRNAs and riboswitches in the modulation of *L. monocytogenes* gene expression is supported by increasing evidence (Cossart and Lebreton, 2014; Xayarath and Freitag, 2009). Firstly, long untranslated regions (UTRs) harbouring secondary structures have been identified in numerous virulence genes, such as *prfa*, *hly*, *actA*, and *mpl* (Shen and Higgins, 2005; Toledo-Arana et al., 2009; Wong et al., 2004). The integrity of the 5'-UTRs of these genes affect the stability of the mRNA and influence the translation of proteins (Loh et al., 2006).

Early study identified 3 Hfq (a RNA-binding protein that contributes to stress tolerance and virulence)-binding sRNAs using immunoprecipitation approach in *L. monocytogenes* (Christiansen et al., 2006). The sRNAs were expressed when *L. monocytogenes* replicated within mammalian cells inferring their associations with virulence. Shortly after this discovery, *in silico* analysis identified 12 sRNAs, 3 of which were antisense RNAs (Mandin et al., 2007). The crucial findings in the regulatory RNAs was from a study of Toledo-Arana and colleagues in 2009 (Toledo-Arana et al., 2009). They newly identified numerous sRNAs including antisense RNAs (asRNAs) by comparing a complete transcriptome between *in vitro*, *ex vivo* and *in vivo* growth conditions. Moreover, several sRNAs that are absent in *L. innocua*, a non-pathogenic species, exhibited expression pattern similar to that of protein-coding virulence genes. Using a tiling microarray, they built the complete operon map of *L. monocytogenes* which was shown to harbour 50 sRNAs. Among those sRNAs, 29 were newly identified sRNAs, and 7 were predicted to be cis-acting asRNAs. Besides, 40 riboswitches were found that showed 'on' and 'off' modes upon transition into different environments, among which functioned as terminators for upstream genes. In 2011, a study compared transcriptome profiles especially of lower molecular weight (< 500 nucleotides in length) between extracellularly growing bacteria and intracellularly growing *L. monocytogenes* in macrophages (Mraheil et al., 2011).

They identified 71 new regulatory sRNAs among which 29 including asRNAs were specifically expressed intracellularly. In sum, the increasing resolution in transcriptome data resulted in discovering a large set of conserved non-coding RNAs. Finally, 305 noncoding RNAs exist in *L. monocytogenes* which decompose into 154 trans-acting sRNAs, 46 cis-regulatory RNAs and 104 asRNAs (Bécavin et al., 2014).

Interestingly, unlike other riboswitches located in 5'-UTRs, sRNA *Rli39* is located at the 3'-end of a gene which is in antisense orientation to the downstream gene *pocR*, which encodes transcriptional regulator PocR for genes engaged in propanediol pathway. Propanediol catabolism requires B12 as a cofactor and is important for the pathogenesis of intestinal pathogens (Mellin et al., 2013; Sampson and Bobik, 2008). In *Listeria*, riboswitch *Rli39* controls the transcription of a noncoding RNA *AspocR*, which is an asRNA to *pocR*, and thereby regulates PocR depending on the availability of B12 (Figure 7).

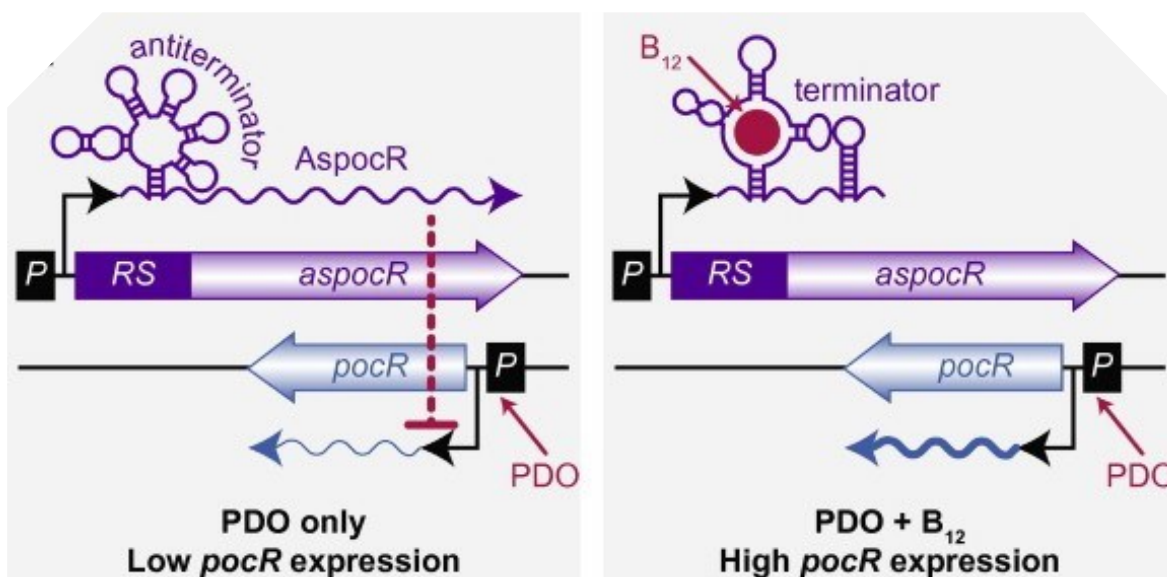


Figure 7. Model for the B12-dependent regulation of *pocR* via *AspocR*. (Left) In absence of B12, *AspocR* is transcribed and inhibits *pocR* expression by base-pairing with PocR mRNA. (Right) In presence of B12, binding of this ligand to the riboswitch (RS) triggers the premature transcription termination of *AspocR*; as a consequence, PocR mRNA can be produced. Note that transcription of *pocR* is also dependent on propanediol (PDO) (Cossart and Lebreton, 2014).

1.5.5 Virulence assay

The pathogenicity is defined as an overall ability of a bacteria to cause disease in host and virulence is the measurement of a level of pathogenicity which is comparable between

different strains. *L. monocytogenes* isolates are heterogeneous in virulence. From a risk assessment perspective, it is important to understand the virulence potential of *L. monocytogenes* strains. Numerous methods have been developed to investigate the virulence potentials of pathogens including *L. monocytogenes*. The aim of virulence assays is to determine either the number of bacteria or the time required to cause disease and death. One of the most widely used measurements is to express the differences in virulence by median Lethal Dose (LD50), the number of bacterial cells to kill half of the members of a tested population or median Lethal Time (LT50), the time to kill half of the members of a tested population.

1.5.5.1 *In vivo* assay

1.5.5.1.1 Mammalian model

Using a human model is excluded because *L. monocytogenes* infection causes high fatality. Primarily, animal models including laboratory mice and guinea pigs have been widely used for virulence assays since they were first described as host animals for *L. monocytogenes* (Cabanès et al., 2008; Murray et al., 1926). The first systematic murine infection model was reported in the early 1960s (Mackaness, 1962). The animals infected with *L. monocytogenes* either intragastrically or intravenously, and virulence is evaluated by several methods. Difference in virulence between strains are compared by LD50 or LT50 values as well as the number of bacteria colonized within infected target organs by enumerating them.

In nature, *L. monocytogenes* causes diseases through gastrointestinal tract by ingestion of contaminated foods. The process of the bacteria infection in intestinal epithelial cells requires an interaction of InlA expressed on bacterial cell surface and epithelial cadherin (E-cadherin) of host epithelial cells (Gaillard et al., 1991). However, murine E-cadherin poses a difference in an amino-acid sequence which in turn does not interact with internalin. Thus, mice are relatively resistant to intestinal infection making the oral transmission of *L. monocytogenes* in mice model inefficient (Lecuit et al., 2001). The major differences in the *in vivo* infection mechanism concerning InlA and InlB among different species including human and the most widely used animal models such as mice, guinea pigs, rats, gerbils and rabbits are compared in Figure 8. For example, in species that possess E-cadherin, such as humans or guinea pigs, the bacteria primarily invade the epithelium of the intestinal villi through interaction with InlA and replicate in the underlying *lamina propria*. In contrast, in species deficient of functional E-cadherin such as mice, *L. monocytogenes* translocates through M-cells, phagocytic cells in the Peyer's patches of the ileum (Lecuit, 2005). Similarly, the bacteria show direct invasion of endothelial cells including those in the blood-brain barrier through interaction of *inlB* with MetC receptors in host such as humans and mice (Parida et al., 2002). However, for MetC

deficient species such as guinea pigs, phagocytic cells such as macrophages (Kupffer cells in liver) indirectly mediate cell-to-cell spread.

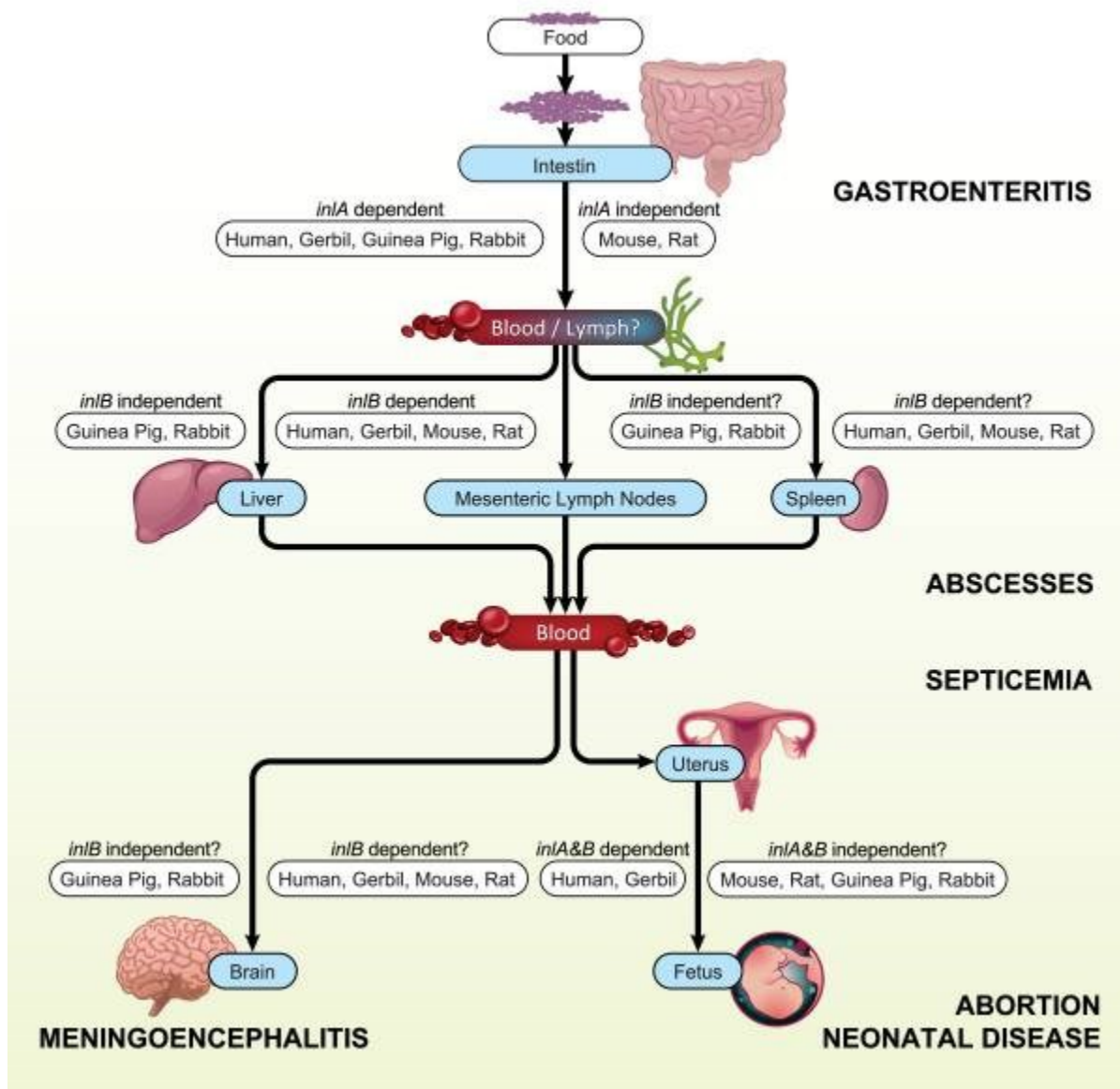


Figure 8. Physiological differences among laboratory animal species as well as humans and their importance in *L. monocytogenes* infection (Hoelzer et al., 2012).

1.5.5.1.2 *Galleria mellonella* model

Non-mammalian animal models were introduced to increase the screening power and avoid ethical problems in using mammalian hosts for pathogenesis studies, toxicology tests or

drug screening (Freires et al., 2017). The examples of these alternatives include roundworms (*Caenorhabditis elegans*) (Charão et al., 2015), fruit flies (*Drosophila melanogaster*) (Mansfield et al., 2004) and greater wax moth (*Galleria mellonella*) (Martinez et al., 2017). Utilization of *G. mellonella* larvae for testing virulence has been reported in a wide range of pathogens from eukaryotic to prokaryotic species (Fallon et al., 2012; Joyce and Gahan, 2010; Olsen et al., 2011; Seed and Dennis, 2008; Wagley et al., 2018; Wand et al., 2013; Wuensch et al., 2018).

There are numerous advantages in non-mammalian hosts (Mansfield et al., 2004). For example, they are often easier to manipulate than mammalian tests requiring less specialized handling techniques. It is more economical for testing a large panel of strains because the cost per animal as well as necessary facilities including animal husbandry is undoubtedly competitive. Additionally, one of the important positive prospects of *G. mellonella* as an *in vivo* model for evaluating virulence of human pathogens is the conserved innate immune response to microbial infections between insects and mammals. The immune system of *G. mellonella* larvae shows high structural and functional similarity to the innate immune response of mammals (Binder et al., 2016; Pereira et al., 2018; Tsai et al., 2016). The cuticle of the insect is the first barrier to pathogens as is the skin in mammalian hosts. The basic immune system is structured in hemolymph, analogous to mammalian blood, which contains hemocytes, comparable to mammalian neutrophils. The hemocytes show phagocytotic activity including phagocytosis of pathogens and destruction of them by superoxide production (Slepneva et al., 1999).

Finally, another advantage that make this animal model more favorable is that the larvae can be reared at 37°C which mimics the human core-temperature. Human pathogens are adapted to this temperature for expressing virulence determinants, therefore, incubation of the larvae at 37°C allows the analysis of microorganism behaviour at mammalian temperature and, more importantly, temperature-dependent virulence associated transcription regulators such as PrfA and σ B in *L. monocytogenes* (Ivy et al., 2010).

The application of *G. mellonella* virulence tests shows high conformity in *L. monocytogenes* studies. A correlation was found between the virulence of a strain in *G. mellonella* and that in mice (Mukherjee et al., 2010). Production of LLO was required for bacterial toxicity and growth in the larvae (Joyce and Gahan, 2010). Similarly, isogenic mutants with the deletions in core virulence genes (*prfA*, *plcA*, *hly*, *actA* and *virR*) genes, revealed significantly higher LT50 than the wild type strain (Martinez et al., 2017).

1.5.5.2 *In vitro* assay-cell culture models

It is amenable to compare the virulence potential of *L. monocytogenes* strains using *in vitro* models of infection because the bacteria invade a broad range of tissue culture cells (Marquis, 2006; Portnoy et al., 2002). One of the most well-established models is Caco-2 cells, a human

colon enterocyte-like cell line, first introduced in 1987 (Gaillard et al., 1987). The study showed that only pathogenic species (*L. monocytogenes* and *L. ivanovii*) induced their own phagocytosis by Caco-2 cells, as opposed to non-pathogenic species (*L. seeligeri*, *L. welshimeri*, and *L. innocua*). High congruency was observed between the Caco-2 cell line and mouse model in infection characteristics such as adhesion, invasion, and translocation (Jaradat and Bhunia, 2003). Other human intestinal tissue derived cell lines have been applied for *in vitro* assays in *L. monocytogenes* such as Int-407 from jejunum, HT-29 from colon, and HCT-8 from ileocecal epithelial cells (Araujo et al., 2018; Jagadeesan et al., 2011; Jaradat et al., 2003; Larsen et al., 2010). Also, due to the capacity of *L. monocytogenes* to invade and infect various cell types, cell lines derived from other tissues than intestinal epithelial cells or immune cells from different animals have been used as follows: HepG-2 cells from human liver (Kortebi et al., 2017); Vero cells from monkey kidney (Khan et al., 2014); CHO cells from hamster ovary (Alvarez-Domínguez et al., 1997); HeLa cells from human cervix (Weiglein et al., 1997); and BeWo cells from trophoblasts in human placenta (Lecuit et al., 2004). Another widely employed tissue culture is various macrophages cell lines (Ohya et al., 1998). Macrophage-like cell lines can internalize up to 20 bacteria per cell. The critical difference of macrophage cell lines is that they actively uptake the *L. monocytogenes* cells while the aforementioned epithelial cell lines require active invasion of *L. monocytogenes*. Therefore, an adequate *in vitro* culture type must be employed depending on the research aim regarding the step of the infection to be characterized.

However, the challenge in tissue culture models aroused with the growth of *L. monocytogenes* in the culture media as it is a facultative pathogen. To overcome the problem, the aminoglycoside antibiotic gentamicin is supplemented to infected cells subsequent to bacterial internalization at a bactericidal concentration in order to prevent extracellular bacterial replication (Jaradat and Bhunia, 2003). On the other hand, such membrane-impermeable antibiotics can also interfere with the results because it can enter the *in vitro* tissue cells and kill intracellular bacteria (Drevets et al., 1994). It was shown that while a comparatively high concentration of gentamicin (higher than 50 µg/ml) is bactericidal for extracellular bacteria, no measurable effect was observed on intracellular bacteria during the first 8 h of infection in an early study using the mouse macrophage-like cell line J774 (Brundage et al., 1993).

Intracellular growth rate of wild-type *L. monocytogenes* is comparable to extracellular growth rate in rich media which is equivalent to doubling times of ≈ 40 min. Invasion and internalization in a host cell followed by intracellular proliferation is the first step in infection. The bacteria start cell-to-cell spread to neighboring cells, propagating infection. The measurement of virulence *in vitro* is realized by plaque forming assay that measures the diameter of macroscopic plaques formed in monolayers of cells (Sun et al., 1990). This enables

the quantification of intracellular growth as well as cell-to-cell spread. *In vitro* virulence level measured using plaque forming assay showed a high correlation with mice infection model (Roche et al., 2001).

I.5.5.3 Phenotypic tests

A number of phenotypic tests have been developed to interpret virulence level by measuring the production of certain virulence factors in *L. monocytogenes*. The most crucial virulence factor is hemolysin called Listeriolysin O (LLO) and encoded by *hly* gene. The activity of LLO can be assessed by measuring the diameter of a hemolytic zone on blood agar (Dubail et al., 2000). This approach distinguishes the LLO mutant strains from a wild type strain. However, it is difficult to interpret among various strains with different LLO activities because the quantification may not be homogeneous due to the varying intensity of the hemolysis also because some strains produce very small zones which may be undetectable. In 1986, a microplate technique using erythrocyte suspensions was developed for the typing of *Listeria* species between hemolytic and nonhemolytic strains (Dominguez Rodriguez et al., 1986).

Similarly, the level of the two phospholipases C, phosphatidylinositol phospholipase C (PI-PLC) and phosphatidylcholine phospholipase C (PC-PLC), encoded by *plcA* and *plcB* genes respectively, can be used as a substitute method to estimate the virulence level (Goldfine and Knob, 1992). The phospholipases mediate the phagosomal lysis along with LLO in infected host cells. The method measures the phospholipases expressed in bacterial suspensions which are filtered and titrated. A study revealed that the phospholipases activity was correlated to cell infection phenotype to some extent (Roche et al., 2005).

The phenotypical methods for measuring virulence level have become secondary to high throughput genotypic assays, such as DNA microarray, because of their low sensitivity in discriminating between strains.

1.6 *Listeria monocytogenes* in foods

Some microorganisms such as *Salmonella*, *Campylobacter*, and *Listeria* pose pathogenic properties through contaminated food products, thus represent a considerable concern within the food industry due to their potential to establish infections in humans. As discussed earlier, *L. monocytogenes* is widely distributed in nature including soil, water, and vegetation as well as human carriers, all of which can contribute to food contaminations (Zhu et al., 2017). Moreover, sea water being suspected to be another major source of contamination, regulation of *L. monocytogenes* in fresh seafoods and related food products seems to be challenging (Leong et al., 2014).

Theoretically, food contamination by *L. monocytogenes* can occur at any point in the food chain, from raw food materials on farms, in food processing plants, in retail establishments and in the consumer's home. The first passage of *L. monocytogenes* to cause food contamination in food processing plants is to be carried by raw materials from natural environment including soil, vegetation and animal host to food processing facilities. Then by direct and indirect contact, including human interventions, the pathogen is delivered to final food products. The post-processing exposure of *L. monocytogenes*, such as at retails or home, is widely recognized as another predominant source of food contaminations (Jofré et al., 2016; Lakicevic et al., 2015).

A wide variety of foods have risks of carrying *L. monocytogenes* among which the most frequently associated foods are RTE deli meats and hot dogs, refrigerated pâtés or meat spreads, refrigerated smoked seafood, raw sprouts, unpasteurized milk and dairy products such as soft cheese made with unpasteurized milk (queso fresco, Feta, Brie, Camembert) (EFSA and ECDC, 2018). Recent report from the EFSA revealed that RTE food categories are typically associated with human listeriosis (Ricci et al., 2018). Despite the regulation on RTE foods (EU Regulation (EC) No 2073/2005 on microbiological criteria, <https://eur-lex.europa.eu/eli/reg/2005/2073/oj>) (European Commission, 2005), human listeriosis caused by RTE foods is significant increasing (Ricci et al., 2018). The fundamental reason is because most of RTE foods do not require any heat treatment such as heating in microwave or cooking on pan or in oven which could reduce number of live bacterial cells. Along with the demands from consumers on RTE foods which are mildly treated, fresh and with high nutritional value, there is increasing chance of contamination to evoke listeriosis.

L. monocytogenes is known to survive over long period of time in FPE, and it is often believed to be persistent strain in FPE that result recurring contamination in foods. Various molecular subtyping methods permitted identification of a persistent strain. A particular subtype that is re-isolated over an extended period of observation time is defined as persistent strain (Ferreira et al., 2014; Keto-Timonen et al., 2007). However, determining an

isolate as a persistent strain is difficult. Firstly, it is not feasible to discriminate a persisting strain in specific FPE from isolates with the identical subtype that are reintroduced at different times via contaminated incoming raw materials. For example, a contaminated personnel, equipment or material can repetitively introduce the same strain from outside the FPE. On the contrary, persistent strains could have been mis-categorized as a non-persistent or sporadic strain due to a non-compliance between the introduction of the strain to FPE and the observation period. Also, real persistent clones may have been isolated only sporadically because it is not physically possible to sample all bacteria present in FPE. Consequently, only a subset of the population is sampled by random sampling practices and persistent strain could be omitted or taken as a sporadic strain. It is also disputed whether certain *L. monocytogenes* subtypes colonize specific favorable niches in FPE and thus persist over a long period, however, there has been no report of persistent-associated genotype (Ferreira et al., 2014). Therefore, categorizing strains into persistent or sporadic can be a challenging task.

I.7 Foods related stress response determinants

Microorganisms are continuously exposed to environmental perturbations which are considered as stresses in broad term. A mild stress means a stress that causes reduced growth rate while a severe stress refers to a stress that negatively impact on cell survival (NicAogáin and O'Byrne, 2016). It requires extra energy for cells to keep homeostasis and adapt to the stress conditions to which they are exposed. The extra costs include synthesis of new cell components or macromolecules to protect themselves from the adverse condition.

In FPE and food matrices, *L. monocytogenes* is exposed to a number of stress factors including cold temperatures, osmolar shock, acids, disinfectants treatments, etc. The adaptation ability of *L. monocytogenes* to these stresses promotes its survival and transmission in the food chain. Several hypotheses were proposed to explain the growth of *L. monocytogenes* in food industry including colonization of niches, biofilm formation, and activation of resistance mechanisms (Bergholz et al., 2018). The presence of the general stress response attributes to the stress tolerance in *L. monocytogenes*. Under a stress condition, σ^B mediates transcriptional responses to provide homeostatic and protective functions (Guldimann et al., 2016).

A large-scale study using 166 strains was performed in order to find potential relationships between *L. monocytogenes* genotypes and food-related stress tolerance phenotypes including tolerances to cold, salt, acid, or desiccation stresses. Interestingly, it found some overlapping stress tolerance phenotypes: salt and acid sensitive ($n = 10$), salt sensitive and desiccation tolerant ($n = 6$), cold and acid tolerant ($n = 5$), and cold tolerant and salt sensitive ($n = 5$). A whole genome single-nucleotide-variants phylogeny found the close relatedness among sensitive and tolerant isolates implying that minor genetic differences can influence the stress tolerance of *L. monocytogenes* (Hingston et al., 2017b).

I.7.1 Osmotic Shock

Various salts including NaCl are commonly used in food products to repress the bacterial growth. The most relevant example is RTE foods including cheese or daily meat products which have long shelf lives. However, *L. monocytogenes* is highly tolerant to salt stress demonstrating survival under 40% NaCl and growth under 13% NaCl (Liu et al., 2005; Shabala et al., 2008). Studies showed the phylogenetic variations in the salt tolerance which further depends on other growth conditions. In a study using 40 strains, lineage I strains were shown to be more salt tolerant (6% NaCl) than Lineage II strains at 37°C but not at 7°C (Bergholz et al., 2010). Another study also revealed different salt tolerance levels among serotypes under various conditions using 138 isolates. At pH neutral (pH 7-4) and mild acidic conditions (pH 5-5) serotype 4b strains showed highest tolerance to high NaCl at 30°C while serotype 1/2b showed

the highest tolerance to high NaCl at 7°C (Veen et al., 2008). A study of Hingston et al. (2017b) using 166 strains demonstrated a varying level of salt tolerance among CCs: in 6% NaCl, CC7 (1/2a) isolates were salt sensitive while CC2 (4b) and CC11 (1/2a) were salt tolerant demonstrating the existence of genetic variation on salt resistant trait at the clonal level rather than the serotype level.

As a primary response of *L. monocytogenes* to hyperosmotic shock, the bacteria accumulate potassium (K⁺) and its counterion glutamate in cytoplasm (Patchett et al., 1992). This response under hyperosmotic shock depends not only on the genetic composition of the strain but also on the surrounding availability of osmoprotectants in the food material (de Zwart et al., 2003). Osmoprotectants or compatible solutes are utilized in osmoadaptation such as glycine betaine, carnitine, proline, glycerol, and trehalose that can be found in foods at varying levels (Inguglia et al., 2017). The transfer of solutes is mediated by compatible solute systems such as glycine betaine porter I (BetL), glycine betaine porter II (Gbu), and the carnitine transporter OpuC in *L. monocytogenes* (Sleator et al., 2003).

Transcriptional analyses are providing more information on genes that are responsible for the response against salt stress. Bergholz et al. (2012) found a large set of transcripts that were altered during the adaptation to salt stress (6% NaCl). The majority of these changes initiated by osmotic stress were temperature-dependent, observed at 2 distinct growth temperatures at 37°C and 7°C, indicating that the mechanism to adapt to osmotic stress differs in a temperature-dependent manner. At both temperatures, short term transcriptional change upon salt stress included increased transcript levels of σ B and σ B-regulated genes. They observed significant upregulation of 55 σ B genes by salt stress at both 7°C and 37°C which had similar patterns of induction over time. Similarly, they observed increased expression of *mrpABCDEFG*, encoding a sodium/proton antiporter, and deletion mutation of the antiporter resulted in a longer lag phase indicating its role in adaptation to salt stress at both temperatures. Another study showed that the transcriptional levels of genes associated with a phosphoenolpyruvate-dependent sugar phosphotransferase system were dependent on NaCl concentrations (2.5, 5, and 10%) in *L. monocytogenes* (Bae et al., 2012).

1.7.2 Cold shock

L. monocytogenes is one of the few psychrotrophic pathogens that contributes significantly to the risk of food safety. It is less competitive at low temperatures than some psychrotrophic food spoilage germs such as several *Pseudomonas* species, however, it is still able to multiply at refrigeration temperatures. Aforementioned study by Hingston et al. (2017b) compared cold tolerance capabilities across different genotypes of *L. monocytogenes* strains to find no significant difference, however, in general serotype 1/2c revealed lower cold tolerance than others even though there existed inter-strain variation. A study revealed that

the level of cold tolerance at 4°C was associated with expression of cold tolerance genes, including putative cold shock protein A (*CspLA*) and cyclic-di-AMP phosphodiesterase (*pgpH*) (Arguedas-Villa et al., 2010). Cold tolerant strains expressed higher transcriptional activation of *cspLA* and *pgpH* after exposure to cold stress compared to the cold sensitive strains. Several mechanisms involved in *L. monocytogenes* response to cold have been implicated including cell membrane-based responses, accumulation of low molecular weight solutes, Csps, cold acclimation proteins (Caps), adaptive regulatory proteins, general stress response proteins, and so on (Tasara and Stephan, 2006).

Membrane fluidity is affected by environmental temperatures and bacteria modify the composition of the membrane, particularly in terms of lipid content to maintain the bacterial homeostasis. The process includes a change in the fatty acid chain lengths, an alteration in the degree of fatty acid unsaturation, and a change in the type of branching at the methyl end of the fatty acids (Suutari and Laakso, 1994). A recent study revealed that the principal in altering fatty acid composition of cell-membrane lipids in *L. monocytogenes* is by desaturation of existing fatty acids (Hingston et al., 2017a).

Csps, Caps and other adaptive regulatory proteins play a role in cold adaptation of *L. monocytogenes* (Bayles et al., 1996). Csp family consists of small, highly conserved, and structurally related nucleic acid binding proteins widely distributed among prokaryotes. CspLA, CspLB, and CspD were found in *L. monocytogenes* and their role in cold tolerance as well as osmotic stress tolerance were evaluated (Schmid et al., 2009). The result demonstrated different functional importance in response to those stresses: CspLA > CspD > CspLB in response to cold stress versus CspD > CspLA/CspLB in response to osmotic stress. Another study found overexpression of a low molecular mass protein when transferring *L. monocytogenes* from 30 to 5°C. It is the case for the ferritin-like protein (Flp), a polypeptide composed of six 18 kDa-subunits able to oxidize and sequester numerous iron atoms and the *flp* transcripts were overexpressed upon thermal stresses including cold stress (30 to 4°C) as well as heat stress (30 to 49°C) (Hébraud and Guzzo, 2000).

One of the mechanisms used by *L. monocytogenes* to combat cold shock is the accumulation of low molecular weight solutes including glycine betaine and carnitine which are abundant in food matrices. This method also conferred resistance to osmotic stress. The increase in interacellular solute levels as cryoprotectants may help to decrease loss of intracellular water from the cell when temperatures decrease. A study showed that when *L. monocytogenes* was incubated in the presence of compatible solutes, bacterial generation time decreased significantly at 4°C. Especially, Gbu-mediated glycine betaine uptake at 4°C significantly promoted chilled-cell growth (Angelidis and Smith, 2003).

The role of σ B in adaptation to cold stress is controversial. A study found both σ B-dependent and σ B-independent mechanisms on cold adaptation of *L. monocytogenes* (Chan

et al., 2007). Even though σ B activity was induced during the first 30 min of cold shock (37 to 4°C) in BHI medium, it did not induce σ B-dependent and σ B-independent genes. Expressions of cold stress genes *ltrC* and *bsh* were partially σ B-dependent in stationary phase at 4°C, however, expressions of *opuCA*, *fri* (also called *flp* above), and *oppA* were σ B-independent during growth at 4°C. Moreover, the study found that σ B was not required for *L. monocytogenes* growth at 4°C by demonstrating that σ B deletion mutant did not show reduced growth at 4°C compared to the wildtype.

Other systems have been suggested to play a role in cold stress adaptation of *L. monocytogenes*. In the genome of EGDe, there are 16 two-component regulatory systems, among which 15 are complete signaling systems and 1, encoded by *Imo2512 (degU)*, is an orphan response regulator (Glaser et al., 2001). Pöntinen et al. (2015) found that histidine kinases, belonging to two-component regulatory system was important for the growth and adaptation of *L. monocytogenes* under cold temperatures, and also found the histidine kinases encoding genes, *yycG* and *lisk*.

1.7.3 Acid shock

L. monocytogenes has been isolated from several food products with acidic pH indicating its ability to tolerate low pH and its ability to tolerate acid varies among strains (Koutsoumanis et al., 2003). Studies found various mechanisms of *L. monocytogenes* that cope with acid stress including the glutamate decarboxylase (GAD) system, adaptive acid tolerance response (ATR), and the arginine deaminase (ADI) system.

One of the most well-known acid tolerance mechanisms in *L. monocytogenes* is the GAD system. It is proposed that the GAD system relies on the glutamine/ γ -aminobutyric acid (GABA) antiport system as well as an intracellular decarboxylation reaction of glutamate into GABA that consumes protons and, therefore increase the internal pH of the organism to facilitate pH homeostasis. A study demonstrated that the acid resistance of a strain was linked to different regulation of the genes encoding the decarboxylase and transporter (Feehily et al., 2014). The study also found that the GAD system plays a significant role in the overall virulence in mice model which is relevant to the low pH condition in host body such as gut environment.

The ADI system is involved in a variety of Gram-positive microorganisms for an increased survival at acidic environments (Cunin et al., 1986). The ADI pathway consists of three enzymes: ADI encoded by *arcA*, ornithine carbamoyl-transferase encoded by *arcB*, and carbamate kinase encoded by *arcC*. Arginine is transported into the cells via a membrane antiporter *arcD* then converted to ornithine, CO₂, ammonia and ATP by *arcABC* genes. During this process, the by-product ammonia can form NH₄⁺ in association with intracellular protons which lead to an increase in the cytoplasmic pH. A study showed a functional ADI system in *L. monocytogenes* that is implicated in survival at low pH and virulence *in vivo* and found a

putative activator of ADI genes, namely ArgR as a regulator of the ADI system (Ryan et al., 2009). Interestingly, the transcription of *arcA* and *argR* were both σ_B and PrfA-dependent suggesting a role for the ADI system in both stress response and virulence.

A study confirmed the presence of the ATR system in *L. monocytogenes* and showed that pre-exposure to sub-lethal pH (pH 5.0-5.5) increased survival in lethal pH (pH 3.0-3.5) condition (Davis et al., 1996). Pre-exposure to sublethal acid (pH 5.0) stress at 37°C or 22°C significantly induced acid-stress (pH 3.5) adaptation in tryptic soy broth supplemented with 0.6% yeast extract, however, no acid-stress adaptation was induced at 4°C (Shen et al., 2013). Some studies showed that this protective effect was extended to other stresses such as heat and osmotic shock (Lou and Yousef, 1996; O'Driscoll et al., 1996). Ferreira et al. (2003) showed that survival rate of *sigB* deletion mutant was lower than the wild-type strain after being pre-exposed to sub-lethal pH (pH 2.5), however, the σ_B activity on acid resistance was growth phase dependent demonstrating that σ_B -independent mechanism(s) regulates growth phase-dependent ATR.

1.7.4 Disinfectants and heavy metal

Adaptation of *L. monocytogenes* to food processing plants is also associated with resistance to disinfectants used in the food industry. The difference in MIC level shows sensitivity between strains of *L. monocytogenes* to disinfectants (Aase et al., 2000). The decreased susceptibility of *L. monocytogenes* to quaternary ammonium compounds (QACs) was at least partially caused by activation of efflux pumps that reduced intracellular accumulation of QACs (Romanova et al., 2006). However, a study revealed that all *L. monocytogenes* isolates carried the *mdrL* gene which encodes a multidrug efflux pump, and the *orfA* gene, a putative transcriptional repressor of *mdrL*, independent of QAC sensitivity indicating that those ubiquitous genetic elements are not responsible for the resistance to QACs (Mereghetti et al., 2000). Another study found that the expression of *mdrL* was significantly increased upon adaptation to BC, the most widely used QAC, in originally sensitive *L. monocytogenes* isolates, while originally tolerant strains expressed low to intermediate levels of *mdrL* indicating its partial role in adaptation to BC (Romanova et al., 2006). The originally tolerant strains to BC could be due to the intrinsic resistance attributed to modifications in cell wall such as thickness and the degree of cross-linking of peptidoglycan in the cell wall (McDonnell and Russell, 1999).

Aforementioned LGI-1 which contributes high virulence specific to CC8 in a large outbreak in Canada also plays a role in stress resistance (Gilmour et al., 2010). LGI-1 carries *emrE* gene, encoding a small multidrug-resistant efflux pump, which is responsible for the increased tolerance to QACs that are often used as sanitizing agents in the food processing industry. In the presence of BC, the expression level of *emrE* was upregulated demonstrating the possible

adaptation of *emrE* harbouring strains in FPE (Kovacevic et al., 2016). Other genetic elements associated with BC tolerance such as plasmid-born *bcrABC* resistance cassette (Elhanafi et al., 2010) and novel transposon Tn6188 (Müller et al., 2013) were identified. The *bcrABC* sequence was highly conserved among strains and vast majority of BC resistant strains were discovered to harbour *bcrABC*, regardless of serotype or source (Dutta et al., 2013). Tn6188 also confers increased tolerance towards other QACs and it was particularly abundant among ST121 strains suggesting clonal structure of *L. monocytogenes* population with regard to stress resistance phenotype (Rychli et al., 2017).

Stress resistance as a way of environmental adaptation also involves resistance to heavy metals, mostly cadmium and arsenic (McLauchlin et al., 2004). Evidences show that resistance to heavy metals are associated with resistance to QACs. In a study using 192 *L. monocytogenes* strains, all BC-resistant strains were also resistant to the heavy metal cadmium (Mullapudi et al., 2008). This arose from the fact that the same plasmid (e.g., pLM80) that carries *bcrABC* also harbours the cadmium efflux determinant *cadA2* (Katharios-Lanwermyer et al., 2012). Other *cad* genes including plasmid-borne *cadA1* and chromosomal *cadA3* and *cadA4* also confer the resistance to cadmium. Interestingly, *L. monocytogenes* virulence study using *G. mellonella* model showed negative effect of *cadA4* gene on virulence, although it showed positive effect on biofilm formation (Parsons et al., 2017).

I.8 Regulation and surveillance of *L. monocytogenes*

As a foodborne pathogen, *L. monocytogenes* demands attentive control for its contamination in foods. The European Commission Regulation No. 2073/2005 established microbiological criteria for foods applicable from 2006 based on which food business stakeholders should ensure food safety at each point of the food chain, 'from farm to fork' (European Commission, 2005).

In case of *L. monocytogenes*, there are three main categories proposed specially for RTE foods as detailed in Table 4.

Table 4. Food safety criteria (modified from European Commission, 2005). CFU: Colony Forming Unit.

Food category	Limits	Analytical reference method	Stage where the criterion applies
Ready-to-eat foods intended for infants and ready-to-eat foods for special medical purposes	Absence in 25 g	EN/ISO 11290-1	Products placed on the market during their shelf-life
Ready-to-eat foods able to support the growth of <i>L. monocytogenes</i> , other than those intended for infants and for special medical purposes	100 CFU/g	EN/ISO 11290-2	Products placed on the market during their shelf-life
	Absence in 25 g	EN/ISO 11290-1	Before the food has left the immediate control of the food business operator, who has produced it
Ready-to-eat foods unable to support the growth of <i>L. monocytogenes</i> , other than those intended for infants and for special medical purposes	100 CFU/g	EN/ISO 11290-2	Products placed on the market during their shelf-life

Australia and New Zealand apply the same policy for the control of *L. monocytogenes* under the scheme 'Standard 1.6.1' in RTE foods which are divided into two criteria based on whether growth of *L. monocytogenes* will or will not occur in the RTE food (Australian Government). In USA, Food and Drug Administration have kept a conservative approach in

regulation of *L. monocytogenes* called 'zero tolerance'. According to the policy, for the RTE foods that support the growth of *L. monocytogenes*, the complete absence of the pathogen is required and this action seems to be maintained in the future (Archer, 2018).

Surveillance of human listeriosis is managed at national and international level which focused on invasive forms of *L. monocytogenes* infection, mostly manifested as septicemia, meningitis or spontaneous abortion.

Since 1999, it has been mandatory to report human listeriosis to public health agencies in France (Goulet et al., 2008). The National Public Health Agency collects epidemiologic data including food consumption histories from all patients by using a specific hypothesis-generating questionnaire with laboratory-confirmed infection of *L. monocytogenes*. At the National Reference Centre for *Listeria*, all human and food isolates are characterized to detect clusters of genetically related strains (Moura et al., 2017). To identify the original source of a listeriosis case, food and environmental investigations are conducted systematically, for example, in refrigerators of patients with neurolisteriosis or in hospital kitchens if the listeriosis is suspected to be hospital-acquired. Once incriminated food products are identified, the Ministry of Agriculture conducts investigations in the producers of the foods.

In EU, listeriosis is monitored in most of the European countries by EFSA and the European Centre for Disease Prevention and Control (ECDC) (EFSA and ECDC, 2018). The invasive forms of listeriosis are reported and data are available on ECDC website (<https://ecdc.europa.eu/en/home>). Monitoring of *L. monocytogenes* in RTE food is conducted in several points along with the food chain. The Figure 9 shows different monitoring points that are carried out by various agencies.

	PRIMARY PRODUCTION ^a	HARVEST & PROCESSING	RETAIL
Sampler & context	Clinical investigations in animals by veterinarians Monitoring & Surveys by CA, veterinarians and academia	Official sampling by CA Industry sampling by FBO ^p HACCP & own checks CA investigations, border inspection & Surveys	Official sampling by CA Surveys by CA and academia Monitoring & Surveys by CA, and academia
Objective & methods	Isolation of <i>Listeria</i> spp. in animals Microbiological Lm isolation protocols	Detection and/or enumeration of Lm in raw materials, intermediate, final products, environmental samples (surfaces, equipment) ISO 11290-1&2 or validated equivalent methods	Detection and/or enumeration of Lm in batches or single samples of RTE foods ISO 11290-1&2 or validated equivalent methods
Usefulness of data collected	Diagnosis of listeriosis in animals Occurrence of <i>Listeria</i> spp. in livestock/feed	Compliance verification by CA with the Reg 2073/2005 Corrective actions by FBO ^p and decisions by FBO ^p & CA Occurrence of Lm in RTE foods	Compliance verification by CA with the Reg 2073/2005 Corrective actions by FBO and decisions by FBO ^p & CA Occurrence of Lm in RTE foods
2017 data	19,295 samples; 14 MS	80,044 samples; 25 MS	

CA: competent authorities; FBO^p: food business operator; HACCP: Hazard Analysis and Critical Control Points; RTE: ready-to-eat; Lm: *Listeria monocytogenes*; MS: Member State in European countries; FBO^p, Food Business Operator

(a): Primary production sector: samples from animals and feed.

Figure 9. Overview of *L. monocytogenes* testing along the food chain according to the sampling stage, the sampler and the objective of the sampling (EFSA and ECDC, 2018).

II Bacterial biofilm

II.1 General features

The first documented discovery of microbial biofilm dates back to 17th century by Van Leeuwenhoek, who observed the microbial biofilms on tooth surfaces using his microscope (Donlan, 2002). In 1940, Heukelekian and Heller (1940) discovered that growth and activity of *E. coli* were substantially enhanced in the presence of solid surfaces. Zobell (1943) observed that the bacteria population on solid surfaces was dramatically denser than in the surrounding medium.

Biofilm is a community of microbial sessile cells that aggregate on a biotic or abiotic substratum, sometimes at a solid-liquid interface, often embedded in self-produced of extracellular polymeric matrix. Biofilm formation is a cooperative group behaviour that engages a comprehensive crosstalk within a bacterial population allowing them to behave like a multi-cellular organism. Microorganisms form biofilms on a wide range of surfaces, including living tissues, indwelling medical devices, industrial piping systems, natural aquatic systems, food processing equipment, or sewage. The most notable physiological change observed in bacterial cells growing in biofilm is the change in composition of the bacterial membrane. Different fatty acids contents of cells within a biofilm as compared to their planktonic growing counterpart were observed (Dubois-Brissonnet et al., 2016; Gianotti et al., 2008). The content of saturated fatty acids increased in biofilm cells compared to planktonic cells and branched-chain fatty acids decreased concomitantly in Gram-positive bacteria (*L. monocytogenes* and *Staphylococcus aureus*). This change in membrane lipid composition enhances bilayer stability and increases membrane phase transition temperature resulting in a higher density of packing (Denich et al., 2003). These physiological changes occurring during biofilm formation allow the bacteria better equipped for stressful conditions encountered in their environment.

Biofilm mode is the most common and successful way of life for microorganisms in nature (Flemming et al., 2016). Few reasons have been proposed to explain the formation of microbial biofilms (Jefferson, 2004). Firstly, biofilms are a way of microbial defense mechanism that increases survival in nature. Biofilms are resistant to physical forces such as the shear forces produced, for example, in pipes or ducts or by flow of blood or saliva that could otherwise remove cells. Cells in biofilms can also resist phagocytosis by protozoa and immune cells and delay the penetration of toxic substances such as antimicrobial reagents. Cells in biofilms can withstand adverse changes such as nutrient deprivation or exposure to extreme pH changes. These advantages could have served as an evolutionary force for microorganisms to build biofilms in order to improve the chances of survival. Second, microorganisms form biofilms in order to allow cells to remain in a favorable niche. Human and animal bodies are a favorable habitat for bacteria because it is nutrient rich and relatively

stable concerning water content, oxygen availability, and temperature. Also, in nature, on abiotic surfaces in flowing systems, biofilms fix bacterial cells where nutrients are abundant and constantly being replenished. Third, biofilms are formed in order to allow cells to live in close association with each other. The cells in community can facilitate nutrient and genetic exchange by cell-to-cell communication which increase chances for survival in general. Upon change in their surroundings, the cells in biofilms exert phenotypic heterogeneity similar to cellular differentiation seen in multicellular organisms. This behaviour enables cells in biofilms to adjust their metabolic processes and defend themselves from deleterious conditions.

II.1.1 Formation steps

Biofilm formation takes place as a sequence of continuous steps which can be categorized into, for example, three steps including adhesion, maturation, and dispersal or five steps including reversible attachment, irreversible attachment, maturation I and II, and dispersion (Monroe, 2007; Stoodley et al., 2002b; Vogelee et al., 2014). Each step of this process depends on various factors such as the microbial species, physiological status of the microorganism, characteristics of substratum as well as environmental conditions. Quorum sensing, a cell–cell communication mechanism, plays a crucial role in biofilm formation. As it requires cooperative bacterial interaction, quorum sensing synchronizes gene expression in response to population cell density and coordinates the switch from planktonic to sessile lifestyles and *vice versa* (An et al., 2006; Li and Tian, 2012; Solano et al., 2014). Figure 10 visualizes the biofilm forming steps.

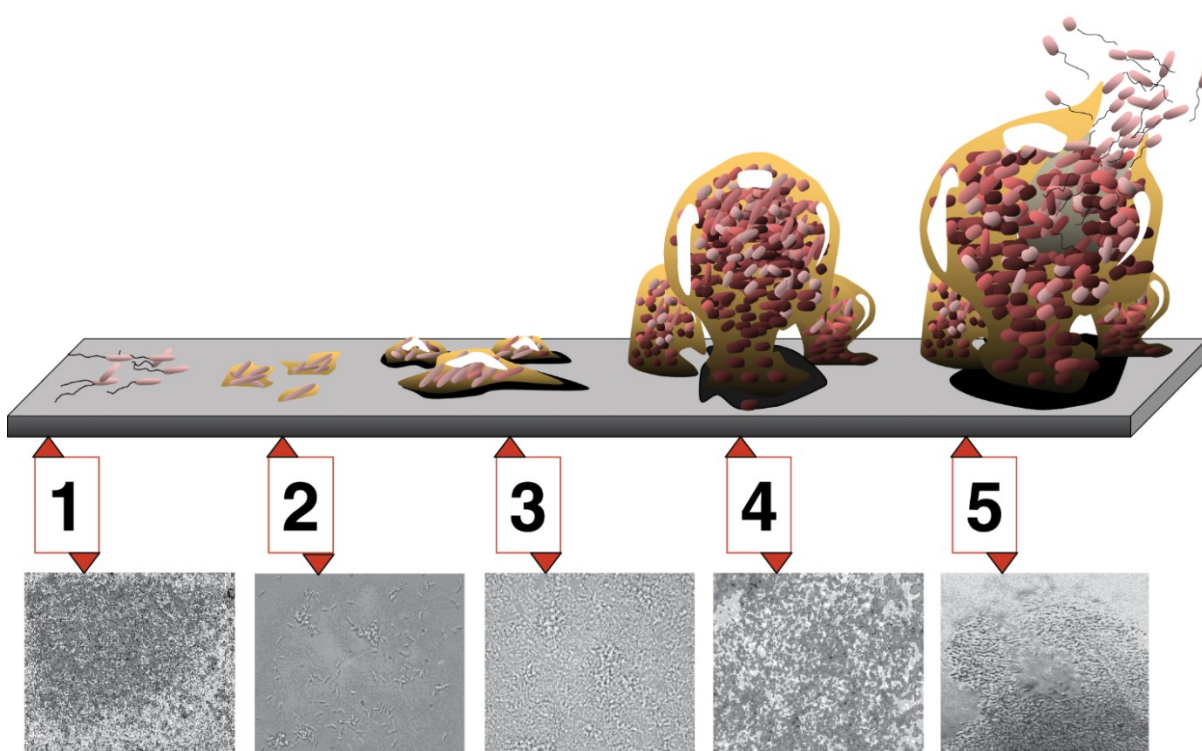


Figure 10. The five stages of biofilm development (Monroe, 2007). Stage 1, initial attachment: Planktonic bacteria adhere to surface. Stage 2, irreversible attachment: Cells aggregates form micro colonies and excrete extracellular polymeric substances. Stage 3, maturation I: A biofilm starts to mature with cells arranged in multi-layered clusters. Stage 4, maturation II: Three-dimensional (mushroom-like) structure and further maturation of the biofilm. Stage 5, dispersion: Cells in the biofilm disperse into planktonic bacteria, ready to colonize other surfaces. Each stage of development is paired with a photomicrograph of a developing *P. aeruginosa* biofilm. All photomicrographs are shown to same scale. Image Credit: D. Davis

In general, the initial step is the colonization of abiotic and biotic surfaces by planktonic cells which is called adhesion. There exist several terms to describe the first step of the biofilm formation including adhesion, attachment, or adsorption. Attachment of a cell to a surface is termed adhesion while cell to cell attachment is called cohesion (Garrett et al., 2008). Fletcher described that adsorption is the accumulation of a microorganism on a substrate which followed by attachment, consolidation of the interface between the organism and the surface (Fletcher and Loeb, 1979). In liquid, microbial cells move toward a surface either by physical force including gravitation or voluntary movement propelled by bacterial appendages such as flagella. When bacteria reach the surface, various factors play a role in the adsorption process such as available energy, surface functionality, bacterial orientation, temperature and

pressure conditions (Garrett et al., 2008). The initial and reversible interaction between a bacterial cell and a surface involves non-specific Lifshitz-van der Waals, Lewis acid-base, and electrostatic forces (Renner and Weibel, 2011; van Oss, 1993).

The reversible attachment is strengthened by adhesins presented on the bacterial cell surface or on cellular appendages such as pili and fimbriae (Rosan and Lamont, 2000). Once cells adhere or irreversibly attached to a surface, they are not washed away by gently washing. Adhered cells often produce extracellular polymeric substances (EPS) that form matrix between a cell and surface as well as between adjacent cells. Also, the sessile cells multiply in numbers. As the matrix and cells accumulates, the biofilm architecture begins to establish and become mature. The developed mature biofilms contain millions of tightly packed cells that are represented by pillar- and mushroom-shaped structures that project into the surrounding medium (Hall-Stoodley et al., 2004).

The last step of biofilm development is the detachment of cells from the biofilm to disperse into the environment. The dispersal of biofilm cells is an essential stage that contributes to transmission of bacteria from environmental reservoirs to human hosts biological dispersal, bacterial survival, and disease transmission (Kaplan, 2010). Dispersal is an elaborated process that involves environmental signals, signal transduction pathways, and effectors. The mechanism of dispersal includes synthesis of enzymes that degrade adhesins, recovery of cell motility, surfactant production, cell lysis and swimming out of motile cells from the inner region of microcolony called 'swarming dispersal' (Karatan and Watnick, 2009). One example of initiating biofilm dispersal is a change in surrounding nutrient level (Sauer et al., 2004). Both decreases and increases in environmental nutrients composition induce dispersal of biofilm cells.

II.1.2 Matrix

In most biofilms, matrix accounts for over 90% of total mass most of which are highly hydrated (Flemming and Wingender, 2010). The matrix consists of various types of biopolymers, known as extracellular polymeric substances (EPS). Initially, EPS indicated 'extracellular polysaccharides' due to the abundance of polysaccharides in the matrix. However, EPS became to define extracellular polymeric substances since studies revealed that other components such as extracellular proteins, nucleic acids, lipids and other biopolymers such as humic substances are produced by microorganisms to form matrix of biofilms (Flemming et al., 2007; Flemming and Wingender, 2010). Most of the components including exopolysaccharides, extracellular proteins, and DNA are hydrophilic molecules that provides highly hydrated environments to cells in biofilms. Various studies indicate that biofilms are hydrogels meaning that polymer chains trap water in order to protect the biofilms from fluctuations in water availability and shear stresses in the environment. This allows protection

of bacterial cells in biofilms from surroundings and thus increase the survival. As a respond to desiccation stress, bacteria actively produce EPS and a study revealed that *L. monocytogenes* in biofilms was highly resistance to desiccation stress (Hansen and Vogel, 2011; Roberson and Firestone, 1992).

Exopolysaccharides were believed to be major composition of the EPS, however, in environmental biofilms, polysaccharides contributed to only a minor part in the matrix (Frølund et al., 1996). Polysaccharides, with a molecular mass of $0.5 - 5 \times 10^6$ Da, can be visualized by electron microscopy as a fine strand attached to the cell surfaces. Exopolysaccharides may either be homopolymeric or heteropolymeric in composition. However, most polysaccharides are heteropolysaccharides, a mixture of neutral and charged sugar residues varying in size from disaccharides to heptasaccharides. Most studied exopolysaccharides include alginate, xanthan and dextran, cellulose, and colanic acid (Nwodo et al., 2012). In general, polysaccharides in EPS provide diverse benefits including adhesion to surfaces, protection from various stresses, and structuring and maintaining biofilms (Limoli et al., 2015). Neutral polysaccharides function as structural components while charged or hydrophobic polysaccharides are involved in ion exchange and sorption (Flemming et al., 2007).

Extracellular proteins are present in considerable amount in biofilm matrix which was reported to exceed the content of polysaccharide on a mass basis (Conrad et al., 2003), especially in environmental biofilms such as sludge and biofilms in sewers (Jahn and Nielsen, 1998). Various extracellular enzymes are detected which are involved in the degradation of biopolymers including water soluble and insoluble compounds and organic particles. The enzymes include protease, peptidase, endocellulase, chitinase, lipase, phosphatase and so on. Some enzymes degrade EPS components to produce low-molecular products that can be utilized as carbon and energy sources. Other enzymes have a function in dispersal step of biofilms to release sessile cells into planktonic cells or a function as virulence factors in infection process. There are also non-enzymatic proteins that are involved in structuring the matrix. Several lectins and lectin-like proteins were reported for their function in stabilization of the matrix network in several species for example, *Streptococcus* mutants (Lynch et al., 2007), *Azospirillum brasilense* (Mora et al., 2008) and *Pseudomonas aeruginosa* (Diggle et al., 2006).

Various species produce extracellular DNA in their biofilm matrix which, in some species, such as *S. aureus* and *P. aeruginosa*, plays an integral role as a major matrix component (Montanaro et al., 2011). The common mechanism to release eDNA is by cellular autolysis, however, some studies found that biofilm eDNA is different from genomic DNA implying that eDNA is actively produced and transported to extracellular biofilm matrix (Böckelmann et al., 2006).

II.1.3 Localization

II.1.3.1 Natural environment

There are fossil records that show evidences of biofilm formations which date back to few billion years (Rasmussen, 2000; Westall et al., 2001). The evidences are found particularly in hydrothermal environments. Comparable morphological similarity was observed between fossil biofilms and modern biofilms found in hot springs or deep-sea vents (Reysenbach and Cady, 2001; Taylor et al., 1999). It is plausible that hostile and fluctuating environmental conditions of primitive earth promoted biofilm formation as an adaptive response that could provide microorganisms homeostasis. It was believed that bacterial planktonic mode of life proceeded sessile mode of life. However, concurrent evolutionary development of both sessile and planktonic forms has been suggested evidenced by fossil biofilms as well as catalytic and protective conditions offered to sessile microorganisms (Stoodley et al., 2002b).

The structural features of biofilms are found to be generally isotropic in diverse environments (Hall-Stoodley et al., 2004). Moreover, *in vitro* grown biofilms by single species and biofilms formed by mixed species in nature exhibited similar overall structural characteristics (Costerton et al., 1995). In quiescent waters where shear force is not apparent, biofilms tend to form mushroom or mound-like structures (Stoodley et al., 2002b). However, under high unidirectional flows, the biofilm cell clusters elongate in the downstream direction to form filamentous streamers (Stoodley et al., 1999). The highly hydrated structure of biofilms grants viscoelastic behaviour when grown under flow either in nature or *in vitro* (Stoodley et al., 2002a). This allows biofilms to withstand water fluctuation and shear stresses that occurs periodically in nature due to seasonal and weather changes.

Microbial biofilms are often found in extreme environments, such as in acid mine drainage (at a pH of 0) where the acidophiles contribute to acid mine drainage and presumably iron and sulfur cycles as well (Edwards et al., 2000). In thermal springs, cyanobacterial biofilms are extensively observed (Ward et al., 1998) and biofilms are also observed in the desert-like lake ice cover in Antarctica (Paerl and Priscu, 1998). Various biological processes were observed including photosynthesis, nitrogen fixation and fermentation in the biofilms formed in these extreme environments. In the marine environment, floating biofilms which are not bound to surfaces, often referred to as marine snow, are investigated (Caron et al., 1986). These macroaggregates are an assembly of bacterial cells, organic and inorganic materials that are involved in biogeochemical transformation of particulate organic carbon in the pelagic environment.

II.1.3.2 Medicine domain

Various bacteria adhere and form biofilms inside or on the surface of host tissues and some of them lead to deleterious infections. The profound knowledge of biofilm formation from environmental studies helped understanding biofilm infections. Now, it is well recognized that biofilm formation is a crucial aspect of many bacterial infections, including urinary tract infections, native valve endocarditis, osteomyelitis, dental caries, middle ear infections, medical device-related infections, ocular implant infections, and chronic lung infections in cystic fibrosis patients (Donné and Dewilde, 2015). It is more challenging to treat infections established in the format of biofilms, because biofilms tolerate antimicrobial agents at concentrations of 10 to 1,000 times higher than that are needed to kill isogenic planktonic bacteria.

Complex interactions between biofilm pathogens and the host inflammatory response are involved in order to modify the host environment and alter the phenotype of the bacteria that contribute to the pathogenesis of biofilm infections (Hall-Stoodley et al., 2004).

One thoroughly documented example is cystic fibrosis pneumonia, an autosomal recessive disease caused by mutations in the cystic fibrosis transmembrane conductance regulator (CFTR) gene (Høiby et al., 2010). This results in dysfunction of electrolyte secretion and absorption primarily manifesting dysfunction in respiratory system. Main features include more viscous respiratory mucous layer and impaired mucociliary clearance due to the reduced hydration of the airway surface fluid. It leads to subsequent airway obstruction and progressive destruction of the airway epithelium developing to respiratory failure. Colonization of the lower respiratory tract of CF patients begins with *S. aureus* and *Haemophilus influenzae* in childhood and transfer to *P. aeruginosa* from early adulthood (Koch and Høiby, 1993). *P. aeruginosa* in lung grows in biofilms that cause persistent chronic infections due to their increased tolerance to antibiotics, resistance to phagocytosis and other innate and the adaptive immune system. This leads to immune complex-mediated chronic inflammation manifested by polymorphonuclear leukocytes which causes damages in the lung tissue. In cystic fibrosis, *P. aeruginosa* biofilms establish antibiotic resistant through several mechanisms including chromosomal β -lactamase, upregulated efflux pumps, and mutations of antibiotic target molecules in the bacteria (Høiby et al., 2010).

Implant contaminations are another main infection caused by biofilms. The causative medical devices include intravenous catheters, peritoneal dialysis catheters, cardiac pacemakers, prosthetic heart valves, joint prostheses, cerebrospinal fluid shunts and endotracheal tubes (Hall-Stoodley et al., 2004). The most frequently associated bacteria are *S. epidermidis*, *S. aureus*, *P. aeruginosa* and other opportunistic bacteria that infect compromised host under invasive medical intervention. The infection caused by biofilm

formed on medical implants is termed as 'polymer-associated infections' (Eiff et al., 1999; von Eiff et al., 1999). The most profound feature of biofilms produced by staphylococci is abundant amount of EPS encasing cells to protect against host immune defences and antibiotic treatment.

II.1.3.3 Food industry

Microbial contamination of food products is of great concern for public health. Contamination of foods with microorganisms occurs when food comes in contact with contaminated surfaces increasing the food safety risk. It is proposed that the microorganisms that persist by forming biofilms lead to repeated food contaminations.

Linked to the food industry, the most studied bacteria forming biofilms are *P. aeruginosa*, *Bacillus cereus* (which secretes toxins that can cause diarrhea and vomiting symptoms), *E. coli* (which may include enterotoxigenic and even enterohemorrhagic strains), *S. aureus* (known for its numerous enteric toxins), *Salmonella enterica* (which, when contaminating a food pipeline biofilm, may induce massive outbreaks and even death in children and elderly), *Campylobacter jejuni*, *Vibrio cholerae*, and *L. monocytogenes* (Coughlan et al., 2016; EFSA and ECDC, 2018; Galié et al., 2018). It is believed that the pathogenic bacteria enter FPE via flows of raw materials, working personnel as well as food processing equipment. Studies demonstrated that in food processing industry, bacterial biofilm was found on various surfaces and crevices of many equipment including stainless steel pipes, vessels, valves, tables, drains and conveyors (Austin and Bergeron, 1995; Marchand et al., 2012). Attached bacteria were also found in liquids contact surfaces such as milking equipment and milk tanks (Latorre et al., 2010). Once biofilm is formed on food contact surfaces, it becomes highly resistant to disinfectants and other cleaning agents compared to the cells in planktonic form (Chmielewski and Frank, 2003; Pan et al., 2006). Moreover, microorganisms existing in biofilms exert higher resistance to other environmental stress factors related to food industry such as cold temperatures, shear force, nutrient deprivation, low water availability, and desiccation stress (Esbelin et al., 2018; Wong, 1998). This higher stress resistance of microorganisms in biofilm is presumed to lead them to colonize, multiply, and persist in FPE including food processing equipment over extended periods and increase the chance of repeated food contaminations (Colagiorgi et al., 2017; Fratamico et al., 2009; Lappi et al., 2004).

II.1.3.4 Others

Dental biofilm, termed dental plaque, is primarily composed of microorganisms community found on a tooth surface embedded in a matrix of organic and inorganic materials derived from saliva, gingival crevicular fluid and bacterial products (Saini et al., 2011). Early colonizer of tooth surfaces are *streptococci* (for example, *Streptococcus mitis* and *S. oralis*)

that bind to acquired pellicle, a thin film of active proteins that coat tooth surfaces. With time, the early colonizers make the environment more anaerobic and other obligate anaerobes multiply and produce EPS to consolidate the biofilm (Huang et al., 2011; Marsh, 2010).

Marine biofilm, termed biofouling, is the colonization of submerged surfaces by microorganisms and is detrimental for devices used in different fields including shipbuilding and aquaculture industries. Microfouling formed by bacteria and microalgae leads to the adhesion of larger organisms including algae, mussels and barnacles causing macrofouling (Carvalho and R, 2018). On the hull surfaces of ships immersed in seawater, biofouling diminishes their hydrodynamic performances. Moreover, the US Navy estimated that the overall cost related to hull fouling for the entire US Navy surface fleet was calculated to be 180–260 million dollars (Schultz et al., 2011).

Biofilms in water distribution systems including pipes can lead to chlorine demand, pipe corrosion and degrading water taste and odor (Hallam et al., 2001). Biofilm built in water pipelines consists of bacterial populations within a slime layer that is in contact with water. Even though water is disinfected before distribution in treatment plants by water authorities, by the time it reaches end point users the quality may decrease dramatically due to contamination of water pipes with biofilms (Mahapatra et al., 2015). A study conducted in UK showed that bacterial communities were highly variable and fluctuating with season and pipe material (Douterelo et al., 2016).

II.2 Regulation of biofilm formation

Biofilm formation is a string of simultaneous processes engaging various steps as well as diverse physiological cellular states. High throughput studies conducted on cells growing in biofilms pointed out time-dependent differential genes expression patterns in various bacterial species (Sauer, 2003). For example, in *Bacillus subtilis* using microarrays for comparison of planktonic *versus* biofilm cells after 8, 12, and 24 h growth, a total of 519 genes were identified as differentially expressed during the time-course of which more than 55% were expressed at only one of the three time points (Stanley et al., 2003). This result indicates temporal and stochastic regulation of genes expression during different biofilm formation steps. Similar findings were observed in *Porphyromonas gingivalis* (Yamamoto et al., 2011) and *L. monocytogenes* (Prakash and Tirumalai, 2012). Together, these findings support the fact that divergent modules of genes are involved in each step of biofilm formation, thus, analyzing a snapshot of bacterial expression patterns may not represent well the regulatory networks involved in biofilm formation at each step. Herein, we will discuss the well described microbial biofilm regulators and discuss further about specific regulators for *L. monocytogenes* biofilm formation later in 'Chapter II.4.1 Specific regulation of *L. monocytogenes* biofilm formation'.

II.2.1 Cyclic-di-GMP

In 1987, bis-(3',5')-cyclic diguanosine monophosphate (c-di-GMP) was first reported in *Acetobacter xylinum* as an allosteric activator for cellulose synthase (Ross et al., 1987). As one of the major second messengers, c-di-GMP mediates wide signaling pathways modulating a large range of bacterial behaviours (Hengge et al., 2016). It was demonstrated that GGDEF and EAL domains, consisting sensor kinases in bacterial two component regulatory systems, regulate the expression of c-di-GMP (Galperin et al., 2001; Ryjenkov et al., 2005; Schmidt et al., 2005) (Figure 11).

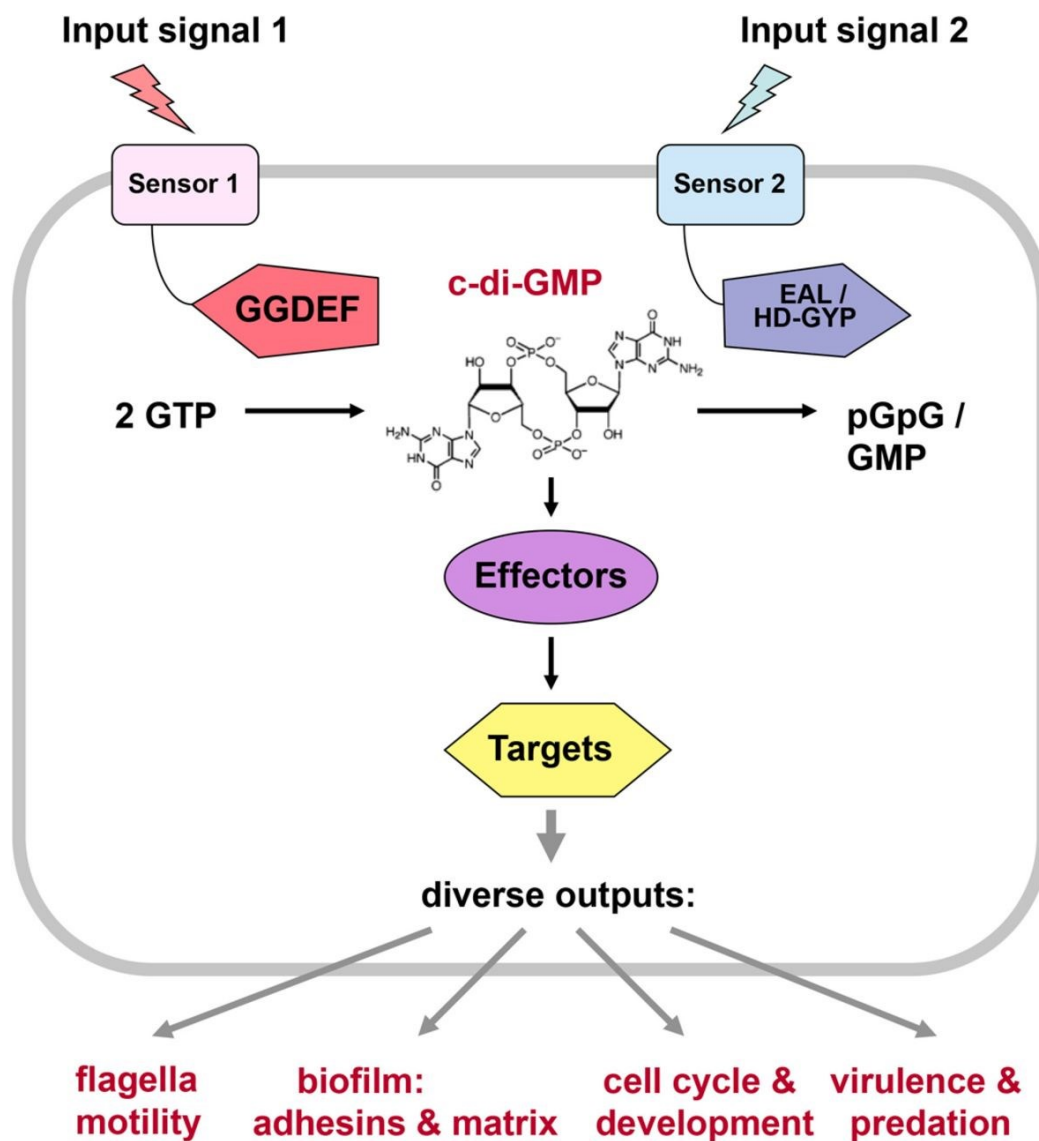


Figure 11. General scheme of production, degradation, mechanism of action, and physiological target processes of the second messenger c-di-GMP (Hengge et al., 2016).

Proteins with GGDEF domain demonstrate diguanylate cyclase (DGC) activity which produces the c-di-GMP while proteins with EAL and HD-GYP domains, which are distinct families of c-di-GMP-specific phosphodiesterases (PDEs), degrade it. The expression of these domains and subsequent c-di-GMP signaling pathway are ubiquitous in bacteria. The domains, often bound to bacterial membrane, sense environmental and intracellular signals such as light (Tschowri et al., 2012), oxygen (Schmidt et al., 2016), membrane-derived signals and other small ligands (Furukawa et al., 2012) and change the c-di-GMP levels, which in turn regulate bacterial lifestyle. One of the well-known functions governed by this cascade is the establishment of a sessile lifestyle by inhibiting motility and increasing biosynthesis of

exopolysaccharides and biofilm formation in various proteobacterial species (Ryjenkov et al., 2005). Implication of this signaling pathway in exopolysaccharide production and biofilm control was demonstrated in *A. xylinum* (Ross et al., 1987), *V. cholerae* (Bomchil et al., 2003), *P. aeruginosa* (D'Argenio et al., 2002), *Pseudomonas fluorescens* (Spiers et al., 2003), *Agrobacterium tumefaciens* (Ausmees et al., 2001), *S. enterica* and *E. coli* (Branchu et al., 2013; Lindenberg et al., 2013; Richter et al., 2014, 4; Simm et al., 2004). In *L. monocytogenes*, c-di-GMP-inducible exopolysaccharide caused cell aggregation and enhanced bacterial tolerance to disinfectants as well as desiccation stress, however, it did not promote biofilm formation on abiotic surfaces (Chen et al., 2014).

II.2.2 RpoS Activity

Bacteria growing in biofilms exhibit physiological behaviours similar to stationary-phase growing cells expressing molecular signals for stress conditions and slow growth. In this regard, the role of a stationary-phase sigma factor RpoS has been implicated in biofilm production in Gram-negative bacteria (Symposium et al., 2000). As a general stress-response regulator, RpoS activates a large number of genes, (23% of genes were regulated in the *E. coli*) in response to various stressful environments to adapt to changing conditions and confer stress tolerance (Wong et al., 2017). As a consequence, RpoS plays a major role in entire cell physiology under suboptimal conditions (Landini et al., 2014). Expression of RpoS is correlated with repression of bacterial motility and transition into sessile mode of life (Adnan et al., 2017; Corona-Izquierdo and Membrillo-Hernández, 2002). The expression of RpoS induces a key transcriptional regulator CsgD at the transcriptional level which determines switch between planktonic and sessile modes of growth (Chambers and Sauer, 2013). It was shown that the RpoS-CsgD cascade enhanced adhesion and biofilm production by activating the production of curli fimbriae while deregulation the expression of several flagellar biosynthesis genes in *E. coli* and *Salmonella* strains (Barnhart and Chapman, 2006; Ogasawara et al., 2011).

However, heterogeneous results were observed in different bacterial species suggesting a strain-specific role of RpoS with regard to biofilm formation. In an endophytic bacterium *Serratia plymuthica*, mutants of *rpos* resulted in enhanced motility as well as biofilm formation (Liu et al., 2016).

Moreover, the expression of RpoS is differentially regulated depending on cell density by interplay between HapR, the quorum-sensing regulator, and VpsR and VpsT, regulators for modulating expression of *vps* genes which encode matrix proteins and polysaccharides synthesis in *V. cholerae* (Wang et al., 2012) (Figure 12). In the bacteria, enhanced motility induced by RpoS was also observed, together, the removal of RpoS repression from VpsT in biofilms enhances motility thus promoting bacterial detachment (Wang et al., 2014).

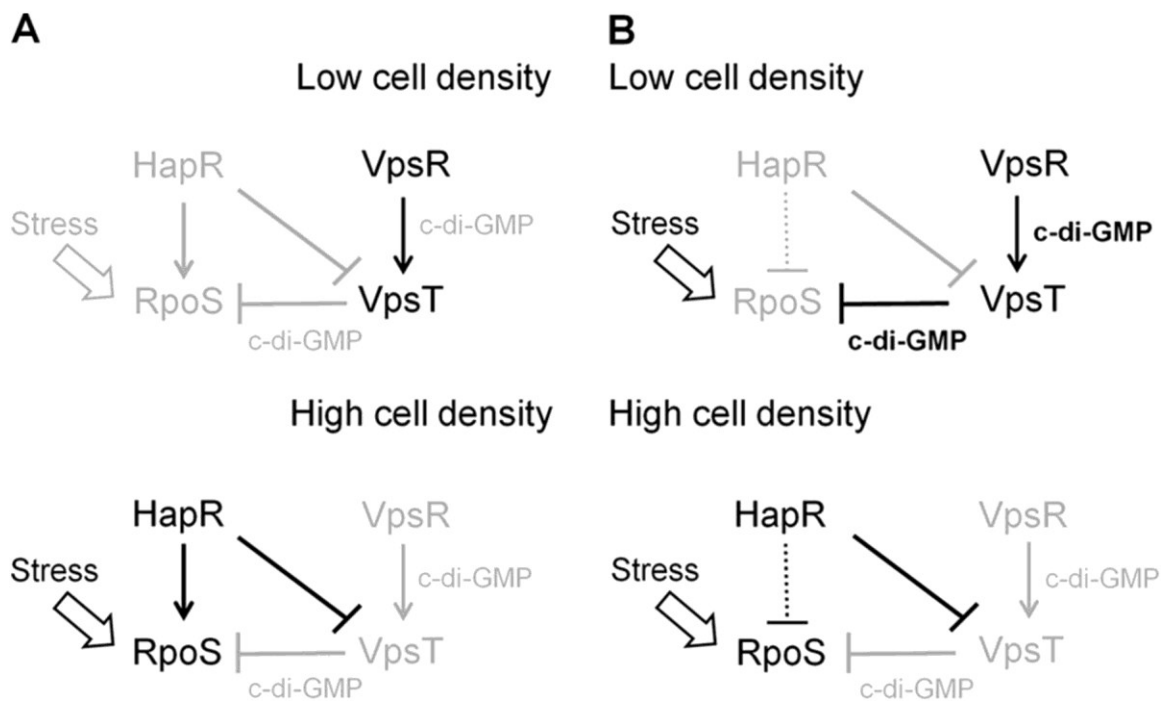


Figure 12. Model for the interplay between HapR and VpsT in the regulation of RpoS expression. Disabled regulations and low c-di-GMP content are represented by lines and fonts in light grayscale. Symbols: \rightarrow , activation; \perp , repression. (A) Planktonic cells. In nutrient-rich medium, the level of c-di-GMP is not sufficiently high for VpsT to repress *rpoS* transcription. HapR enhances *rpoS* in a VpsT-independent manner. (B) Biofilm cells. Biofilm cells can exhibit a higher starting intracellular c-di-GMP level than planktonic cells and experience stress conditions resulting in earlier expression of RpoS. At a low cell density, VpsT represses *rpoS* transcription. At a high cell density, HapR represses VpsT and diminishes the c-di-GMP pool to relieve *rpoS* from VpsT repression. We postulate that in biofilms, HapR could have a negative effect on *rpoS* expression (dotted line) that is masked in the *hapR* mutant due to the much stronger repressive effect of VpsT (Wang et al., 2014).

II.2.3 Others

As the first step of biofilm formation, adhesion plays a critical role in determining the overall path of sessile format of lifestyle. Notably, several bacterial cell surface structures function as adhesins in this initial step. Some well described bacterial appendages important for adhesion are capsules, fimbriae, pili and flagella. Capsulation occurs in certain bacterial species which protect the pathogens from host defense mechanisms. The capsular polysaccharides were shown to enhance adhesion in *Klebsiella pneumoniae* (Wang et al., 2015). For pathogenic bacteria, fibrillar structures such as fimbriae and pili serve bacterial

adhesion and colonization or invasion of host tissues (Finlay and Falkow, 1997). It was observed in diverse species, such as *E. coli* (Lasaro et al., 2009), *Proteus mirabilis* (Scavone et al., 2016), and *K. pneumoniae* (Schroll et al., 2010) where fimbriae contribute to adhesion and biofilm maturation. Accumulated data show that various types of fimbriae differentially regulated biofilm construction. Similarly, flagellum-mediated adherence was also reported (Girón et al., 2002). Furthermore, a study showed that flagella and type 1 fimbriae served as integral components for adhesion and invasion of intestinal epithelial cell line in *E. coli* strain LF82 (Barnich et al., 2003; Boudeau et al., 2001). The two components were shown to be regulated in a coordinate manner. However, contradictory findings were reported regarding the role of flagella in biofilm formation depending on the experimental settings. Flagellar motility showed a critical role in biofilm formation in *L. monocytogenes* (Lemon et al., 2007) and transposon mutagenesis screening identified that genes involved in flagellar motility (*fliQ*, *flaA*, *fli1*, *motA* and *lrmg_00396*) were necessary for biofilm formation, especially for early adhesion to surfaces (Alonso et al., 2014). Unlike the static cultivation used in those studies, a study using a flow cell demonstrated that motility mutants produced more biofilms (Todhanakasem and Young, 2008). Similarly, a study demonstrated that flagella in *L. monocytogenes* served for motility but not for adhesion to Caco-2 cells (O'Neil and Marquis, 2006). In *E. coli* K-12 strain, flagellar motility was not required for initial adhesion nor for biofilm development (Prigent-Combaret et al., 2000). Flagella in principal confer swimming locomotion enabling bacteria to move towards favorable responses, for example, nutrients and away from unfavorable stimuli, such as disinfectants. Flagella, therefore, demonstrate a reciprocal balance between motility and adhesion.

Several transcription factors have been identified in the regulatory networks of biofilm-associated gene in different species. In *B. subtilis*, the major early sporulation transcription factor Spo0A plays a central role controlling the expression of more than hundred genes including those required for biofilm matrix formation and sporulation (Hamon and Lazazzera, 2001). A study showed that mutant lacking *spo0A* was capable of adhering to a surface in a monolayer of cells, however, failed to build mature three-dimensional biofilms. Intracellular ratio of phosphorylated Spo0A (Spo0A-P) in comparison to Spo0A determines the bacterial behavioural change between cannibalism, competence or biofilm production (Vlamakis et al., 2013). Biofilm formation and sporulation are repressed when Spo0A-P level is low and biofilm formation is induced when Spo0A is initially phosphorylated as a result of matrix gene expression (Fujita et al., 2005). Higher level of Spo0A-P induces sporulation genes.

Surface proteins and extracellular matrix components are involved in interbacterial adhesion and biofilm structure. Surface proteins are important for promoting bacterial colonization. Among them type V secretion pathway plays an important role in contact-dependent translocation of proteins toward the extracellular medium in *E. coli* (Beloin et al.,

2008). Antigen 43 promotes cell-to-cell adhesion (Kjærgaard et al., 2000). Biofilm Regulator, EbrB modulates biofilm formation and intestinal colonization (Top et al., 2013).

II.3 Biofilm development and stress response

As discussed earlier, in nature habitats most microorganisms live in contact with solid materials. Bacteria have evolved efficient ways to cope with fluctuating and adverse conditions and rapid switch to surface-attached biofilm lifestyle is one of the most advantageous for the survival (Donlan, 2002). In principal, sessile lifestyle is favored for contradictory reasons: while bacteria switch from free-living to biofilm mode of life to colonize and remain in a favorable niche, non-optimal growth conditions also trigger biofilm formation as a defense mechanism (Jefferson, 2004). To support these opposing phenomena, controversial findings were reported regarding the impact of environmental conditions on biofilm formation. For example, nutrient contents in media resulted in different outcomes with regard to biofilm formation. While some studies found that biofilm production was enhanced in nutrient-limited condition (Anutrakunchai et al., 2015), others showed that nutrient rich media produced more biofilms (Stepanović et al., 2004). In fact, the differences were carbon-source specific (Totani et al., 2017) and also species specific (Stepanović et al., 2004).

In cases in which biofilm formation is promoted as defense mechanism, therefore, environmental signals that activate stress responses often lead to biofilm formation. Bacteria growing in biofilms, in turn, exert higher resistance against broad range of stress factors such as antibiotics (Mah and O'Toole, 2001), sanitizers (Chavant et al., 2004), acid (Welin-Neilands and Svensäter, 2007), osmotic, and temperature (Vatansever and Turetgen, 2018) stresses. Several mechanisms underlie the general resistance phenomenon. As mentioned earlier, change in membrane lipid composition in biofilm cells enhances stress resistance. The EPS matrix grant physical resistance to stresses. Finally, metabolic pathways in biofilms share stress response mechanisms. For instance, oxidative stress is one of the most common stresses for microorganisms in nature (Imlay, 2019). Response to oxidative stress in bacteria share common regulatory pathways with biofilm formation of which involve reactive oxygen species (ROS) as a signaling molecule. Bacteria alter their metabolism to avoid cellular damages from ROS. They integrate ROS into several signaling pathways which mediate the transit from planktonic to sessile forms of lifestyle (Cáp et al., 2012). ROS in biofilm cells provoke genetic variabilities and promote programmed cell death in core regions. Also, ROS are involved in other pathways engaged in biofilm formations, such as quorum sensing (Karatan and Watnick, 2009) or indole signaling pathway (Hu et al., 2010). An experimental evolution assay demonstrated that ROS led to the emergence of pro-biofilm cells in *P. aeruginosa* (Chua et al., 2016). Moreover, oxidative stress induced the activation of the DNA repair system such as a DNA double-strand break repair system, resulting in higher phenotypic diversity. This confer readiness on bacteria to adapt to environmental changes also to

withstand environmental stresses (Boles and Singh, 2008). Recent study found that polysaccharides cellulose and alginate in biofilm matrix protected *Pseudomonas putida* against ROS produced under matrix stress and copper exposure (Svenningsen et al., 2018).

Similarly, histidine kinase QseC involved in two-component regulatory system mediates osmotic stress resistance and induces biofilm formation in *Haemophilus parasuis* (He et al., 2018). Also, a study showed that high temperature (40°C) induced RpoS expression which promoted biofilm formation in *P. putida* (Srivastava et al., 2008).

II.4 *Listeria monocytogenes* biofilms

It was suggested that *L. monocytogenes* could only form an attached monolayer of cells on surfaces without growing into mature biofilms, however, recent studies revealed a various degree of maturation in biofilms produced by *L. monocytogenes* (Borucki et al., 2003; Lee et al., 2017; Rieu et al., 2008). *L. monocytogenes* exhibits a capacity to adhere to a wide range of materials after a short contact time such as stainless steel, polypropylene, glass or rubber which implicate the capacity of this pathogen to colonize equipment used in FPE (Beresford et al., 2001; Chavant et al., 2002; Mafu et al., 1990).

Using microscopy such as scanning electron microscopy (SEM) or confocal laser scanning microscopy (CLSM), *L. monocytogenes* biofilm architecture can be visualized. Diverse biofilm structures exist ranging from flat multilayers to complex honeycomb-like structures decorated with hollow voids among *L. monocytogenes* strains (Guilbaud et al., 2015).

In the *L. monocytogenes* biofilm matrix, various EPS were detected including polysaccharides and proteins as well as extracellular DNA (Colagiorgi et al., 2016). Among them, teichoic acid is the major polysaccharide which has the same origin as cell wall teichoic acid (Brauge et al., 2016). Study using 80 *L. monocytogenes* strains revealed that all strains were able to produce exopolysaccharide and the level of production was correlated with cell adherence for high biofilm formers (Borucki et al., 2003).

Under various conditions, one *L. monocytogenes* strain demonstrated significant variation of biofilm production indicating that intra-strain phenotype changes were dependent on experimental settings (Nowak et al., 2015). Interestingly, nutrient deprivation enhanced biofilm formation in microfluidic conditions, however, under static incubation, nutrient restriction resulted in less biofilms (Cherifi et al., 2017; Guilbaud et al., 2015). Moreover, inter-strain variability of biofilm formation has been extensively studied, however, no conclusive agreement was made on describing biofilm forming capacities of *L. monocytogenes* in relation to their origins or serotypes. While some studies found higher biofilm production with serotype 1/2a and 1/2c strains (Borucki et al., 2003; Nilsson et al., 2011), others demonstrated the opposite result showing greater biofilm production capacity of serotype 4b strains (Djordjevic et al., 2002). Moreover, a study using 143 strains implied the impact of experimental settings in finding such a relation (Kadam et al., 2013). In the study, the effect of serotypes on biofilm formation was influenced by growth media which, at the same time, differently affected the kinetics of total biomass measured by crystal violet staining during different incubation time. Another study using 98 *L. monocytogenes* strains could not observe any relation between serological groups and biofilm production (Doijad et al., 2015).

II.4.1 Specific regulation of *L. monocytogenes* biofilm formation

The molecular basis that governs biofilm formation of *L. monocytogenes* are not completely elucidated. However, recent studies identified numerous factors that play a certain role through a screening of insertion mutant libraries (Gorski et al., 2003; Taylor et al., 2002) and proteomic approaches (Helloin et al., 2003; Trémoulet et al., 2002). Trémoulet and colleagues (2002) found that two key enzymes, pyruvate dehydrogenase and 6-phosphofructokinase, involved in global carbon metabolism, were increased in biofilm formation in *L. monocytogenes*. Also, 22 and 9 proteins were up- and down-regulated, respectively, among which diverse functions were observed. For instance, ribosomal proteins YvyD and rpsB that may act as sensors to detect physical or chemical change, SOD and CysK that may be involved in quorum sensing, RecO conferring DNA repair and protection and DivIVA which controls cellular division were upregulated in biofilms.

A surface protein called Biofilm-associated protein (Bap) is involved in biofilm formation in several bacterial species. A protein showing Bap-like structural features was identified in *L. monocytogenes* and thereby designated as BapL (Jordan et al., 2008). Though BapL contributed to adherence on abiotic surfaces, it was not an essential requirement since non-BapL possessing strains revealed attachment to comparable extent. Another study found the deletion of *relA* and *hpt* induced impaired growth of biofilms due to lack of accumulation of guanosine pentaphosphate in response to amino acid starvation (Taylor et al., 2002). Biofilm formation related genes were newly found at 15°C which represent a temperature close to that found in food production environments (Piercey et al., 2016). The study performed insertional mutagenesis and found the following genes that resulted higher biofilm formation at 15°C: *Imo2572*, *Imo2488* (*uvrA*), *Imo1224*, *Imo0434* (*inlB*), *Imo0263* (*inlH*), *Imo0543*, *Imo0057* (*esaA*), *Imo2563*, and *Imo0453*. Also, transcriptional regulator DegU was found to be directly mediating biofilm formation of *L. monocytogenes* (Gueriri et al., 2008). Among one of the many two-component systems involved in response to fluctuating environmental conditions including stress stimuli, the accessory gene regulator *agr* influences adhesion in *L. monocytogenes* (Williams et al., 2005a). Mutants lacking *agrA* and *agrD* showed impaired adhesion but did not affect mature biofilm formation (Rieu et al., 2007).

II.4.2 *L. monocytogenes* biofilms and stress factors

As a foodborne pathogen, numerous studies investigated the susceptibility of disinfectants in *L. monocytogenes*, especially with respect to biofilm cells. Pan and colleagues (2006) designed a simulated food processing experimental setting to compare the resistance of *L. monocytogenes* between biofilm cells pre-exposed and non-exposed to peroxide sanitizers. The results showed that biofilm cells that were repeatedly exposed to the peroxide agent

developed resistance to it as well as other sanitizing compounds including QACs and chlorine (Pan et al., 2006). However, the resistance of cells detached from peroxide pre-exposed and non-exposed biofilm cells did not differ significantly suggesting that the resistant may be attributed to extracellular polymeric substances. Similarly, another study mimicking a sanitation regime applied in real food processing premises showed that *L. monocytogenes* in biofilm could tolerate disinfectants treatment suggesting that biofilms make the sanitary regime inefficient for preventing bacterial food contaminations (Fagerlund et al., 2017).

One of the most predominant factors related to FPE is the low temperature. Most of the studies assessed the influence of different temperatures on biofilm formation. In general, as the temperatures decrease under optimal growth temperature (around 30-37°C), the total biomass also decreases (Nilsson et al., 2011). However, the different growth kinetics were not taken account, therefore, it is not clear whether the bacteria may reach the same maturity of biofilm achieved at optimal temperatures if the growth rate is compensated by longer incubation time at lower temperatures. Our study revealed that cold stress enhanced adhesion of bacteria to abiotic surfaces as a transient phenotype change (Chapter III). Another study showed that cold-adapted *L. monocytogenes* strains by storing at -20°C for 6 and 24 months increased adhesion and biofilm formation on various surfaces (Slama et al., 2012). Interestingly, cross adaptation to a different stress was observed; for example, influence of temperature on chitosan resistance. Chitosan resistance was compared between biofilm cells produced at 20°C or 4°C. The morphology of the chitosan injuries and viability recovery rate of *L. monocytogenes* showed that cold stress increased the tolerance to the chitosan (Puga et al., 2016).

Biofilms formed on equipment in FPE are regularly exposed to desiccation stress. A study performed desiccation stress (43% relative humidity) at 15°C for 23 days on biofilm cells to examine survival and subsequent transfer to salmon products (Hansen and Vogel, 2011). The cells in biofilms were significantly protected against the desiccation treatment compared to the planktonic cells. Moreover, cells adapted to 5% NaCl produced a biofilm that showed significantly increased survival against a long-term (49 days) desiccation. As a result of the enhanced tolerance to desiccation, more bacteria from cells grown in biofilms survived after transfer to salmon products. A recent study compared the difference in desiccation resistance among 14 strains and found the most resistant strains harboured Stress Survival Islet 1 genetic marker which, however, was not a major determinant of survival during desiccation, exposure BC, as well as biofilm formation (Piercey et al., 2017).

II.4.3 Persistence and biofilms of *L. monocytogenes*

Development in molecular subtyping methods such as PFGE and MLST allowed observation of specific subtypes of *L. monocytogenes* that survive over long periods of time in

food production facilities. To explain the persistence trait of certain *L. monocytogenes* subtypes, studies investigated the association of persistence with phenotypic characteristics including tolerance to food related-stresses, desiccation stress, resistance to disinfection processes as well as biofilm formation (Ferreira et al., 2011; Holah et al., 2002; Lundén et al., 2008). It is hypothesized that a higher biofilm forming ability might cause strain persistence in FPE. Borucki et al. (2003) demonstrated the differences in biofilm formation among persistent and non-persistent isolated from bulk milk samples. They revealed that the persistent strains were more efficient in biofilm formation than non-persistent strains. Similarly, Lundén et al. (2000) found that persistent strains were more efficient in adherence after short contact times. Norwood and Gilmour (2001) also showed that the adhesion of persistent strains was superior than that of sporadic strains. However, other studies revealed conflicting results. Djordjevic et al. (2002) found no relationship between persistence of a strain and biofilm formation. A study from Jensen et al. (2007) also revealed no significant relation between adherence and persistence. Similarly, conflicting results were observed between persistent and non-persistence strains with respect to food associated stress factors and susceptibility to disinfectants or sanitizers (Fagerlund et al., 2017; Heir et al., 2004; Holah et al., 2002; Magalhães et al., 2016). In sum, accumulating data disclose diverse phenotypic and genetic characteristics in persistent *L. monocytogenes* suggesting that it is unlikely that biofilm forming capability underlie persistence of *L. monocytogenes* in FPE (Ferreira et al., 2011).

The discrepancies can be ascribed to the different experimental settings between studies including sample size and methodology for quantifying biofilms. Also, the *in vitro* measurements may not reflect well the real environmental conditions that might induce different bacterial behaviours. Moreover, an identification of persistent strains could have been mistaken. A persistent strain, defined as a particular subtype that is re-isolated from the same environment over an extended observation period, is often difficult to determine for several reasons as discussed earlier (Chapter 1.6 *Listeria monocytogenes* in foods). Also, discrepancies were observed among studies in discriminating a persistent subtype from sporadic isolates. For example, variations in the observation period or the minimum number of isolations for a subtype to be determined as persistent or sporadic may have caused biases. Moreover, it is disputed as to whether particular *L. monocytogenes* subtypes can persist or they incidentally colonize specific niches in FPE. More investigations are required in this topic regarding whether a genotype associated with persistence exists or an isolate colonize specific favorable niches in FPE conferring, what we define as persistence.

II.5 Some methods for biofilm study

As the concept of a microbial biofilm became concrete, researchers developed numerous techniques or adapted new technologies to investigate biofilms in several aspects. The most widely applied basic method is counting the colony forming units (CFU) on agar media. Microbial cells in biofilms are detached from an adhering surface using sonication or mechanical disruptions then are subjected to serial dilutions which are spread on an agar plate to numerate the CFU after an adequate incubation (Bjerkan et al., 2009). The CFU approach, affordable and available in every microbiology lab, however, revealed some limitations (Li et al., 2014). There exists a status of microbial cells called viable but non-culturable (VBNC) that are still viable but not able to resuscitate and grow over the given condition of incubation to be counted as a colony. Stressful conditions such as osmotic, oxidative or starvation can trigger transition of bacterial cells to VBNC status which leads to an underestimation of total viable cells in samples. Moreover, the CFU does not represent the entire amount of biofilm including dead cells and EPS components.

Colorimetric methods were developed primarily based on staining of biomass with appropriate dyes. For instance, crystal violet (CV) staining is most widely used in laboratories for measuring total biomass and Alcian Blue or Ruthenium red staining can be used for staining the EPS matrix (Borucki et al., 2003; Sohm et al., 2011). Stained biofilms can be either observed using microscopy or quantified by measuring optical density of destained solution using spectrophotometer. More recently, a method specialized to measure adhesion capacity of microorganism called Biofilm Ring Test (BRT) was developed which is manifested by less manipulations and faster result acquisition (Azeredo et al., 2017).

II.5.1 Microtiter plate assay

The Microtiter plate assay (MPA) is most widely used as a quantitative method. The method was first introduced in 1997 to assess the attachment of a marine *Pseudomonad* (Fletcher, 1977). The MPA was successfully applied in *L. monocytogenes*, and numerous studies utilized the method (Borucki et al., 2003; Djordjevic et al., 2002; Moltz and Martin, 2005). CV stains both living and dead cells as well as some matrix components thus it represents the best the total amount of biofilm (Azeredo et al., 2017). In the classical protocol, biofilms are grown on a sterile polystyrene plate, the most used cell culture plate in laboratories. The material of plates as well as size of a well could be of any kind corresponding to the interest of a study. Using the conventional cell culture plates, MPA measures biofilms formed on the bottom and walls of the plate, which may include cells that were sedimented due to gravity or loss of cell vitality and embedded in biofilm matrix. To avoid this problem and measure solely the actively produced biofilms, Calgary biofilm device was developed (Ceri

et al., 1999). The device is characterized by pegs under the lid that protrude into wells of a microtiter plate. This device allows the selection of biofilms actively produced by microorganisms that adhere to the pegs only.

The first step of conventional MPA is to grow biofilms in microtiter plate under a condition designed for aims of a study. When the incubation ends, medium is emptied by flipping the plate upside down or pipetting carefully without disturbing biofilms and washed with distilled water or saline for a few times to wash out unattached planktonic cells. Optionally before staining, the sessile cells are fixed using 95% ethanol. Next, biofilms are dried then subjected to 0.1-1% CV staining, often filtered before use. Unbound dye is removed by rinsing with distilled water by flipping the plate or pipetting several times. After drying, the CV is solubilized with 33% acetic acid or 70-95% ethanol. The optical density of each well is quantified using spectrophotometry plate reader at an absorbency of 570-630 nm.

In general, a condition includes triplicate wells as well as negative controls containing no microorganism resulting in slight staining due to the impact of media on surfaces that must be subtracted from absorbency of samples. The method is advantageous over other methods because it is affordable and it does not require much proficiency in performance. However, the method often produces results with poor reproducibility among independent replicates or individuals who are performing MPA and it is assumed to be originated from multiple manipulation steps. Moreover, as seen in the protocol, there are variations in each step across the laboratories such as way of washing wells, inclusion of fixation step, percentage and volume of CV for each well, type and volume of destaining solution, and optical density for spectrophotometry. These inconsistencies render the method unharmonized that may lead to biased interpretation of data from different laboratories.

II.5.2 Microscopy

As microscopic technology developed, researchers became to make use of various microscopy tools to study biofilms. Numerous methods were discussed in a review on biofilm methods including light microscopy, CLSM, SEM, other SEM-derived microscopies, and atomic force microscopy (Azeredo et al., 2017). Here, we will discuss the most widely used methods: light microscopy, CLSM and SEM.

Above all, light microscopy is the most useful tool to provide visualization of biofilms due to its high accessibility in laboratories accompanied with affordable cost. A range of dyes are used in this technique including: CV stain as utilized in MPA, Periodic acid–Schiff, Alcian Blue and Ruthenium red dyes for staining EPS, Hematoxylin and eosin stain for staining nuclei and cytoplasm of bacteria and so on (Sohm et al., 2011). Stained biofilms are observed under a light optical microscope that gives two-dimensional images in comparatively low magnification. The structural organization in biofilms can be detected by this method. For

example, Harvey et al. (2007) observed that *L. monocytogenes* formed networks of microcolonies in biofilm formation. In our experiments, we observed varying size of microcolonies and some regions showed higher intensity of CV stain in the images indicating multi-layer cellular structures (Figure 13).

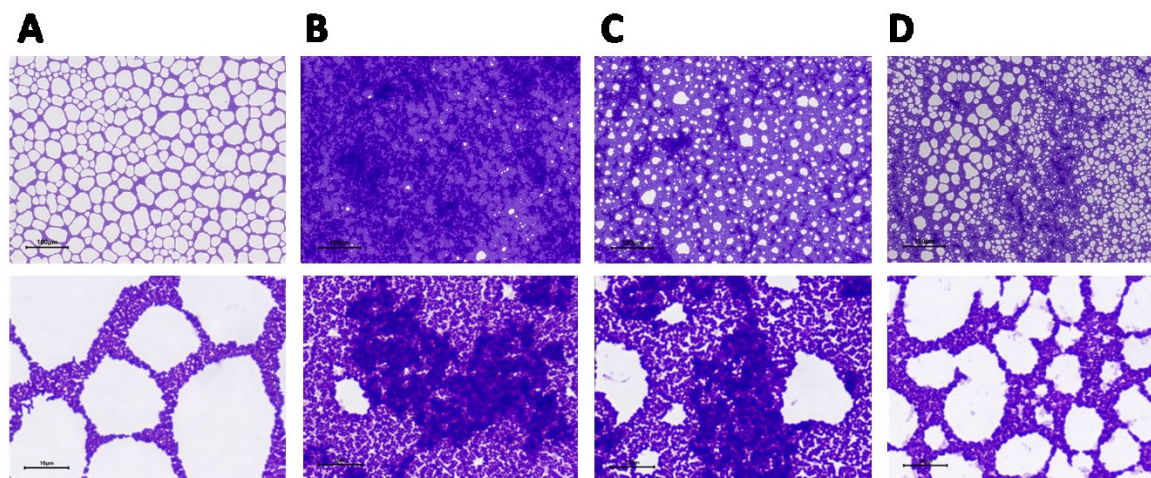


Figure 13. Micrographs of *L. monocytogenes* biofilms stained with crystal violet and observed by light optical microscopy. Cells were grown in BHI media for 24 h at 37°C with additional NaCl concentrations at (A) 0%; (B) 0.85%; (C) 2%; (D) 5%. Scale bars, 100 μ m in upper figures, and 10 μ m in lower figures (unpublished data).

The limitation of light microscopy such as a two-dimensional observation and low magnification can be overcome by CLSM or SEM. CLSM is advantageous in visualizing a three-dimensional spatial structure of biofilm. In CLSM, biofilms are labeled with various fluorescent probes. The most widely applied dyes are cell permeant nucleic acid dyes, for example, SYTO-9 and SYBR-Green (Neu and Lawrence, 2014). Along with these green fluorescent markers, red cell impermeant marker such as propidium iodide can be accompanied for a live/dead viability test (Bogachev et al., 2018) that calculate the ratio of live/dead cells (Figure 14). On top of the visualization, quantitative parameters of biofilms can be obtained such as biovolume, substratum coverage, thickness and roughness using a software, making CLSM an attractive method (Bridier et al., 2010; Xavier et al., 2003).

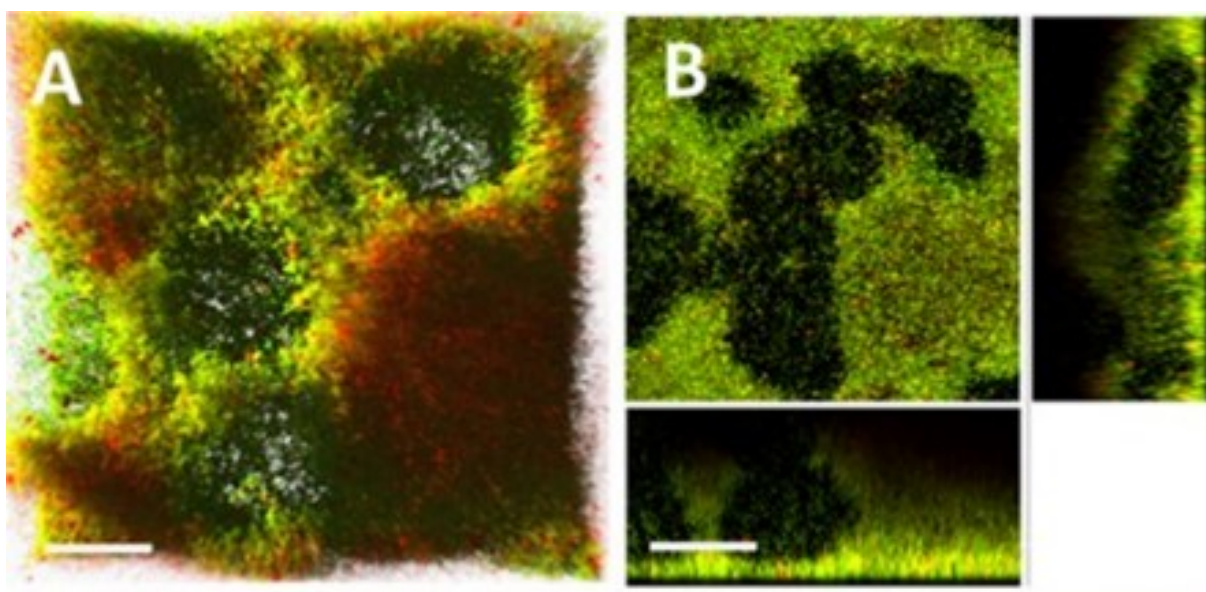


Figure 14. A representative of motile *L. monocytogenes* strains forming biofilms with a honeycomb morphotype. An isosurface representation (A) and section view (B) of CLSM images from biofilms forming honeycomb-like structures stained in green with SYTO-9 and in red with propidium iodide. The scale bars represent 30 μm (Guilbaud et al., 2015).

SEM also provides visualization of a spatial three-dimensional architecture of biofilms at varying resolution which can go up to around 100 nm scale. It is a preferable method in that it can detect EPS matrix produced by microorganisms. In literature, SEM is often performed in parallel with a quantitative biofilm detection method such as MPA. However, sample preparation process is time-consuming involving fixation, dehydration and coating. To gradually replace water with organic solvents, dehydration step is performed with a series of ascending concentrations of acetone or ethanol and samples are dried completely which might form artifacts (Hannig et al., 2010). For coating step, samples are often sputtered with conductive material, for example, gold, to create a thin conductive layer to inhibit charging and thermal damage as well as to improve secondary electron signal required for topographic examination in SEM. Under high vacuum condition, electrons from electrons beam interact with atoms in the sample and secondary electrons emitted by atoms are detected to produce images. SEM, however, is not a routine laboratory method due to its high cost and limited accessibility to the equipment and trained personnel who can manipulate this technology.

II.5.3 Biofilm Ring Test

Adhesion is the first step in biofilm formation which is manifested by irreversible attachment of bacterial cells to biotic or abiotic surfaces. BRT is a comparably new analysis

that is specialized in detecting the adhesion step and is provided in a form of kit comprising mainly BHI media, microtiter plate, and magnetic beads (Figure 15) (Chavant et al., 2007).

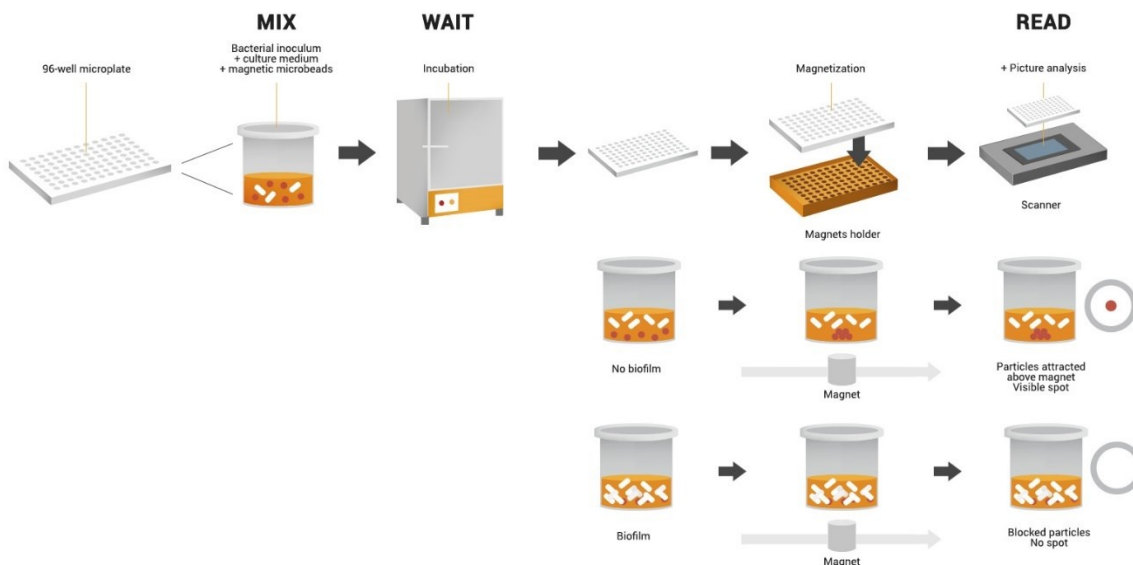


Figure 15. The BRT workflow (The BRT technology, n.d.). Microorganism of interest is suspended in a well with magnetic beads and incubated until they form the first layer of biofilms on the bottom of microtiter plate. After incubation, the wells are placed on the Magnets holder for 1 min to apply magnetic fields at the center of all wells. The movement of sedimented magnetic beads are subsequently blocked by sessile cells which adhere on the bottom, thus the degree of mobile beads depends on the extent of sessile cells. Then the bottom of plate is scanned with the Plate Reader and analyzed by a software provided with the kit. The software calculates the size and intensity of the pulled beads in the middle of the well and outputs numeric values of each well called the BioFilm Index (BFI) ranging from 0 to 20. A BFI around 20 resulted from a high mobility of magnetic beads implies no biofilm was formed in the well, in comparison to a lower or near zero BFI which is resulted from an immobilization of beads by sessile cells in biofilms.

There are two protocols in BRT used for comparing biofilm forming abilities among different microorganisms. First protocol is to diversify the concentration of microorganisms used for inoculation, for example, serial 10-fold or 5-fold dilutions are performed starting from a same bacterial number determined by optical density (Di Domenico et al., 2016). Each dilution point of strains is inoculated on a same microplate displaying, for instance, serial dilutions by row and different strains by column. This enables comparison of BFIs in each inoculum of various bacteria to further discriminate strong biofilm formers from weak biofilm

formers. Second protocol is to make multiple plates and read a plate every 2 to 3 hours making a kinetic analysis (Olivares et al., 2016). If some bacteria form biofilms after a shorter incubation time than the others with same initial inoculum, they can be considered to be more efficient in the early phases of adhesion and biofilm formation.

The technique is especially interesting for high-throughput screening tests, for example, anti-biofilm reagents screening test. In clinics, the application of BRT was introduced as 'antibiofilmogram' as a complementary examination to widely practiced antibiogram in order to aid antibiotic selection in biofilm related bacterial diseases (Tasse et al., 2016). The utilization of this method in normal microbiology lab, however, is limited because it requires specific devices such as Magnets holder or Plate Reader.

III References

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Chapter III

*Increased adhesion of *Listeria monocytogenes* strains to abiotic surfaces under cold stress*

I Preface

One of the most prominent environmental factors affecting physiology of *L. monocytogenes* in food chains is the temperature. The bacteria are capable of producing biofilms at refrigerating temperatures even though the amount of total biomass reduces as incubation temperatures decrease under optimal growth temperature (Kadam et al., 2013; Nilsson et al., 2011). It is primarily because the microbial metabolism is highly dependent on the incubation temperatures. Therefore, from the data available in literature, it is presumed that the total biomass obtained at different temperatures reflect the bacterial metabolic rates before the biofilms are oversaturated and start the dispersal step. Meanwhile, as discussed in 'Chapter II.3 Biofilm development and stress response', the transition of planktonic to sessile form of life is promoted by environmental stimuli, both favourable and unfavourable. However, there was no report on whether a sudden downshift in temperature promotes sessile growth. To elucidate this question, total 22 isolates with different origins and serogroups were adapted to cold (4°C). The cells were determined as cold-adapted when they reached stationary phase growth after several days of incubation at 4°C. Concurrently, the same strains grown at optimal (37°C) temperature for overnight were included in the test. The two types of cells exhibited a significant difference in adhesion level measured by BRT. Non-cold-adapted cells, termed cold-stressed cells, transited to sessile cells upon sudden exposure to cold more efficiently than cold-adapted counterparts which preferred to grow in free-living form. This is the first report of enhanced adhesion by sudden cold stress in *L. monocytogenes*. We further examined how the cell surface physicochemical properties, such as hydrophobicity was related to the level of adhesion.

II Article

Increased Adhesion of *Listeria monocytogenes* Strains to Abiotic Surfaces under Cold Stress

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Increased Adhesion of *Listeria monocytogenes* Strains to Abiotic Surfaces under Cold Stress

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Food contamination by *Listeria monocytogenes* remains a major concern for some food processing chains, particularly for ready-to-eat foods, including processed foods. Bacterial adhesion on both biotic and abiotic surfaces is a source of contamination by pathogens that have become more tolerant or even persistent in food processing environments, including in the presence of adverse conditions such as cold and dehydration. The most distinct challenge that bacteria confront upon entry into food processing environments is the sudden downshift in temperature, and the resulting phenotypic effects are of interest. Crystal violet staining and the BioFilm Ring Test[®] were applied to assess the adhesion and biofilm formation of 22 listerial strains from different serogroups and origins under cold-stressed and cold-adapted conditions. The physicochemical properties of the bacterial surface were studied using the microbial adhesion to solvent technique. Scanning electron microscopy was performed to visualize cell morphology and biofilm structure. The results showed that adhesion to stainless-steel and polystyrene was increased by cold stress, whereas cold-adapted cells remained primarily in planktonic form. Bacterial cell surfaces exhibited electron-donating properties regardless of incubation temperature and became more hydrophilic as temperature decreased from 37 to 4°C. Moreover, the adhesion of cells grown at 4°C correlated with affinity for ethyl acetate, indicating the role of cell surface properties in adhesion.

Keywords: *Listeria monocytogenes*, cold stress, adhesion, biofilm, BRT[®], crystal violet staining, MATS, SEM

INTRODUCTION

In recent decades, the foodborne pathogen *Listeria monocytogenes* has become a notable threat to food manufacturers, particularly those making ready-to-eat (RTE) foods (Jofré et al., 2016; Vongkamjan et al., 2016). Infection with this saprophytic and psychrotrophic gram-positive pathogen results in a high mortality rate, especially in susceptible groups such as pregnant women or senior populations (Orsi et al., 2011).

Listeria monocytogenes efficiently survives under extreme conditions, such as 40% w/v NaCl or pH 3.0 (Liu et al., 2005). The risk of listeriosis has increased with growing consumption of RTE foods or frozen foods requiring minimal heat treatment before consumption because food processing plants often utilize adverse conditions such as refrigeration, high salt concentration,

or low pH to preserve foods. Moreover, *L. monocytogenes* persists by adhering to food contact surfaces, causing the contamination of final food products (Ferreira et al., 2014). A biofilm is a sessile community of bacterial cells embedded in a matrix of self-produced extracellular polymeric substances (EPS), including proteins, polysaccharides, and extracellular DNA. According to recent studies, the composition of EPS in the *L. monocytogenes* biofilm matrix is dominated by teichoic acids (Brauge et al., 2016; Colagiorgi et al., 2016). Biofilms are often multi-species in nature, and interactions with other bacteria may benefit biofilm formation by *L. monocytogenes* (Giaouris et al., 2015). Although maturity may vary depending on environmental conditions, fundamental biofilm growth involves bacterial adhesion to surfaces (Garrett et al., 2008).

Given increasing concerns that biofilms in food premises lead to food contamination with *L. monocytogenes*, studies have primarily compared the effects of temperature on biofilm formation by growing bacteria at different temperatures, most frequently ranging from 4 to 37°C, and demonstrated that bacteria survive and form biofilms at low temperatures (Di Bonaventura et al., 2008; Nilsson et al., 2011). In general, total biomass production by *L. monocytogenes* strains is augmented with increased incubation temperature, regardless of the adhesion surface, including hydrophilic stainless-steel coupons and hydrophobic polystyrene culture plates. One study showed that storage of *L. monocytogenes* strains at -20°C for 6 and 24 months increased adhesion and biofilm formation on various surfaces, including polystyrene microtiter plates and stainless-steel (Slama et al., 2012). Given its exceptional adaptive ability to mitigate and survive harsh environments, biofilm formation by *L. monocytogenes* may be an adaptation response to stress (Tasara and Stephan, 2006). However, direct observation of cold stress-induced biofilm production by *L. monocytogenes* has not been reported to date.

In this study, a total of 22 *L. monocytogenes* strains of diverse origins and serogroups were investigated to elucidate the impact of cold on phenotypic changes. Cells acclimatized at 37 and 4°C were exposed to cold to evaluate the effects of cold stress on bacterial adhesion and biofilm formation on polystyrene and stainless-steel surfaces using the BioFilm Ring Test® (BRT®), crystal violet (CV) staining, and scanning electron microscopy (SEM). Furthermore, microbial affinity to solvents (MATS) analysis was performed to assess cell surface physicochemical properties and their relationship to surface adhesion characteristics.

MATERIALS AND METHODS

Listeria monocytogenes Isolates and Culture Conditions

A panel of 22 isolates of *L. monocytogenes* from human listeriosis cases, animals, foods and food-related premises were used in this study (Table 1). All strains were analyzed by the Institut Pasteur (Paris, France) for serogrouping using a multiplex PCR assay (Doumith et al., 2004). Serogroup IVb includes serovars 4b, 4d, and 4e; serogroup IIb includes serovars 1/2b, 3b and 7; serogroup

IIa includes 1/2a and 3a; and serogroup IIc includes serovars 1/2c and 3c.

Strains were stored in Brain-Heart Infusion (BHI) broth (Laboratorios Conda, Spain) with 8.3% glycerol at -20°C, and each set of experiments was conducted with freshly recovered isolates on BHI agar (Laboratorios Conda, Spain). Strains were maintained on BHI agar for at least 2 days at 37°C by sub-culturing daily onto a fresh agar plate.

Sample Preparation

Several colonies were harvested using a sterile inoculating loop, suspended in 20 ml of BHI broth and grown at 37°C with shaking at 100 rpm to reach stationary phase. After incubation for 15 h, stationary cells were pelleted by centrifugation at $5,000 \times g$ for 10 min at room temperature, dispersed in 5 ml of fresh BHI broth by vortexing, and utilized for different experiments. Some cells were incubated at 37 and 4°C and were denoted positive control and cold-stressed cells, respectively (Figure 1, box A). A portion of the culture was diluted in 20 ml of BHI medium pre-cooled to 4°C to obtain an optical density at 600 nm (OD_{600}) of 0.1 and brought to 4°C to grow under shaking at 100 rpm for 4 to 7 days until the cells reached stationary phase. Stationary cells were harvested by centrifugation at $5,000 \times g$ for 10 min at 4°C and suspended by vortexing in fresh pre-cooled BHI broth for use as cold-adapted samples (Figure 1, box B). Some cold-adapted cells were streaked onto BHI agar with a sterile inoculating loop and incubated at 37°C overnight. This culture was then exposed to sudden cold stress as described above and designated cold-stressed cells² (Figure 1, box C).

Viable Cell Counts

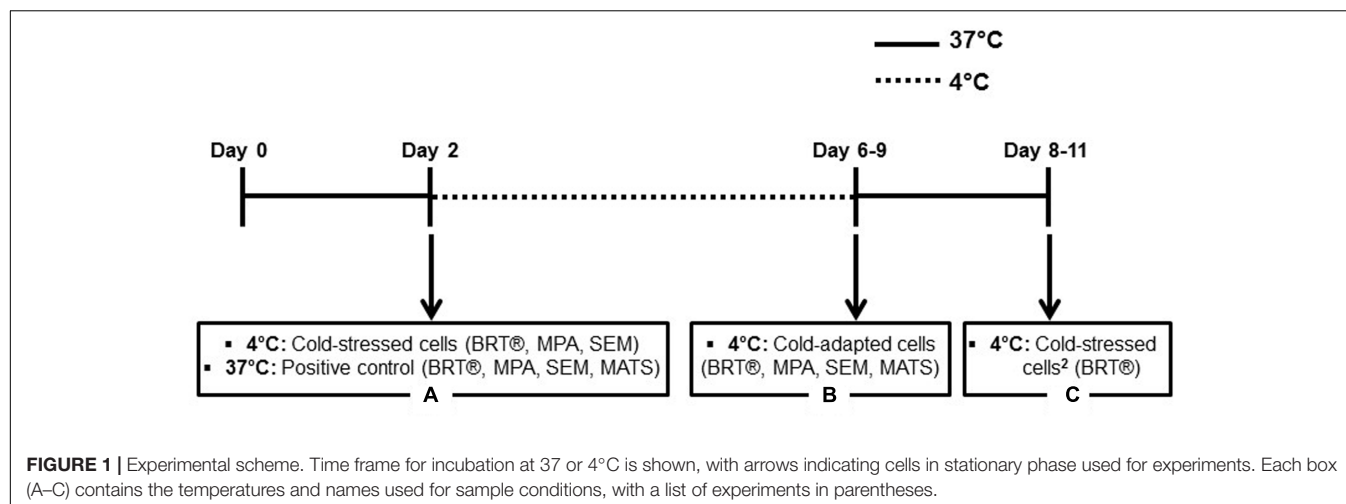
Portions of the positive control (precultured at 37°C) and cold-adapted cells (precultured at 4°C) were used to obtain viable cell counts. After measuring OD_{600} with a spectrophotometer (Biomate3, Thermo Scientific, United States), 50 µl of culture was transferred to tryptone salt (TS) solution containing 0.1% w/v tryptone (Conda, Spain) and 0.85% w/v NaCl (Sigma-Aldrich, France) and 10-fold serially diluted in TS solution. From each dilution, 100 µl was spread on a BHI agar plate using sterile glass beads in triplicate. After overnight incubation at 37°C, colonies were counted to calculate colony forming units (CFU) per ml. Total CFU of 30 to 300 per plate were considered valid data.

Two experiments were performed for each condition.

BRT®

The BRT® assay was performed in a polystyrene 96-well microplate (BRT kit C004, BioFilm Control, France) as described by Chavant et al. (2007).

A freshly prepared culture was measured at OD_{600} to obtain a final OD_{600} of 0.5 (approximately 1.2×10^9 CFU/ml) in BHI broth kept at two temperatures: 4°C for cold-stressed and cold-adapted conditions, and room temperature for a positive control. A portion of the suspension was used to perform a threefold dilution to obtain an OD_{600} of 0.17 (approximately 3.8×10^8 CFU/ml). Toner 4 (magnetic beads) was added to



a final concentration of $10 \mu\text{l ml}^{-1}$. After homogenization of these mixtures, $200 \mu\text{l}$ of each bacterial suspension was deposited in each well of the microplate in triplicate. Wells containing only BHI broth with magnetic beads were added as negative controls.

Microplates were kept static for 24 h at 4°C for cold-stressed (precultured at 37°C) and cold-adapted (precultured at 4°C) conditions and at 37°C for the positive control. After incubation, wells were covered with a few drops of Liquid Contrast (inert

and non-toxic oil), and the plates were placed on a magnetic block with 96 mini-magnets centered under the 96 wells of the microplate for 1 min to apply magnetic fields that attracted mobile beads, creating a quantifiable spot above each mini-magnet. The bottoms of the plates were scanned with a plate reader and analyzed using BFC elements 3[®] software (BioFilm Control, France) to obtain a numerical value termed the BioFilm Index (BFI) for each well, which ranged from 0 to 20 depending on the size and intensity of the spot. A BFI of approximately 20 corresponded to high magnetic bead mobility, implying no or very few sessile cells, while a lower BFI or a value of zero resulted from the immobilization of beads by sessile cells.

At least four experiments were performed, with triplicate wells for each condition.

TABLE 1 | *Listeria monocytogenes* strains used in this study.

Strain	Lineage	Serogroup	Origin	Reference
1	I	IVb	Human, epidemic (pasteurized milk)	ScottA
2	I	IVb	Human, epidemic (hot dog)	
3	I	IVb	Meat (sausage)	
4	I	IVb	FCS ^a in FPE ^b	
5	I	IIb	Cow	
6	I	IIb	Human, sporadic	EGDe
7	I	IIb	Chocolate milk, epidemic	
8	I	IIb	FCS in FPE	
9	I	IIb	Lean meat	
10	II	IIa	Not known	
11	II	IIa	Cow	
12	II	IIa	Hot dog, sporadic	
13	II	IIa	Human, sporadic (hot dog)	
14	II	IIa	Meat (batter)	
15	II	IIa	Meat (sausage)	
16	II	IIa	FCS in FPE	
17	II	IIa	FCS in FPE	
18	II	IIa	Meat (cured ham)	
19	II	IIa	Meat (batter)	
20	II	IIc	Rabbit	
21	II	IIc	FCS in FPE	
22	II	IIc	Human	LO28

^aFCS: food contact surface ^bFPE: food processing environment The contaminated food sources of certain epidemic and sporadic cases are specified.

Microtiter Plate Assay (MPA)

The procedure to prepare a 96-well microplate for microtiter plate assay (MPA) was the same as that described above (BRT[®]), except that no Toner 4 was added. The assay was performed as previously described by Doijad et al. (2015), with slight modifications. After static incubation for 24 h, the absorbance values of negative controls and total cell densities, including sessile and planktonic cells, were measured using a microplate reader (EL800, BioTek, United States) at OD₆₀₀.

Plates were inverted, and the media and planktonic cells were discarded via gentle tapping. To remove loosely attached bacteria, wells were washed twice with $300 \mu\text{l}$ of sterile saline solution (8.5 g of NaCl per l). Sessile cells were fixed with $300 \mu\text{l}$ of 96% ethanol (Sigma–Aldrich, France) for 20 min and air-dried for 2–3 h at room temperature after removal of the ethanol until no standing moisture was visible. To stain the bacterial biomass, a 0.1% w/v CV (Merck KGaA, Germany) solution was filtered (0.22- μm filter, Millipore, France), and $220 \mu\text{l}$ was added to each well. After static incubation for 30 min, CV solution was removed by sharply flicking the plates while upside down. Wells were washed three times with $300 \mu\text{l}$ of saline, followed by tapping them upside down on paper towels. Plates were air-dried for 3–4 h, filled with $150 \mu\text{l}$ of 33% v/v acetic acid

TABLE 2 | Viable cell counts of six strains grown at stationary phase at two temperatures.

Strain	37°C	4°C
1	9.36 ± 0.03	9.46 ± 0.05
4	9.33 ± 0.03	9.50 ± 0.05
6	9.30 ± 0.03	9.45 ± 0.03
11	9.27 ± 0.06	9.43 ± 0.01
14	9.24 ± 0.01	9.33 ± 0.02
20	9.22 ± 0.04	9.35 ± 0.20

Data are presented as the mean log CFU/ml ± standard deviation at an OD₆₀₀ of 1.

(Sigma–Aldrich, France) and placed on a plate shaker with slight agitation for 10 min to completely destain CV and obtain a homogenized solution. Destained CV levels were determined using a microplate reader at OD₆₀₀.

At least four experiments were performed, with triplicate wells for each condition.

Physicochemical Experiments

The MATS partitioning method (Bellon-Fontaine et al., 1996) was performed to define bacterial cell surface properties. This method involves comparing the affinities of microbial cells for pairs of monopolar and nonpolar solvents, which have similar van der Waals surface tension components. In this study, the following sets of solvents were used: (i) chloroform, an acidic solvent (electron acceptor), and hexadecane, a nonpolar *n*-alkane, and (ii) ethyl acetate, a basic solvent (strong electron donor), and decane, a nonpolar *n*-alkane (Sigma–Aldrich, France).

Cultures grown until stationary phase at 37 and 4°C were pelleted by centrifugation at 5,000 × *g* for 10 min at room temperature and 4°C, respectively. Sterile 0.15 M NaCl (Sigma–Aldrich, France) solutions pre-incubated at 37 and 4°C were used to wash pellets, in compliance with the original culture temperatures, followed by centrifugation. Bacterial suspensions were prepared to obtain an OD at 400 nm (OD₄₀₀) of approximately 0.6 to 0.7, and the initial OD₄₀₀ was measured as [A₀]. A suspension in a volume of 2.4 ml was vortexed for 60 s with 0.4 ml of each solvent in a glass tube. The mixture was allowed to stand static for 15 min to ensure the complete separation of both phases. The absorbance of the aqueous phase was measured at OD₄₀₀ [A]. The percentage of cells in each solvent was calculated using the following equation: percent affinity = [1 – (A/A₀)] × 100.

Each experiment was performed in quadruplicate with independently grown bacterial cultures.

SEM

Biofilms were grown on sterile stainless-steel coupons to visualize adhesion patterns, biofilm architecture, and cell morphologies via SEM with positive control, cold-stressed, and cold-adapted cells.

Fresh cultures in BHI broth were prepared to obtain an OD₆₀₀ of 0.5, and 7 ml of each bacterial suspension was poured into

a petri dish (55-mm diameter) containing a sterile stainless-steel coupon (AISI 304, mean roughness = 0.064) and statically incubated for 24 h at 37°C for a positive control and at 4°C for the cold-stressed and cold-adapted conditions. After removing the cultures using a pipette, the coupons were gently washed twice by filling the petri dishes with sterile saline solution to remove nonadherent cells. Sessile cells and biofilms were fixed on each coupon in 10 ml of a solution containing 3% glutaraldehyde in 0.2 M cacodylate buffer (pH 7.4) in a 50-ml glass beaker at 4°C for a minimum of 1 h to overnight. Coupons were washed three times for 15 min each via immersion in cacodylate buffer, followed by dehydration using a graded ethanol series (70, 90, and 100%) three times for 15 min each. Further dehydration was performed in a 50:50 mixture of ethanol:hexamethyldisilazane (HMDS) three times for 10 min each. Samples were immersed in pure

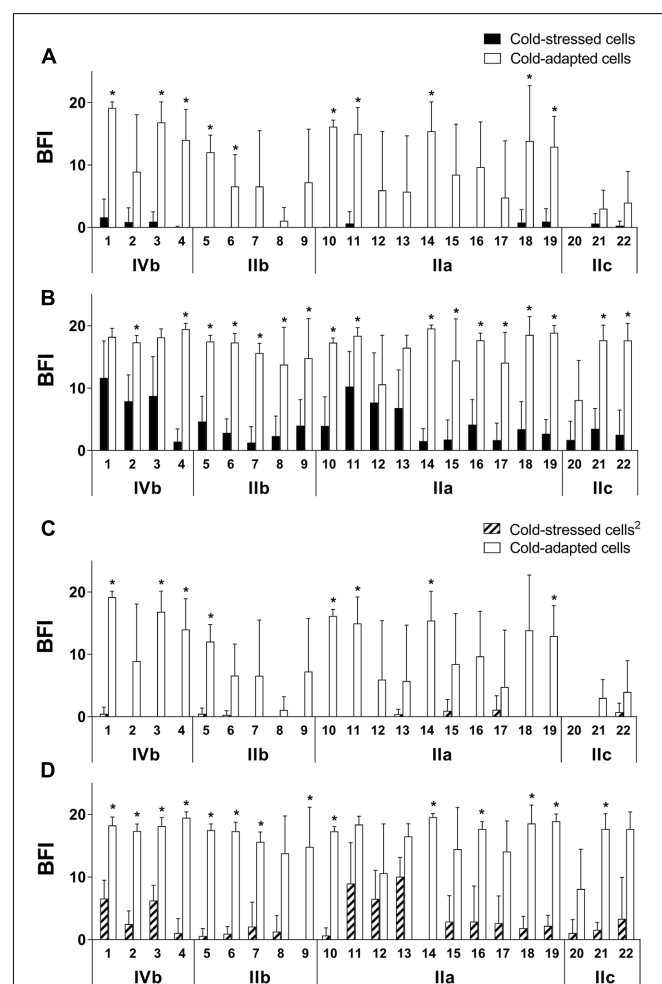


FIGURE 2 | Increased adhesion of cold-stressed cells compared to cold-adapted cells, measured by BRT®. Sudden exposure to cold for the first time was denoted as cold-stressed cells (A,B), and exposure for a second time was denoted as cold-stressed cells² (C,D); initial inocula were at an OD₆₀₀ of 0.5 (A,C) and 0.17 (B,D). Strains and serogroups are indicated on the X-axis, and data are presented as the mean ± standard deviation of the BFI. A BFI of 0 represents full blockage of the magnetic beads. **p* < 0.05.

HMDS (Delta Microscopies, France) twice for 10 min, followed by air-drying overnight at room temperature. Coupons were mounted on stubs using adhesive carbon tabs, sputter-coated with gold-palladium (JFC-1300, JEOL, Japan) and observed with a scanning electron microscope (JEOL 6060-LV, JEOL, Japan) at 5 kV in high-vacuum mode.

Statistical Analysis

A *t*-test was performed on data comparing cold-stressed and cold-adapted cells or positive control and cold-adapted cells to test for statistically significant differences. Correlations were evaluated to identify any effects of cell surface properties on bacterial adhesion and biofilm formation by calculating the Pearson's correlation coefficient. All data were analyzed using Prism 7 software (Graphpad software Inc., United States), and significance was assigned at $p < 0.05$.

RESULTS

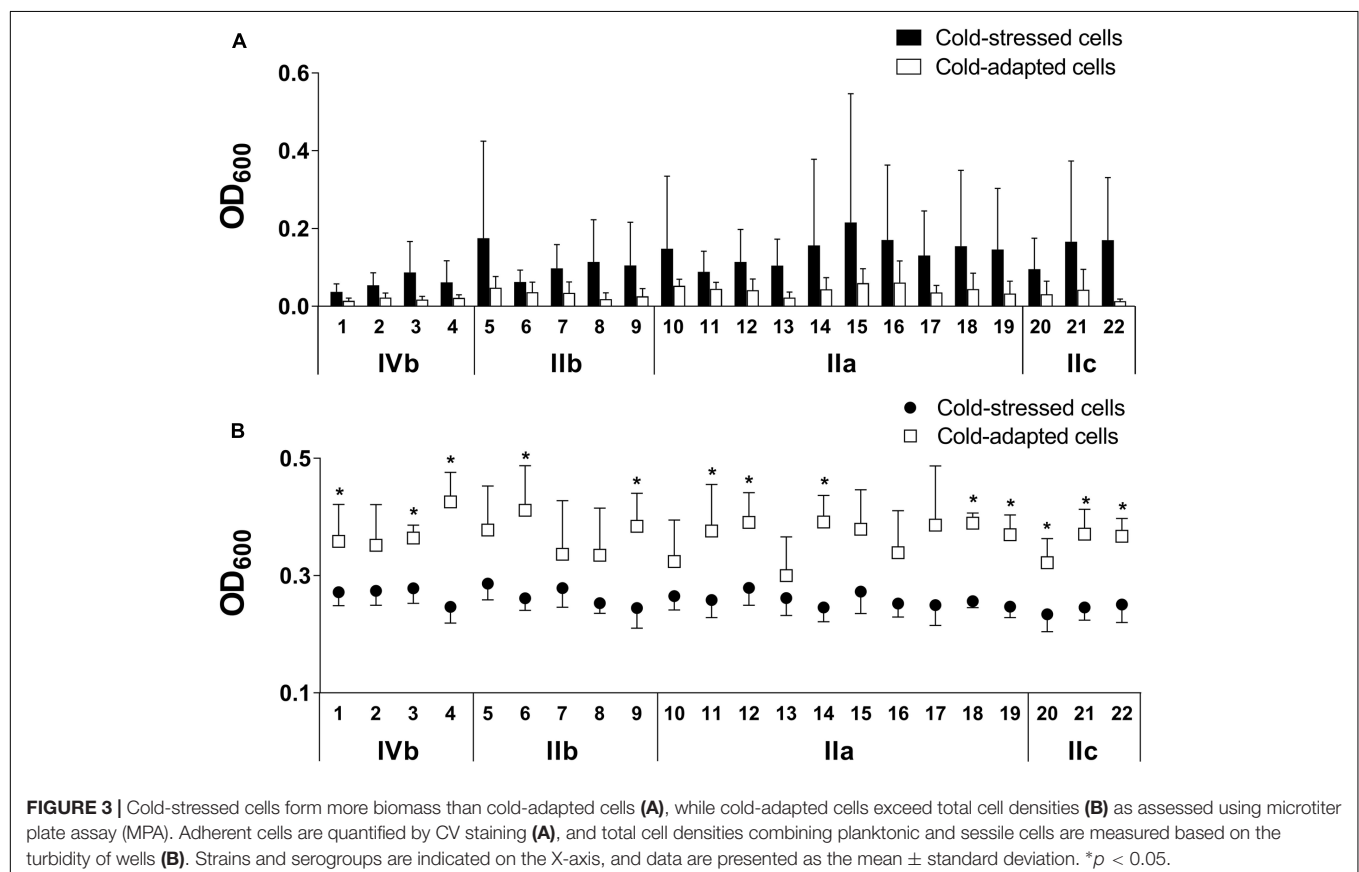
Viable Cell Counts

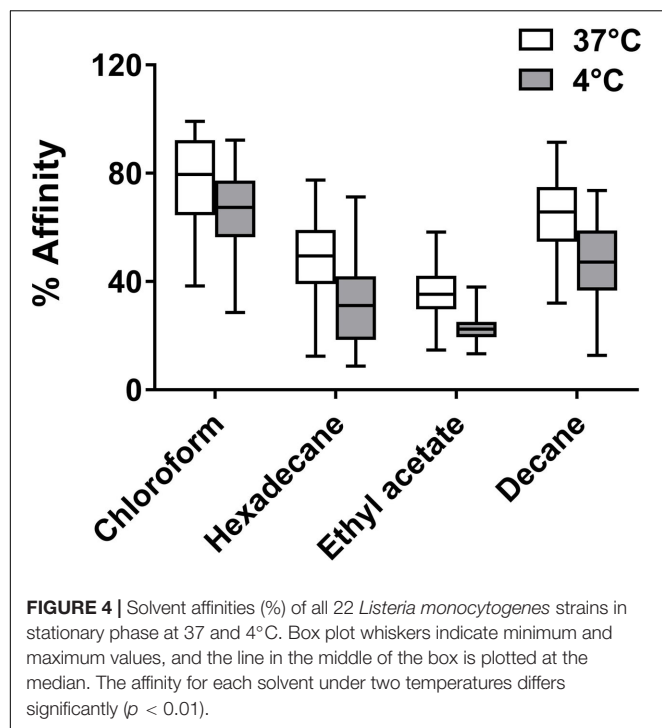
Six strains composed of four different serogroups with diverse origins were selected for viable cell count tests to verify the relationship between OD₆₀₀ values and viable cell numbers. As shown in Table 2, the two stationary cultures acclimated to 37 and 4°C resulted in comparable numbers of viable cells, with no significant differences.

Evaluation of Adhesion and Biofilm Formation on a Polystyrene Surface BRT®

The ability of 22 *L. monocytogenes* strains to adhere to an abiotic surface was analyzed using BRT®. BFI, with a value ranging from 20 to 0, is associated with the extent of blockage of magnetic beads (Toner 4) by sessile bacterial cells at the bottom of polystyrene microplate wells. Therefore, differences in BFI are caused by varying abilities to adhere. All strains exhibited higher adhesion ability when exposed to cold shock by demonstrating lower BFI scores (Figure 2). Statistical differences ($p < 0.05$) in BFI values between cold-stressed and cold-adapted cells were observed for 19 strains in either of the two inocula (Figures 2A,B). Further tests were performed to verify whether this adhesion phenomenon was reversible. Cold-adapted cells were cultured at 37°C and re-exposed to a sudden temperature downshift (cold-stressed cells²). Interestingly, the same response was observed for adhesion profiles (Figures 2C,D). No significant difference was observed for any strain between cells that were exposed to sudden cold shock for the first time (cold-stressed cells) and the second time (cold-stressed cells²), demonstrating that enhanced adhesion upon cold exposure represents a transient phenotype switch (Supplementary Figure 1).

When positive control cells were incubated at 37°C, all strains completely blocked the beads, resulting in a BFI of 0 for all inocula (data not shown).





MPA

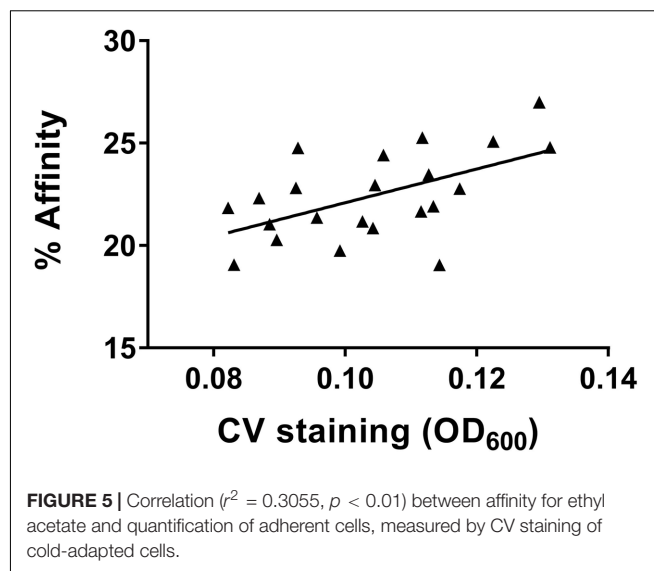
Microtiter plate assay was performed to assess sessile biomasses and total cell densities after incubation for 24 h at 4°C for cold-stressed and cold-adapted conditions and at 37°C for positive control. Much greater biomass quantities were obtained by CV staining for the positive control than for cold-stressed or cold-adapted cells (Supplementary Figure 2).

Cold-adapted cells showed overall higher total cell densities than cold-stressed cells; 13 of the 22 strains were statistically significant ($p < 0.05$, **Figure 3B**). Cold-stressed cells, however, resulted in more sessile bacterial communities than cold-adapted cells (no significance found) as quantified by CV staining (**Figure 3A**). The higher total cell densities obtained for cold-adapted cells were primarily attributable to planktonic cells. Based on these findings, increased cell numbers in cultures did not result in bacterial adhesion, indicating that enhanced adhesion is a distinct feature of cold-stressed cells.

Cell Surface Physicochemical Properties

Positive control and cold-adapted cells, grown at 37 and 4°C until stationary phase, respectively, were prepared for the MATS test to compare the surface physicochemical properties of cells that acclimated to different temperatures. The MATS results obtained for all 22 *L. monocytogenes* grown at 37 and 4°C until stationary phase in BHI media are shown in Supplementary Figure 3.

As shown in **Figure 4**, the general affinity of the 22 *L. monocytogenes* for chloroform (an electron-acceptor solvent) was higher than the affinity for hexadecane (a non-polar solvent), regardless of the culture temperature, indicating the strong electron donor nature of these bacteria. Likewise, bacterial affinity for ethyl acetate (an electron-donating solvent) was lower than

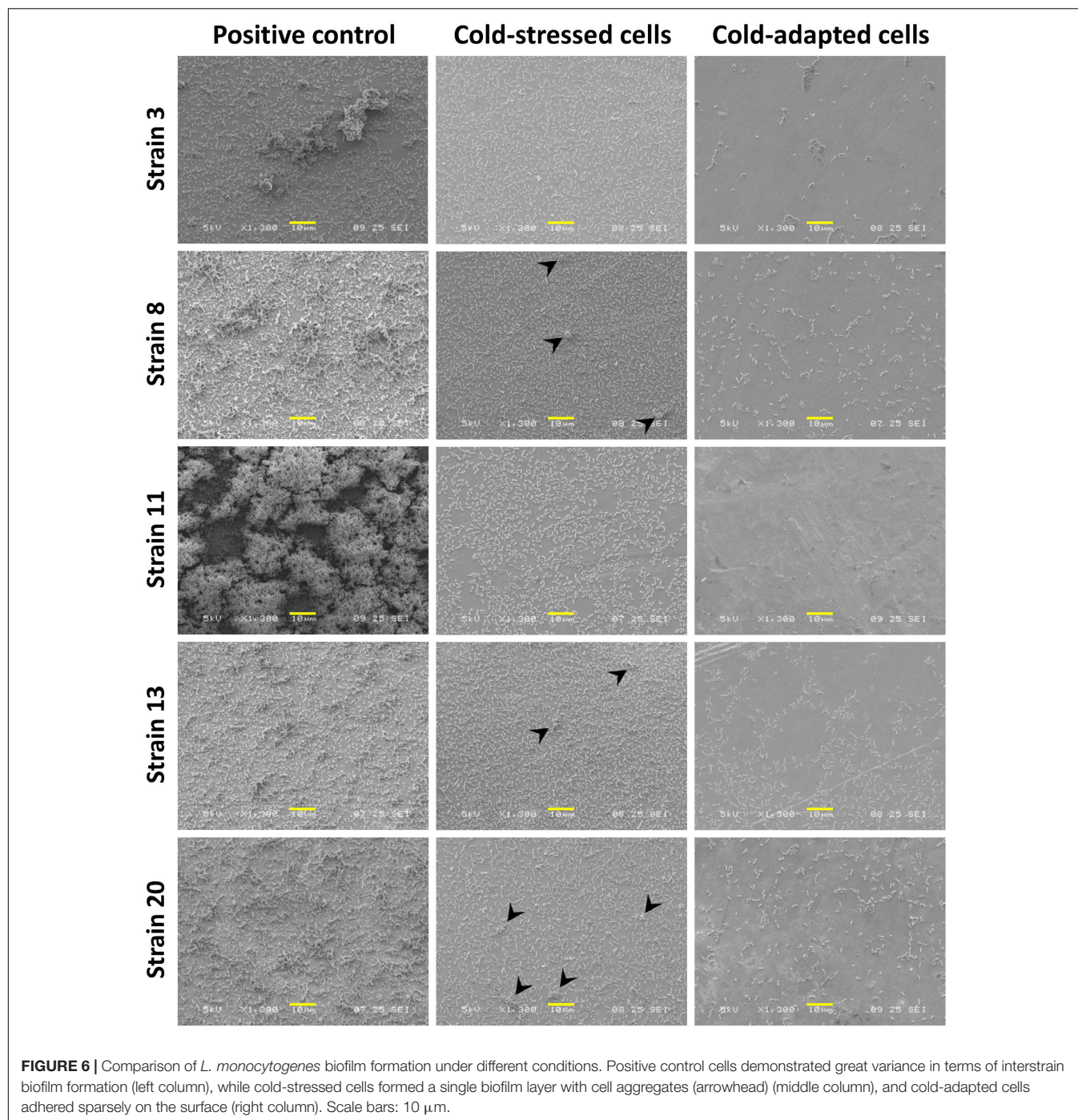


for decane (a nonpolar solvent), indicating that the electron-accepting nature of the bacteria grown at either temperature was weak. Affinity for hexadecane decreased from $49 \pm 14\%$ at 37°C to $32 \pm 15\%$ at 4°C ($p < 0.01$), demonstrating that cell surfaces became relatively more hydrophilic as cells adapted to cold temperature.

Relationships between the affinities for the four solvents and adhesion data obtained via two methods, CV staining and BRT, were evaluated using Pearson's correlation coefficient (r^2). A positive correlation was identified between the adhesion results obtained from CV staining and the affinity for ethyl acetate obtained from the MATS test for cold-adapted cells grown at 4°C ($r^2 = 0.3055$, $p < 0.01$) (**Figure 5**).

SEM Observation

Scanning electron microscopy images of cells grown under all three tested conditions (positive control, cold-stressed, and cold-adapted cells) were obtained to analyze surface colonization patterns and biofilm structures as well as the morphologies of individual cells. Low to high magnifications were applied over several zones. There was greater variance in the maturity of biofilms among strains grown under positive control conditions (**Figure 6**, left column), showing that the biofilm-forming capability of *L. monocytogenes* is strain-dependent. Conversely, under cold-stressed and cold-adapted conditions, the variance among strains was less obvious, primarily because no homogeneous mature biofilms were produced. However, cold-stressed cells underwent surface colonization with cell aggregates (arrowhead) resulting from sessile cell division (**Figure 6**, middle column), while analysis of cold-adapted cells revealed the attachment of individual cells in the absence of noticeable cell clusters (**Figure 6**, right column). Extracellular matrix was observed at high magnification (X 9,000 and higher) among individual cells and between cells and the stainless-steel surface (**Figure 7**, red circle). Irregular cell sizes were observed under all conditions, but significant cell elongation was more



frequently noted among cold-stressed and cold-adapted cells (Figure 7, arrow). This result may be because positive control cells formed more complex biofilm structures that limited the distinction of individual cell morphologies. Similar to a previous report by Harvey et al., spatial colonization was observed, constituting a network of microcolonies (Figures 7E,I) (Harvey et al., 2007). Cells were often found in indented substrate surfaces resulting from scratches on the coupons (Figure 7, arrowhead).

DISCUSSION

Certain bacteria adapt to inhabit environments by assuming different forms that are favorable to survival, such as planktonic cells, sessile biofilm communities or spore formation. Biofilms of *L. monocytogenes* in food processing environments are of great concern for food contamination. *L. monocytogenes* adapts to the harsh environments employed by food processing facilities, such as antibacterial agents or refrigeration, and reports have

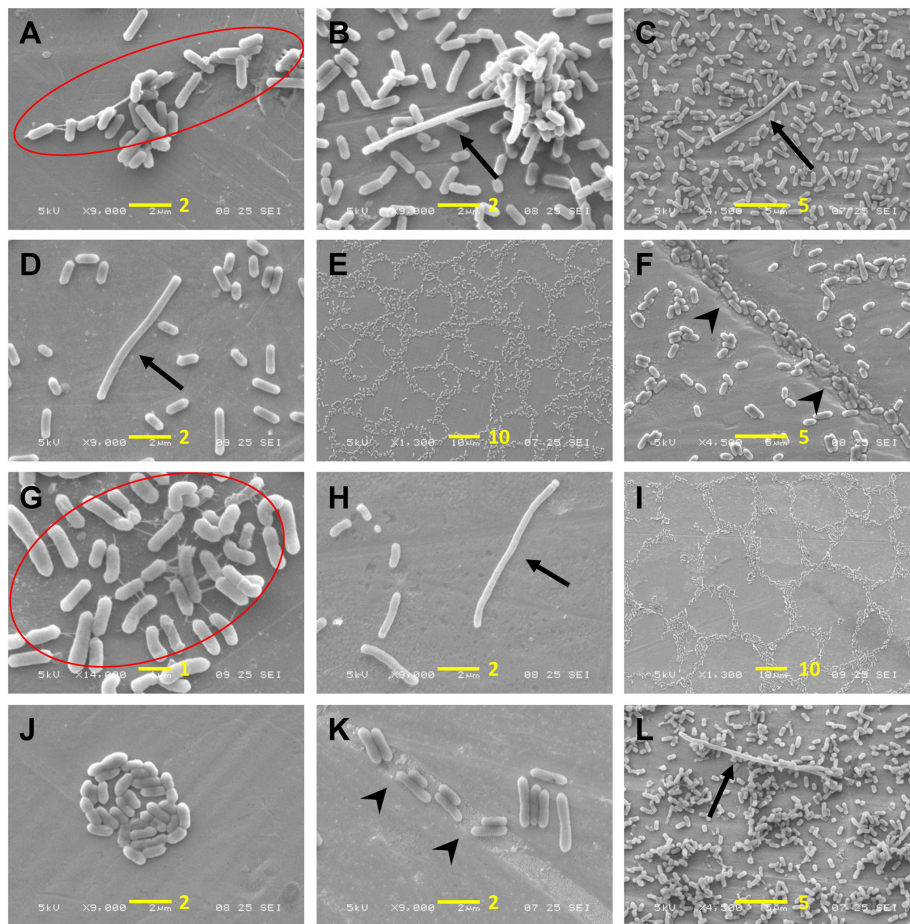


FIGURE 7 | Observation of *L. monocytogenes* adhesion patterns and cellular morphology. (A–F) Cold-stressed cells; (G–K) cold-adapted cells; (L) positive control cells. EPS are marked in red circles, arrows indicate elongated cells and arrowheads indicate cells in crevices. A scale bar (length in μm) is indicated in yellow in each figure.

demonstrated that exposing bacteria to sublethal stress leads to cross-protection or cross-adaptation to various stresses and lethal factors (Lou and Yousef, 1997; Lundén et al., 2003). Biofilm production by *L. monocytogenes* is stimulated to protect against various stressful conditions, making bacterial elimination a serious challenge at food processing facilities (Giaouris et al., 2014).

Significant variation in biofilm production under various conditions was observed for one *L. monocytogenes* strain, indicating that intra-strain phenotype changes are dependent on experimental settings (Nowak et al., 2015). Moreover, the interstrain variability of biofilm formation has been extensively studied with a focus on its relationships to serogroups or persistence in the food industry. However, a study employing 143 *L. monocytogenes* strains indicated that experimental settings such as temperature and culture media affect the comprehension of biofilm formation and its relationship to serotype or origin (Kadam et al., 2013). Recently, a study of 98 *L. monocytogenes* strains revealed no correlation between serological groups and biofilm production (Doijad et al., 2015).

Numerous methods and devices have been developed to detect or quantify biofilms, including staining-based quantification methods, visual identification by microscopy, viable and culturable cell counts, and devices to test bacterial adhesion (Azeredo et al., 2017). BRT[®] is a microbial adhesion test that is primarily used to assess the simultaneous phenotype switch from planktonic cells into sessile cells. In BRT[®], microorganisms are added to microplate wells in planktonic form, some of which adhere to the bottoms of the wells during incubation and switch to a sessile form that hinders the magnetic beads attracted to the magnetic block. Results vary with experimental conditions that affect the process, including planktonic cell growth and adhesion to polystyrene microplates, as well as sessile cell growth. Recently, a new approach to BRT[®], designated cBRT[®], was developed using serial 10-fold dilutions of bacterial suspensions to better discriminate biofilm-forming abilities among strains (Di Domenico et al., 2016). However, in the current study, all 22 *L. monocytogenes* strains revealed homogenous adhesion behavior that was not discernible by cBRT[®] under the same experimental conditions, i.e., cold-adapted or cold-stressed

conditions or incubation at 37°C. Nevertheless, cBRT® was sensitive for discriminating between cold-stressed and cold-adapted cells in terms of bacterial adhesion.

Cells undergo cold shock when subjected to a sudden downshift in temperature. Such a rapid environmental change induces modifications in bacterial cell surface proteins and lipid composition to maintain membrane fluidity homeostasis, which presumably facilitates adhesion as an adaptation strategy against adverse conditions. This behavior may be advantageous for bacterial survival in FPEs where cells might be exposed to sudden cold shock. The current study employed preculture temperatures of 37 and 4°C to compare differences in adhesion characteristics upon further exposure to 4°C. BRT® and MPA results revealed that cold-stressed cells (precultured at 37°C) are more efficient at forming biofilms, while cold-adapted cells (precultured at 4°C) favor growth in the planktonic state. *L. monocytogenes* cells entering the food processing chain are exposed to temperature downshifts, such as ambient temperature in outdoor food materials or optimal temperature in infected animals to refrigeration temperatures used during food processing or storage. When introduced to the food processing chain, *L. monocytogenes* adhesion to food contact surfaces is potentially fortified by cold shock, which will increase the chance of food product contamination. Once adapted to the cold, the bacteria in final food products will proliferate to hazardous levels during distribution and storage.

The heterogeneity of a population contributes to the adaptation of *L. monocytogenes* to sublethal conditions, accompanied by phenotypic and genetic changes (Abee et al., 2016). When cold-adapted cells were returned to 37°C and re-exposed to cold, they exhibited the same enhanced adhesion, which was indistinguishable by BRT® (Supplementary Figure 1), demonstrating that this transient trait was reacquired when cold stress was removed.

All 22 strains retained basic (electron-donating) properties (a higher affinity for chloroform than hexadecane), regardless of growth temperature, and became more hydrophilic with decreased temperature, as previously described (Chavant et al., 2002). The adhesion data obtained from CV staining of all 22 *L. monocytogenes* correlated best with cell affinity for ethyl acetate under cold-adapted conditions (Figure 5). This finding aligned with that of Briandet et al., who observed a linear correlation between listerial adhesion to stainless-steel and an affinity for ethyl acetate at different temperatures (37, 20, 15, and 8°C) in the presence of NaCl (Briandet et al., 1999). Physicochemical properties, including the hydrophobicity of bacterial cells versus that of a substratum, affect the interfacial interactions involved in bacterial attachment to abiotic surfaces. Nonetheless, this trait is negligible in the context of building a mature biofilm structure that is highly dependent on bacterial growth kinetics and EPS production, thus explaining the absence of an obvious relationship between cellular surface properties and biofilm formation at 37°C in the current study and in the literature (Cunliffe et al., 1999; Chmielewski and Frank, 2003).

Scanning electron microscopy observations supported the quantitative results obtained with CV staining and BRT®. Figure 6 shows variable biofilm maturity among the strains. This

variability may be attributable to differential biofilm production capabilities, although divergent biofilm kinetics among strains are unable to be excluded. Some strains may have already begun to disperse, while others were still in the process of structuring mature biofilms. SEM observation confirmed the higher bacterial adhesion of cold-stressed cells, along with the formation of cellular aggregates, while cold-adapted cells were only able to form a single sparse layer of adherent cells. This finding aligns with the BRT® results, demonstrating that BRT® is applicable for testing the early step of biofilm formation. Moreover, our observations of cells that densely accumulated in the crevices and scratches of stainless-steel surfaces strongly support the thorough cleaning of food contact surfaces to eliminate bacteria, although this may also further damage surfaces and create additional niches for bacterial adhesion.

In the current study, enhanced adhesion of sudden cold-stressed *L. monocytogenes* cells was observed for the first time. CV staining and SEM observation revealed that *L. monocytogenes* possesses dramatic interstrain variances in biofilm production, independent of origin or serotype. BRT® is shown to be a sensitive tool to discern the first layer of biofilm formation, facilitating the detection of increased adhesion of cold-stressed cells in the current study. Interestingly, the adhesion of cold-adapted cells correlated with an affinity for ethyl acetate. Further study of cold-stressed cells during cross-adaptation to other stress factors, such as dehydration or antimicrobial agents, will add to our understanding of the behavior of *L. monocytogenes* in the food processing industry.

AUTHOR CONTRIBUTIONS

B-HL conceived, designed, and conducted experiments, analyzed the results, and drafted the manuscript. All authors contributed to the experimental design and reviewed and approved the final manuscript.

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SUPPLEMENTARY MATERIAL

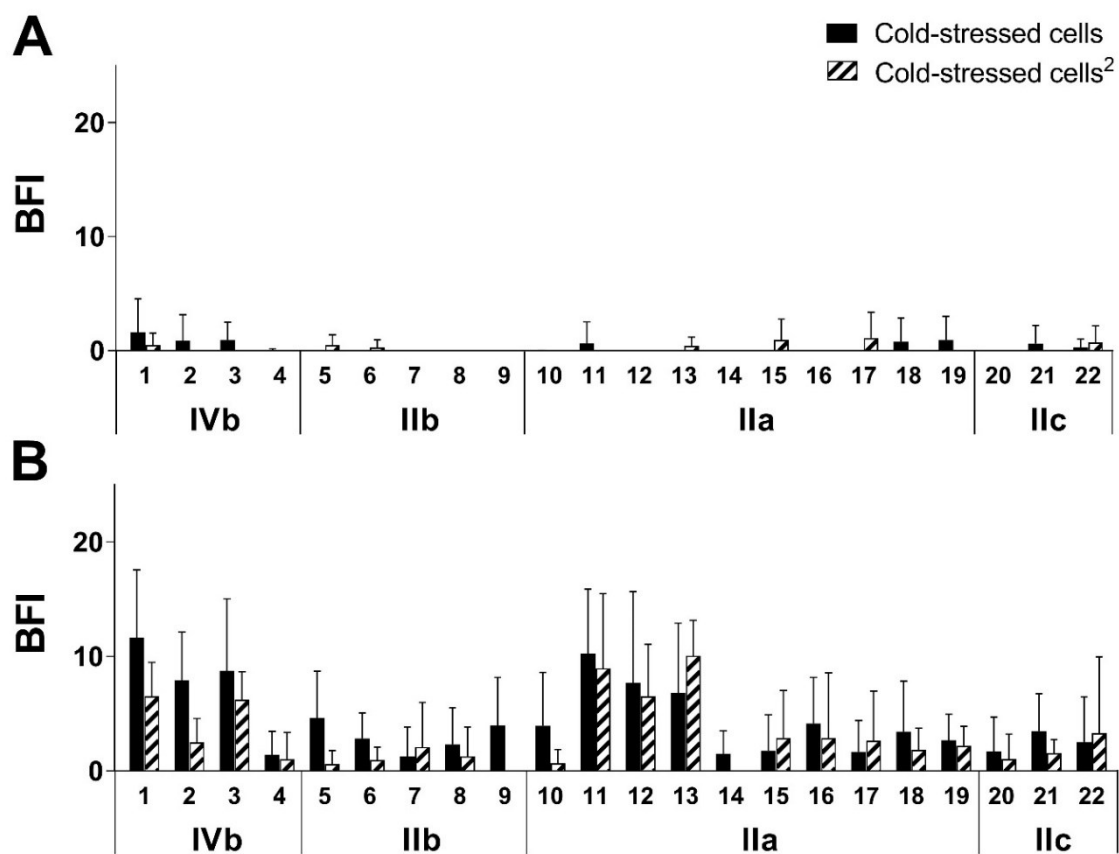
The Supplementary Material for this article can be found online at: <https://www.frontiersin.org/articles/10.3389/fmicb.2017.02221/full#supplementary-material>

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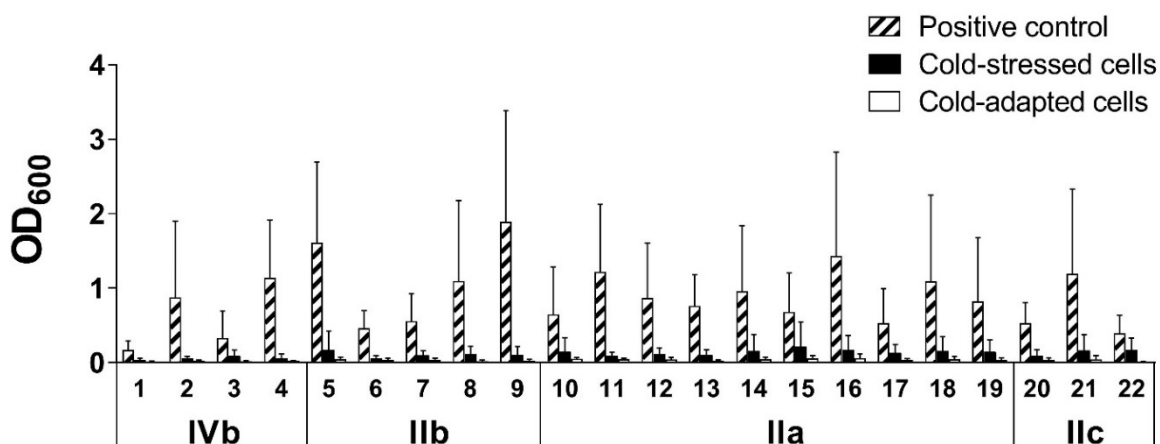
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Conflict of Interest Statement: The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

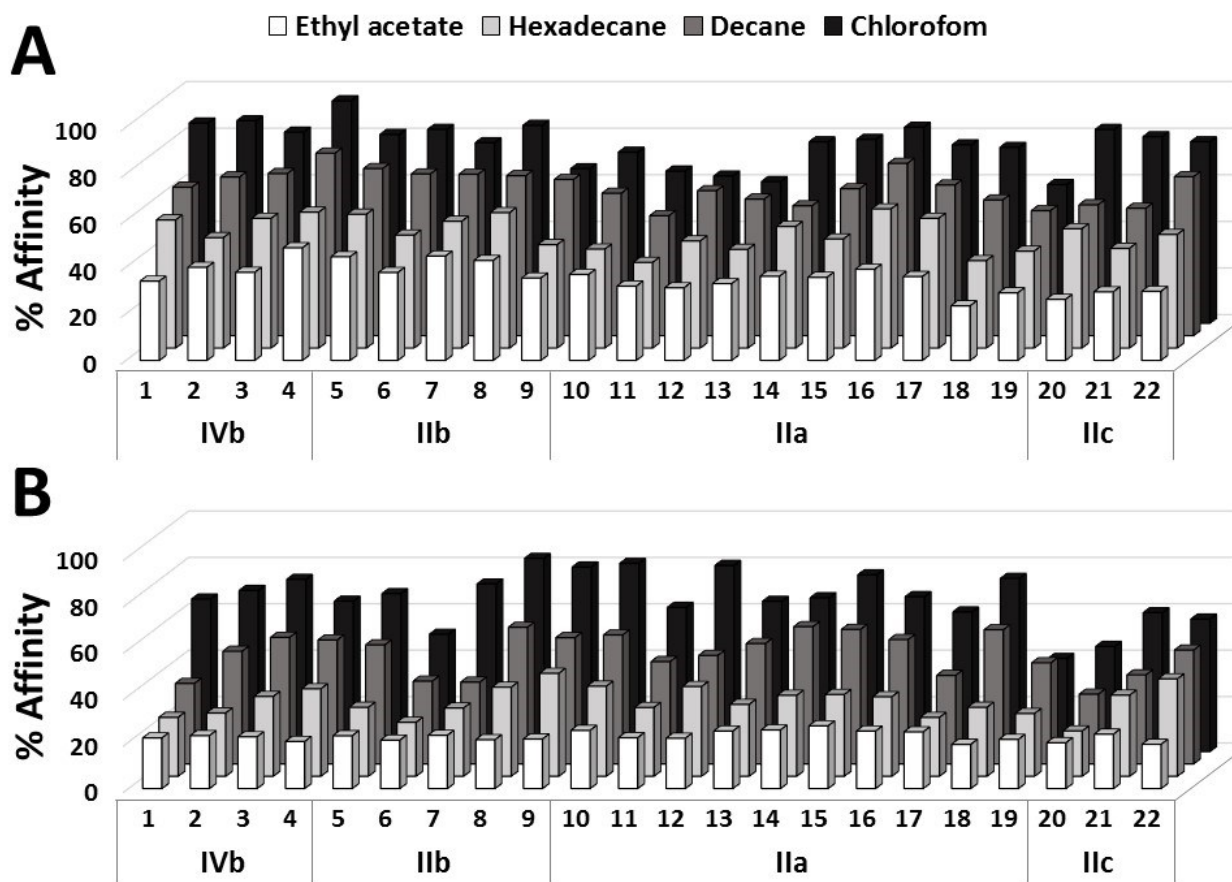
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Supplementary Figure. 1. Recovery of cold shock-induced adherence is demonstrated by BRT®. Cold-stressed cells (exposed to cold shock for the first time) and cold-stressed cells² (exposed to cold shock for the second time) exhibit indistinguishable adhesion profiles. Initial inocula at OD₆₀₀ of 0.5 (A) and 0.17 (B). Data are presented as the mean \pm standard deviation.



Supplementary Figure. 2. Comparison of total biomass measured by CV staining. Data are shown as the mean \pm standard deviation.



Supplementary Figure 3. Affinity (%) of 22 *L. monocytogenes* strains to solvents in stationary phase at 37°C (A) and 4°C (B). Data are shown as the mean of four measurements.

Chapter IV

*Biofilm formation of *Listeria monocytogenes* strains under food processing environments and pan-genome-wide association study*

I Preface

Studies including ours (Chapter III) on biofilm formation in *L. monocytogenes* demonstrated high heterogeneity in the maturity of biofilms among strains (Di Bonaventura et al., 2008; Kadam et al., 2013; Nowak et al., 2017; Rodrigues et al., 2009). In the past, the phenotype diversity was evaluated in association with variables, mainly the phylogenetic position, such as lineages and serotypes. However, contradictory findings were observed which could be attributed to the inter-strain variability and inconsistent experimental settings (Borucki et al., 2003; Djordjevic et al., 2002; Doijad et al., 2015; Nilsson et al., 2011) implying the importance of diversifying a strain panel and experimental conditions for unbiased analysis.

The French Agency for Food, Environmental and Occupational Health & Safety (Anses), as the French national reference laboratory, has collected a great amount of *L. monocytogenes* isolates from diverse origins over the last two decades. They analysed the genetic diversity among 1,894 *L. monocytogenes* isolates from food products and FPE in France (Henri et al., 2016). Using PFGE and MLST subtyping approaches, the isolates unravelled a highly diversified clonal population structure. Furthermore, distribution frequencies of the genotypes were compared to select representative panels of prevalent and rare isolates for the present study. On top of this selection, persistent isolates were added, making up the complete list of three distinct groups, 19 persistent, 20 prevalent and 19 rare isolates exclusively from food and FPE. To obtain a comprehensive view of *L. monocytogenes* biofilm phenotypes using these isolates, we diversified the following factors: (i) Growth conditions mimicking environments that *L. monocytogenes* may encounter in food chain (ii) Analysis aspects from divergences of lineages, serogroups, MLST genotypes to isolate categories (persistent, prevalent, and rare) (iii)

Observation points of biofilm forming process, namely adhesion measured by BRT and total biomass by MPA. The results revealed that high biofilm productivity of clonal complex 26 was magnified at cold temperature. Moreover, importantly, the current study documented a nonlinear positive effect of nutrient deficiency and NaCl supplementation in mature biofilm production.

Furthermore, the total biomasses under different conditions were evaluated in relation to the genomic composition by pan-genome-wide association study (pan-GWAS) for the first time. Pan-GWAS assessed association of accessory genome contents with biofilm phenotypes converted into binary formats. Some difficulties were encountered in applying this tool. Firstly, interpreting the empirical observation of total biomass expressed in continuous values by MPA in binary format was not straightforward. In the current study, hierarchical clustering was applied for unbiased division of strains into strong and weak biofilm formers. Even though our study included numerous strains that showed a wide range of capacity in biofilm production, one cannot exclude the possibility that binary clustering may result in different outcome if the panel of strains expands to encompass more variations. Another difficulty was that differences of genes presence/absence rate between strong and weak biofilm formers were not always pronounced. It may be attributed to a complexity in biofilm formation and its steps that may occur simultaneously in a population of *L. monocytogenes* cells.

II Article

Biofilm Formation of *Listeria monocytogenes* Strains under Food Processing Environments and pan-Genome-Wide Association Study

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Nicolas Krezdorn, Michel Hébraud, Thierry Bernardi, Ibrahim Sultan,
Pascal Piveteau*

Biofilm formation of *Listeria monocytogenes* strains under food processing environments and pan-genome-wide association study

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Abstract

Concerns about food contamination by *Listeria monocytogenes* are on the rise with increasing consumption of ready-to-eat foods. Biofilm production in the food chain is presumed to be one of the ways that confer increased resistance and persistence to this pathogenic bacterium. In this study, a collection of isolates representing persistent, prevalent, and rarely detected *L. monocytogenes* in foods and food processing environments was evaluated for biofilm forming capacities including adhesion and total biomass production under diverse environmental conditions. Depending on the growth conditions, high variability was observed in total biomass within and among lineages, serotypes as well as genotypes but association of clonal complex 26 genotype with biofilm production was evidenced under cold temperature. In general, isolates revealed heterogeneous relative biofilm productivities across growth conditions. There were no clear associations between biofilm formation and persistent or prevalent genotypes suggesting that biofilm production capacity may not be the main driver of *L. monocytogenes* persistence in food chains. Distinct extrinsic factors affected specific

steps of biofilm formation. Sudden nutrient deprivation enhanced cellular adhesion while a prolonged nutrient limitation impeded biofilm maturation. Salt addition exhibited a positive effect, moreover, nutrient limitation supplemented by salt significantly stimulated biofilm formation. Pan-genome-wide association study assessed genetic composition with regard to biofilm phenotypes for the first time. The number of reported genes varied depending on the growth conditions and the number of shared genes was low. However, a broad overview of the ontology contents revealed a similar pattern regardless of the conditions. Functional analysis showed that functions concerning surface proteins including internalins, and competence genes were highly enriched.

1. Introduction

Listeria monocytogenes is a psychrotolerant Gram-positive, rod shaped saprophytic bacterium. As a non-fastidious organism, it can tolerate a range of stressful conditions. Its resistance to high osmolarity was demonstrated by growth up to 13% NaCl and survival under 40% NaCl (Liu et al., 2005; Shabala et al., 2008). *L. monocytogenes* can grow at low temperatures (Junttila et al., 2008) and its minimal growth temperature is expected to be at -2°C (Augustin et al., 2005). It can withstand acidic or alkaline environments as well as low water activity levels (Liu et al., 2005; Nolan et al., 1992). Moreover, exposure to a stress factor provided cross-adaptation to subsequent exposure to other stresses (Begley et al., 2002; Bergholz et al., 2012).

L. monocytogenes inhabits a broad range of environments such as soil, silage, vegetation, sewage or river (Garrec et al., 2003; Vivant et al., 2013; Welshimer and Donker-Voet, 1971). The pathogenic bacterium is responsible for the foodborne, life-threatening disease listeriosis. In the European Union (EU) in 2017, a total of 2,480 confirmed invasive human listeriosis were reported by 28 member states, corresponding to an EU notification rate of 0.48 cases per 100,000 population and a fatality rate of 13.8% (EFSA and ECDC, 2018). As a foodborne pathogen, introduction of *L. monocytogenes* to food processing environments (FPE) imposes a huge burden not only to food premises but also to the whole society. Indeed, evidence suggests that FPE is the most likely source of contamination of *L. monocytogenes* in different types of foods (Pérez-Rodríguez et al., 2008) and growth of biofilms in FPE is considered to be one of the main sources of repeated food contaminations (Colagiorgi et al., 2017; Giaouris et al., 2014). Biofilms are the common form of bacterial development in nature represented by bacteria adhering to surfaces and growing in sessile communities. Materials widely used in FPE such as stainless steel, polypropylene, glass or rubber can support *L. monocytogenes* colonisation (Beresford et al., 2001; Chavant et al., 2002; Mafu et al., 1990). Because bacteria are embedded in self-produced extracellular polymeric matrix that confers higher resistance to external stress factors such as desiccation, nutrient deprivation, or disinfectant treatment (Bridier et al., 2011; Esbelin et al., 2018), it is a great challenge to eliminate biofilms in FPE. Despite an early belief that *L. monocytogenes* could only form monolayer biofilms, later studies evidenced various degrees of maturation in biofilms (Borucki et al., 2003; Guilbaud et al., 2015; Lee et al., 2017).

Pulsed-field gel electrophoresis (PFGE), the gold standard for the last two decades for epidemiology and intraspecific diversity analyses (Félix et al., 2014; Graves and Swaminathan, 2001), enabled identification of persistent isolates. In parallel, multi-locus sequence typing (MLST) has emerged as a key method to investigate the genomic relatedness among *L.*

monocytogenes isolates (Stessl et al., 2014). A prominent advantage of MLST is that it can be derived from whole genome sequence analysis and provides reproducible data across laboratories. High congruence between PFGE and MLST results allowed successful conversion of PFGE profiles into MLST data, thus enabling utilization of PFGE databases for investigation of population genetics and clonal structure of *L. monocytogenes* (Félix et al., 2018; Maury et al., 2016).

In the past, attempts to correlate biofilm phenotype to serotype, origin or persistence gave conflicting results depending on the studies and experimental conditions. Such comparisons can now be addressed at the level of the genome. Indeed, Genome-wide association study (GWAS) is a top-down approach that involves testing a large number of genetic variants in a population of individual organisms with a given phenotype. The application of GWAS in microbiology has slowly emerged (Falush, 2016; Falush and Bowden, 2006) and application of GWAS to *Campylobacter* successfully identified genetic factors responsible for adaptation to different host animals (Sheppard et al., 2013). While most association studies are investigating clinical phenotypes, GWAS dealing with food-related phenotypes was recently applied to *L. monocytogenes* traits associated to cold, salt, acid and desiccation stresses (Fritsch et al., 2019; Hingston et al., 2017).

A collection of 58 isolates was built to represent the diversity and frequency of detection of *L. monocytogenes* in the food industry. These isolates were selected from a panel of 1667 strains isolated from foods and food premises. Based on the distribution of PFGE pulsotypes, the most and least frequent pulsotypes were determined, from which 20 prevalent as well as 19 rare isolates were selected, respectively. Additionally, 19 persistent isolates were included in the strain collection in order to investigate the following questions: (i) Does high biofilm forming capacity underlies persistence as well as prevalence of specific genotypes in FPE and related food products (ii) How environmental conditions affect biofilm forming capacity among genotypes (iii) Can modules of genes be linked to biofilm formation. We evaluated the sessile growth at low temperature, under nutrition deprivation and exposure to salt, mimicking environmental conditions frequently encountered in food premises. To our knowledge, this is the first study that assessed adhesion capacity and biofilm formation at multiple levels including intergroups (persistent, prevalent, and rare isolates), lineages, serogroups, as well as genotypes. Pan-GWAS further highlighted genes that could affect the ability of *L. monocytogenes* to form biofilms under various conditions.

2. Materials and Methods

2.1. *L. monocytogenes* isolate collection, inoculum preparation and growth media

Fifty-eight isolates were selected from the strain collection of Anses (French Agency for Food, Environmental and Occupational Health & Safety, Maisons-Alfort, France), in order to represent the genetic diversity of *L. monocytogenes* isolated from foods and FPE (Table 1). Based on a multiplex PCR assay (Doumith et al., 2004), these 58 isolates were typed into 4 serogroups, IIa (serotype 1/2a and 3a), IIb (serotype 1/2b, 3b, and 7), IIc (serotype 1/2c and 3c) and IVb (serotype 4b, 4ab, 4d, and 4e). They consisted of 43 lineage II strains (40 serogroup IIa and 3 serogroup IIc strains) and 15 lineage I strains (5 serogroup IIb and 10 serogroup IVb strains). The selection criteria were first of all the phylogenetic position of each isolate determined by its pulsotype and MLST clustering (Henri et al., 2016). The second criterion was the frequency of isolation of the genotypes. Three categories, prevalent, persistent and rare isolates were considered according to the frequency of detection of the genotypes. The group of prevalent strains was composed of 20 isolates from the 9 most dominant MLST clusters. Nineteen rare strains were selected from 15 minor clusters. Persistence was defined as isolates of the same pulsotype being isolated at least 3 times over an extended observation period (1 to 5 years) from the same food premise (A, B, C and D) in France or Norway. With these criteria, 19 isolates grouped within 4 MLST clonal complexes (CCs) were selected as persistent strains. As a whole, the strain collection was distributed into 27 different genotypes (CCs and sequence types, STs); 12 singletons, 9 genotypes represented by 2 isolates, 3 genotypes represented by 3 isolates, and 3 genotypes represented by 4, 7, and 8 isolates, respectively (Table 1). The genomes of 57 strains were available from a previous study (Henri et al., 2016).

A working stock was prepared in Brain-Heart Infusion (BHI) broth (Laboratorios Conda, Spain) with 8.3% glycerol (Sigma-Aldrich, France) and stored at -20°C. Bacteria were sub-cultured twice on BHI agar at 37°C. Overnight grown colonies were harvested and homogenized in BHI and 1:10 diluted BHI (dBHI). When required, 0.85% (w/v) NaCl (Sigma-Aldrich) was added to the growth medium.

2.2. Assessment of adhesion capacity: Biofilm Ring Test® (BRT)

The BRT assay (KitC004, BioFilm Control, France) was carried out in polystyrene 96-well microplates as described by Chavant *et al.*³⁵ with slight modifications.

Fresh overnight grown colonies on BHI agar plates were harvested and homogenized in dBHI. Absorbance (OD₆₀₀) was measured to calibrate initial inocula at an OD₆₀₀ of 0.2 in BHI and dBHI broths, each containing magnetic beads (Toner4) at a final concentration of 10 µl ml⁻¹.

According to the BRT technology, a series of inocula, from OD₆₀₀ of 0.2 to 0.0002, was prepared in order to work within the detection range of the system whatever the conditions tested in order to increase the range of detectable phenotypes. In a microplate, 200 µl of each solution was transferred into triplicate wells. Negative controls composed of BHI or dBHI broths with magnetic beads were included in each plate in triplicate. For each strain, duplicated plates were prepared and incubated statically at 10 or 37°C for 5 h. After incubation, few drops of Liquid Contrast (inert and non-toxic white oil) were deposited in the wells and the plates were placed on the Block Test for 1 min to apply magnetic fields at the centre of each well. The bottom of the plates was scanned with the Plate Reader and analysed by BFC elements 3[®] software to obtain the numeric values of each well called the BioFilm Index (BFI) ranging from 0 to 20. With this measurement, absence of biofilm formation in a well results in high mobility of magnetic beads and a BFI around 20. In contrast, immobilization of beads by sessile cells results in a lower BFI or zero value.

At least three experiments were performed for each condition with independently grown bacterial cultures.

2.3. Biofilm quantification with Microtiter Plate Assay

The Microtiter Plate Assay (MPA) was performed as previously described by Lee *et al.* (Lee *et al.*, 2017) with slight modifications. Inocula were prepared as described above. Briefly, overnight grown colonies were diluted to obtain OD₆₀₀ of 0.1 in each growth medium and 200 µl of bacterial solution was transferred in triplicate wells in 96-well microplates. Growth media were added as negative controls. The effect of 3 factors on biofilm formation was tested: nutrient availability (BHI or dBHI), salt content (0 or 0.85% (w/v) NaCl), and temperature (10 or 37°C). Microtiter plates were incubated statically for 24 h at 37°C or 10°C. Plates were inverted and the media and planktonic cells were removed by gently tapping off. To remove loosely attached bacteria, wells were washed twice with 300 µl of sterile saline solution (8.5 g NaCl per litre). Then biofilms were fixed with 300 µl of 96% ethanol (v/v) (Sigma-Aldrich) for 20 min and air-dried completely at room temperature after removal of the ethanol. For staining bacterial biomass, 220 µl of a 0.1% (w/v) solution of crystal violet (CV, Merck KGaA, Germany) was added per well and the plates were incubated static for 30 min. Then the solution was removed by sharply tapping the plates upside down. Wells were washed 3 times with 300 µl of saline and air-dried completely before filling with 150 µl of 33% v/v acetic acid (Sigma-Aldrich). The plates were placed on a plate shaker with slight agitation for 10 min to completely dissolve CV and get homogenized solutions. The amount of destained CV was determined by reading OD₆₀₀ in a Microplate Reader (EL800, BioTek, USA).

At least three experiments were performed for each condition with independently grown bacterial cultures.

2.4. Scanning electron microscopy (SEM) of biofilms

Overnight grown cells were suspended to obtain an OD₆₀₀ of 0.1 in 4 different growth conditions: 0 or 0.85% NaCl in BHI or dBHI broths at 37°C. Seven millilitres of each bacterial suspension were poured into a Petri dish (55-mm diameter) containing a flat stainless-steel coupon (AISI 304, mean roughness = 0.064, 2.5 cm X 1 cm). After 24 h incubation at 37°C under static conditions, coupons were gently washed twice with sterile saline solution. Sessile cells and biofilms were fixed on the coupons with a solution of 3% glutaraldehyde in 0.2 M cacodylate buffer (pH 7.4) then kept at 4°C for a minimum of one hour to overnight. Before dehydration steps, coupons were washed three times with cacodylate buffer for 15 min each. Coupons were dehydrated using a graded ethanol series (70, 90, and 100%) three times, 15 min each and dehydrated further in a 50:50 mixture of ethanol:hexamethyldisilazane (HMDS, Delta microscopies, France) three times for 10 min each. Samples were immersed twice for 10 min each in pure HMDS followed by air-drying at room temperature and sputter-coated with gold (JFC-1300, JEOL, Japan) and observed with a scanning electron microscope (JEOL 6060LV, JEOL, Japan).

2.5. Pan-Genome-Wide Association Study

Total biomasses measured by MPA under 8 different growth conditions were classified into binary phenotypes, strong or weak biofilm formers. This clustering of strains was established based on OD values with function `hclust` in R version 3.4.2 with the complete linkage method for hierarchical clustering.

A pan-GWAS based on the accessory gene content of the 57 *L. monocytogenes* de novo assemblies was performed. First, draft genomes were obtained based on the SPAdes algorithm (Bankevich et al., 2012) after quality check of Illumina reads using FASTQC (Andrews, 2010). Then, whole genome annotation was carried out using Prokka (Seemann, 2014) with default parameters. Prokka uses the assemblies as input and produces GFF3-files, including sequences and annotations, which were used to extract the pangenome of the 57 *L. monocytogenes* isolates with the software Roary (Page et al., 2015). Finally, gene-based GWAS was performed using Scoary (Brynildsrud et al., 2016) by following the instructions provided on <https://github.com/AdmiralenOla/Scoary>. Scoary helped to assess presence/absence patterns of genes in binary phenotypes. The genes with significant association ($p < 0.05$) were reported. Percentage of strains between strong versus weak biofilm formers carrying each gene in the genomes was calculated. For example, % of a gene in strong biofilm formers was

determined as follows: (number of strains carrying the gene in their genomes among strong biofilm formers) X 100 / (total number of strains grouped into strong biofilm formers).

Information regarding gene name, protein name, accession number and Gene Ontology were retrieved from the Universal Protein Resource database (<https://www.uniprot.org/>). Sequence with no BLAST hit (0.79%) were excluded from further analysis. To obtain a visualized dataset on selected genes, Gene Ontology (GO) enrichment analysis was performed using PANTHER Version 14.0 (<http://pantherdb.org/>). Selected sequences were annotated according to *L. monocytogenes* EGDe genome (Refseq accession NC_003210.1) and compared to the functional classification retrieved from ListiList (<http://genolist.pasteur.fr/ListiList/>).

2.6. Phylogenetic analysis

A variant calling analysis was performed using iVarCall2 (Felten et al., 2017). Using this pipeline, paired-end reads were aligned against the reference genome EGDe to identify single-nucleotide polymorphisms (SNPs) and small insertions/deletions by local de novo assembly. Phylogenomic reconstruction based on core-genome SNPs was carried out with RAxML (Randomized Axelerated Maximum Likelihood) (Stamatakis, 2014). The phylogenetic inference was performed with bootstrap analysis and searching for the best-scoring Maximum Likelihood tree with General Time-Reversible model of substitution and the secondary structure 16-state model.

2.7. Statistical analyses

One-way analysis of variance (ANOVA) with Tukey's multiple comparison test was applied to determine statistically significant differences in the level of adhesion and biofilm production within lineages, serogroups, groups (persistent, prevalent, and rare) or genotypes. Dunnett's multiple comparison test was applied for testing the significance of changes in biofilm production caused by alteration of growth conditions (T°C or NaCl) in comparison to the standard BHI or dBHI condition. Multiple t-test was applied to assess the statistical significance of changes in adhesion measured by BRT. All differences are reported at a level of significance of 0.01 or 0.05.

3. Results

3.1. Environmental conditions affect biofilm production

Biofilm production by 58 strains was evaluated at 37°C, its optimal growth temperature, and 10°C, a low temperature close to that of FPE. For each temperature, 4 culture media were tested: BHI as a control, dBHI representing a nutrient-deprivation medium, and both media with addition of 0.85% (w/v) NaCl to assess impact of salt. Temperature played a major role in determining the total biomass; in general, biofilm production was more than 5 times greater at 37°C than at 10°C with the exception of dBHI broth in which the total biomass produced at both temperatures was similar (Figure 1; Table 2).

Similar trends upon changes in media composition were observed at both temperatures. Nutrient deficient condition (dBHI) induced a significant decrease in total biomass compared to BHI condition, notably the effect was more prominent at 37°C (Figure 1). In contrast, addition of 0.85% NaCl induced a significant increase in biofilm production under both nutrient rich (BHI + NaCl) and poor (dBHI + NaCl) conditions (Figure 1; Table 2). This effect was significantly stronger in nutrient poor condition than in nutrient rich condition. Supplementation of dBHI broth with NaCl resulted in 23.4 and 4.5 times higher total biomass at 37°C and 10°C, respectively while 1.7 times increase was observed in BHI broth at both temperatures. It is noticeable that the combination of two factors, addition of salt and deprivation of nutrient, exerted a nonlinearly positive effect on biofilm production. Approximate osmolarity, calculated based on the literature (Takahashi et al., 1981) and molarity of NaCl showed that addition of 0.85% NaCl to dBHI medium increased its osmolarity from 36 to 327 mOsm/L, i.e. comparable to that of BHI medium (360 mOsm/L). However, the bacteria produced significantly more biomass in dBHI + NaCl compared to that in BHI suggesting that the nutrient deprivation stimulates biofilm production provided the appropriate osmotic environment is supplied.

SEM observations of strain 13 (persistent group) showed several biofilm structures from monolayers of cells to mature 3-D biofilms according to environmental conditions (Figure 1B). These observations were in accordance with MPA biomasses quantifications (Table 2). Cells grown in BHI media uniformly colonized the surface with small cellular aggregates and addition of salt increased the volume and frequency of cell clusters. When deprived of nutrients (dBHI), the surface was only sparsely colonized with no visible aggregate. However, addition of salt in dBHI medium dramatically improved biofilm construction and dense, three-dimensional mature biofilms were observed.

3.2. Association of biofilm phenotypes with phylogenetic division

The associations between phylogenetic attributes and biofilm formation were evaluated (Figure 2). Lineage II strains were statistically more efficient than lineage I strains in producing biofilms under 3 (BHI, BHI + NaCl, and dBHI + NaCl at 37°C) out of 8 conditions. However, opposite results were observed after incubation in dBHI broth at both temperatures. No significant differences were observed under the other conditions tested. Comparative analysis at the level of serogroups revealed that, at 37°C, serogroup IVb strains produced significantly less biofilm than serogroup IIa and/or IIb strains under 3 conditions (BHI, BHI + NaCl, and dBHI + NaCl). On the contrary, IVb strains formed higher biofilms under dBHI medium at 37°C. These differences are concordant with the differences observed at lineage levels; for example, the significant differences between serogroup IIa and IVb strains at 37°C are consistent with the differences observed between lineage I and II strains. However, some significant differences were also detected within lineage I, concurrently between serogroups IIb and IVb strains (BHI and BHI + NaCl at 37°C).

3.3. Intra- and Inter-genotype biofilm phenotype variations

The genotypes represented by at least 3 isolates (28 isolates in total) were selected to assess intra- and inter-genotypic variances. Intra-genotype variations were observed except for CC7 and CC26. At least two isolates within genotypes CC121, CC11, CC155, and CC9 showed statistically different biofilm phenotypes under one or more growth conditions (Supplementary Figure 1). Considering the inter-genotype variations, it was manifest that isolates from CC26 formed distinctively more biofilm than other CCs at 10°C (Figure 3). Multiple comparison test confirmed that CC26 formed statistically more biofilms than the other 5 genotypes under all 4 different conditions at 10°C while at 37°C differences were significant under only one condition (dBHI + NaCl) implying that the cold temperature capitalized the biofilm forming trait of genotype CC26.

3.4. Biofilm formation of persistent, prevalent, and rare isolates

To test the hypothesis whether higher biofilm forming capacity could underlie persistence or frequent isolation of specific genotypes, we evaluated the total biomass produced under diverse conditions among persistent (group 1, n=19), prevalent (group 2, n=20) and rare (group 3, n=19) isolates (Figure 4; Table 1). Group 1 strains showed higher biofilm formation only in BHI at 37°C while group 2 strains were not more efficient than others under any condition tested. Interestingly, biofilms produced by isolates of group 3 were significantly more abundant than biofilms produced by isolates of the other two groups under numerous conditions. These observations suggest that, under the conditions tested, biofilm production cannot discriminate persistence or distribution frequency of genotypes in foods and FPE.

3.5. Nutrient deficient stress induces higher adhesion

Adhesion is the first step of biofilm formation manifested by attachment of bacterial cells to biotic or abiotic surfaces. The adhesion capacity measured by BRT is computed as BFI, a parameter inversely proportional to the level of adhesion. The BFI values, measured in nutrient deprived cells (dBHI) were lower than that of control cells (BHI) demonstrating an enhanced adhesion upon exposure to nutrient starvation after 5 h (Figure 5A). The positive effect of nutrient starvation on adhesion was observed regardless of the incubation temperature. At 37°C, the first two high inoculums gave results out of range (BFI = 0). A nearly complete blockage of beads resulted from full coverage of sessile cells at the bottom of the plate. However, significant differences were observed between BHI and dBHI at only one lower inoculum (OD₆₀₀ of 0.002; app. 4E⁺⁰⁶ cells/ml). By contrast, at 10°C, the highest inoculum of OD₆₀₀ of 0.2 (app. 4E⁺⁰⁸ cells/ml) showed the impact of nutrient stress while no adhesion could be recorded with a lower inoculum.

To further examine the increased adhesion under low nutrient conditions, ΔBFI was calculated by subtracting BFI of cells incubated in dBHI broth from that of BHI broth. ΔBFI was compared among the 3 groups (persistent, prevalent, rare) as well as 4 serogroups and no significant differences was found (Figure 5B and C) indicating that the enhanced adhesion was a universal phenotype transition. Furthermore, BFI values collected from BHI and dBHI media were compared among the 6 genotypes represented by at least 3 isolates. No evidence of genotype-specific predisposition in adhesion characteristics could be recovered (Figure 5D). In summary, enhanced adhesion of *L. monocytogenes* was a global cellular response to hypoosmotic shock triggered by nutrient deprivation.

3.6. Phylogenetic analysis of relative biofilm productivity

The total biomasses of 57 isolates were displayed in colour scale with binary transformation into strong or weak biofilm formers under different growth conditions and grouped according to their phylogenetic positions (Figure 6). The same colour gradient scheme was applied to a range of MPA values obtained under each growth condition in order to reflect relative biofilm productivity. The result showed that biofilm productivity varied inconsistently within each isolate depending on growth conditions except for certain isolates. For example, isolates belonging to CC7 and CC26, which previously revealed homogenous intra-genotype traits under each condition (Supplementary Figure 1), manifested overall low and high biofilm productivities, respectively across all the conditions. On the other hand, high variations in biofilm productivity were observed between closely related strains, including isolates of the same genotypes.

By binary transformation, only 2 and 6 isolates were consistently classified as strong and weak biofilm formers, respectively regardless of the growth conditions.

3.7. Putative determinants of biofilm formation detected by pan-GWAS

Pan-GWAS identified genes whose presence or absence were significantly ($p < 0.05$) related to the binary biofilm phenotype in 57 strains. The sets of significant genes varied greatly according to the growth conditions. As temperature is the critical environmental signal for *L. monocytogenes*, the sets of genes were compared at each temperature. There were 283, 692, 551, and 674 genes in BHI, dBHI, BHI + NaCl, and dBHI + NaCl media at 37°C, respectively and 319, 676, 281, and 65 genes at 10°C, respectively (Figure 7A and 7B). Among the 1360 genes specifically identified at 37°C, only 50 genes (3.68%) were found in more than 3 conditions. In a similar way at 10°C, 59 genes (5.62%) were found in more than 3 conditions among 1050 genes specifically identified at 10°C. The lists of genes under each condition can be found in supplementary tables 1 to 8. Globally, considering all 8 conditions, 37% of the genes identified by pan-GWAS had no predicted protein function. In order to compare the occurrence of pan-GWAS-identified genes between weak and strong biofilm formers, the percentage of strains carrying the genes was calculated in the two categories (Supplementary Tables 1 to 8). Depending on the genes and conditions, the difference of occurrence between weak and strong categories varied from 15 to 63% and the overall average difference of occurrence on the full set of pan-GWAS genes was 29%.

PANTHER GO-Slim analysis was applied to investigate the distribution of genes under each condition. We found 34, 273, 122, and 286 genes at 37°C, and 80, 262, 46, and 10 genes at 10°C enriched in BHI, dBHI, BHI + NaCl, and dBHI + NaCl media, respectively. Among the GO category “molecular function”, the most enriched classes were “catalytic activity” (GO:0003824) followed by “binding” (GO:0005488), and “transporter activity” (GO:0005215) (Figure 7C). In the category “biological process”, the “metabolic process” (GO:0008152) class was overrepresented followed by “localization” (GO:0051179), “cellular component organization or biogenesis” (GO:0071840), and “biological regulation” (GO:0065007) classes (Figure 7D). In the “cellular component” category, the most prevalent class was “cell” (GO:0005623) followed by “protein-containing complex” (GO:0032991) and “membrane” (GO:0016020) classes (Figure 7E).

Because the enriched GO terms were similar regardless of the growth conditions, the whole list of genes identified by pan-GWAS was subjected to functional analysis. In total, 2105 genes (genes observed in several conditions were counted several times for enrichment purposes) were annotated to the genome of *L. monocytogenes* EGDe. Within each functional category, fold enrichment was calculated as % in identified genes / % in whole genome of *L.*

monocytogenes EGDe (Figure 8). Functional categories highly enriched belonged predominantly to “Cell envelop and cellular processes”, for example “cell surface proteins” (3.39 fold-enriched), “soluble internalin” (2.03 fold-enriched), “transformation/competence” (3.00 fold-enriched) and “cell wall” (1.31 fold-enriched). In “Intermediary metabolism” category, “metabolism of phosphate” (1.58 fold-enriched) was overrepresented while “metabolism of nucleotides and nucleic acids” (0.22 fold-enriched) and “metabolism of lipids” (0.33 fold-enriched) were comparatively underrepresented. Among the other functional categories, “phage-related functions” (1.52 fold-enriched), “similar to unknown proteins from *listeria*” (2.00 fold-enriched) and “no similarity” (1.9 fold-enriched) were overrepresented. On the other hand, “protein synthesis” (0.09 fold-enriched) was underrepresented.

4. Discussion

Complex mechanisms regulate bacterial sessile growth and biofilm formation from adhesion to maturation and dispersal. Each step is affected by intrinsic and extrinsic factors. In this study, 58 *L. monocytogenes* strains isolated from food and FPE were evaluated for biofilm forming traits including adhesion and total biomass production. Under all conditions studied, all isolates adhered and developed as biofilms. Diverse growth conditions reflecting food and FPE such as changes in salt content, nutrient availability and temperature significantly affected biofilm production. Temperature was the most influencing factor for biofilm production as observed in previous studies (Di Bonaventura et al., 2008; Kadam et al., 2013; Rodrigues et al., 2009). Despite its capacity to survive and grow at low temperatures, growth rate of *L. monocytogenes* falls when temperatures decrease below optimal range (Murphy et al., 1996) which explains the significant differences between the total biomass obtained at optimal (37°C) and cold (10°C) temperatures during the 24 h of incubation. It needs to be investigated whether or not similar mature biofilms would be produced at 10°C if the incubation period was prolonged as shown for other strains (Chavant et al., 2002; Zameer et al., 2010).

In food industry, salt is the most widely applied natural preservative for foods especially in processed foods including RTE products (Intake et al., 2010). However, *L. monocytogenes* efficiently adapts to changes in water activity in surrounding environments (Sleator et al., 2003) and NaCl induces biofilm production. Indeed higher biomass was quantified when NaCl concentration increased from 0.5% to 2% at 22.5, 30 and 37°C in tryptic soy broth (TSB) containing 0.6% yeast extract (Pan et al., 2010). Similarly, in another study, addition of 2 to 5% NaCl in TSB caused a dramatic increase in aggregation of *L. monocytogenes* (Jensen et al., 2007). The present study demonstrated that addition of salt at saline concentration (0.85% NaCl) induced a significant increase in biofilm formation under both nutrient rich (BHI) and poor (dBHI) conditions. Besides, our results disclosed, for the first time, a dramatic nonlinear effect of salt addition and nutrient deprivation on biofilm production. Positive effect of NaCl on biofilm maturation was significantly intensified by nutrient deprivation.

L. monocytogenes isolates in FPE are likely to encounter nutrient deprivation or hypo-osmotic stress. To avoid cell lysis caused by massive influx of water into the cell when subjected to sudden hypo-osmotic shock, bacteria have evolved several mechanisms including mechanosensitive or stretch-activated channels that mediate efflux of cytoplasmic solutes and water channels such as aquaporins (Sleator and Hill, 2002). Our study found that when cells were exposed to sudden nutrient deprivation stress, the initial step of adhesion to microtiter plate was enhanced at both optimal (37°C) and cold (10°C) temperatures. This finding is in agreement with our previous study that demonstrated enhanced adhesion of *L.*

monocytogenes upon sudden cold stress (Lee et al., 2017). Both studies were aligned in the fact that the increase in adhesion upon sudden stresses was not related to serotype, origin or genotype of strains as previously reported in the literature (Kalmokoff et al., 2001). Physicochemical properties such as hydrophobic interactions and interfacial forces between a substratum and a bacterial cell influence cell attachment to a surface (Renner and Weibel, 2011). Our previous study found a correlation between cell surface properties and adhesion levels (Lee et al., 2017). Similarly, the sudden hypo-osmotic shock accompanied by nutrient stress could have induced alterations in cell surface properties resulting in increased adhesion as a stress response. However, the mechanisms behind this observation remain to be elucidated. Furthermore, the increased adhesion upon nutrient stress did not lead to the construction of mature biofilms suggesting that each step of biofilm formation is differently affected by environmental factors.

L. monocytogenes shows high intraspecific diversity. To date, studies that evaluated intraspecific diversity of biofilm phenotype in this species focused on associating phenotypes with genetic lineages, serotypes or origins. However, discrepancies among studies were reported. For example, conflicting results were reported on the association of lineages or serotypes with biofilm production (Borucki et al., 2003; Djordjevic et al., 2002; Doijad et al., 2015). These inconsistencies could be ascribed to differences of experimental setups (Kadam et al., 2013). Similarly, in the present study, some significant differences in biofilm production were observed among serotypes, though the associations were not consistent throughout the different growth conditions. Moreover, lineages seem to be a spurious indicator for biofilm formation in *L. monocytogenes* as both serogroup IIb and IVb belonging to lineage I, showed significant differences in biofilm formation under some conditions. The results suggest that these criteria may not reflect the actual diversity of biofilm formation in *L. monocytogenes*. Instead, more closely related isolates identified by molecular subtyping methods such as MLST could divulge stronger phenotype-genotype associations. Some studies on population genetics highlighted a distinct clonal structure of *L. monocytogenes* strains within distinct phylogenetic lineages (Bakker et al., 2010; Ragon et al., 2008). Interestingly, recent studies reported heterogeneous distribution of genotypes among a large panel of food and clinical isolates of *L. monocytogenes* (Maury et al., 2016; Painset et al., 2019). According to the studies, CC121 and CC9 accounted for most of food isolates, whereas CC1, CC2, CC4, and CC6 were highly associated with a clinical origin and higher virulence potentials *in vivo*. Similarly, associations between genotypes and stress tolerance traits in *L. monocytogenes* has been documented (Hingston et al., 2017) showing that genotype associations levelled out further associations at serotype level. In the current study, interestingly, three isolates of CC26 produced more biofilms than other CCs at 10°C. It is assumed that core genetic features of

CC26 have contributed to the exceptional behaviour of these isolates under cold stress resulting in higher biofilm production. By contrast, high intra-genotype variations observed in some CCs suggests that minor genetic variants within a genotype may impact biofilm phenotype.

In addition, our data suggest that high ability to adhere to surface or to produce sessile biomass may not be a prerequisite to persistence or prevalence of *L. monocytogenes* in FPE. Other traits associated with stress factors in food chain such as increased resistance to disinfectants or desiccation treatments need to be investigated to understand the characteristics of *L. monocytogenes* stratifying the current population structure. As a matter of fact, except for 8 isolates of CC7 (persistent subgroup 'D') which showed similar phenotypes, other persistent clones (subgroup 'A' 'B', and 'C') expressed biofilm phenotypes significantly different under some growth conditions. In the current study, persistence was defined when the same genotype was re-isolated at least 3 times from the same FPE or related food products over a timespan of more than 1 year. Apparently, there exists a limitation in discriminating different strains belonging to a same genotype defined by subtyping methods such as PFGE or MLST. Moreover, it is difficult to discriminate real persistent clones from non-persistent ones reintroduced into FPE regularly and supposed persistent clones could be mis-categorized as a sporadic strain on multiple sampling occasions (NicAogáin and O'Byrne, 2016).

The pan-GWAS analysis on total biomasses produced under various growth conditions identified a large number of genes from the accessory genome of 57 strains. Results depended on the experimental conditions and the combinations of nutrient stress, NaCl addition and temperature. Generally, the number of shared genes was low among different growth conditions due to high genomic variation. However, GO enrichment revealed that the distribution of modules of genes found by pan-GWAS was comparable regardless of the growth conditions suggesting that overall patterns of genes involved in biofilm production are homogeneous.

Several studies investigated putative biofilm determinants using transposon mutagenesis (Alonso et al., 2014; Chang et al., 2012; Piercey et al., 2016; Yong et al., 2012). Among the wide spectrum of functions reported in these studies, "cell wall component" (teichoic acid metabolism and peptidoglycan synthesis), "membrane proteins" (lipoprotein assembly), "flagella and motility", "cell signalling", "energy generation and intermediary metabolism", "biosynthesis" and "gene regulations" were the most prevalent ones. Genes encoding virulence related surface proteins such as internalins and cell wall anchor proteins were also found to be engaged in biofilm formation (Franciosa et al., 2009; Jordan et al., 2008; Popowska et al., 2017) and in cold adaptation (Fritsch et al., 2019). Similar findings were observed among

the genes identified by pan-GWAS in the current study. For example, functions including cell surface proteins, internalins and cell wall were overrepresented.

Interestingly, functional category “metabolism of phosphate” was enriched in the set of genes. Previously, phosphate-dependent biofilm production was suggested in *Pseudomonas fluorescens* (Navarro et al., 2011; Newell et al., 2011). Change of phosphate level in the surrounding environment modulated expression of the surface adhesin through a cyclic dimeric GMP (c-di-GMP) signaling pathway mediating the lifestyle switch between motile planktonic cells and biofilm formers. As an important second messenger, c-di-GMP plays a role in the complex regulation of broad bacterial behaviours including biofilm formation and exopolysaccharide synthesis in *L. monocytogenes* and in a wide variety of bacteria (Hengge et al., 2016; Köseoğlu et al., 2015; Valentini and Filloux, 2016). Phosphate is the incorporated form of phosphorous in nucleic acids and phospholipids which take up a substantial part of the cell. However, the effect of phosphate on specific phenotypes as well as phosphate metabolism has not been studied in depth.

Another highly enriched function was “transformation/competence”. In *Streptococcus pneumoniae* biofilm maturation is dependent on allelic variants of *comC*, the gene encoding competence-stimulating peptide (Carrolo et al., 2014). Moreover, significantly higher competence induction and transformation efficiencies accompanied by upregulation of competence genes was described during sessile growth (Marks et al., 2012). In this regard, the exact role of extracellular DNA, an essential part of the matrix in *L. monocytogenes* biofilms (Harmsen et al., 2010), needs to be investigated.

However, a limitation of the pan-GWAS approach was a lack of straightforward associations of presence/absence of genes with strong or weak biofilm formers because occurrence between two binary traits was obscure in general (the mean difference in gene occurrence was about 29%). This may be explained by the difficulty to convert a linear trait into binary format which may have affected the results. Secondly, biofilm formation is a string of simultaneous processes engaging various steps as well as diverse physiological cellular states. The number of genes identified by pan-GWAS may reflect this complexity. Transcriptomics studies conducted on cells growing in biofilms pointed out time-dependent, differential gene expression patterns in *L. monocytogenes* and other bacteria (Stanley et al., 2003; Tirumalai and Prakash, 2012; Yamamoto et al., 2011). It supports the hypothesis that divergent modules of genes are involved in each step of biofilm formation. Thus, engagement of a gene in one step of biofilm formation might have been masked by its irrelevance during later steps which might affect pan-GWAS results.

5. Conclusion

This study is the first attempt to correlate biofilm traits of food-related *L. monocytogenes* isolates with diverse characteristics such as persistence and frequency of distribution of genotypes as well as genetic composition. Our results suggest that the ability of some isolates to be persistent or prevalent in FPE is not depending on the biofilm formation efficiency. The current distribution of genotypes in FPE and foods could be the result of their corresponding heterogeneous distribution in natural environments which, unfortunately, is difficult to investigate due to the lack of appropriate databases. Biofilm productivity exhibited profound inter- and intra-strain variations depending on growth conditions which resulted in inconsistent associations between biofilm formation and lineages or serotypes throughout the different growth conditions. Interestingly, we observed a temperature-dependent association of genotype with biofilm production asserting genotype as a better predictor of bacterial phenotypes. While salt addition enhanced biofilm production, nutrient deprivation impaired it. Importantly, a marked nonlinear effect of both treatments was documented for the first time in *L. monocytogenes*. Supplementation of NaCl in nutrient deprived cells significantly increased biofilm maturity regardless of temperature. Pan-GWAS was successfully applied on biofilm data and the module of genes were found to be comparable across different growth conditions in spite of the small number of shared genes. Cell surface proteins and transformation/competence related functions were highly enriched among the total list of identified genes. Further investigations on genes of unknown function that accounted for a third of all genes as well as a time-course transcriptome analysis will help decipher the complex mechanisms of the biofilm formation.

Author contributions

B-H.L. and P.P. conceived the project. B-H.L. designed the experiments and analysed and interpreted the data. S.B., M.H., and T.B. supervised the experiments concerning biofilm phenotypes conducted by S.C. and B-H.L. L.G. performed the phenotype clustering and the GWAS and B.F. selected the strains. N.K. performed annotation on EGDe and I.S. performed functional analysis. B-H.L. and P.P. wrote the manuscript and all authors reviewed and approved the final manuscript.

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Data availability

The authors declare that the data supporting the findings of this study are available within the paper and its supplementary information files. The paired-end reads of the strains used in the study are available under the ENA bio-projects (<https://www.ebi.ac.uk/ena/data/view/PRJEB15592> and <http://www.ebi.ac.uk/ena/data/view/PRJEB32254>).

Figures and Tables

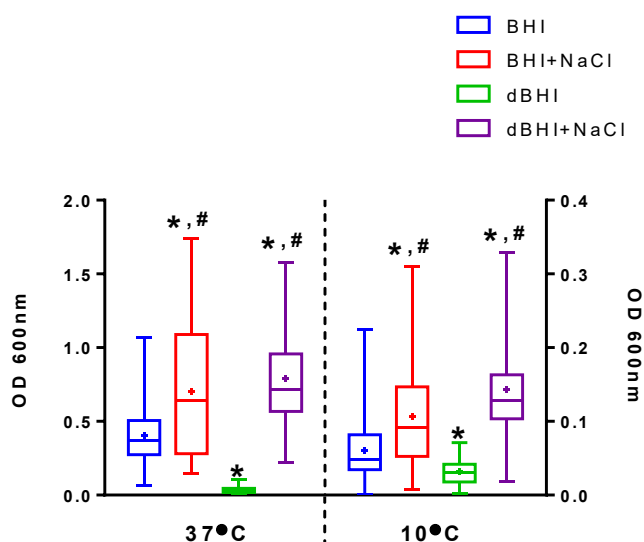
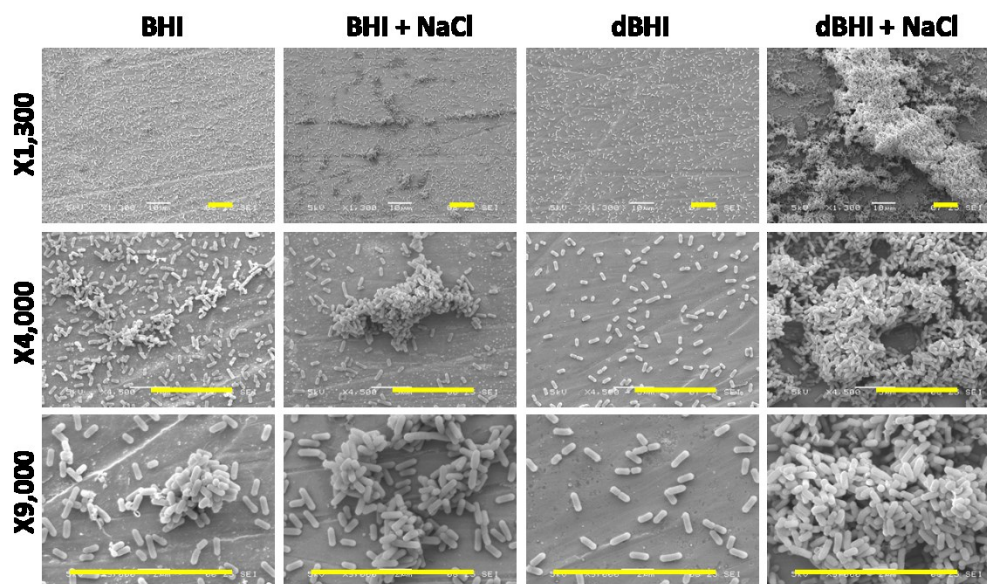
A**B**

Figure 1. Effect of various growth conditions on biofilm formation. (A) Total biomasses of all 58 isolates measured by MPA at 37°C and 10°C are plotted on the left and right Y-axes respectively. Whiskers extend to minimum and maximum values, and the horizontal line and the dot in the box represent the median and mean values, respectively. Statistical significance was assessed using One-way ANOVA and Dunnett's multiple comparison tests, * $p < 0.01$ compared to BHI medium, # $p < 0.01$ compared to dBHI medium. (B) Examples of SEM observation at low, middle, and high magnifications (row) for strain 13 (persistent group) biofilm formation at 37°C according to the growth conditions. Scale bars: 10 µm.

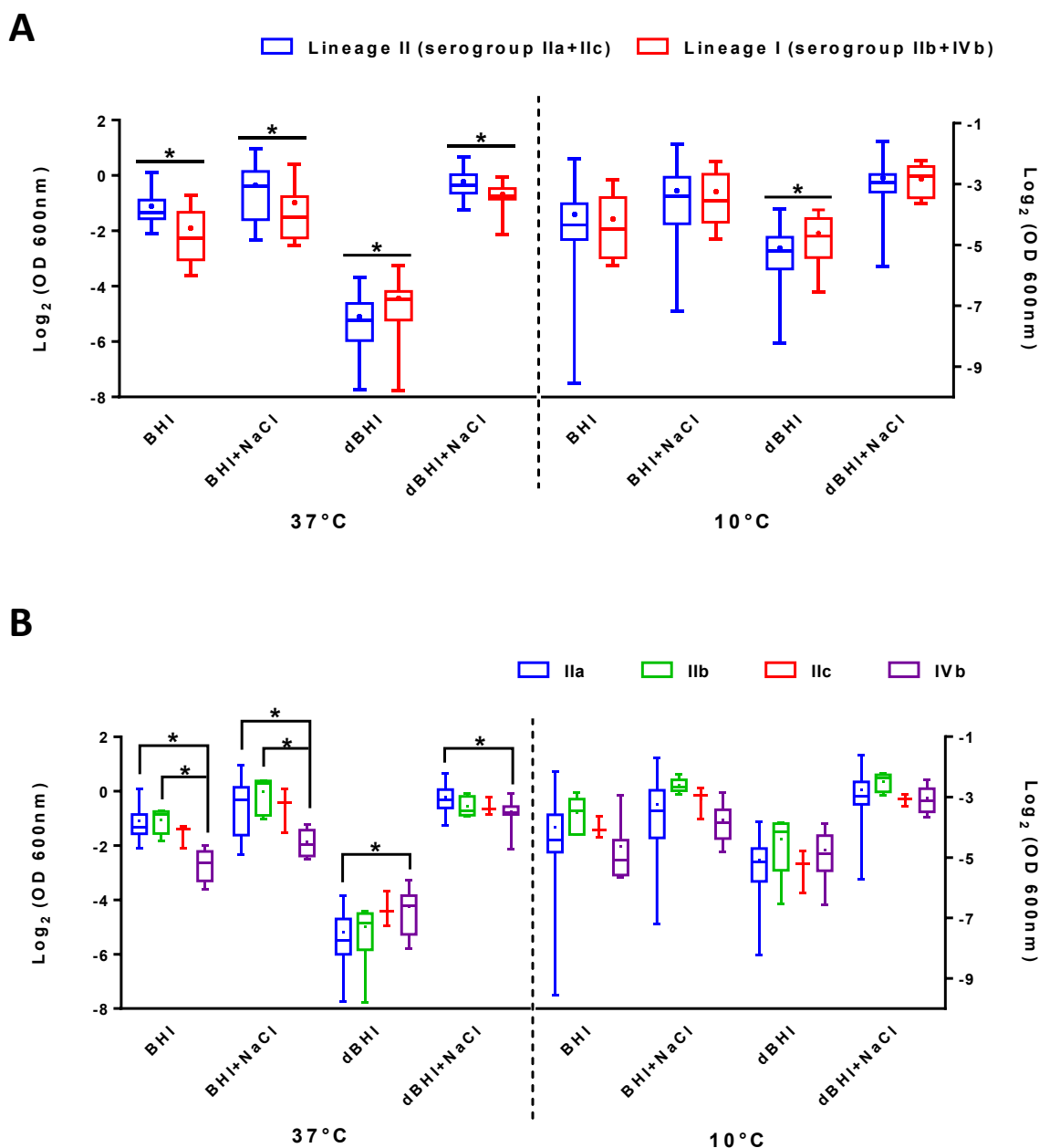


Figure 2. Comparative analysis of biofilm formation among lineages and serogroups. Data obtained from MPA are grouped by lineages (A) and serogroups (B). Total biomasses produced at 37°C and 10°C are plotted on left and right Y-axes, respectively. Whiskers extend to minimum and maximum values, and the horizontal line and the dot in the box represent the median and mean values, respectively. Data were analysed using One-way ANOVA and Turkey's multiple comparison tests, * $p < 0.05$.

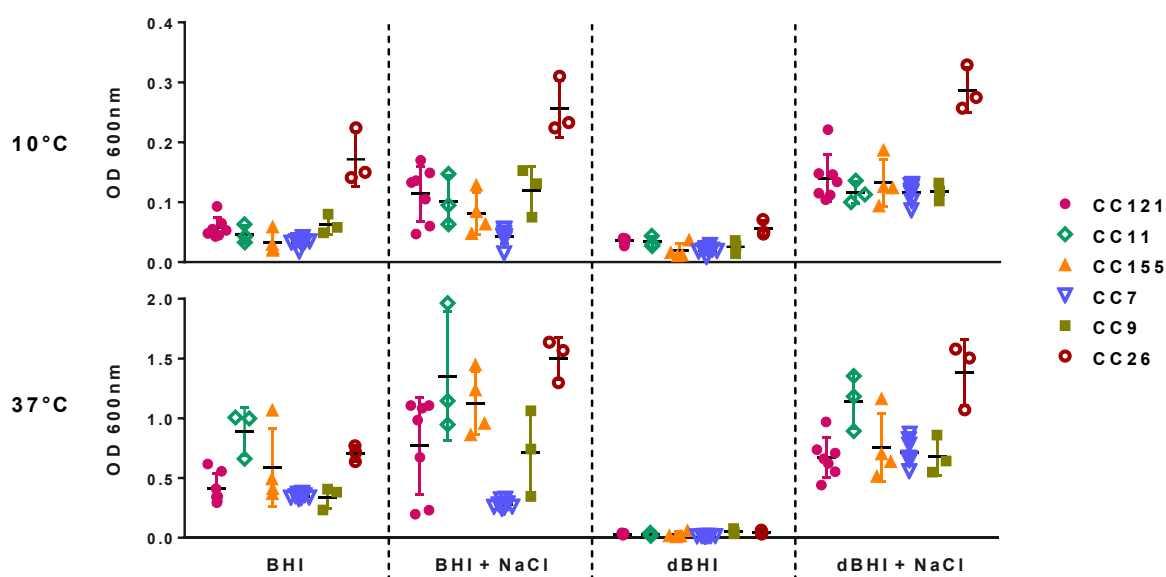


Figure 3. Inter- and intra-genotype variation in biofilm formation. Isolates are grouped according to their phylogenetic position and 6 genotypes comprising 28 *L. monocytogenes* isolates are shown; CC121 (n=7), CC11 (n=3), CC155 (n=4), CC7 (n=8), CC9 (n=3), and CC26 (n=3). Only CCs represented by at least 3 isolates are plotted. Upper and lower graphs show MPA results at 10°C and 37°C, respectively. Each dot represents one isolate; vertical lines indicate SD and horizontal bars the mean values. Data were analysed using One-way ANOVA and Turkey's multiple comparison tests, $p < 0.05$. CC26 formed statistically more biofilms than other genotypes in all media conditions at 10°C and dBHI + NaCl medium at 37°C.

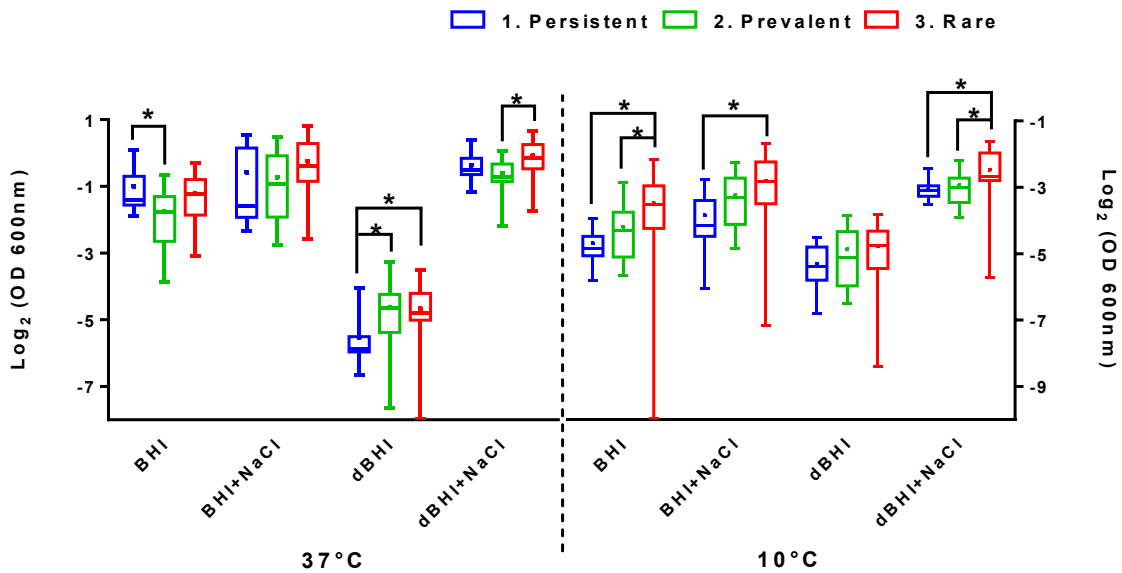


Figure4. Comparative analysis of biofilm formation among persistent (group 1), prevalent (group 2), and rare (group 3) isolates. Total biomasses measured by MPA at 37°C and 10°C are plotted on left and right Y-axes, respectively. Whiskers extend to minimum and maximum values, and the horizontal line and the dot in the box represent the median and mean values, respectively. Data were analysed using One-way ANOVA and Tukey's multiple comparisons test, * $p < 0.05$.

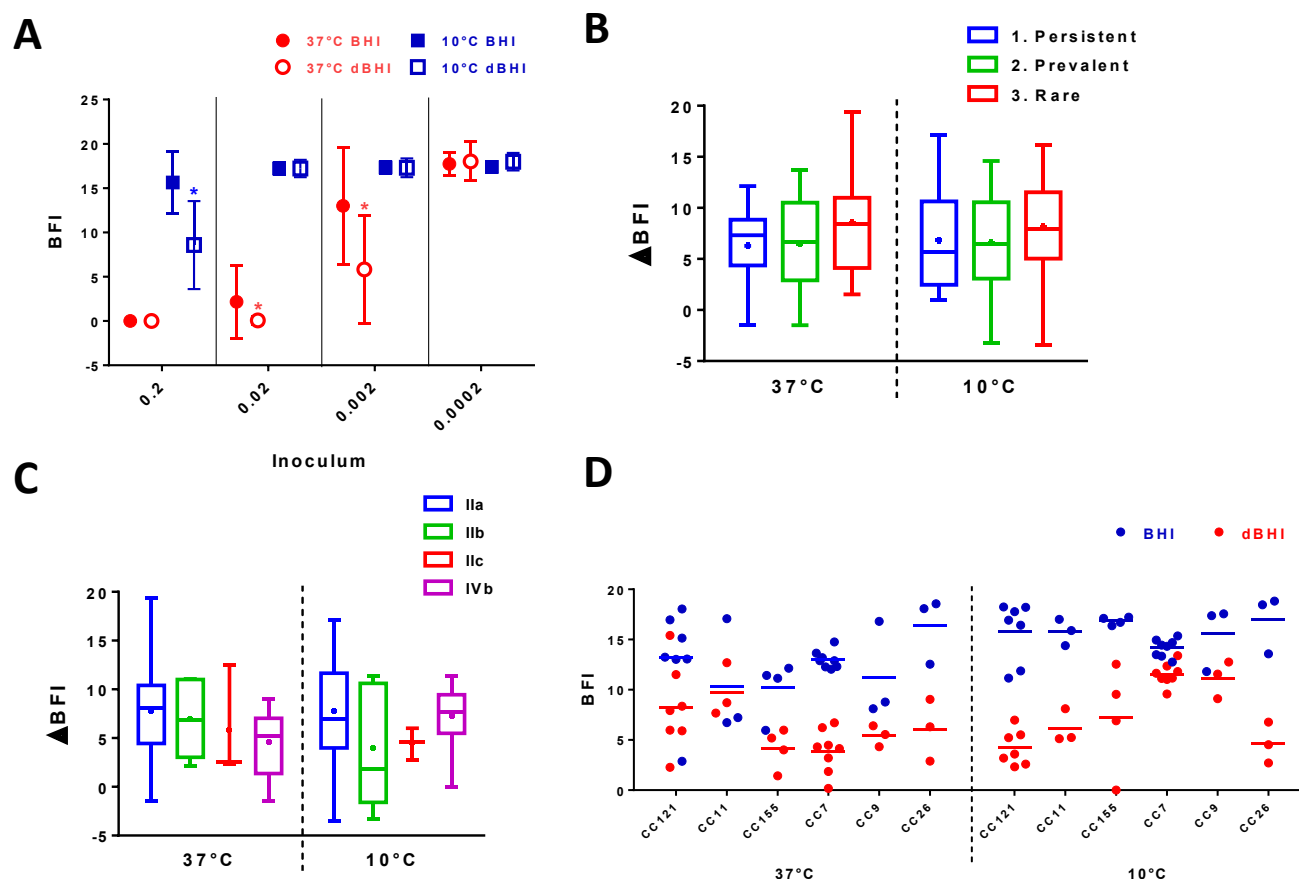


Figure 5. Enhanced adhesion of *L. monocytogenes* upon nutrient stress measured by BRT. (A) BRT results of all isolates under 4 different conditions (symbols) at different inoculum concentrations (X-axis). Data are presented as mean \pm SD and statistical significance was determined by multiple t-test, $*p < 0.05$ compared to BHI at each temperature. Delta BFI (Δ BFI) presented by groups (B) and serogroups (C). Whiskers extend to minimum and maximum values, and the horizontal line and the dot in the box represent the median and mean values, respectively. Data were analysed using One-way ANOVA and Tukey's multiple comparisons test, $*p < 0.05$. (D) BFI values under BHI and dBHI broths are shown for six genotypes containing more than 3 isolates. Each dot represents one isolate and horizontal bars the mean value. BRT results of cells inoculated at OD₆₀₀ of 0.002 were used for 37°C and 0.2 for 10°C (B-D).

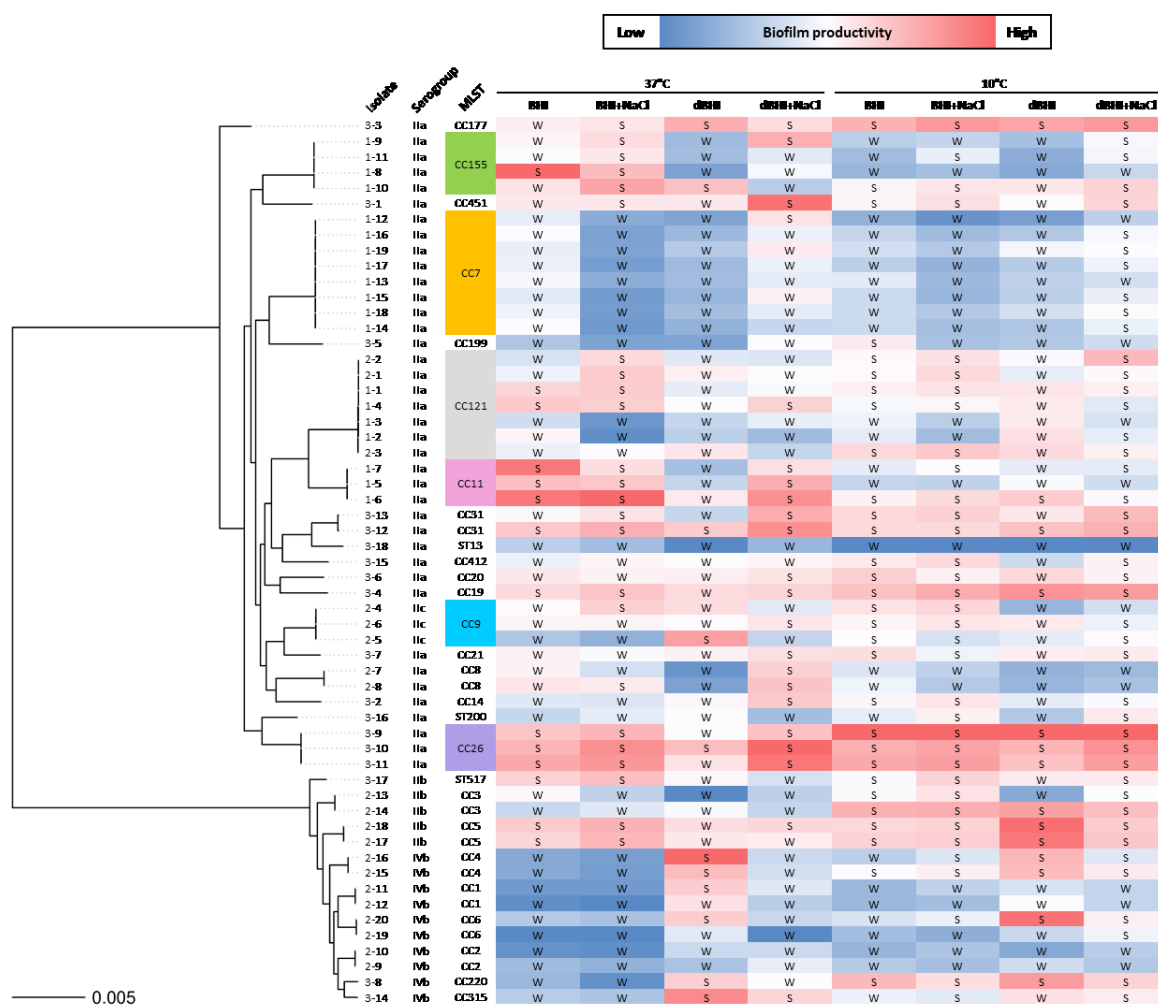
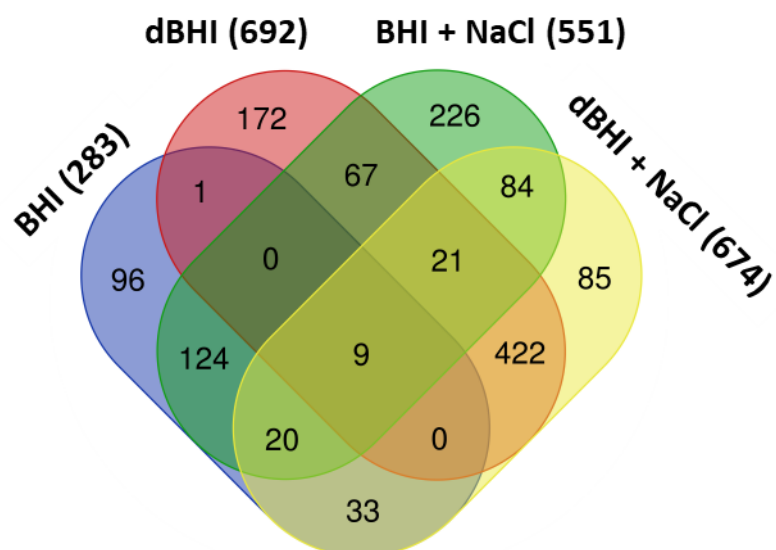
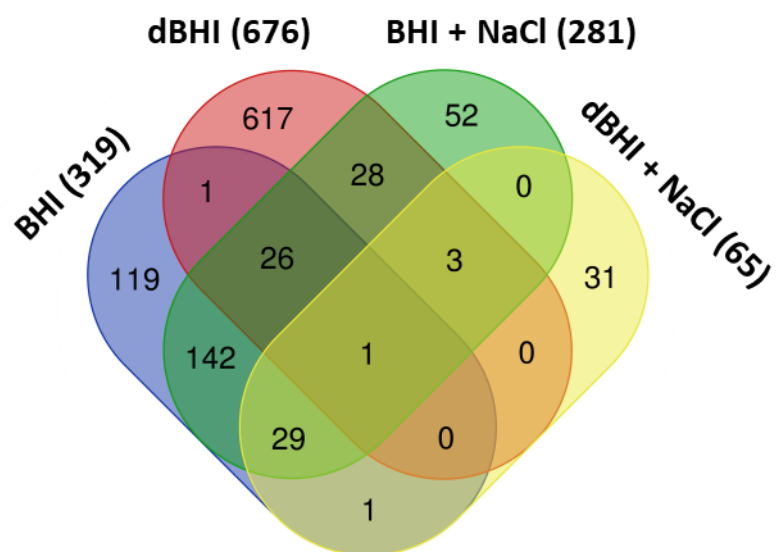


Figure 6. Phylogenetic tree of 57 *L. monocytogenes* isolates with biofilm phenotype. A colour scale is applied to MPA results within each growth condition to reflect relative biofilm productivity. The isolate names are shown as group numbers (1, persistent; 2, prevalent; 3, rare) hyphenated with isolate numbers. Binary transformation of the isolates based on MPA results is indicated as S, strong and W, weak biofilm former.

A**B**

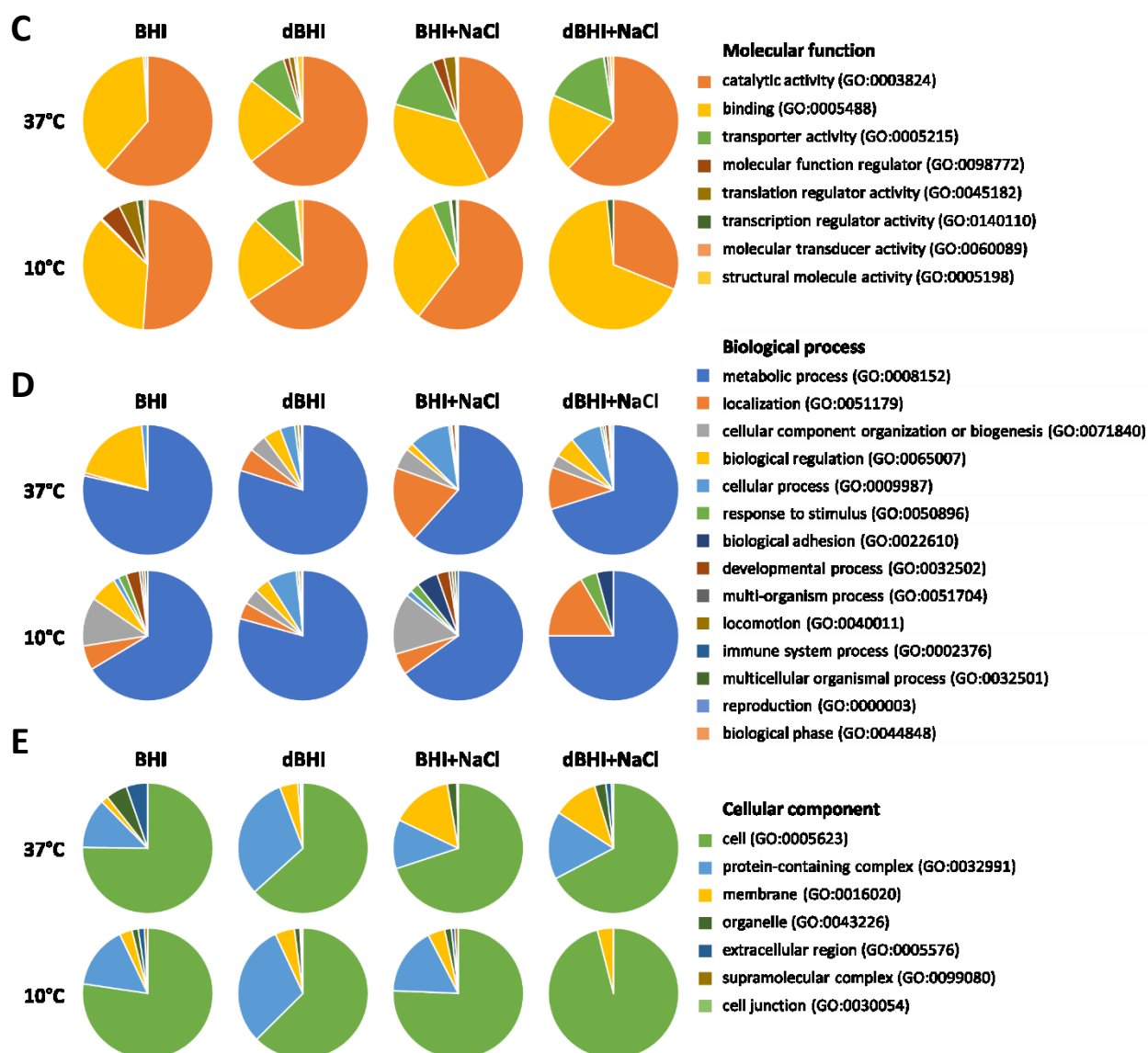


Figure 7. Genes identified by pan-GWAS and Gene Ontology (GO) analysis under different growth conditions. Venn diagrams show number of genes related to each condition at 37°C (A) and 10°C (B). PANTHER derived GO-slim categories for molecular function (C), biological process (D), and cellular component (E) are presented in pie charts.

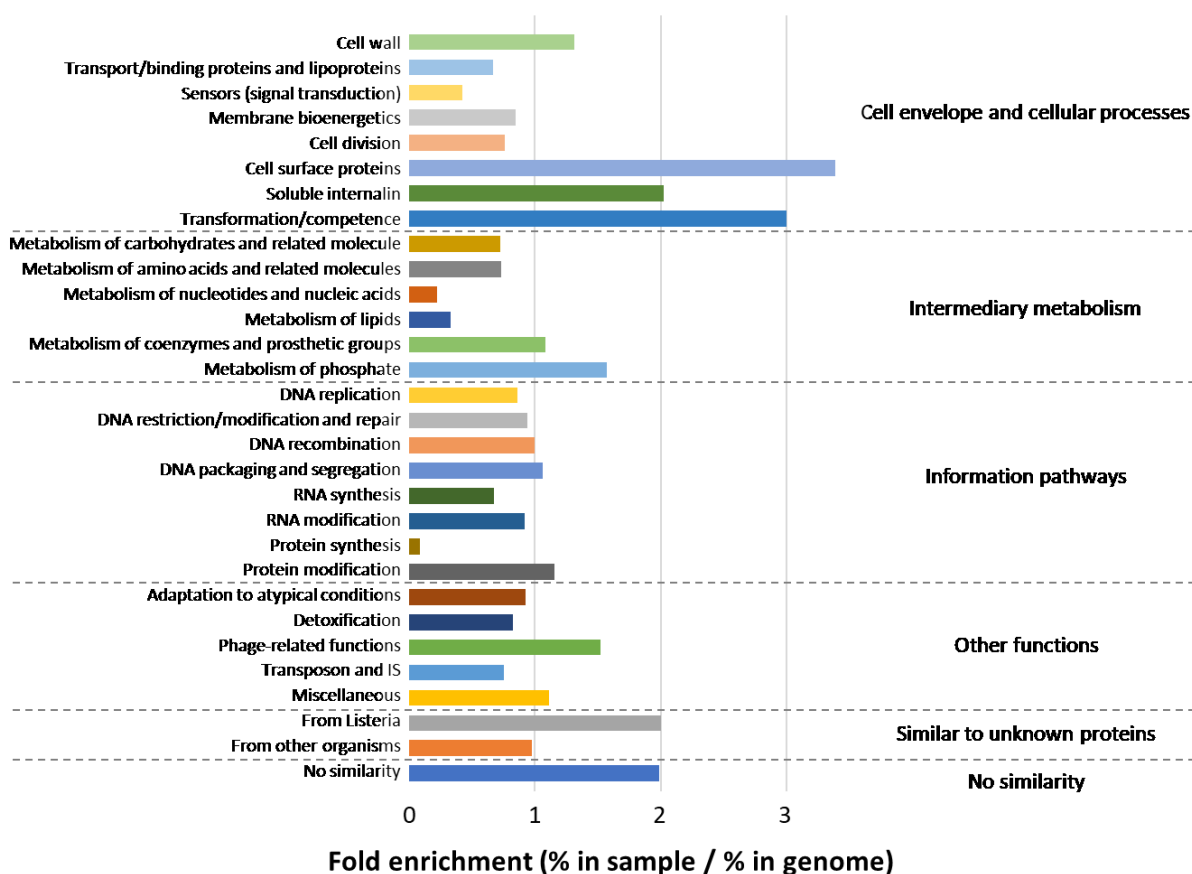


Figure 8. Functional enrichment analysis. Among the total list of genes identified by pan-GWAS, 2105 genes were annotated to *L. monocytogenes* EGDe and compared to the functional classification retrieved from ListiList (<http://genolist.pasteur.fr/ListiList/>). Fold enrichment of each functional category was performed as follow: Fold enrichment = % in annotated genes / % in whole genome of EGDe. Functional categories are presented in super- and subclass on the right and left of the figure, respectively.

Table 1. *L. monocytogenes* strains used in this study (Henri *et al.*, 2016).

Group	Subgroup†	Isolate	Origin	Detail	Serogroup‡	Lineage	MLST
Persistent	A	1	Food	Smoked-salmon	IIa	II	CC121
		2	Food	Catering plate	IIa	II	CC121
		3	FPE	Wipping of ground	IIa	II	CC121
		4	FPE	Wipping of food contact surface	IIa	II	CC121
	B	5	FPE	Food conveyor	IIa	II	CC11
		6	FPE	Wipping of chain	IIa	II	CC11
		7	FPE	chain bracket	IIa	II	CC11
	C	8	FPE	Sewer	IIa	II	CC155
		9	FPE	Before cleaning procedure	IIa	II	CC155
		10	FPE	Sewer on floor	IIa	II	CC155
		11	Food	Sandwich (ham and butter)	IIa	II	CC155
	D	12	FPE	Factory environment	IIa	II	CC7
		13	FPE	Factory environment	IIa	II	CC7
		14	FPE	Slicer machine before use	IIa	II	CC7
		15	FPE	Factory environment	IIa	II	CC7
		16	FPE	Factory environment	IIa	II	CC7
		17	FPE	Factory environment	IIa	II	CC7
		18	FPE	Factory environment	IIa	II	CC7
		19	FPE	Factory environment	IIa	II	CC7
Prevalent		1	Food	Sandwich (ham and cheese)	IIa	II	CC121
		2	Food	Sliced tomato	IIa	II	CC121
		3	Food	Ham	IIa	II	CC121
		4	Food	Cheese (Gouda)	IIc	II	CC9
		5	Food	Spinach	IIc	II	CC9
		6	Food	Sausage (Merguez)	IIc	II	CC9
		7	Food	Frozen onions	IIa	II	CC8
		8	Food	Sausage meat	IIa	II	CC8
		9	Food	Smoked-haddock	IVb	I	CC2
		10	Food	White chocolate mousse	IVb	I	CC2
		11	Food	Grilled vegetables	IVb	I	CC1
		12	Food	Goat milk	IVb	I	CC1
		13	Food	Vacuum-packed goose breast fillet	IIb	I	CC3
		14	Food	Pastrami	IIb	I	CC3
		15	FPE	Rag for surface wipping	IVb	I	CC4
		16	Food	Red pepper	IVb	I	CC4
		17	Food	Salad (Piedmontese)	IIb	I	CC5
		18	Food	Sausage meat with vegetable	IIb	I	CC5
		19	Food	Potatoes	IVb	I	CC6
		20	Food	Frozen tomatoes	IVb	I	CC6

Rare	1	Food	Cheese (Munster)	Ila	II	CC451
	2	Not Known	Not Known	Ila	II	CC14
	3	Food	Cheese	Ila	II	CC177
	4	Food	Salmon steak	Ila	II	CC19
	5	Food	Cheese	Ila	II	CC199
	6	Food	Cheese	Ila	II	CC20
	7	Food	Cheese (Cantal)	Ila	II	CC21
	8	Food	Salmon	IVb	I	CC220
	9	Food	Cheese	Ila	II	CC26
	10	Food	Cheese	Ila	II	CC26
	11	Food	Cheese	Ila	II	CC26
	12	Food	Salad (rice, corn, pepper and ham)	Ila	II	CC31
	13	FPE	Not known	Ila	II	CC31
	14	Food	Sandwich (smoked-salmon and mimolette cheese)	IVb	I	CC315
	15	Food	Cheese	Ila	II	CC412
	16	Food	Soy bean sprouts	Ila	II	ST200
	17	Food	Cheese (Morbier)	IIb	I	ST517
	18	Food	Not Known	Ila	II	ST13
	19	Food	Duck liver (foie gras)	Ila	II	ST13

† Presumed persistent clones

Table 2. Impact of growth condition on biofilm production quantified by MPA. Total biomasses of 58 strains produced under 8 conditions are shown in means + SD, rounded to two decimal places.

	BHI (373.5†)	BHI + NaCl (664.4)	dBHI (37.4)	dBHI + NaCl (328.2)
37°C	0.41 + 0.21	0.71 + 0.44	0.03 + 0.02	0.79 + 0.30
10°C	0.06 + 0.04	0.11 + 0.06	0.03 + 0.02	0.14 + 0.06

† Osmolarity is presented in parentheses, mOsm/L

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- ❖ **Supplementary materials for this article can be found at the end of the thesis.**

Chapter V

Exploring Listeria monocytogenes transcriptomes in correlation with divergence of lineages and virulence measured in Galleria mellonella

I Preface

L. monocytogenes is a causative agent for listeriosis which affects the most vulnerable groups such as pregnant women and senior population with a high fatality rate (EFSA and ECDC, 2018; Schuchat et al., 1991). However, apart from the host susceptibility, intraspecific variation in virulence potential has been evidenced which contributes largely to the development of *L. monocytogenes* infection. Accumulated epidemiological data clearly demonstrate the difference in virulence potential between major phylogenetic lineage I and II which reflect the difference observed at serological level: serotype 4b strains of lineage I are more virulent (Orsi et al., 2011; Ward et al., 2008). Recent studies further disclosed the variation in virulent potential among certain subtypes of strains, namely MLST-derived clonal complexes (Maury et al., 2016 and 2017). This distinct imbalance of virulence phenotype between *L. monocytogenes* isolates have led to ample findings of virulence factors and virulence-associated genetic contents (Glaser et al., 2001; Radoshevich and Cossart, 2018). Furthermore, complex regulatory networks modulate the genes expression upon transition from saprophytic to intracellular lifestyle and *vice versa* (Chapter I.5.4 Virulence factors and their regulation).

A few studies revealed differential basal transcript patterns of conserved genomic elements between pathogenic and non-pathogenic strains implying that the fine-tuning of the transcriptional network may play a significant role in determining virulence (Severino et al., 2007; Wurtzel et al., 2012; Couto et al., 2016; Biller et al., 2010). To investigate the whole transcriptome profiles of *L. monocytogenes* from various aspects, the current study included 33 isolates with diverse characteristics and their transcript levels under optimal *in vitro* culture condition were analysed. Firstly, we described in detail the analytical approaches applied to

refine the datasets in order to remove experimental noise and improve statistical power. The results showed that basal transcript levels were highly heterogeneous but arranged to some extent by transcriptional factors such as σB , PrfA, and CodY which play important roles in virulence regulation. Secondly, using the refined large transcriptomes, we performed correlation analyses with respect to phylogenetic division, virulence-associated genotypes as well as *in vivo* virulence level measured in *G. mellonella*. The results revealed that transcript patterns support the evolutionary divergence of the isolates as well as the epidemiological evidence of virulence potential. Furthermore, the study was a pioneer in that it attempted to correlate the basal transcriptome profiles with large-scale *in vivo* study. We hope that this study will serve as guidance for future investigations that will integrate more concrete epidemiological and experimental data with other omics approaches in order to unveil the *L. monocytogenes* physiology including virulence.

II Article

Exploring *Listeria monocytogenes* Transcriptomes in Correlation with Divergence of Lineages and Virulence Measured in *Galleria mellonella*

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Exploring *Listeria monocytogenes* transcriptomes in correlation with divergence of lineages and virulence measured in *Galleria mellonella*

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Abstract

As for many opportunistic pathogens, virulence potential of *Listeria monocytogenes* has been reported to be highly heterogeneous between isolates and correlated, to some extent, with phylogeny and gene repertoires. In sharp contrast with copious data on intraspecies genome diversity, little is known about transcriptome diversity despite the role of complex genetic regulations in pathogenicity. The current study employed RNA sequencing to characterize the transcriptome profiles of 33 isolates under an optimal *in vitro* growth condition. Transcript levels of conserved single copy genes were comprehensively explored from several perspectives including phylogeny, in silico virulence category based on epidemiological MLST data, and virulence phenotype measured in *Galleria mellonella*. Comparison of baseline transcriptomes between isolates proved intrinsically more complex than genome comparison because of inherent plasticity of gene expression in response to the environmental conditions. We show that the relevance of correlation analyses and their statistical power can be enhanced by using Principal Component Analysis to remove a first level of irrelevant, highly coordinated changes linked to growth phase. Our results highlight the contribution of transcription factors with key roles in virulence to the diversity of transcriptomes. Divergence

in the basal transcript levels of a substantial fraction of the transcriptome was observed between lineage I and II echoing previously reported epidemiological differences. Correlation analysis with *in vivo* virulence identified numerous sugar metabolism-related genes suggesting pathways that might play roles in the onset of infection in *G. mellonella*.

Importance

Listeria monocytogenes is a multifaceted bacterium able to proliferate in a wide range of environments from soil to mammalian host cells. The accumulated genomic data underscores the contribution of intraspecies variation in gene repertoire to differential adaptation strategies between strains, including infection and stress resistance. It seems very likely that the fine-tuning of the transcriptional regulatory network is also a key component of the phenotypic diversity, albeit more difficult to investigate than genome content. Some studies reported incongruity in basal transcriptome between isolates suggesting a putative relationship with phenotypes, but small isolate numbers hampered proper correlation analyses with respect to their characteristics. The present study is the embodiment of the promising approach that consists in analysing correlations between transcriptomes and various isolate characteristics. Statistically significant correlations were found with phylogenetic groups, epidemiological evidence of virulence potential, and virulence in *Galleria mellonella* larvae used as an *in vivo* model.

1. Introduction

The genus *Listeria* currently groups 20 species among which *L. monocytogenes* and *L. ivanovii* are considered pathogenic (Leclercq et al., 2019; Orsi and Wiedmann, 2016). *L. monocytogenes* is found in a wide range of habitats including soil, vegetation, water, and food processing environments and as a facultative intracellular pathogen in mammal and non-mammal hosts (Sauders et al., 2012; Vivant et al., 2013). This bacterium also stands as an important model to study host-pathogen interactions (Radoshevich and Cossart, 2018). In humans, *L. monocytogenes* is the causative agent of listeriosis, a foodborne disease resulting from ingestion of contaminated food products, especially ready-to-eat foods (Buchanan et al., 2017). Symptoms of listeriosis range from febrile gastroenteritis, if any, in healthy people to meningitis, meningoencephalitis, and septicaemia with high fatality rate in immunocompromised individuals. In pregnant women, perinatal infections can lead to miscarriage, stillbirth or premature birth (Charlier et al., 2017).

Isolates of *L. monocytogenes* are grouped in four phylogenetic lineages. Most isolates belong to lineage I (serotypes 4b, 1/2b, 3b, 4d, 4e, and 7) and lineage II (serotypes 1/2a, 1/2c, 3a and 3c) while lineages III and IV (serotypes 4a, 4c, and 4b) appear to be smaller groups. Overrepresentation of serotypes 1/2a, 1/2b, 1/2c, and 4b is observed from food and clinical isolates among which serotype 4b accounts for the majority of human listeriosis (Orsi et al., 2011; Ward et al., 2008). Additionally, Multilocus sequence typing (MLST) unravelled clonal structure (Ragon et al., 2008) and uneven distribution of clonal complexes (CCs) between clinical and food isolates in which hyper- and hypovirulent clones were further identified (Maury et al., 2016; Painset et al., 2019). The onset of infection relies on expression of virulence factors (Glaser et al., 2001), many of which are clustered in the *Listeria* pathogenicity islands (LPIs), whose distribution is phylogenetically distinctive (Clayton et al., 2014; Maury et al., 2016; Vázquez-Boland et al., 2001).

In parallel to genome diversity studies, transcriptome profiling evidenced global transcriptional reshaping during infection and a large set of virulence-associated genes were identified (Camejo et al., 2009; Toledo-Arana et al., 2009). A complex network of transcription factors tightly coordinate virulence-related genes expression. PrfA, the master activator of virulence factors, the alternative sigma factor B (σ^B), the major regulator of stress responses, AgrA, the response regulator of the Agr system, and several non-coding RNAs are part of this regulatory network (Autret et al., 2003; Kazmierczak et al., 2003; Lebreton and Cossart, 2016; Nadon et al., 2002).

Importantly, several studies reported differential expression of conserved genes between pathogenic versus non-pathogenic isolates (Wurtzel et al., 2012; Severino et al., 2007; Couto

et al., 2016; Biller et al., 2010) which could reflect the contribution of the regulatory network to fine-tuning gene expression of virulent isolates straight after ingestion and in the gastrointestinal tract, therefore maximising their fitness in the host system (Gahan and Hill, 2014). However, as most studies were restricted to a limited number of strains, the weight of intraspecific diversity tended thus to be overlooked. To overcome this limitation, a collection of 91 phylogenetically divergent isolates from diverse origins were processed in *G. mellonella* virulence assay in order to compare their virulence potential. A subset of 33 isolates was then analysed by high-throughput RNA sequencing (RNA-seq) to explore transcriptome heterogeneity according to phylogenetic distance and virulence potential.

2. Material and Methods

2.1. Isolates collection and culture condition

A collection of 91 *L. monocytogenes* isolates from various origins, serogroups and genotypes were used in the current study (Table 1) (Henri et al., 2016; Olier et al., 2003). Each experiment was performed with freshly prepared cultures from a stock kept at -80°C in Brain Heart Infusion (BHI) broth (AES laboratoire, France) with 8.5% glycerol (Sigma-Aldrich, France). After overnight incubation on BHI agar (AES laboratoire, France) at 37°C, few colonies were suspended into BHI broth and grown overnight at 37°C. Consecutive subculture (16 h, 37°C) was performed to prepare stationary phase cells (mother culture) for infection. Cells were centrifuged (5,000 g, 5 min, room temperature) and pellets were washed twice with PBS. Washed cells were suspended in PBS and calibrated to obtain an optical density at 600 nm of 0.1. Part of the suspension was used for enumeration by serial dilutions in PBS and plating onto BHI agar to retrospectively determine the bacterial counts used for injection. Colony forming units (CFU) were counted after overnight incubation at 37°C.

2.2 Whole genome sequencing and Phylogenetic analysis

The genome of 15 isolates had been sequenced in a previous study (Henri et al., 2016). The paired-end reads of the strains used in the study are available under the ENA bio-projects as follows; PRJEB15592 (<https://www.ebi.ac.uk/ena/data/view/PRJEB15592>) and PRJEB32254 (<http://www.ebi.ac.uk/ena/data/view/PRJEB32254>).

We sequenced additional isolates for phylogenetic analysis. Genomic DNA was isolated from exponential cells harvested by centrifugation at 5,000g for 10 mins. Cells were washed twice with TE buffer (10 mM Tris-HCl, pH 7.5, 1 mM EDTA in nuclease free water). Pelleted cells were resuspended in TE buffer and cell walls were disrupted by sonication using Bioruptor® (Diagenode). The cells were sonicated for 56 cycles of 30 s on and 30 s off at low frequency at 4°C with several spin-downs at intervals. Fragmented DNA was purified using Nucleospin® PCR cleanup kit (Macherey-Nagel) and its quality and size were confirmed on Labchip GX II bioanalyzer. End repair was performed followed by ligation of adapters (Illumina) and the final product was purified using MagSi-NGSPrep Plus (AmsBio). Concentration of each library was measured using Qubit™ dsDNA HS Assay (Thermo Fisher Scientific) and pooled libraries were subjected to additional purification using MagSi-NGSPrep Plus. Sequencing was carried out on the Illumina NextSeq 500 platform (single-end, 1 X 75 bp per read). After quality control and trimming, *de novo* gene assembly was performed using SPAdes (Bankevich et al., 2012) for each genome library.

The 2,867 CDSs annotated in EGDe (GenBank accession No. NC_003210, length 2,944,528 bp) were mapped on the 33 assembled genomes to retrieve their pattern of presence/absence as well as all their allelic variants. For this purpose, we used “tblastn” version 2.6.0+ with options ‘-task tblastn -evalue 1e-10 -seg no’ (Camacho et al., 2009) and cut-offs corresponding to 80% identity at the amino-acid sequence and minimum coverage of 80% of the query. This procedure identified a total of 2,456 conserved single copy genes whose amino-acid sequences were subjected to separate multiple sequence alignments using “muscle” version v3.8.31 with default parameters (Edgar, 2004). Custom Perl scripts were used for conversion to nucleotide sequences, concatenation, and gap removing. The resulting alignment of 2,241,553 bp containing 167,253 SNPs served for phylogenetic tree reconstruction using “Phyml” version 20120412 with default parameters (Guindon and Gascuel, 2003).

2.3. *Galleria mellonella* injection and virulence assay

G. mellonella larvae in their final instar stage were used (Sud Est Appats Sarl, Queige, France). Each larva was injected with 10 µl (app. 1.6×10^6 CFU) directly to the larval hemocoel via the last left proleg using ultra-fine (29 gauge) needle insulin syringes. Ten larvae were injected per isolate. After injection, larvae were incubated at 37°C and monitored for survival at daily intervals post-infection up to day 5. Larvae showing no movement in response to external stimuli such as shaking of the Petri dish and touching with a pipette tip were considered dead and the time necessary to kill more than or equal to 50% of larvae (LT50) was recorded. Every trial included 10 larvae injected with PBS as negative control in order to confirm their viability. Any experiment which resulted in more than 20% mortality in control larvae were excluded. Assays were repeated at least three times.

2.4. RNA extraction and DNase I treatment

Mother cultures (see above) were inoculated into fresh BHI broth and grown at 37°C for 5-6 h to reach exponential phase. RNAProtect (Qiagen) was immediately added and cultures were vortexed followed by incubation at room temperature for 5 min. The mixtures were pelleted by centrifugation (5,000g, 10 min, room temperature) and pellets were suspended in 5M Guanidine thiocyanate (Roth) lysis buffer with 10 µl/ml 2-Mercaptoethanol (Sigma-Aldrich). To lyse cell walls, 0.5mm glass beads (Roth) were added and bacterial cells were homogenized using Tissulyser (Qiagen) at a frequency of 30^{-1} for 6 min. After centrifugation (16,000g, 30 s, room temperature) supernatants were collected and RNA was purified using column-based RNA Clean & Concentrator-5 kit (Zymo Research). Quality of extracted RNA was assessed using Labchip GX II bioanalyzer (Perkin Elmer). To remove DNA contamination, total RNA was incubated with Baseline-Zero DNase (Epicentre) in the presence of RiboLock RNase inhibitor (40U/µl) (Thermo Fisher Scientific) for 30 min at 37°C followed by purification using RNA Clean

& Concentrator-5 kit. RNA concentration was measured using fluorescence-based Qubit™ RNA HS Assay (Thermo Fisher Scientific).

2.5. Library preparation and sequencing

To enrich mRNA and remove ribosomal RNA (rRNA), total RNA was treated with Ribo-Zero rRNA removal kit (Illumina). Briefly, beads were washed twice and hybridized with probes at 68°C for 10 min. Five hundred ng of total RNA was added to the mixture and incubated at RT and 50°C for 5 min each. rRNA bound to the beads was separated from mRNA using a magnetic stand. Enriched mRNA was then purified with RNA Clean & Concentrator-5 kit and rRNA depletion was confirmed on Labchip GX II bioanalyzer (Perkin Elmer).

Preparation of cDNA fragment libraries was performed using the NEBNext® Ultra™ II Directional RNA Library Prep Kit for Illumina® (Illumina) with slight modifications. Briefly, the enriched mRNA was fragmented for 15 min at 94°C and reverse transcribed to synthesize the first-strand cDNA followed by second strand cDNA synthesis. Double-stranded cDNA (ds cDNA) was purified using NucleoMag (Macherey nagel) SPRI selection. End repair was performed on the ds cDNA library followed by ligation of adapters. High fidelity PCR was performed using KAPA Hifi polymerase (Kapa Biosystems) and NEBNext Multiplex Oligos for Illumina (Dual Index Primers) to selectively enrich library fragments. The PCR products were purified twice using NucleoMag SPRI beads and the quality of the final library was assessed on Labchip GX II bioanalyzer. Indexed and purified libraries were sequenced on Illumina NextSeq 500 platform (paired-end, 2 X 75 bp per read).

2.6. Exploratory transcriptomic analysis

RNA-seq was performed in duplicate on a collection of 33 isolates with independently grown bacterial cells. Sequencing quality was assessed using FastQC, and Illumina adapter sequences and some low-quality base pairs were removed using “cutadapt” version 1.9 (Martin, 2011). Reads were further trimmed in 3’ using “sickle” program version 1.33 with option -x and default values for all other parameters (implying Phred quality cut-off of 20). The cleaned reads were then mapped against the whole repertoire of allelic variants for the 2,867 CDSs annotated in EGDe found in the 33 genomes using “bowtie2” version 2.2.6 (Langmead and Salzberg, 2012) with options ‘-N 1 -L 16 -R 4’ and converted to bam format using “samtools” version 1.9 (Li et al., 2009). Read counts on each allelic variant were obtained using “htseq-count” version 0.10.0 (Anders et al., 2015) with options ‘-s reverse --nonunique all -a 1’. Read counts associated with all allelic variants were summed up to obtain a single read count per gene per sample. Importantly, “bowtie2” as used here mapped each read on a single allelic variant ensuring that each read could not be counted more than once and “htseq-count”

options allowed to retrieve the reads that mapped equally well on several sequences as expected given the redundancy of the repertoire of allelic variants.

All subsequent analyses and graphical representations were conducted with R. Read counts were normalized with the function “estimateSizeFactors” provided in the R package “DESeq2” (Love et al., 2014) version 1.20.0 based on the behaviour of the 2,456 conserved single copy genes (option ‘controlGenes’) and expressed as rpkm (reads per kilo base per million mapped reads) using as library size the median number of reads aligned on conserved single copy genes. Expression levels were converted to log₂-scale after adding a pseudo-count of 10 which corresponded approximately to the 10% quantile of rpkm values obtained for the conserved single copy genes. The RNA-seq datasets generated for this study can be found in the Gene Expression Omnibus GSE129537.

Principal Component Analysis (PCA) used function “prcomp” in R package “stats” on centered but non-scaled variables corresponding to the expression values in log₂-scale, i.e. log₂(rpkm+10). Hierarchical clustering analyses were performed with function “hclust” in R package “stats” using average link aggregation method based on Pearson distance (1-r where r is the pairwise correlation coefficient). Pearson and Spearman’s rank correlation coefficients (denoted r and ρ, respectively) as well as the p-values associated to the PCs presented in Fig. 5B and C were obtained with function “cor” in R. Heatmaps were drawn with function “heatmap.2” provided by R package “gplots”. Quantiles corresponding to the values of ρ under the null hypothesis of no statistical association between transcript levels and isolate characteristics (lineage, Maury’s classification of genotypes, and LT50) were obtained by 25,000 random permutations of isolate labels that preserved the correlation between biological replicates. Quantiles were converted to p-values of a two-sided test designed to reject the null hypothesis of random association by applying the transformation $1-2|x-0.5|$. These p-values served to estimate false discovery rates (q-values) using R function “fdrtool” version 1.2.15 (Strimmer, 2008b).

The functional classification was downloaded from ListiList (<http://genolist.pasteur.fr/ListiList/>) which consists of 43 functional categories including 3 non-informative classes (unknown protein functions) for genes found in *L. monocytogenes* EGDe.

3.Result

3.1. Intraspecific virulence phenotype monitored in the *G. mellonella* virulence assay

The virulence of a collection of 91 isolates was assessed using *G. mellonella* virulence assay. To verify the relevance of the protocol, the bacterial loads used for assays of 63 isolates were compared. CFUs ranged from a minimum of 0.70×10^6 to a maximum of 2.37×10^6 with mean value 1.53×10^6 and standard deviation 0.35×10^6 . Grubb's test identified no outlier and D'Agostino-Pearson omnibus normality test did not reject normality ($k^2=0.711$, $p = 0.701$) suggesting that the number of injected bacteria was comparable between isolates. Survival of larvae post-infection was monitored daily and the time (day) needed to kill more than 50% of the insects (LT50) was calculated. All isolates were capable of killing larvae but their observed LT50 varied greatly (Fig. 1). While 1 isolate killed more than 50% of larvae within the first 24 h post-infection (LT50 of 1), 8 isolates did not reach 50% death by 5 days post-infection (LT50 > 5, encoded as 6). A majority of isolates (72.4%) showed LT50s of 2 to 3 days (37 and 28 isolates, respectively). The rest showed LT50s of 4 and 5 days (8 and 9 isolates, respectively).

The 89 isolates with known lineage were grouped according to their LT50 (Table 1). No significance (Fisher's exact test, $p = 0.93$) was observed implying no association between lineage and LT50 measured in *G. mellonella*. Similarly, no relation was found ($p = 0.83$) between LT50 values and epidemiological backgrounds (clinical, faecal or food-related samples).

A sub-collection of 33 isolates was selected to explore the diversity of transcriptomes of *L. monocytogenes* with respect to three isolates' classifications: lineage II versus lineage I, LT50 measured in *G. mellonella*, and CC-based virulence level. The latter, hereafter referred to as Maury's classification, establishes 3 CC-based virulence groups (hypo-virulent, intermediate or unknown, and hyper-virulent) based on a comprehensive analysis of population clonal structure in relation to isolates' origin and further *in vivo* assay confirmation (Maury et al, 2016). Figure 2 shows the 3 classifications superimposed onto a phylogenetic tree reconstructed after complete genome comparison of the 33 isolates. This representation highlights the tight connection between Maury's classification and lineage since all genotypes of hypervirulence (CC1, CC2, CC4 and CC6) were closely distributed in lineage I while those of hypovirulence (CC9 and CC121) were grouped in lineage II.

3.2. Exploratory analysis of RNA expression

3.2.1. Global variations in transcript expression and PCA analysis

A total of 66 transcriptome profiles were obtained from duplicated exponential cultures of 33 isolates grown at 37°C. Transcript levels of 2,456 conserved single copy genes demonstrated large variations across samples which delineated groups of genes with highly correlated expression profiles (left dendrogram in Fig. 3A). Intriguingly, transcriptome profiles were not always consistent between duplicates suggesting sources of variability that may complicate comparisons between isolates. To further investigate the patterns of variations, PCA was applied to project the 66 transcriptomes, each characterized by the levels of 2,456 transcripts, onto spaces of smaller dimensions. It revealed that coordinates of the samples on a single axis (the first of the PCA, hereafter referred to as PC1) was able to explain 48.4% of the total variance. Figure 3 shows that PC1 identified the existence of a continuum of transcriptome profiles that was not directly connected to the isolates' characteristics.

To understand the source of this heterogeneity, the genes which contributed the most to PC1 were checked for their functional category. Loading values for PC1 were calculated for each gene and 100 genes positioned at both extreme positive and negative ends of PC1 were examined for the distribution of functional categories (Fig. 4). Functions involved in exponential growth (e.g. 'Cell division', 'RNA synthesis' and 'Protein synthesis') were negatively linked with position on PC1. On the other hand, functions related to the transition to stationary phase were positively linked with position on PC1 (e.g. 'Intermediary metabolism', 'Adaptation to atypical conditions' and 'Detoxification'). In sum, PC1 represented transcriptome differences caused by transition from exponential to early stationary phase.

PC2 explained 11.2% of the total variance and other axes explained less than 10% fraction of variance. In total, 89.2% of variance were explained by 15 axes (Fig. 5A). Correlation analyses were performed to identify the contextual variables captured by the different PCs underlying heterogeneity. The coordinates of the two biological replicates (BR1 and BR2) were more consistent for some PCs than for others as reflected in the variation of the Pearson correlation coefficient (r) computed between the vectors of 33 coordinates available for each biological replicate (Fig. 5B). In particular, coordinates on PC2 exhibited little correlation between the two biological replicates ($r=0.17$) whereas the highest level of correlation was reached for PC3 ($r=0.88$). Computation of Spearman's rank correlation coefficient (ρ) served as a generic approach to assess relationships between coordinates on each PC and ordinal (LT50, Maury's classification) or binary (lineage, BR) covariates (Fig. 5C). Among the PCs, coordinates on PC3 and PC5 revealed the highest correlations with *in vivo* virulence (LT50) ($\rho=0.26$ and $\rho=0.33$, respectively). Concomitantly, Maury's classification of the genotypes exhibited positive correlations with PC1 ($\rho=0.33$) and PC5 ($\rho=0.39$), reflecting a trend for higher coordinates on these axes for samples corresponding to hypervirulent genotypes, and negative correlation

with PC4 ($\rho=-0.47$). The exact opposite pattern was observed with respect to the division between lineages I and II: PC1 ($\rho=-0.31$) and PC5 ($\rho=-0.76$) exhibited negative correlations reflecting a trend for lower coordinates for samples corresponding to lineage II, whereas PC4 exhibited positive correlation ($\rho=0.46$). This result was expected because of the aforementioned exclusive distribution of hyper- and hypovirulence genotypes in lineage I and II, respectively. Furthermore, in conjunction with the lower correlation between the coordinates of two biological replicates on PC2, it showed that PC2 tended to separate the two biological replicates ($\rho=0.65$), with a trend for higher coordinates for samples corresponding to the BR2.

Dissimilarity between BRs was further investigated by analysing the new transcriptome datasets generated by removing the variations captured by preceding PCs (Fig. 5D). The result revealed that jointly filtering out the variations captured by PC1 (reflecting transition of growth phases) and by PC2 (reflecting a difference between the two BRs) globally decreased the distance between the two transcriptome profiles (BRs) available for each isolate.

3.2.2. Construction of a new dataset with improved statistical power

Because large variations in transcriptome profiles related to transition of growth phase and systematic differences between BRs can mask more subtle variations associated with the characteristics of the isolates, a refined transcriptome dataset was generated by filtering out variations captured by PC1 and PC2 from the original dataset. Technically, this dataset consisted in the residuals of the PCA projection on the subspace formed by PC1 and PC2. This processing step increased reproducibility of the transcriptome profiles between biological replicates (Fig. 6A) as predicted by the Pearson correlation analysis (Fig. 5C). We also confirmed that it increased significantly the statistical power of some correlation analyses between transcript levels of individual genes and phenotypic values such as LT50 (Fig. 7). Namely, we examined the distribution of Spearman's rank correlation between each individual gene (i) and each of the three isolates characteristics (LT50, Maury's classification, and lineage number), denoted by c . This was done in terms of quantiles corresponding to the values of $\rho_{i,c}$ under the null hypothesis of no statistical association between transcript levels and covariate values such that departure from the uniform distribution is the landmark of the presence of statistically significant associations and can be directly used to estimate false discovery rates as summarized in q-values (Strimmer, 2008a). While no statistical association between gene and LT50 was found with the original data (lowest q-value 0.18; Supplementary Table 4), 25 genes were attributed q-values below 0.10 based on the new dataset. Not surprisingly given the correlation between PC1 (growth phase) and the two other characteristics (Maury's classification of genotypes and lineage number), filtering out the

variations captured by PC1 and PC2 slightly decreased the number of statistically associations. However, we reasoned that statistical association between growth phase and Maury's classification (more advanced for hypervirulent genotypes) and lineage (less advanced for lineage II) could still be considered a confounding factor when pinpointing out associations between them and individual genes which also justifies to work with the new dataset. In sum, removing variations captured by PC1 and PC2 reduced protocol-driven noise and thereby increased statistical significance and biological relevance of correlations.

3.2.3. Comparison to known regulons

Genes were clustered according to the similarity in expression patterns based on the refined dataset (left dendrogram in Fig. 6A). Clusters of highly correlated genes (defined by average pairwise Pearson correlation greater than 0.6) were numbered according to their sizes. Summarizing for each gene the level of variability by the maximum log₂-fold change between any pair of samples pinpointed 12 main clusters of genes with highly variable transcription levels (Fig 6B and Supplementary Table 4). Each of these clusters, contained at least 8 genes, half of these genes with maximum log₂-fold change higher than 4. Taken together, they encompassed 11.5% (283 genes) of the core genome: 101 genes in cluster 1; 48 genes in cluster 3, 26 genes in cluster 4, and from 17 to 8 genes in the remaining clusters. The gene-content of these 12 clusters were investigated in details since they reflected the main components of transcriptome plasticity. Clustered genes were compared to previous knowledge of the regulons of 32 transcription factors in order to scrutinize the regulatory networks. Regulons of 8 transcription factors including 4 Sigma factors (Chaturongakul et al., 2011; Palmer et al., 2011), CtsR (Hu et al., 2007), CodY (Bennett et al., 2007), VirR (Mandin et al., 2005), and PrfA (Scortti et al., 2007) were collected from the literature and regulons of the 24 phylogenetically conserved transcription factors were retrieved from RegPrecise database (34, http://regprecise.lbl.gov/RegPrecise/genome.jsp?genome_id=210). Potentially σ^B regulated genes accounted for 86% of cluster 1 and 88% of cluster 4 which is consistent with the proximity of the two clusters in the hierarchical clustering tree (left dendrogram in Fig. 6A). At distance in the tree, cluster 30 and 45 also included 67% and 50% of genes previously linked to σ^B . In sum, 8 clusters contained 41% (130 genes) of the core genome genes previously reported as probable members of the σ^B regulon. Clusters 14, 45, 3, and 30 were dispersed throughout the tree and included 54%, 50%, 35%, and 22% of genes previously reported as regulated by CodY, respectively. Altogether, they accounted for 42% (30 genes) of the genes previously associated with CodY regulon. In cluster 26, 70% of the genes were probable members of the ArgR regulon which accounted for the whole list of genes linked to this transcription factor. Concurrently, 6 core PrfA virulon (*plcB*, *actA*, *mpl*, *hly*, *pclA*, and *inlC*) accounted for 75% of the genes of cluster 41 (Scortti et al., 2007). Log₂ transcript levels of

these core PrfA virulon genes are represented in Supplementary Figure 1. In total, taking into account other PrfA-regulated genes sparsely located in clusters 1, 4, and 7, 40% of the genes linked to PrfA were detected after clustering. Finally, 52 genes previously identified as virulence-related (Wurtzel et al., 2012) were highlighted in the heatmap (Fig. 6A). Their dispersed position implies heterogeneous expression patterns among samples.

3.2.4. Correlation with phylogeny and virulence potential based on genotypes and phenotypes

The refined dataset was further exploited to delineate set of genes whose transcript levels was correlated with lineage, Maury's classification, and experimental virulence phenotype (LT50). The number of genes whose expression levels were highly correlated ($|p| \geq 0.4$) with each of these characteristics was computed (Table 2).

A total of 473 genes and 222 genes correlated to lineage and Maury's classification, respectively (Supplementary Table 2 and 3). Among the 111 genes positively correlated with Maury's classification (higher transcript levels in more virulent CCs), 77% were overlapped in the set of 261 genes negatively correlated with lineages (higher transcript levels in lineage I). Similarly, 80% of the 111 genes negatively correlated with Maury's classification were present in the set of 212 genes positively correlated with lineage. As mentioned earlier, this high congruency is ascribable to the exclusive distribution of the hyper- and hypovirulent genotypes in lineages I and II, respectively. Only 7 and 3 of the genes known to be linked with virulence in *L. monocytogenes* (Wurtzel et al., 2012) were identified in the sets of lineage- and Maury's classification-associated genes, respectively. Heatmap representation of the transcription levels of the set of genes that were the most correlated to lineage and Maury's classification were able to discriminate the two lineages and were able to group together the isolates with similar virulence potential according to Maury's classification (Fig. 8A).

The sets of lineage- and Maury's classification-correlated genes were further examined in light of the functional categories (Fig. 9). Due to the overlap between lineage and Maury's classification of genotypes, the two correlation analyses tended to reveal similar enrichment patterns with respect to functional categories. Transcripts showing increased expression in lineage II ($p \geq 0.4$) were enriched (more than 1-fold enrichment) in functional categories 'Transformation/competence' and 'DNA recombination'. Categories 'Sensors (signal transduction)', 'Metabolism of phosphate' and 'Detoxification' exhibited the same trend, albeit to a lesser extent. In contrast, transcripts showing increased expression in lineage I ($p \leq -0.4$) were enriched in functional categories 'Soluble internalin' and 'RNA modification'. Of note, the functional categories 'Protein modification' and 'Protein folding' were more than 1-fold enriched in both analyses, however, they were more highly enriched in genes with increased expression in lineage I. Additionally, Hypervirulence ($p \geq 0.4$) was correlated to

'Protein secretion', 'Cell division', 'Metabolism of lipids', 'Metabolism of coenzymes and prosthetic groups', 'Metabolism of phosphate', 'DNA packaging and segregation', and 'Similar to unknown proteins from *Listeria*'. Categories 'Metabolism of amino acids and related molecules' and 'Protein folding' were associated with hypovirulence ($p \leq -0.4$).

3.2.5. Transcripts whose expressions are correlated with virulence level measured in *G. mellonella*

Because higher LT50 means lower virulence, negative p indicates positive correlation between *in vivo* virulence and transcript level. A total of 56 genes were identified ($|p| \geq 0.4$) of which 39 with $p \geq 0.4$ and 17 with $p \leq -0.4$ (Fig. 8B). None of these genes (Table 3) were previously reported as directly virulence-associated (Wurtzel et al., 2012). Total 14 genes belonged to 'Cell envelope and cellular processes', 11 to 'Intermediary metabolism', 3 genes in 'Information pathways', 2 genes in 'Other functions'. For 26 genes of unknown function ('Similar to unknown proteins', and 'No similarity or information not available') online HHpred suite was used to search for possibly remote homology to known protein structures (Zimmermann et al., 2018). Diverse functions were predicted such as carbohydrate transport and metabolism (*Imo0635*, *Imo0879*, and *Imo2832*), defence mechanisms (*Imo0375* and *Imo1963*), lipid metabolism (*Imo1862* and *Imo1863*), histidine triad protein (*Imo2216*), energy production (*Imo1050*), translation and posttranslational modification (*Imo2078* and *Imo2127*), and permease (*Imo0831*). In addition, the 56 genes were compared to the list of virulence genes from PATRIC database (<https://www.patricbrc.org/>) and two potential virulence factors: *Imo0763*, a serine/threonine phosphatases (Schauer et al., 2010) and *Imo0540*, a penicillin-binding protein (Guinane et al., 2006) were identified. The heatmap representation (Fig. 8B) roughly split the samples conforming to the PCA result which highlighted that lineages and LT50 were both correlated to PC5 (Fig. 5C).

Among the 56 genes, 3 operon structures were identified based on the published operon map (17). Full operons 064 (*Imo0372*, *Imo0373*, and *Imo0374*) and 224 (*Imo1389*, *Imo1390*, and *Imo1391*) as well as 2 out of 6 genes in operon 330 (*Imo1858* to *Imo1863*) were found in the list. Moreover, among genes previously not identified in operon structure, 4 sets of genes at close loci displayed similar expression patterns across samples: *Imo0034* and *Imo0035*; *Imo1147* and *Imo1149*; *Imo2567* and *Imo2568*; *Imo2836*, *Imo2838* and *Imo2839*.

4. Discussion

To date, all *L. monocytogenes* isolates are considered to be equally virulent by regulatory agencies, which, however, is contradicted by accumulating evidence (Fritsch et al., 2018; Maury et al., 2016). Virulence of *L. monocytogenes* is determined by its capacity to circumvent innate host barriers such as microbiota (Rahman et al., 2018; Zhang et al., 2017) and its ability to hijack host cell functions during its intracellular life cycle (Cossart, 2011; Radosheвич and Cossart, 2018). Numerous virulence attributes were discovered during the last few decades. The 9-kb chromosomal pathogenicity island (LPI1) contains *prfA*, *plcA*, *hly*, *mpl*, *actA*, and *plcB* encoding the key virulence factors required for intracellular lifestyle (Vázquez-Boland et al., 2001). The aforementioned master virulence regulator PrfA coordinates expression of a set of genes in LPI1 and at other loci, such as *bsh* (Dussurget et al., 2002), *inlC* (Gouin et al., 2010), and *hpt* (Chico-Calero et al., 2002). Additional pathogenicity islands (Cotter et al., 2008; Maury et al., 2016), antibiotic resistance plasmids (Hadorn et al., 1993; Poyart-Salmeron et al., 1990) and an internalin-carrying plasmid (den Bakker et al., 2012) were reported as extra virulence determinants. Moreover, reports on the direct and indirect involvement of several small non-coding RNAs in pathogenesis have increased in the last decade (Bécavin et al., 2014; Cerutti et al., 2017; Lebreton and Cossart, 2016; Toledo-Arana et al., 2009).

A range of molecular markers were proposed to approximate virulence potential of *L. monocytogenes* isolates (Maury et al., 2017; Olier et al., 2003; Port and Freitag, 2007) on the basis of genomic analysis. As an example, detection of point mutations in *inlA* was tested to predict non-invasive isolates (Rousseaux et al., 2004). Similarly, multiplex PCR detecting *inlA*, *inlC*, and *inlJ* as biomarkers was proposed to assess virulence potential (Liu et al., 2007). However, because of the high degree of intraspecific genetic diversity and the complex mechanisms leading to infection in host, estimating virulence by analysing a discrete number of genes may yield unsatisfactory results (Olier et al., 2005; Roberts et al., 2009). Moreover, a recent study showing epistatic control of fosfomycin resistance by *prfA* and *hpt* during infection supports complex genotype-phenotype associations (Scotti et al., 2018).

Transcriptional reshaping is the cornerstone of the transition from saprophytism to infection (Toledo-Arana et al., 2009). Interestingly, evidence suggests that assessment of *in vitro* basal transcription of some bacterial pathogens could be informative of their level of virulence. For example, transcriptional profiling of methicillin-resistant and -susceptible cultures of *Staphylococcus pseudintermedius* identified differentially expressed genes such as surface proteins, toxins, and prophage genes that might contribute to virulence (Couto et al., 2016). In the current study, we produced a comprehensive transcriptome dataset from which basal transcription patterns were analysed in multiple aspects. Since exponentially grown cells in

BHI at 37°C were reported to be the closest to *L. monocytogenes in vivo* (Camejo et al., 2009), total RNA was extracted under this laboratory condition. Part of the core transcriptome variations was explained by slight differences in growth stage at time of harvest. This variation was captured by PC1 (48.4%) that discriminated samples according to the transition from exponential to early stationary phase. Functional analysis revealed that while transcript levels of genes involved in protein synthesis reflected exponential phase, those involved in carbohydrate metabolism could be linked to transition to early stationary phase. Indeed, transition from glycolysis to gluconeogenesis was reported as the most important metabolic rearrangement at the end of exponential growth in various organisms (Shimizu, 2013). Further systematic experimental noise between BRs was captured by PC2. Exclusion of these variations improved correlations and increased robustness of the conclusions drawn between transcript levels and covariates. Even though PC1 showed significant correlations with some covariates (Maury's classification and lineage), the improved statistical power of correlation analyses supported the rationale for using the new dataset. This approach of using PCA to filter noise is reminiscent to its well-established use in genome-wide association studies to search for disease markers. In this context, PCA serves to overcome potentially confounding effects of population stratification from geographical attributes by allowing to adjust genotypes and phenotypes using the main axes of variations (Price et al., 2006, 2010).

The statistical treatment unveiled significant correlations between large sets of genes with phylogenetic divergence. Among the most prominent differences in functional analysis 'Transformation/competence' and 'DNA recombination' were overrepresented in lineage II isolates. It supports the current evolutionary history of *L. monocytogenes* characterized by higher recombination potential in lineage II than lineage I isolates which may have promoted successful adaptation of lineage II isolates to diverse environments (Orsi et al., 2011). In contrast, functions related to pathogenicity were overrepresented in lineage I isolates. For instance, 'Soluble internalin' was enriched only in lineage I and functions related to posttranslational modifications, namely 'Protein modification' and 'Protein folding', were enriched more in lineage I than II isolates by 1.7- and 2.8-fold, respectively. Posttranslational modification is one of the crucial strategies employed by pathogens to modify activity of virulence factors as well as to modulate host cell pathways to their benefit (Ribet and Cossart, 2010). A previous study using macroarray compared transcriptomes of 6 isolates (2 lineage II and 4 lineage I) during late-exponential growth in defined medium supplemented with 1% glucose (Severino et al., 2007). The lack of overlap with the genes identified in the present study may be ascribed to differences in the experimental design and in statistical approaches. Technical variations in obtaining the expression values may also have contributed to the differences. Indeed, the current study used RNA-seq while previous study relied on a noisier

technology. Moreover, investigating a larger collection of isolates allowed here to better capture intraspecific diversity.

In spite of the high congruence between the set of transcripts correlated with lineage and Maury's classification of genotypes, functional analyses highlighted some differences. Genotype-specific features were mainly found in intermediary metabolisms: while 'Metabolism of lipids', 'Metabolism of coenzymes and prosthetic groups', and 'Metabolism of phosphate' were highly enriched in CC1, CC2, CC4 and CC6, 'Metabolism of amino acids and related molecules' was highly enriched in CC121 and CC9. It is tempting to suggest that these differences in basal metabolism may be linked to niche-specific adaptation strategies which led to the current distribution of these CCs from clinical and environmental sources.

In our data, isolates were clustered according to genes sharing similar transcription patterns. Interestingly, 64% of these clustered genes were found to belong to published lists of regulons, among which were the core PrfA virulon. Considering that the published lists that we analysed accounted for only 26% of the genes of *L. monocytogenes* EGDe, our clustering reflects the strong contribution of the known transcription factors to variability of gene expression during optimal growth.

The conserved innate immune response to microbial infections between insects and mammals as well as its cost efficiency and comparably lesser ethical concerns than with mammals makes *G. mellonella* an attractive *in vivo* model for evaluating virulence in bacteria (Scully and Bidochka, 2006; Tsai et al., 2016) and it was successfully applied to *L. monocytogenes* (Joyce and Gahan, 2010; Mukherjee et al., 2010). In the present study, Spearman correlation analysis identified 56 genes whose transcript levels were positively or negatively correlated with *G. mellonella in vivo* virulence. None of the obvious virulence factors were represented among them, confirming that transcription of virulence genes strictly restricted to host cell invasion are poor markers of virulence potential. Among the correlated genes were phosphatases that broadly modulate activity of pathogenic bacteria and promote their intracellular growth (Sajid et al., 2015). Similarly, lipid metabolism is important for intracellular lifecycle, for example, to make use of host lipids as energy sources and to modulate host immune responses (Rameshwaram et al., 2018). Recent studies found existence of several type II toxin-antitoxin systems in *L. monocytogenes* connected to stress conditions (Curtis et al., 2017; Kalani et al., 2018), though their role in virulence need further investigations. Two competence genes (*Imo2189* and *Imo1397*) were positively correlated while one (*Imo1346*) was negatively correlated to virulence level. The Com system of *L. monocytogenes* is required to promote escape from phagosome during infection (Rabinovich et al., 2012). The exact role of these competence proteins in virulence requires to be explored in depth. One of the negatively

correlated genes was *lmo0540* which encodes a penicillin-binding protein. Although disruption of *lmo0540* did not alter resistance to penicillin G and cephalosporins, insertion mutant led to virulence attenuation *in vivo* (Guinane et al., 2006). On the contrary, other penicillin-binding proteins were reported to induce attenuation of virulence in some bacterial pathogens (Beceiro et al., 2013; Rieux et al., 2001; Rudkin et al., 2012) even though antibiotic resistance is evolutionarily intertwined with bacterial virulence. Likewise, negative correlations between transcript levels of *lmo0540* and *lmo1963* (hypothetical lantibiotic-exporting membrane permease) and virulence in *G. mellonella* may suggest complex relationships between virulence and drug resistance. Other transcripts negatively correlated with virulence included genes involved in sugars transport (*lmo0034*, *lmo0373*, *lmo0374*, *lmo1389*, *lmo1390*, *lmo1391*, *lmo2838*, and *lmo2839*) and metabolism (*lmo0035*, *lmo0372*, *lmo0557*, *lmo2836*, *lmo0635*, *lmo0879*, and *lmo2832*). PrfA-mediated repression of virulence gene expression by specific carbohydrates is one of the subtle mechanisms that control the onset of infection (Aké et al., 2011; Milenbachs Lukowiak et al., 2004). Correspondingly, PrfA overexpression interferes with glucose uptake which resulted in impaired growth (Marr et al., 2006). In this regard, the current study showing lower basal transcript levels of those genes in more virulent isolates grown in nutrient rich BHI media suggests further connections between central metabolism and infection. Detailed investigations of bacterial metabolism during infection must be assessed to explore possible links between bacterial fitness and virulence potential.

As a whole, our data evidenced vast variations in virulence phenotype and transcriptome profiles. PCA successfully filtered noise from RNA-seq dataset and strengthened experimental reproducibility. Clustering of several regulons across samples featured the role of key transcription factors such as σ B, PrfA, and CodY in the observed transcriptome diversity. The phylogenetic position appeared as a major factor underlying transcriptome diversity since as much as 19% of the genes differentially transcribed correlated with lineage. This result documents a genome-wide physiological differentiation during evolution that parallels previously reported epidemiological differences. Although correlations between virulence determined in *G. mellonella* and transcriptomes were evidenced it is challenging to identify molecular markers whose transcript levels could predict virulence. We hope that the present study can help for the design of future analyses, at even more ambitious scale, that are needed to tackle the challenges of integrating epidemiological or experimental data on virulence with transcriptome data. Despite the high interest for this idea, it remains unclear at this stage if transcriptomics could become useful as a predictive tool for virulence that could be applied to large collections of isolates.

Author contributions

B-H.L., P.N., and P.P. conceived the project. L. Gal, D.G., and B-H.L. performed *in vivo* and *in vitro* experiments. C.G. processed the RNA-seq raw data. B-H.L. and P.N. performed analysis of the data and interpreted the results. L. Guillier provided isolates with genome sequences. A.R. and B.R. guided the RNA-seq libraries preparation carried out by B-H.L. B-H.L., P.N. and P.P. wrote the manuscript and all authors reviewed and approved the final manuscript.

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Figures and Tables

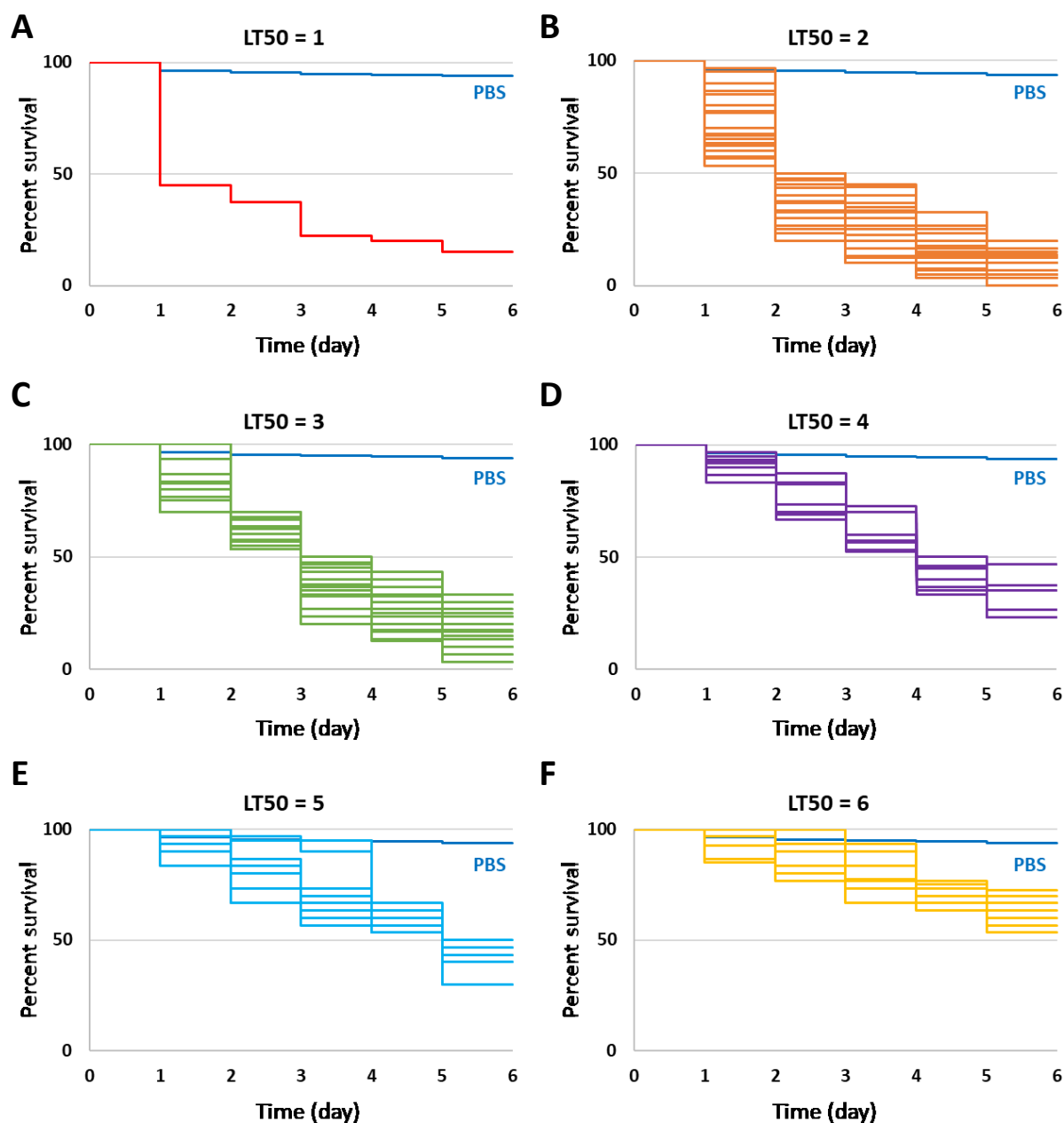


Figure 1. Varying virulence levels of 91 *L. monocytogenes* isolates in *G. mellonella*. Isolates are grouped by post-infection incubation time (day) required to observe 50% or more death of larvae (LT50). Larvae injected with PBS served as negative controls. (A) to (E) show isolates with LT50 of days 1 to 5, respectively and (F) shows isolates that did not reach 50% death by day 5 post-infection (LT50 > 5).

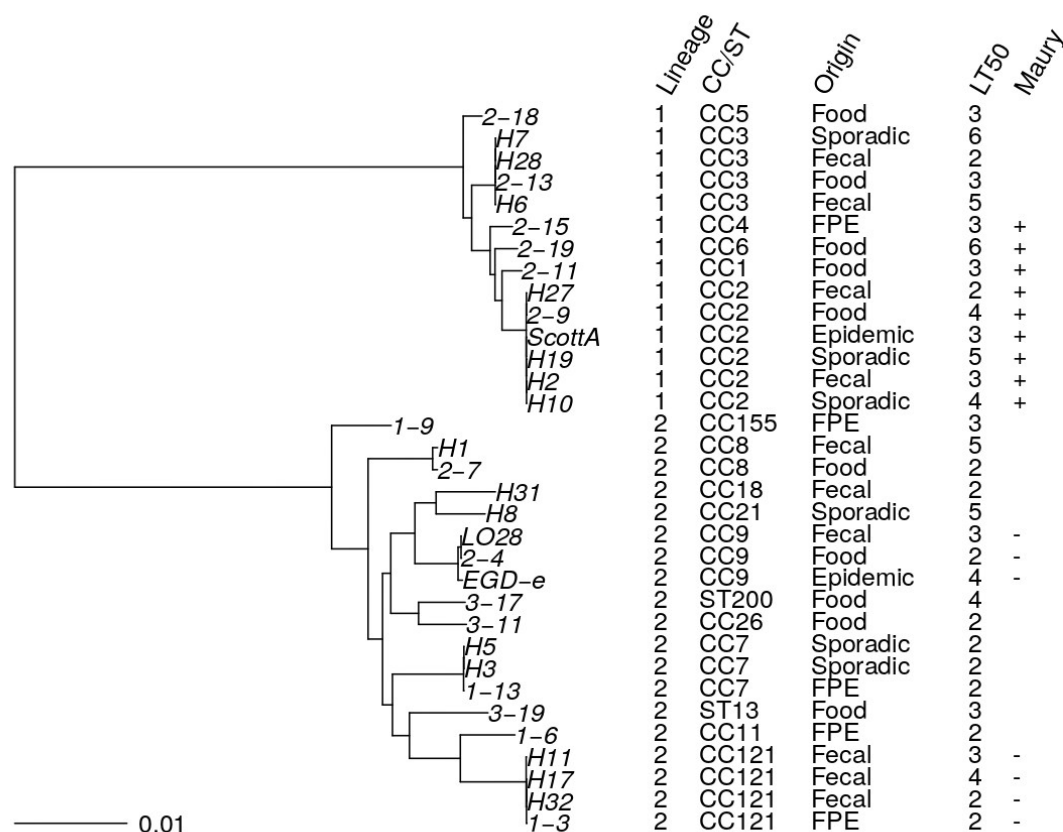
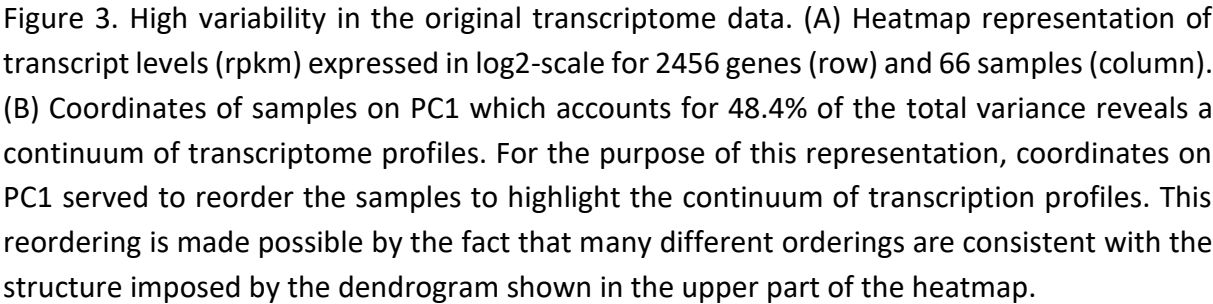


Figure 2. Phylogenetic tree reconstructed on the basis of whole-genome sequences for the 33 *L. monocytogenes* isolates selected for transcriptome profiling. Columns on the right side show lineage, MLST genotype (CC, clonal complex; ST, sequence type), origin, virulence level expressed as LT50 measured in *G. mellonella*, and Maury's classification (virulence-associated genotypes: +, hypervirulence; -, hypovirulence) (Maury et al., 2016). Branch length represents the expected number of substitutions per base.



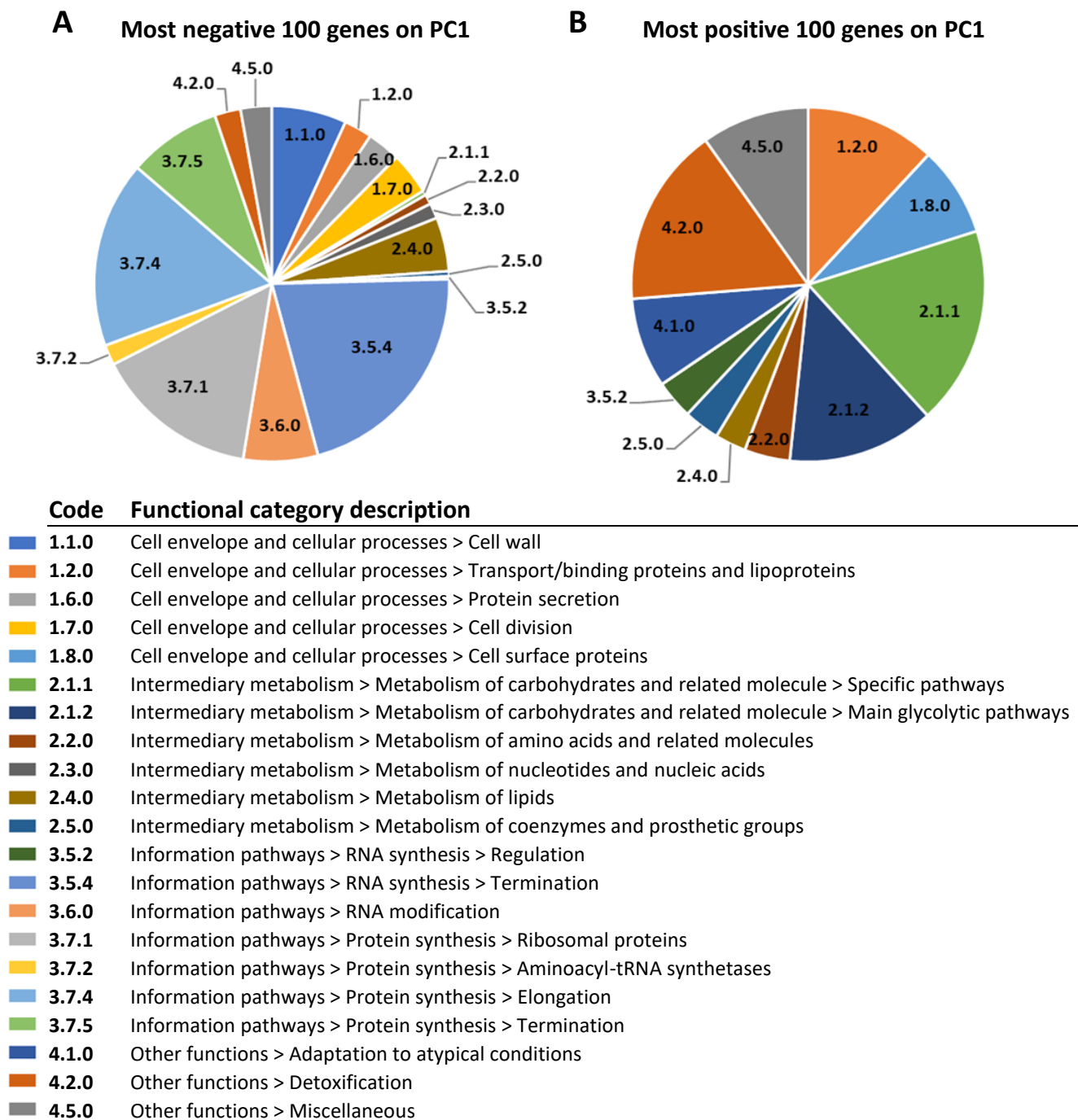
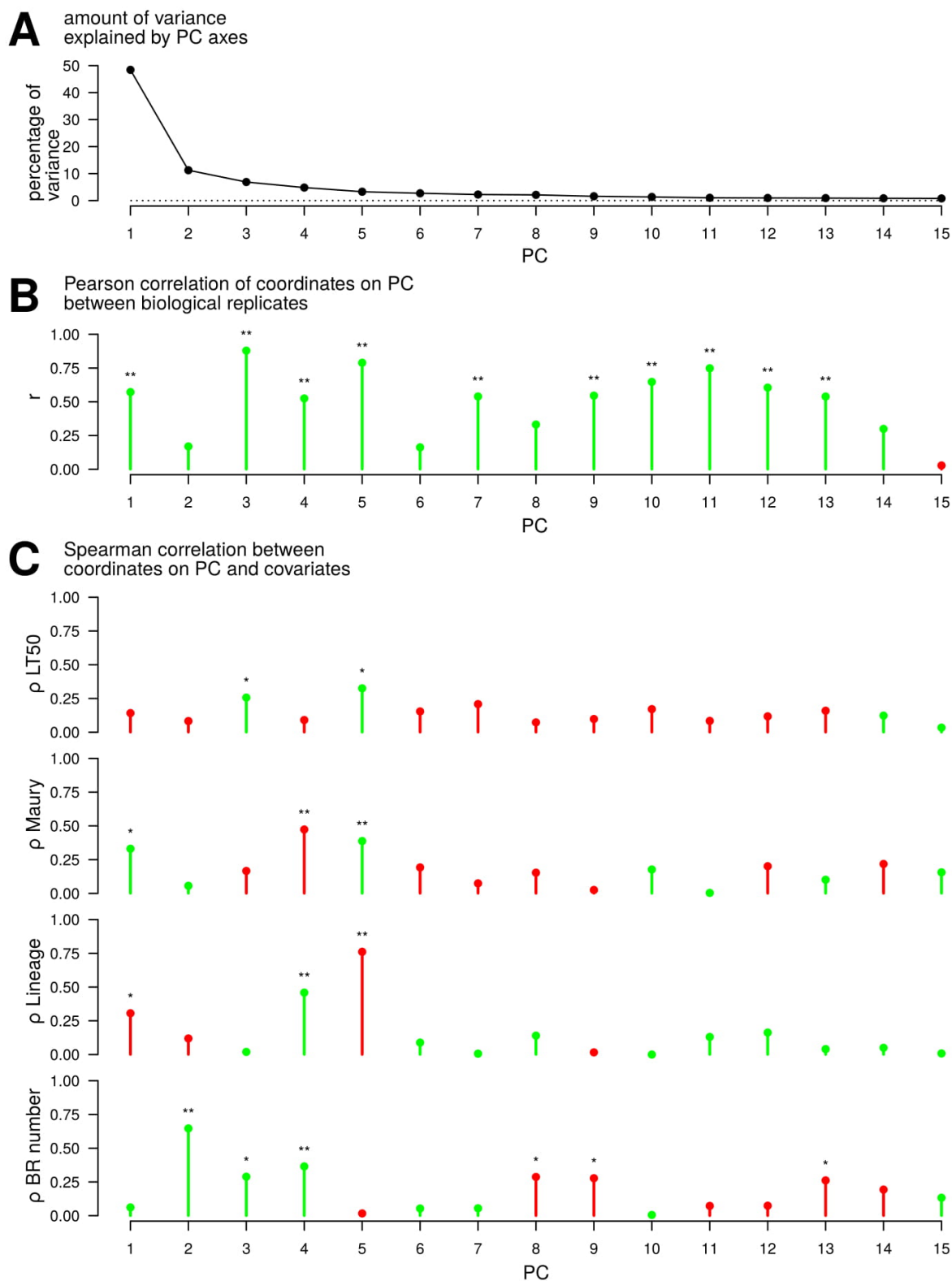


Figure 4. Principal component axis 1 (PC1) distinguishes variations arising from changes in growth stage. Distribution of functional categories among genes that contribute most to the PC1 is displayed in the pie chart. (A) Most negative 100 loading values and (B) most positive 100 loading values are selected and relative ratio (number in 100 genes / number in whole genome) of each functional category is calculated. Uninformative categories are excluded in the analysis.



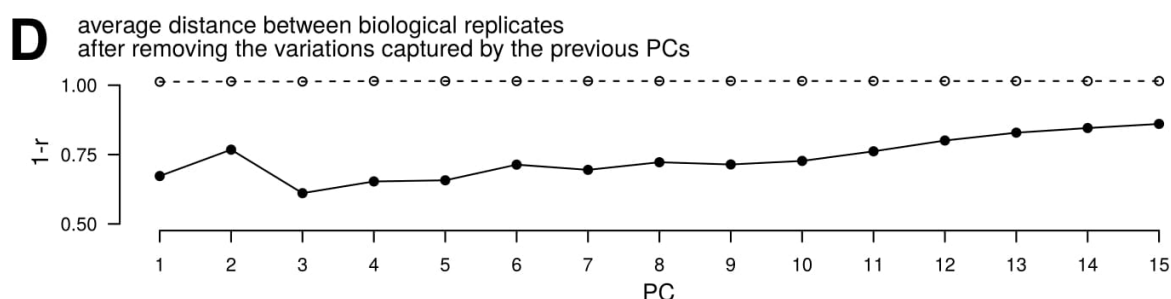


Figure 5. Principal components axes (PCs) explain relationships between transcriptomes and variables. (B) Variance in transcriptomes captured by each PC are expressed in percentage. The first two axes, PC1 and PC2 express 59.6% of total dataset inertia. (B) Pearson correlation coefficient (r) is measured between coordinates of biological replicates (BRs) on each PC. (C) Spearman correlations coefficient (ρ) is measured between coordinates on each PC and the original covariates as follows: virulence measured in *G. mellonella* ('LT50'), genotypes related to hyper- or hypovirulence ('Maury'), phylogenetic division ('lineage'), and sets of BR ('BR number'). Green and red colours indicate positive and negative correlations, respectively. (D) After eliminating the variations captured by preceding PCs, average distances between BR are calculated as ' $1-r$ ' (r , Pearson correlation coefficient). For example, point PC3 on x-axis shows average distance after removing variations captured by PC1 and PC2. *, $p \leq 0.05$; **, $p \leq 0.005$.



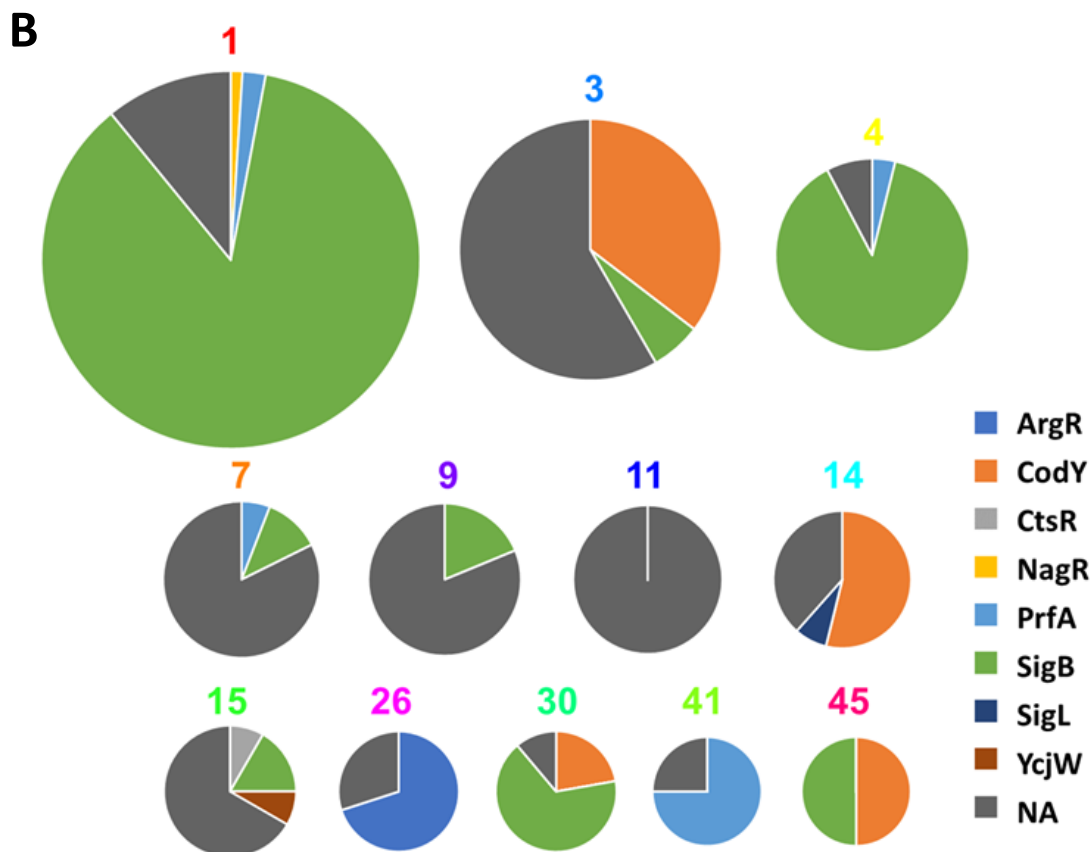


Figure 6. Analysis of the refined transcriptome dataset created by filtering out the variations captured by PC1 and PC2. (A) Heatmap representing transcript levels (rpkm) in log2-scale expresses for 2,456 genes (row) and 66 samples (column). Cut-off at Pearson correlation coefficient of 0.6 identifies 12 clusters with more than 8 genes and fold change ≥ 4 . The clusters are indicated in coloured bars with cluster identification numbers to the left of the dendrogram. Genes with known link to virulence (Wurtzel et al., 2012) are shown in the bars to the right of the heatmap and core PrfA virulon (Scortti et al., 2007) are indicated. (B) are indicated. (B) Relative abundance of regulons belonging to each cluster is expressed in the pie chart. Cluster number is marked on the top of each circle whose area is proportional to the number of genes composing the cluster. A complete list of the genes can be found in Supplementary Table 1. NA, information not available.

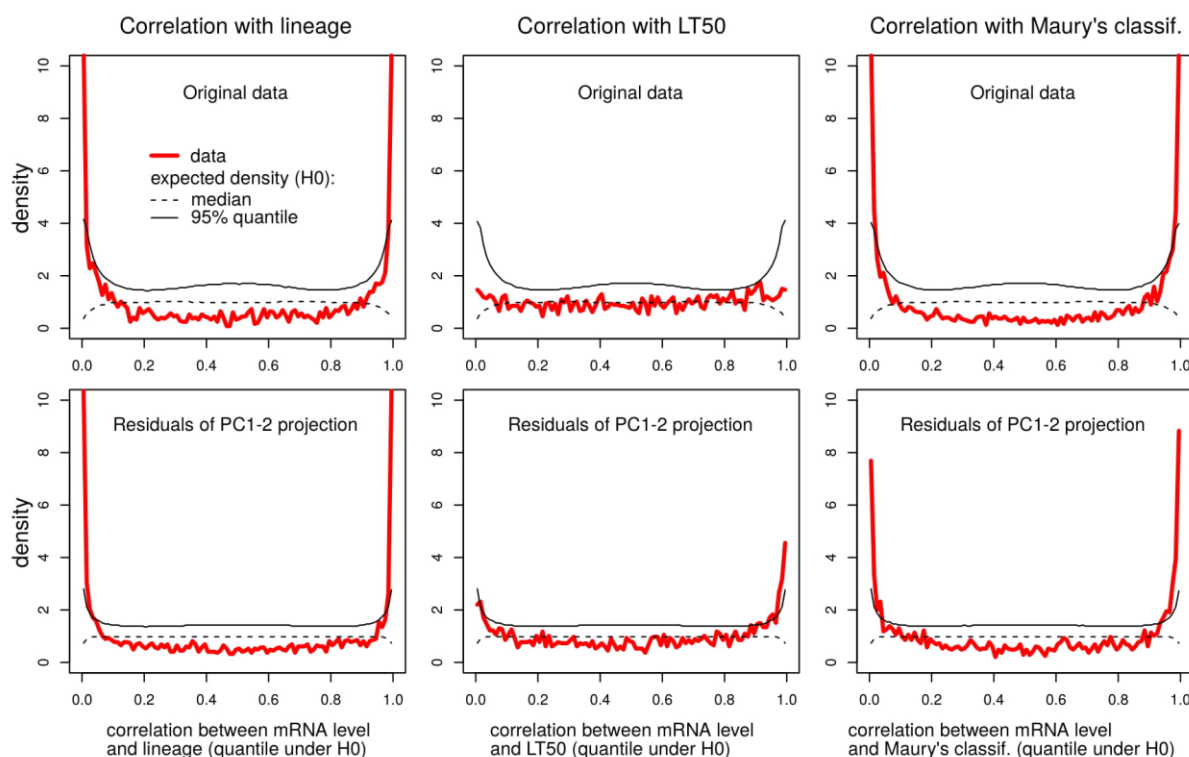
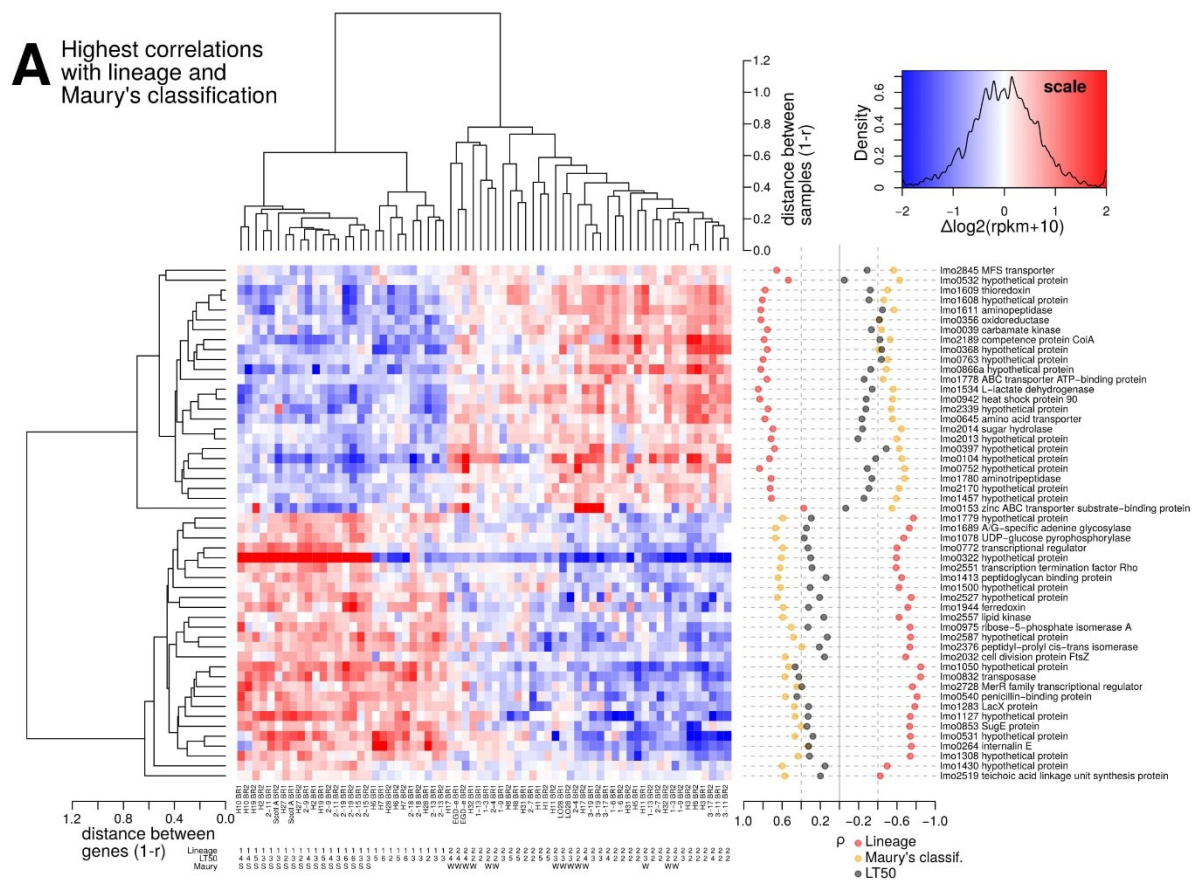


Figure 7. Impact of removing PC1 and PC2 on the correlation analysis between transcriptome profiles and isolate characteristics. For each correlation analysis, a plot shows the distribution of the Spearman correlation coefficients expressed in terms of quantile under the null hypothesis of no-association (i.e. random permutations of the isolate labels) such that deviation from the uniform reflects statistical significance, values near 0 correspond to negative correlations and near 1 to positive correlation. Distribution of the correlation coefficients for the actual dataset (red line) is plotted along with the median (50% quantile, dashed black line) and the 95% quantile (black line). Distribution of quantiles for the adjusted dataset (bottom row) reveals enhanced statistical power in Spearman correlation analysis compared to the original dataset (top row).



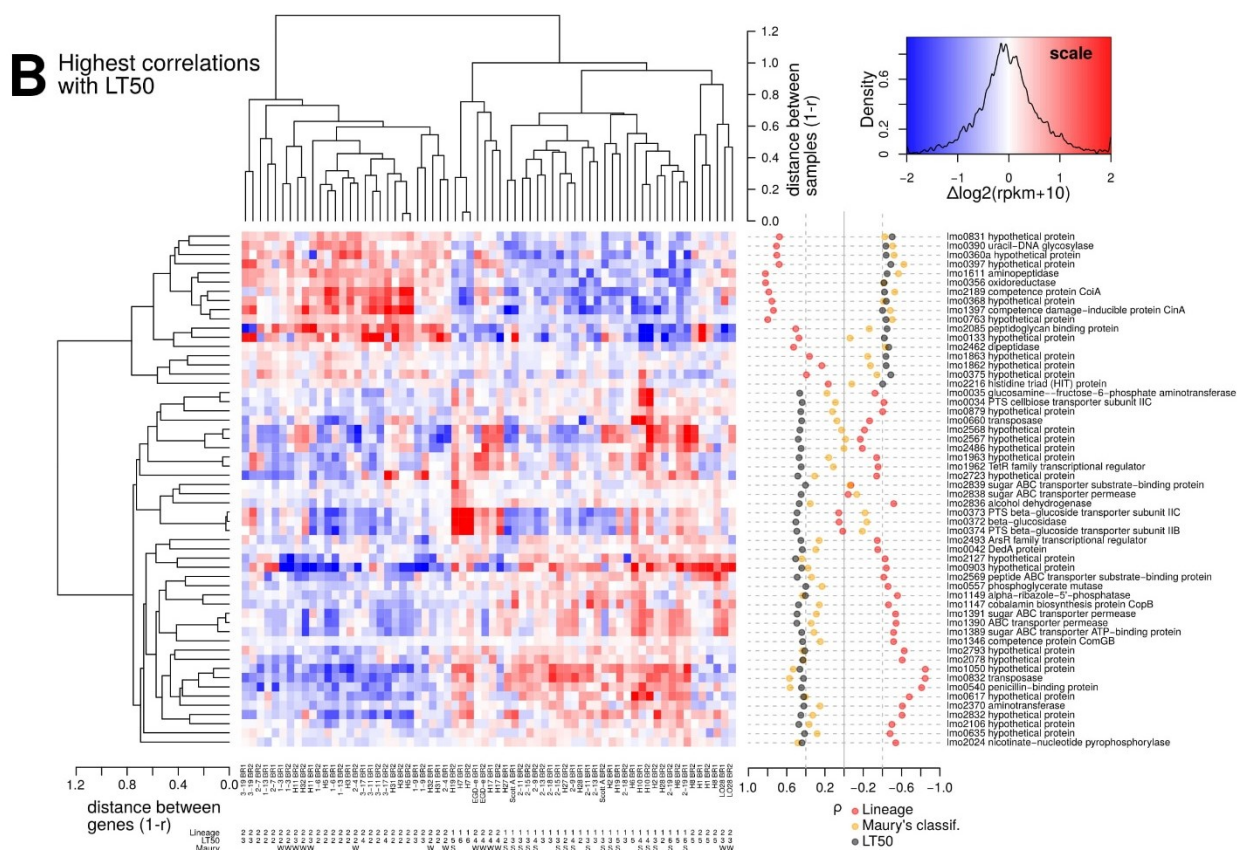


Figure 8. Highest correlation between transcript levels and covariates. (A) Transcripts corresponding to the 15 most extreme negative or positive p values with lineages (30 genes) and with Maury's classification of virulence genotypes (30 genes). Due to overlaps, the union between these sets resulted in 52 genes. The figure combines an heatmap representation of transcript levels in log2-scale, with a graphical representation of the Spearman correlation coefficients with each covariate as semi-transparent dots (red for lineage; orange for Maury's classification; black for LT50 measured in *G. mellonella*). (B) 56 transcripts corresponding to the highest correlations ($|\rho| \geq 0.4$) with virulence level determined in *G. mellonella* (LT50). Lists of the genes can be found in Table 3, Supplementary Table 2 and 3.

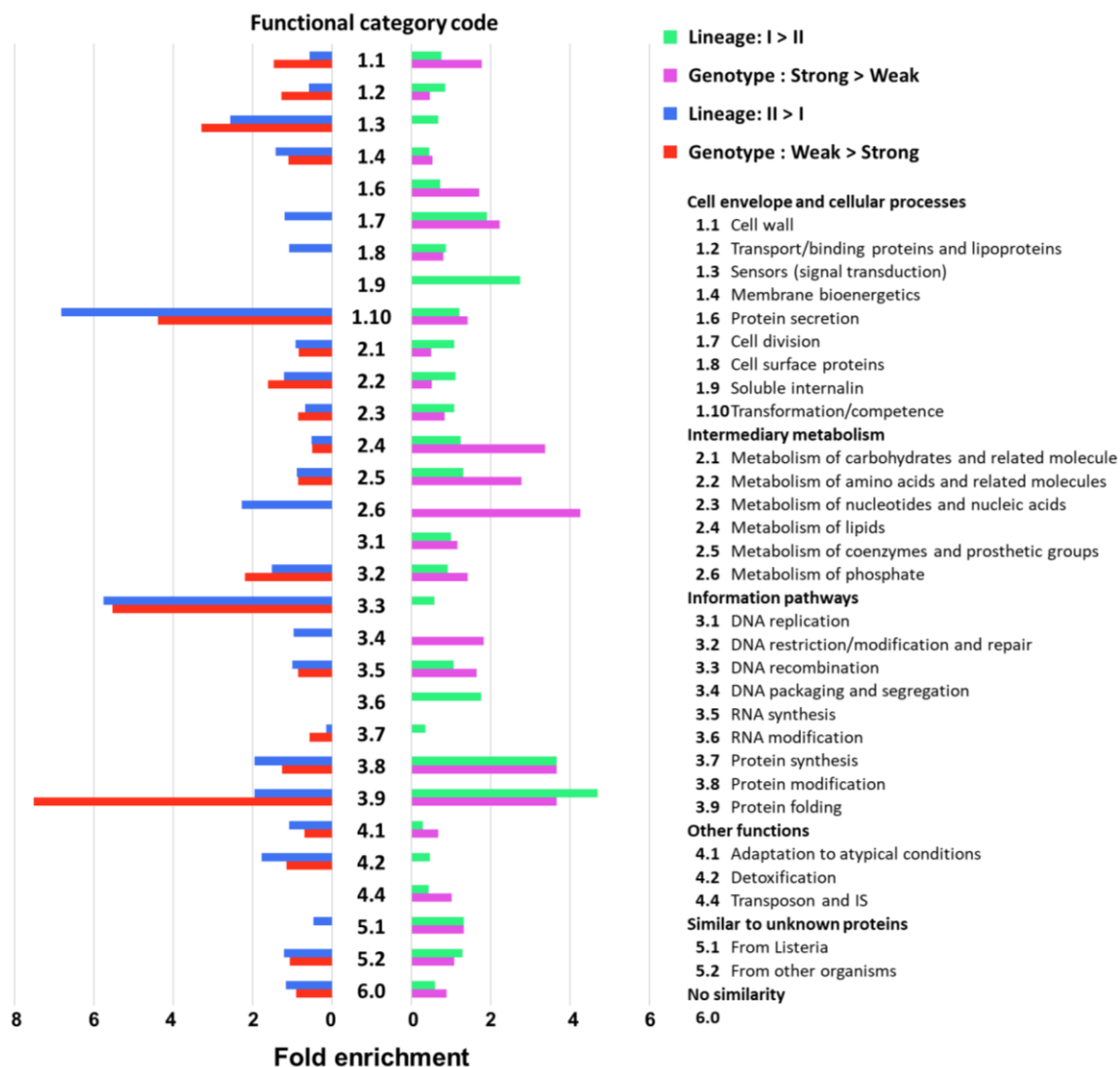


Figure 9. Functional classification of transcripts whose expression are correlated to division of lineages and Maury's classification. Among the lists of genes selected by Spearman's rank correlation analysis ($|p| \geq 0.4$), total 467 (99%) and 219 genes (99%) were designated to one of the categories, which is present in two higher hierarchies. Fold enrichment was calculated for each category as follows: Fold enrichment = % in annotated genes / % in whole genome of EGDe.

Table 1. Characteristics of *L. monocytogenes* strains used in the study.

Isolate	Origin	MLST	Maury's classification §	LT50	Lineage *	RNA-seq **	Reference
H1	Fecal	CC8	Strong	5	II	yes	Olier et al., 2003
H2	Fecal	CC2		3	I	yes	Olier et al., 2003
H3	Sporadic	CC7		2	II	yes	Olier et al., 2003
H5	Sporadic	CC7		2	II	yes	Olier et al., 2003
H6	Fecal	CC3	Strong	5	I	yes	Olier et al., 2003
H7	Sporadic	CC3		6	I	yes	Olier et al., 2003
H8	Sporadic	CC21		5	II	yes	Olier et al., 2003
H9	Sporadic	CC88		2	I		Olier et al., 2003
H10	Sporadic	CC2	Strong	4	I	yes	Olier et al., 2003
H11	Fecal	CC121	Weak	3	II	yes	Olier et al., 2003
H13	Sporadic	CC7	Strong	2	II		Olier et al., 2003
H14	Sporadic	CC1		3	I		Olier et al., 2003
H15	Sporadic	CC8		3	II		Olier et al., 2003
H16	Sporadic	CC7		2	II		Olier et al., 2003
H17	Fecal	CC121	Weak	4	II	yes	Olier et al., 2003
H18	Sporadic	CC3	Strong	3	I		Olier et al., 2003
H19	Sporadic	CC2		4	I	yes	Olier et al., 2003
H21	Sporadic	CC1		2	I		Olier et al., 2003
H22	Sporadic	CC1		2	I		Olier et al., 2003
H23	Sporadic	NA †	Strong	2	NA		Olier et al., 2003
H24	Sporadic	CC6		3	I		Olier et al., 2003
H25	Sporadic	CC18		2	II		Olier et al., 2003
H27	Fecal	CC2		2	I	yes	Olier et al., 2003
H28	Fecal	CC3	Strong	2	I	yes	Olier et al., 2003
H31	Fecal	CC18		2	II	yes	Olier et al., 2003
H32	Fecal	CC121		2	II	yes	Olier et al., 2003
H34	Fecal	CC121		2	II		Olier et al., 2003
H35	Fecal	CC3	Strong	2	I		Olier et al., 2003
H36	Epidemic	CC1		2	I		Olier et al., 2003
H38	Fecal	CC37		2	II		Olier et al., 2003
LO28	Fecal	CC9	Weak	3	II	yes	Olier et al., 2003
Scott A	Epidemic	CC2	Strong	3	I	yes	Olier et al., 2003
EGD-e	Epidemic	CC9	Weak	4	II	yes	Olier et al., 2003
1-1	Food	CC121	Weak	3	II		Henri et al., 2016
1-2	Food	CC121	Weak	6	II		Henri et al., 2016
1-3	FPE ‡	CC121	Weak	2	II	yes	Henri et al., 2016
1-4	FPE	CC121	Weak	5	II		Henri et al., 2016
1-5	FPE	CC11		5	II		Henri et al., 2016
1-6	FPE	CC11		2	II	yes	Henri et al., 2016
1-7	FPE	CC11		6	II		Henri et al., 2016

1-8	FPE	CC155		6	II		Henri et al., 2016
1-9	FPE	CC155		2	II	yes	Henri et al., 2016
1-10	FPE	CC155		6	II		Henri et al., 2016
1-11	Food	CC155		6	II		Henri et al., 2016
1-12	FPE	CC7		5	II		Henri et al., 2016
1-13	FPE	CC7		2	II	yes	Henri et al., 2016
1-14	FPE	CC7		4	II		Henri et al., 2016
1-15	FPE	CC7		2	II		Henri et al., 2016
1-16	FPE	CC7		5	II		Henri et al., 2016
1-17	FPE	CC7		3	II		Henri et al., 2016
1-18	FPE	CC7		2	II		Henri et al., 2016
1-19	FPE	CC7		3	II		Henri et al., 2016
2-1	Food	CC121	Weak	3	II		Henri et al., 2016
2-2	Food	CC121	Weak	3	II		Henri et al., 2016
2-3	Food	CC121	Weak	1	II		Henri et al., 2016
2-4	Food	CC9	Weak	2	II	yes	Henri et al., 2016
2-5	Food	CC9	Weak	3	II		Henri et al., 2016
2-6	Food	CC9	Weak	2	II		Henri et al., 2016
2-7	Food	CC8		2	II	yes	Henri et al., 2016
2-8	Food	CC8		2	II		Henri et al., 2016
2-9	Food	CC2	Strong	4	I	yes	Henri et al., 2016
2-10	Food	CC2	Strong	3	I		Henri et al., 2016
2-11	Food	CC1	Strong	3	I	yes	Henri et al., 2016
2-12	Food	CC1	Strong	2	I		Henri et al., 2016
2-13	Food	CC3		3	I	yes	Henri et al., 2016
2-14	Food	CC3		3	I		Henri et al., 2016
2-15	FPE	CC4	Strong	3	I	yes	Henri et al., 2016
2-16	Food	CC4	Strong	3	I		Henri et al., 2016
2-17	Food	CC5		2	I		Henri et al., 2016
2-18	Food	CC5		3	I	yes	Henri et al., 2016
2-19	Food	CC6	Strong	6	I	yes	Henri et al., 2016
2-20	Food	CC6	Strong	4	I		Henri et al., 2016
3-1	Food	CC451		2	II		Henri et al., 2016
3-2	NA	CC14		2	II		Henri et al., 2016
3-3	Food	CC177		2	II		Henri et al., 2016
3-4	Food	CC19		2	II		Henri et al., 2016
3-5	Food	CC199		2	II		Henri et al., 2016
3-6	Food	CC20		2	II		Henri et al., 2016
3-7	Food	CC21		3	II		Henri et al., 2016
3-8	Food	CC220		2	I		Henri et al., 2016
3-9	Food	CC26		3	II		Henri et al., 2016
3-10	Food	CC26		2	II		Henri et al., 2016
3-11	Food	CC26		1	II	yes	Henri et al., 2016
3-12	Food	CC31		2	II		Henri et al., 2016
3-13	FPE	CC31		3	II		Henri et al., 2016

3-14	Food	CC315	3	I		Henri et al., 2016
3-15	Food	CC412	3	II		Henri et al., 2016
3-16	Food	ST200	4	II	yes	Henri et al., 2016
3-17	Food	ST517	3	NA		Henri et al., 2016
3-18	Food	ST13	3	II	yes	Henri et al., 2016
3-19	Food	ST13	6	II		Henri et al., 2016

* Lineage was determined based on the online MLST database for *Listeria monocytogenes*
(<http://bigsd.b.pasteur.fr/Listeria/>)

** Isolates included in RNAseq are noted as 'yes'

§ Classification of genotypes into strong or weak virulence by Maury et al., 2016

† Information not available

‡ Food processing environment

Table 2. Comparison of number of genes selected by Spearman correlation analysis with different variates (lineage, Maury's classification of genotypes, and *in vivo* virulence).

	Lineage ^a		Maury's classification ^b		LT50 ^c	
	Negative	Positive	Negative	Positive	Negative	Positive
Designation	Lineage_N	Lineage_P	Maury_N	Maury_P	LT50_N	LT50_P
Number of genes †	261	212	111	111	17	39
Mean ρ	-0.54	0.55	-0.48	0.48	-0.44	0.45
FDR ‡	0.01	0.01	0.04	0.03	0.18	0.15
Number of shared genes						
Lineage_N	261	0	0	85	0	24
Lineage_P	0	212	89	0	13	0
Maury_N	0	89	111	0	11	0
Maury_P	85	0	0	111	0	9
LT50_N	0	13	11	0	17	0
LT50_P	24	0	0	9	0	39
Virulence genes *						
Number	1	6	3	0	0	0
p-value	0.04	0.45	0.50	0.17	1.00	1.00
Compared to Severino et al., 2007 **						
481 (Lineage II > I)	33	71				
462 (Lineage I > II)	73	22				

a Lineage II versus I in relation to transcript levels

b Hyper- versus hypovirulent genotypes (Maury et al., 2016) in relation to transcript levels

c Higher versus lower LT50 measured in *G. mellonella* in relation to transcripts levels

† Genes having $|\rho| > 0.4$ (ρ , Spearman correlation coefficient)

‡ False discovery rate (FDR) was calculated by averaging the local FDRs

* Compared to the previously identified virulence-related genes (Wurtzel et al., 2012)

** Compared to the previously identified differentially expressed genes (Severino et al., 2007) available in our transcriptomes

Table 3. List of genes whose transcript levels are correlated with virulence measured in *G. mellonella*.

Functional classification §	Locus tag	Spearman correlation			Product HHpred ‡
		Cor †	p value	p-value	
1. Cell envelope and cellular processes	Cell wall				
	<i>lmo0540*</i>	N	0.445	0.007	penicillin-binding protein
	Cell envelope and cellular processes				
	<i>lmo0034</i>	N	0.438	0.003	PTS cellbiose transporter subunit IIC
	<i>lmo0373</i>	N	0.492	0.001	PTS beta-glucoside transporter subunit IIC
	<i>lmo0374</i>	N	0.494	0.001	PTS beta-glucoside transporter subunit IIB
	<i>lmo1389</i>	N	0.443	0.003	sugar ABC transporter ATP-binding protein
	<i>lmo1390</i>	N	0.494	0.001	ABC transporter permease
	<i>lmo1391</i>	N	0.492	0.001	sugar ABC transporter permease
	<i>lmo2569</i>	N	0.491	0.001	peptide ABC transporter substrate-binding protein
	<i>lmo2838</i>	N	0.449	0.001	sugar ABC transporter permease
	<i>lmo2839</i>	N	0.404	0.002	sugar ABC transporter substrate-binding protein
	Cell surface proteins				
	<i>lmo2085</i>	P	-0.448	0.006	peptidoglycan binding protein
	Transformation/competence				
	<i>lmo1346</i>	N	0.433	0.001	comGB; competence protein ComGB
	<i>lmo1397</i>	P	-0.401	0.016	cinA; competence damage-inducible protein
	<i>lmo2189</i>	P	-0.421	0.012	CoiA; competence protein
2. Intermediary metabolism	Metabolism of carbohydrates and related molecule				
	<i>lmo0035</i>	N	0.464	0.001	glucosamine--fructose-6-phosphate aminotransferase
	<i>lmo0356</i>	P	-0.416	0.013	oxidoreductase
	<i>lmo0372</i>	N	0.504	0.001	beta-glucosidase
	<i>lmo0557</i>	N	0.401	0.006	phosphoglycerate mutase
	<i>lmo2836</i>	N	0.469	0.000	alcohol dehydrogenase
	Metabolism of amino acids and related molecules				
	<i>lmo1611</i>	P	-0.449	0.006	aminopeptidase
	<i>lmo2370</i>	N	0.421	0.006	aminotransferase
	<i>lmo2462</i>	P	-0.466	0.001	dipeptidase
	Metabolism of coenzymes and prosthetic groups				
	<i>lmo1147</i>	N	0.477	0.001	CopB; cobalamin biosynthesis protein
	<i>lmo1149</i>	N	0.405	0.005	alpha-ribazole-5'-phosphatase
	<i>lmo2024</i>	N	0.440	0.002	nadC; nicotinate-nucleotide pyrophosphorylase
3. Information pathways	DNA restriction/modification and repair				
	<i>lmo0390</i>	P	-0.436	0.004	uracil-DNA glycosylase
	RNA synthesis				

	<i>Imo1962</i>	N	0.449	0.002	TetR family transcriptional regulator
	<i>Imo2493</i>	N	0.452	0.001	ArsR family transcriptional regulator
4. Other functions	Transposon and IS				
	<i>Imo0660</i>	N	0.444	0.000	transposase
	<i>Imo0832</i>	N	0.425	0.010	transposase
5. Similar to unknown proteins	From <i>Listeria</i>				
	<i>Imo0617</i>	N	0.423	0.007	hypothetical protein
	[PF16729.5_99.2%] DUF5067; Domain of unknown function				
	<i>Imo2568</i>	N	0.462	0.000	hypothetical protein
	[COG5294_99.9%] YxeA; Uncharacterized protein YxeA, DUF1093 family (Function unknown)				
	From other organisms				
	<i>Imo0042</i>	N	0.437	0.001	DedA protein; Uncharacterized membrane protein
	[COG0586_99.8%] DedA; Uncharacterized membrane protein DedA, SNARE-associated domain (Function unknown)				
	<i>Imo0133</i>	P	-0.419	0.009	hypothetical protein
	[COG3592_98.2%] Yjdl; Uncharacterized Fe-S cluster protein Yjdl (Function unknown)				
	<i>Imo0397</i>	P	-0.488	0.003	hypothetical protein
	[cd08899_99.8%] SRPBCC_CalC_Aha1-like_6; Putative hydrophobic ligand-binding SRPBCC domain of an uncharacterized subgroup of CalC- and Aha1-like proteins				
	<i>Imo0635</i>	N	0.414	0.003	hypothetical protein
	[COG0637_99.9%] YcjU; Beta-phosphoglucomutase or related phosphatase, HAD superfamily (Carbohydrate transport and metabolism, General function prediction only)				
	<i>Imo0763*</i>	P	-0.438	0.007	Ser/Thr protein phosphatase family protein
	[COG1408_100%] Yael; Predicted phosphohydrolase, MPP superfamily (General function prediction only)				
	<i>Imo0831</i>	P	-0.502	0.001	hypothetical protein
	[COG0679_100%] YfdV; Predicted permease (General function prediction only)				
	<i>Imo0879</i>	N	0.453	0.003	hypothetical protein
	[COG3623_100%] SgaU; L-ribulose-5-phosphate 3-epimerase UlaE (Carbohydrate transport and metabolism)				
	<i>Imo0903</i>	N	0.443	0.005	hypothetical protein
	[COG1765_99.9%] YhfA; Uncharacterized OsmC-related protein (General function prediction only)				
	<i>Imo1050</i>	N	0.463	0.006	hypothetical protein
	[COG1853_100%] RutF; NADH-FMN oxidoreductase RutF, flavin reductase (DIM6/NTAB) family (Energy production and conversion)				
	<i>Imo1862</i>	P	-0.438	0.001	hypothetical protein
	[cd04506_99.9%] SGNH_hydrolase_YpmR_like; Members of the SGNH-hydrolase superfamily, a diverse family of lipases and esterases				
	<i>Imo1863</i>	P	-0.437	0.003	hypothetical protein
	[COG1307_100%] DegV; Fatty acid-binding protein DegV (Lipid transport and metabolism)				
	<i>Imo1963</i>	N	0.471	0.001	hypothetical protein

[COG4200_99.6%] EfiE; Predicted lantibiotic-exporting membrane pepmease, EfiE/EfiG/ABC2 family (Defense mechanisms)

Imo2078 N 0.432 0.004 hypothetical protein

[COG0802_100%] TsaE; tRNA A37 threonylcarbamoyladenine biosynthesis protein TsaE (Translation, ribosomal structure and biogenesis)

Imo2106 N 0.474 0.000 hypothetical protein

[COG1408_100%] Yael; Predicted phosphohydrolase, MPP superfamily (General function prediction only)

Imo2127 N 0.507 0.001 hypothetical protein

[COG1266_98.9%] YdiL; Membrane protease YdiL, CAAX protease family (Posttranslational modification, protein turnover, chaperones)

Imo2216 P -0.403 0.000 histidine triad (HIT) protein

[COG0537_99.9%] Hit; Diadenosine tetraphosphate (Ap4A) hydrolase or other HIT family hydrolase (Nucleotide transport and metabolism, Carbohydrate transport and metabolism, General function prediction only)

Imo2486 N 0.450 0.000 hypothetical protein

[PF13349.6_99.9%] DUF4097; Putative adhesin

Imo2723 N 0.484 0.002 hypothetical protein

[COG2153_99.8%] ElaA; Predicted N-acyltransferase, GNAT family (General function prediction only)

Imo2832 N 0.452 0.004 hypothetical protein

[COG1929_100%] GlxK; Glycerate kinase (Carbohydrate transport and metabolism)

6. No similarity or No information available

Imo0375 P -0.487 0.003 hypothetical protein

[COG3077_90.9%] RelB; Antitoxin component of the RelBE or YafQ-DinJ toxin-antitoxin module (Defense mechanisms)

Imo2567 N 0.480 0.000 hypothetical protein

[PF13314.6_86.3%] DUF4083; Domain of unknown function

Imo2793 N 0.411 0.005 hypothetical protein

[PF17178.4_80.5%] MASE5; Membrane-associated sensor

Imo0360a P -0.438 0.005 hypothetical protein

[PF14143.6_78.3%] YrhC; YrhC-like protein (Function unknown)

Imo0368 P -0.441 0.008 hypothetical protein

[KOG0142_99.8%] Isopentenyl pyrophosphate:dimethylallyl pyrophosphate isomerase (Secondary metabolites biosynthesis, transport and catabolism)

§ Functional classification for *L. monocytogenes* EGDe (<http://genolist.pasteur.fr/ListiList/>)

* Virulence factors identified from PATRIC (<https://www.patricbrc.org/>)

† Correlation with virulence measured in *G. mellonella*. N, negative correlation; P, positive correlation

‡ Homology detected by HHPred is expressed as: [Identifier_probability %] product (function)

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- ❖ **Supplementary materials for this article can be found at the end of the thesis.**

Chapter VI

Conclusion and perspectives

The current doctoral thesis focused on exploring the biofilm phenotypes and virulence characteristics of the foodborne pathogen *L. monocytogenes* from various perspectives using innovative approaches. Throughout the studies, a large number of isolates were included to reflect intraspecific variations.

Various conditions that *L. monocytogenes* may encounter in food industry were examined for their impact on biofilm formation. The different steps of biofilm formation were observed by BRT and MPA that featured adhesion and maturation steps which were further monitored by microscopic investigations. Regardless of serotype or origin of isolates, sudden cold shock induced cellular adhesion to abiotic surfaces as a transient phenotypic change. A mild but significant correlation was observed between affinity for ethyl acetate and cellular adhesion level acquired at 4°C suggesting that Lewis acid-base interaction was implicated in adhesion step. Similarly, sudden nutrient deprivation (or hypoosmotic shock), triggered by 10-fold dilution of BHI medium, induced bacterial adhesion irrespective of growth temperature. Physicochemical changes including rearrangement of cell membrane composition induced by hypoosmotic stress may have facilitated the bacterial adhesion to abiotic surfaces. The molecular pathways behind the unfavourable stimuli such as cold shock and nutrient stress need further investigation with regard to the bacterial adhesion and transition to sessile mode of life. However, prolonged nutrient deprivation impeded mature biofilm production. Addition of 0.85% NaCl stimulated biofilm production and surprisingly, it significantly intensified biofilm maturation of cells under nutrient-deprived condition. Appropriate salinity seems important for biofilm production since nutrient deficiency resulted in significant differences in mature biofilm production depending on the NaCl contents in growth media. To accurately determine the impact of salinity on biofilm production, growth kinetics under different conditions need to be taken into account when comparing biofilm phenotypes. Also, as environmental conditions differentially affected adhesion and maturation steps, it is necessary to investigate molecular background behind it at each point that represents well adhesion, maturation, and dispersal under various conditions to elucidate the complex mechanisms governing biofilm formation.

Pan-GWAS was applied for the first time to assess presence/absence profiles of genes in association with biofilm production which identified numerous genes. Even though the number of shared genes across the conditions was low due to high genomic variations, patterns of genes were comparable in terms of functions and processes of genetic products. Among the total list of genes functions including 'cell surface proteins', 'soluble internalin', 'transformation/competence', 'metabolism of phosphate', and 'phage-related functions' were more than 50% enriched. Cell surface proteins including internalins as adhesins are previously implicated in cellular adhesion and intercellular interaction during biofilm maturation. The extracellular DNA found in biofilm matrix of *L. monocytogenes* will need further investigation for their role in transformation during biofilm formation. Similarly, phage-related genes will need to be studied for their role in horizontal gene transfer. Comparing biofilm production at each step between a mutant lacking or overexpressing those genes and wildtype bacteria will uncover their role in biofilm formation. The application of GWAS and its derived approaches is of great value as a tool for screening determinants of bacterial characteristics in a heterogeneous species like *L. monocytogenes*. The presented results may expand to future studies that will integrate a larger panel of isolates with more genomic and phenotypic findings. Moreover, improvement of bioinformatic tools which will be able to utilize continuous numerical data such as optical densities from MPA instead of binary conversion of phenotypes will increase reliability of such metadata analysis.

The thesis work could not unravel biofilm phenotypes in association with bacterial characteristics such as persistence or prevalence. First of all, the conventional practice for determining persistent clones is doubted since some isolates belonging to the same persistent clone revealed significant variations in biofilm phenotypes. In the study isolates having the same genotype by PFGE or MLST subtyping method were recognized as persistent clones when they were recovered more than 3 times from the same FPE and related food products over the minimum 1 year of sampling period. However, in reality it is difficult to exclude isolates of the same genotype or even actual clones being re-introduced to the FPE at different times via raw materials or infected personnel. Moreover, it is debated whether a specific subtype persist in FPE or some isolates incidentally colonize specific niches in FPE being interpreted as persistent. In the latter case, research of *L. monocytogenes* behaviours in FPE will need to be redirected toward defining and exploring the niches specific for harbouring the bacterium which in turn will improve regulations and practices concerning food safety against *L. monocytogenes* contamination. Secondly, the frequency of genotypes in food isolates may simply reflect their distribution pattern in nature rather than being selected by certain bacterial characteristics that we attempted to discover. Accumulation and exchange of data regarding the *L. monocytogenes* in natural habitat especially in vegetation sites and

domesticated animals for food sources will answer this question. Lastly, the experimental setups used in the present study for assessing biofilm phenotypes may not reflect well the actual conditions in FPE. Also, other FPE-related factors such as desiccation, disinfectant, or pH stresses need to be investigated with regard to bacterial adaptability and resistance and their impact on bacterial transition into a sessile lifestyle as well as a viable but nonculturable status which is of great concern in food safety.

Copious genomic data highlight the intraspecies variations in gene repertoire that underlies differential adaptation strategies between isolates, including infection and stress resistance to some extent. Moreover, an extensive transcriptional reshaping upon transition from extracellular to intracellular lifestyle evidences the importance of the fine-tuning of the transcriptional regulatory network for the bacterial fitness in the host system and the following onset of infection. Supporting this, some studies reported incongruity in basal transcriptome between isolates that featured characteristics of isolates such as virulence potentials in some pathogenic bacteria. In this regard investigating intraspecific transcriptomic diversity is tempting, however, is more difficult to perform than genomic analyses because *L. monocytogenes* readily alter transcriptome profiles in response to slight environmental changes. Moreover, the concept of deducing relationships between phenotypic observations and basal transcript levels is not yet well established. Therefore, the approach presented by the thesis work which explored the basal transcriptome heterogeneity with regard to virulence characteristics was unconventional and innovative. Also, we performed a high-throughput virulence assay using an alternative *in vivo* model, *Galleria mellonella* larvae to efficiently compare virulence potential among a large set of isolates.

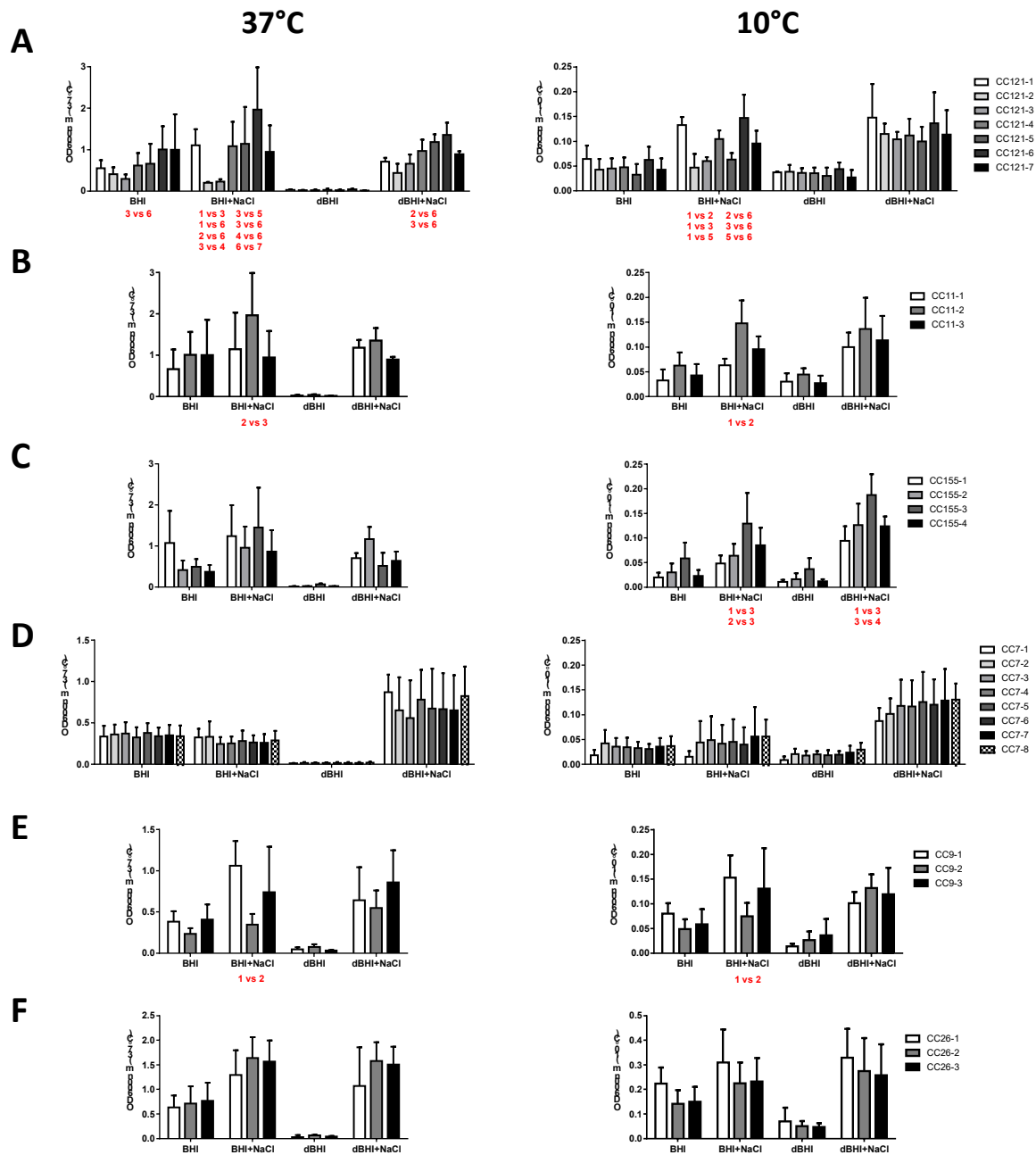
Transcriptomic profiles of 33 distinctive isolates grown in BHI media until exponential phase were analysed in depth by using RNA sequencing. Importantly, the thesis demonstrated the application of Principal Component Analysis and subsequent analytic processes in detail which refined the metadata to strengthen experimental reproducibility and improve statistical power of correlation analyses with covariates. The baseline transcriptomes among isolates proved intrinsically more complex than genome comparison because of inherent plasticity of gene expression in response to the environmental conditions. Certain transcriptional factors with key roles in virulence such as σB , PrfA, and CodY contributed to the major variations in basal transcripts level. High diversity of transcriptomes between lineage I and II as well as hyper- and hypovirulent genotypes supported the evolutionary characteristics that parallels previously reported epidemiological differences. The results underscore the importance of transcriptomic plasticity in the physiology and pathogenesis of *L. monocytogenes*. Transcripts level of numerous genes related to sugar metabolism and transport found to be correlated with *in vivo* virulence potential suggesting the involvement of central metabolic pathways in

the infection in *G. mellonella* model system. In the thesis, the infection in *G. mellonella* was established by injecting bacterial suspension into haemolymph which is equal to blood in vertebrate. However, since the onset of *L. monocytogenes* infection in human is largely dependent on its survival in gastrointestinal track and invasion of intestinal epithelial cells, administration of the bacteria via oral gavage may improve the reliability of the *in vivo* virulence data. Additionally, accumulating epidemiologic data with detailed clinical descriptions can be employed in future analysis.

During the last decades the standard subtyping method for *L. monocytogenes* isolates moved from PFGE to MLST and the recent years witnessed the emergence and prospect of WGS as a tool for routine subtyping method due to its greater discriminatory power accompanied by decreasing cost. Implementation of WGS technique and standardized method for genotyping as the reference in research, clinical and public laboratories will capacitate rapid identification and tracking of a suspected isolate and facilitate efficient communication in case of a listeriosis outbreak. Also, it will enable more accurate detection of persistent, or at least recurrent, isolates in FPE which can be a potential threat for society. Indeed, as asserted by multinational outbreaks, an integrative global effort is inevitable for controlling *L. monocytogenes* as well as other hazardous microbes. In this regard, there is a need for researchers and stakeholders to develop a web-based platform for efficient storing and sharing of various information including metadata which will undoubtedly open a new era. As an early attempt, the thesis work generated invaluable phenotypic, genomic, and transcriptomic datasets and presented innovative approaches to disclose the complex mechanisms behind *L. monocytogenes* intraspecific heterogeneity. The upcoming innovative strategies and integration of other high-throughput omics approaches will continue to complete the understanding of physiology and pathogenesis of *L. monocytogenes*.

Chapter VII
Supplementary materials

Chapter IV



Supplementary Figure 1. Intra-genotype comparison of biofilm formation. MPA results of isolates belonging to the same subtype are presented as mean + SD. Graphs on the left for 37°C and right for 10°C of (A) CC121, (B) CC11, (C) CC155, (D) CC7, (E) CC9, and (F) CC26. The number following the hyphen indicates the strains within each genotype in the legend. Data were analysed using One-way ANOVA and Tukey's multiple comparisons test. Pairs of strains showing significant differences are noted under each growth condition, $p < 0.05$.

Supplementary Table 1. List of genes associated with biofilm phenotype in BHI media at 37°C after pan-GWAS (p < 0.05).

GWAS name	Uniprot Entry	Organism ¥	Gene name	Protein names	Function al category †	% in weak biofilm formers	% in strong biofilm formers
group_1986	UPI00047C87C6			hypothetical protein	4.3.0	2.33	50.00
group_4801	A0A3A2R9E5		<i>D3B46_07385</i>	Uncharacterized protein		0.00	35.71
group_893	Q8Y802		<i>lmo1117</i>	Lmo1117 protein	6.0.0	60.47	7.14
group_5501	A0A392ZMB7		<i>inlA_5</i>	Internalin-A (LPXTG cell wall anchor domain-containing protein)		13.95	64.29
group_3614	UPI000BDFAB31			hypothetical protein		20.93	71.43
group_3690	A0A393TFG3		<i>AF876_00592</i>	Uncharacterized protein		6.98	50.00
group_4887	A0A392Z6S3		<i>ABY94_00615</i>	Uncharacterized protein		6.98	50.00
group_2681	A0A3A2N2S0		<i>D3B30_04480</i>	DUF4274 domain-containing protein		6.98	50.00
group_4899	A0A393JAZ3		<i>inlA_6</i>	DUF5011 domain-containing protein (Internalin-A)		16.28	64.29
group_1913	A0A3A2RAJ4		<i>AF237_14650</i>	Uncharacterized protein		11.63	57.14
marA	Q8Y803		<i>lmo1116</i>	Lmo1116 protein	3.5.2	55.81	7.14
group_5936	A0A394SL40		<i>AF237_14660</i>	Uncharacterized protein		4.65	42.86
group_3668	A0A3A2JQP2		<i>D3B79_08735</i>	PBSX family phage terminase large subunit		4.65	42.86
group_474	A0A393CRL8		<i>AF264_01650</i>	Putative sulfate transporter (SulP family inorganic anion transporter)	1.2.0	44.19	0.00
group_3691	A0A3A2TPS8		<i>D3B72_03010</i>	DUF4274 domain-containing protein		9.30	50.00
group_5935	UPI0005C68DD0			hypothetical protein	4.3.0	0.00	28.57
group_3804	UPI0005DF0EE0		<i>UF18_04880</i>	Uncharacterized protein		0.00	28.57
group_5979	A0A393TCN4		<i>AF828_02778</i>	Uncharacterized protein		0.00	28.57
group_3849	UPI000C82ECAA		<i>AE052_00662</i>	Uncharacterized protein		0.00	28.57
group_513	A0A393M724		<i>DN831_08165</i>	Uncharacterized protein	6.0.0	0.00	28.57
group_6217	UPI00076181B6			hypothetical protein	6.0.0	0.00	28.57
hin	A0A3A2JMV4		<i>hin_1</i>	DNA-invertase hin (Recombinase family protein)	4.3.0	16.28	57.14
group_4197	UPI00098E3EF0			hypothetical protein		48.84	7.14
gadB_2	A0A241SSP1		<i>gadB</i>	Glutamate decarboxylase (EC 4.1.1.15)	2.2.0	90.70	57.14
group_3660	A0A0H3GIL3		<i>LMRG_01530</i>	Gp68		2.33	28.57
group_5631	A0A3A2SG05		<i>AF944_00595</i>	Uncharacterized protein		2.33	28.57
group_3808	A0A3A2SPJ1		<i>AF944_00596</i>	Uncharacterized protein		2.33	28.57
group_5617	A0A394RIH7		<i>AF239_05370</i>	Uncharacterized protein		2.33	28.57
group_5618	A0A394SSM4		<i>AF240_05645</i>	Uncharacterized protein		2.33	28.57
group_1228	A0A2Z5C2Q2		<i>RK57_10170</i>	DUF917 domain-containing protein	5.2.0	97.67	71.43
group_120	A0A3A2RM25		<i>D3B79_08840</i>	Uncharacterized protein	4.3.0	2.33	28.57
xerC_2	A0A393N2F1		<i>DOM71_15540</i>	Site-specific integrase		2.33	28.57
group_672	A0A1B2LR20		<i>pLM-C-273_00081</i>	Uncharacterized protein		30.23	71.43

group_1807	UPI000BE00DE2		hypothetical protein		44.19	7.14
group_4344	Q8YA33	<i>lmo0332</i>	Lmo0332 protein	6.0.0	55.81	14.29
group_904	A0A3A7P9G8	<i>inlJ_10</i>	Class 1 internalin InlL (Internalin-J)	1.8.0	34.88	0.00
group_2741	A0A3A2SDU8	<i>D3B73_13335</i>	SMI1/KNR4 family protein	6.0.0	34.88	0.00
mtlR_4	A0A3A8C544	<i>mtlR_1</i>	Transcriptional regulator MtlR	3.5.2	34.88	0.00
group_489	A0A393SSR6	<i>AF245_00250</i>	SMI1/KNR4 family protein	6.0.0	65.12	100.00
group_4686	A0A393MBE2	<i>cas7i</i>	Type I-B CRISPR-associated protein Cas7/Cst2/DevR		37.21	78.57
group_302	UPI000BE05055		hypothetical protein	5.1.0	62.79	21.43
group_2660	A0A3A7IMJ8	<i>cas8a1</i>	Type I-B CRISPR-associated protein Cas8b1/Cst1		37.21	78.57
group_6207	A0A3A7FSY6	<i>DYZ81_02933</i>	Uncharacterized protein		0.00	21.43
group_6204	A0A393NA30	<i>AB922_02135</i>	Uncharacterized protein		0.00	21.43
group_6218	Q8Y4W6	<i>lmo2313</i>	Lmo2313 protein	4.3.0	0.00	21.43
group_6215	A0A393UIF1	<i>DCT05_15210</i>	DUF1837 domain-containing protein		0.00	21.43
group_5642	A0A3A7KKC0	<i>AB922_01978</i>	DNA helicase (EC 3.6.4.12)		0.00	21.43
group_6211	A0A393N8B1	<i>DCT13_10510</i>	Uncharacterized protein		0.00	21.43
group_6210	A0A247D711		Associated protein		0.00	21.43
group_6212	A0A3A7FBG4	<i>DCT05_15235</i>	Uncharacterized protein		0.00	21.43
yjcD	UPI00093184AE		ATP-dependent helicase		0.00	21.43
group_6222	UPI0001B714EA	<i>AF262_13565</i>	Uncharacterized protein		0.00	21.43
group_6221	A0A393UC33	<i>AEZ78_01333</i>	N4-gp56 family major capsid protein		0.00	21.43
group_6223	UPI00086A6C7E		hypothetical protein		0.00	21.43
group_6224	A0A393MXG5	<i>amid</i>	Amidase (Putative amidase AmiD) (EC 3.5.1.4)		0.00	21.43
group_6225	A0A3A7FQS4	<i>ydde</i>	PhzF family phenazine biosynthesis protein (Putative isomerase YddE) (EC 5.1.-.-)	5.2.0	0.00	21.43
group_5639	UPI0006798459		SLATT domain-containing protein		0.00	21.43
group_5636	UPI000E722DA8	<i>AF269_05195</i>	Uncharacterized protein (Fragment)	5.1.0	0.00	21.43
group_5637	A0A3A7KQ90	<i>AB922_01984</i>	Uncharacterized protein		0.00	21.43
group_6220	A0A393UC43	<i>D3B99_08750</i>	DUF1064 domain-containing protein	4.3.0	0.00	21.43
group_5844	A0A392YQG8	<i>AF844_02972</i>	Uncharacterized protein	6.0.0	0.00	21.43
group_5841	A0A3A7BU98	<i>D3B69_09415</i>	Chorismate synthase	6.0.0	0.00	21.43
group_5840	A0A3A7BL13	<i>D3B69_08805</i>	ATP-binding protein		0.00	21.43
group_5843	A0A3A2R8P7	<i>D3B69_09405</i>	DUF5081 family protein	6.0.0	0.00	21.43
group_5842	A0A3A2NZC0	<i>D3B69_09410</i>	WXG100 family type VII secretion target	6.0.0	0.00	21.43
group_5242	A0A393UDW4	<i>DCT05_12755</i>	Uncharacterized protein	6.0.0	0.00	21.43
group_5643	UPI000E74A098	<i>AF269_05155</i>	ATP-dependent endonuclease (Fragment)		0.00	21.43
bmrR	UPI0000F53E35	<i>ARJ20_03215</i>	MerR family transcriptional regulator	3.5.2	100.00	78.57
group_6208	A0A393VMB4	<i>AF240_14725</i>	Uncharacterized protein		0.00	21.43
group_5833	C6ZXJ8	<i>purM</i>	Phosphoribosylformylglycinamide cyclo-ligase (EC 6.3.3.1) (Phosphoribosyl-aminoimidazole synthetase)	2.3.0	0.00	21.43

group_3866	A0A3A2KPA5	<i>D3C41_12940</i>	DUF1642 domain-containing protein	4.3.0	0.00	21.43
group_123	A0A394WPT0	<i>AF251_11515</i>	Uncharacterized protein	4.3.0	0.00	21.43
group_6214	A0A393UF83	<i>recF_2</i>	ATP-dependent endonuclease (DNA replication and repair protein RecF)		0.00	21.43
group_5641	UPI000BE0786D		hypothetical protein		0.00	21.43
group_5640	A0A3A8A402	<i>AB922_01980</i>	Nucleotidyltransferase		0.00	21.43
spkB_1	UPI0009873B89		pentapeptide repeat-containing protein	6.0.0	0.00	21.43
group_5653	A0A393VB96	<i>AB922_02764</i>	Uncharacterized protein		0.00	21.43
purM	C1KW66	<i>purM</i>	Phosphoribosylformylglycinamide cyclo-ligase (EC 6.3.3.1) (Phosphoribosyl-aminoimidazole synthetase)	2.3.0	100.00	78.57
group_1993	UPI000BE107B2		DEAD/DEAH box helicase		0.00	21.43
group_5638	A0A3A7E261	<i>AB922_01982</i>	XRE family transcriptional regulator		0.00	21.43
group_5835	A0A3A7QPE8	<i>AF840_01803</i>	Uncharacterized protein		0.00	21.43
group_5836	A0A3A2RH67	<i>D3B69_08785</i>	Appr-1-p processing protein		0.00	21.43
group_6216	A0A393VME7	<i>xre_2</i>	HTH-type transcriptional regulator Xre (Helix-turn-helix domain- containing protein)	3.5.2	0.00	21.43
group_6205	A0A3A7PK56	<i>AB922_02136</i>	Uncharacterized protein		0.00	21.43
group_504	UPI000BDE7A67		class 1 internalin InII	1.8.0	0.00	21.43
group_6199	UPI000D735265		DUF1310 family protein	5.1.0	0.00	21.43
group_6202	A0A393WEP5	<i>D3C41_12930</i>	Uncharacterized protein	4.3.0	0.00	21.43
group_2705	A0A394RVL7	<i>AF240_04685</i>	DNA helicase (EC 3.6.4.12)		0.00	21.43
group_5838	A0A3A2NKZ5	<i>D3B79_09090</i>	Uncharacterized protein		0.00	21.43
group_5839	A0A3A2TU61	<i>D3B69_08800</i>	SIR2 family protein		0.00	21.43
group_6206	A0A393E6L1	<i>DCT05_12765</i>	DUF2481 domain-containing protein		0.00	21.43
group_5837	UPI00098E44F1		Appr-1-p processing protein		0.00	21.43
group_6203	UPI000BE0E517		pentapeptide repeat-containing protein	6.0.0	0.00	21.43
group_6200	A0A3A2TUU6	<i>bmrr</i>	MerR family transcriptional regulator (Multidrug-efflux transporter 1 regulator)	3.5.2	0.00	21.43
group_6201	A0A393UPN4	<i>AFX94_02538</i>	Uncharacterized protein		0.00	21.43
group_5509	A0A3A2KDS0	<i>AF273_15200</i>	Uncharacterized protein		18.60	57.14
group_3797	A0A3A2L4U9	<i>AF238_14470</i>	Uncharacterized protein		18.60	57.14
group_673	A0A394V0T8	<i>AF237_14690</i>	Uncharacterized protein		32.56	71.43
group_4631	UPI00074D6448	<i>LM901004_160002</i>	Uncharacterized protein		32.56	71.43
ssb_4	UPI000BE1101C		hypothetical protein		32.56	71.43
group_3636	A0A3A2YAK1	<i>cas5b</i>	Type I-B CRISPR-associated protein Cas5		39.53	78.57
cas1	UPI00092E4084	<i>B0X19_02870</i>	CRISPR-associated endonuclease Cas1		39.53	78.57
cas3	UPI00083D7946		CRISPR-associated helicase/endonuclease Cas3		39.53	78.57
cas2	A0A0E0UTU7	<i>cas2</i>	CRISPR-associated endoribonuclease Cas2 (EC 3.1.-.-)		39.53	78.57
group_2659	A0A3A7SZG9	<i>cas6</i>	CRISPR-associated endoribonuclease Cas6		39.53	78.57

group_481	A0A3A7DXN2	<i>AB922_02752</i>	Uncharacterized protein		6.98	35.71
group_5654	A0A394RQC8	<i>AB922_02753</i>	Ribonuclease BN		6.98	35.71
group_2049	A0A393T6R3	<i>AF818_02839</i>	Uncharacterized protein	4.3.0	6.98	35.71
group_1262	UPI000873C4F1		DUF1310 family protein	5.1.0	20.93	57.14
group_958	UPI00003CA3F3	<i>AF262_13785</i>	Uncharacterized protein		11.63	42.86
group_2733	A0A3A7T550	<i>clpP1</i>	ATP-dependent Clp protease proteolytic subunit		11.63	42.86
group_2178	A0A3A7KNB4	<i>gadB_1</i>	Glutamate decarboxylase (EC 4.1.1.15)	2.2.0	11.63	42.86
group_5457	A0A393UJV3	<i>AF828_00146</i>	Phage gp6-like head-tail connector protein		11.63	42.86
group_4888	A0A393CGK6	<i>AF876_00589</i>	Uncharacterized protein	5.1.0	11.63	42.86
group_5418	A0A393W8P8	<i>AF847_02885</i>	Uncharacterized protein	4.3.0	11.63	42.86
group_2710	UPI00003CA3EB	<i>AE052_00030</i>	DUF3954 domain-containing protein		11.63	42.86
group_5415	A0A394VMA7	<i>AF239_12500</i>	Uncharacterized protein		11.63	42.86
group_1934	A0A392XCY7	<i>AF828_00150</i>	Phage tail protein		11.63	42.86
group_5416	A0A394VX67	<i>AF239_12505</i>	Uncharacterized protein		11.63	42.86
group_2040	A0A3A7F101	<i>AF264_14455</i>	Ribonuclease (EC 3.1.-.-)	5.2.0	58.14	92.86
group_676	Q8Y496	<i>ami</i>	Autolysin, amidase	1.8.0	69.77	100.00
group_2522	A0A3A2PCV4	<i>comEC_1</i>	ComE operon protein 3 (MBL fold metallo-hydrolase)	1.10.0	30.23	0.00
group_2647	A0A3A2YHL0	<i>AF252_05590</i>	ATP-dependent helicase (DEAD/DEAH box helicase)		30.23	0.00
group_131	A0A393RNT2	<i>AF264_14030</i>	Uncharacterized protein	6.0.0	30.23	0.00
group_1298	Q8Y842	<i>lmo1076</i>	Lmo1076 protein	1.1.0	69.77	100.00
group_2523	A0A0B8QZ29	<i>LmNIHS28_01111</i>	ComE operon protein 3	1.10.0	72.09	100.00
group_1062	A0A393CV23	<i>AF264_09920</i>	Glycoside hydrolase family 65 protein	2.1.1	27.91	0.00
group_5799	UPI00092FB1F5		arsenic metallochaperone ArsD family protein		27.91	0.00
group_4465	Q8Y7Z7	<i>lmo1122</i>	Lmo1122 protein	5.1.0	51.16	14.29
group_2122	A0A3A2WTD5	<i>AF264_12285</i>	DUF4969 domain-containing protein	5.2.0	51.16	14.29
group_2594	Q8Y7Z5	<i>lmo1124</i>	Lmo1124 protein	5.1.0	51.16	14.29
group_2805	A0A3A7LSN2	<i>AF818_02838</i>	Uncharacterized protein		16.28	50.00
group_3818	A0A3A7FAB2	<i>inlb_6</i>	Internalin B (LPXTG cell wall anchor domain-containing protein)		4.65	28.57
group_5531	Q2V4W5	<i>pCT0006</i>	Site-specific recombinase, resolvase family		4.65	28.57
group_5704	UPI000E74C0A2		hypothetical protein	5.1.0	4.65	28.57
group_5549	A0A393VTF5	<i>AF236_15595</i>	Uncharacterized protein		4.65	28.57
group_5702	A0A393BLD4	<i>AF840_02465</i>	Cupin domain-containing protein		4.65	28.57
group_5584	UPI000E73B5A8		hypothetical protein		4.65	28.57
group_5586	A0A392WM50	<i>AB922_00582</i>	Uncharacterized protein		4.65	28.57
group_5582	A0A393RIL7	<i>AB922_00586</i>	Uncharacterized protein		4.65	28.57
licA_5	A0A3A6X849	<i>lica_3</i>	Lichenan-specific phosphotransferase enzyme IIA component (EC 2.7.1.-) (PTS lactose/cellobiose transporter subunit IIA)		4.65	28.57
group_5588	A0A3A7P0S6	<i>AB922_00580</i>	Uncharacterized protein		4.65	28.57
group_5589	UPI000BE0B2D8		plasmid replication protein		4.65	28.57

group_5566	A0A393QP03	<i>AF236_15520</i>	Uncharacterized protein	4.65	28.57
group_5562	A0A394RJT3	<i>AB922_00606</i>	Uncharacterized protein	4.65	28.57
group_5563	A0A393TGS3	<i>AB922_00605</i>	DUF87 domain-containing protein	4.65	28.57
group_5560	A0A393PMD5	<i>AB922_00608</i>	Uncharacterized protein	4.65	28.57
group_5561	A0A393VTG5	<i>AB922_00607</i>	Uncharacterized protein	4.65	28.57
group_5568	A0A393QVU4	<i>AB922_00600</i>	Uncharacterized protein	4.65	28.57
group_5569	A0A392WH96	<i>AB922_00599</i>	Uncharacterized protein	4.65	28.57
rsrIM	UPI00003CAA42	<i>pLIS100090</i>	DNA modification methylase	4.65	28.57
bacD	A0A3A6XBZ3	<i>ddaf</i>	ATP-grasp domain-containing protein (Dapdiamide A synthase) (EC 6.3.2.47)	4.65	28.57
group_5585	A0A3A7M9C2	<i>AB922_00583</i>	XRE family transcriptional regulator	4.65	28.57
group_5593	A0A393W756	<i>AB922_00575</i>	Restriction endonuclease	4.65	28.57
group_2737	A0A393FQK7	<i>AF840_02461</i>	Uncharacterized protein	4.65	28.57
group_5591	A0A393QQU6	<i>AB922_00577</i>	Uncharacterized protein	4.65	28.57
group_5594	A0A1X9VTW9	<i>Leuconostoc mesenteroides</i> <i>BSR26_10010</i>	DNA methyltransferase	4.65	28.57
group_5587	UPI000EF5BA74		IS3 family transposase	4.65	28.57
group_5533	Q2V4W3	<i>pCT0008</i>	Cation-transporting ATPase E1-E2 family	4.65	28.57
group_5581	D7V1H8	<i>Listeria grayi</i> <i>HMPREF0556_plasmid12603</i>	Uncharacterized protein	4.65	28.57
group_5575	A0A393NXT1	<i>AB922_00593</i>	Uncharacterized protein	4.65	28.57
group_5574	UPI000EF5AA7F		ImmA/IrrE family metallo-endopeptidase	4.65	28.57
group_3816	A0A393UXZ0	<i>ARL28_13835</i>	MFS transporter	4.65	28.57
group_5571	A0A3A7JXP8	<i>AB922_00597</i>	Restriction endonuclease	4.65	28.57
group_5570	A0A393QNC4	<i>AB922_00598</i>	Riboflavin synthase subunit alpha	4.65	28.57
group_5573	A0A3A7W8P2	<i>AB922_00595</i>	Uncharacterized protein	4.65	28.57
group_5572	A0A393SKE9	<i>AF236_15490</i>	Uncharacterized protein	4.65	28.57
group_5583	A0A3A7W8N1	<i>AB922_00585</i>	Uncharacterized protein	4.65	28.57
group_5579	A0A3A7ST51	<i>AB922_00589</i>	Uncharacterized protein	4.65	28.57
group_5534	UPI000931B2A1		transporter	4.65	28.57
group_5537	S5XI53		Pli0065	4.65	28.57
group_5580	UPI00003CAA45	<i>AJN46_07220</i>	Uncharacterized protein	4.65	28.57
group_5567	A0A393SB73	<i>AB922_00601</i>	Fructose 1,6-bisphosphatase	4.65	28.57
group_5564	A0A3A7VTB4	<i>AB922_00604</i>	Uncharacterized protein	4.65	28.57
gpmA_7	A0A3A7X7L3	<i>pspB</i>	Histidine phosphatase family protein (Putative phosphoserine phosphatase 2) (EC 3.1.3.3)	4.65	28.57
group_5578	A0A3A7K0H3	<i>AB922_00590</i>	Uncharacterized protein	4.65	28.57
nucH	A0A3A7QU08	<i>nucH</i>	Thermonuclease (EC 3.1.31.1)	4.65	28.57

ybbH_3	A0A393LHT2	<i>ybbh_3</i>	MurR/RpiR family transcriptional regulator (Putative HTH-type transcriptional regulator YbbH)	4.65	28.57
group_5700	A0A393I885	<i>AFT78_13605</i>	Uncharacterized protein	4.65	28.57
nanE_2	A0A3A7NDZ8	<i>nanE_1</i>	Putative N-acetylmannosamine-6-phosphate 2-epimerase (EC 5.1.3.9) (ManNAc-6-P epimerase)	4.65	28.57
tnsB	S5XPZ4		Putative transposase	4.65	28.57
group_5592	A0A3A7AMA0	<i>AB922_00576</i>	Site-specific DNA-methyltransferase	4.65	28.57
group_5697	A0A393V6K3	<i>AF840_02454</i>	DUF4127 family protein	4.65	28.57
group_3854	A0A3A7V0R5	<i>AF951_02096</i>	Uncharacterized protein	3.5.2 4.65	28.57
cwI_O_1	A0A3A7JTC0	<i>cwI_O_2</i>	Peptidoglycan DL-endopeptidase CwI_O (EC 3.4.-.-)	4.65	28.57
group_3799	A0A3A7AUB6	<i>AB922_00627</i>	Uncharacterized protein	4.65	28.57
group_5548	A0A393I3M4	<i>AB922_00620</i>	Uncharacterized protein	4.65	28.57
group_5551	D7V1E8	<i>Listeria grayi HMPREF0556_plasmid12573</i>	Uncharacterized protein	4.65	28.57
group_5540	A0A393VTE6	<i>AB922_00629</i>	Uncharacterized protein	4.65	28.57
group_5541	A0A3A7TQJ4	<i>AB922_00628</i>	Uncharacterized protein	4.65	28.57
group_5542	UPI000EF5635A		DUF3324 domain-containing protein	4.65	28.57
copY	A0A392WH77	<i>copy</i>	CopY/TcrY family copper transport repressor (Transcriptional repressor CopY)	4.65	28.57
group_5544	A0A3A7WL76	<i>AB922_00624</i>	Uncharacterized protein	4.65	28.57
group_5545	A0A3A7TAI8	<i>AB922_00623</i>	Uncharacterized protein	4.65	28.57
group_5546	A0A393QVS4	<i>AB922_00622</i>	Putative conjugal transfer protein (Type IV secretion protein)	4.65	28.57
group_5547	A0A3A7NVN4	<i>AB922_00621</i>	Uncharacterized protein	4.65	28.57
yigL	UPI00074D5656	<i>LM701345_50019</i>	Uncharacterized protein	4.65	28.57
group_5543	A0A393N4Q5	<i>AB922_00625</i>	Uncharacterized protein	4.65	28.57
licB_7	A0A3A7FKG5	<i>cela_5</i>	PTS sugar transporter subunit IIB (PTS system cellobiose-specific EIIB component) (EC 2.7.1.205)	4.65	28.57
rhIE	UPI000869703C		hypothetical protein	4.65	28.57
group_5550	UPI000D726E6E		hypothetical protein	4.65	28.57
group_3844	A0A0H3GMQ7	<i>LMRG_01523</i>	Gp45	4.65	28.57
group_5538	A0A393NZ28	<i>AF236_15655</i>	Uncharacterized protein	4.65	28.57
group_5559	A0A3A7MIR8	<i>AB922_00609</i>	Conjugal transfer protein TraG	4.65	28.57
group_5558	A0A393T254	<i>AB922_00610</i>	Uncharacterized protein	4.65	28.57
group_5557	A0A3A7NVP5	<i>AB922_00611</i>	Uncharacterized protein	4.65	28.57
group_5556	A0A393QNZ5	<i>AB922_00612</i>	Uncharacterized protein	4.65	28.57
group_5555	A0A3A7M9E3	<i>AB922_00613</i>	Uncharacterized protein	4.65	28.57
group_5554	A0A393N712	<i>AB922_00614</i>	Uncharacterized protein	4.65	28.57
group_5553	UPI000C86C85D	<i>C1118_15230</i>	Uncharacterized protein (Fragment)	4.65	28.57
group_5552	A0A393QP37	<i>AB922_00616</i>	Sodium:dicarboxylate symporter family protein	4.65	28.57
bin3	A0A3A7R6E9	<i>bin3</i>	DNA-invertase (Recombinase family protein)	4.65	28.57

group_5539	UPI0001B4211E	<i>AB922_00630</i>	Uncharacterized protein	4.65	28.57
group_5596	UPI000D729918		IS6 family transposase	4.65	28.57
group_5532	Q2V4W4	<i>pCT0007</i>	Cadmium efflux system accessory protein	4.65	28.57
group_5535	UPI000D73450A		DNA recombinase	4.65	28.57
group_5536	UPI000C86D6AB		IS6 family transposase	4.65	28.57
group_5924	A0A3A2Y1W1	<i>AF828_02779</i>	Uncharacterized protein	4.65	28.57
group_2739	A0A3A2S9A2	<i>D3B73_14375</i>	Uncharacterized protein	4.65	28.57
group_2736	A0A3A7VMA9	<i>rizA</i>	ATP-grasp domain-containing protein (L-arginine-specific L-amino acid ligase) (EC 6.3.2.48)	4.65	28.57
group_217	A0A3A7KP06	<i>AE052_02425</i>	Uncharacterized protein	4.65	28.57
group_6055	A0A3A7V312	<i>AF951_00084</i>	Uncharacterized protein	4.65	28.57
group_5508	A0A3A7W759	<i>AF951_01101</i>	Uncharacterized protein	34.88	71.43
group_1317	A0A1B2LR19	<i>pLM-C-273_00082</i>	Uncharacterized protein	34.88	71.43
group_494	A0A3A7W452	<i>AF947_01400</i>	Uncharacterized protein	34.88	71.43
group_1914	A0A1B2LR10	<i>pLM-C-273_00079</i>	Uncharacterized protein	34.88	71.43
group_1318	A0A1B2LR12	<i>pLM-C-273_00075</i>	Phage minor capsid protein 2	34.88	71.43
eccCa1	A0A393D7A8	<i>essC</i>	ESAT-6 secretion machinery protein EssC (Type VII secretion protein EssC)	5.2.0	48.84 14.29
group_2474	UPI000D72D1E5		DHA2 family efflux MFS transporter permease subunit	1.2.0	58.14 21.43
group_4470	A0A1D2IW15	<i>pduM</i>	Microcompartment protein PduM	6.0.0	30.23 64.29
group_5453	A0A2A6A785	<i>CDR86_09870</i>	XRE family transcriptional regulator	9.30	35.71
group_5451	A0A2A6A6P5	<i>CDR86_09885</i>	Uncharacterized protein	9.30	35.71
group_5454	A0A2A6A617	<i>CDR86_09865</i>	Uncharacterized protein	9.30	35.71
group_5445	UPI00083E1BDA		hypothetical protein	6.0.0	9.30 35.71
group_3782	A0A2A6A6S9	<i>CDR86_09890</i>	MerR family transcriptional regulator	9.30	35.71
group_3783	A0A2A6A5V6	<i>CDR86_09875</i>	XRE family transcriptional regulator	9.30	35.71
group_3780	A0A3A7G6J0	<i>AF847_01785</i>	DUF3850 domain-containing protein	9.30	35.71
group_903	A0A3A2NUT3	<i>inlJ_11</i>	Internalin-J (Peptidoglycan-binding protein)	1.8.0	9.30 35.71
emrY	A0A3A8BX24	<i>emrY</i>	Putative multidrug resistance protein EmrY	1.2.0	44.19 78.57
group_311	A0A3A7W0T2	<i>AF947_01398</i>	Uncharacterized protein	37.21	71.43
group_1331	A0A394UA13	<i>AF237_14675</i>	Uncharacterized protein	37.21	71.43
group_2567	Q7AP83	<i>lmo0320</i>	Lmo0320 protein	1.8.0	37.21 71.43
group_2636	A0A1B2LR21	<i>pLM-C-273_00076</i>	Uncharacterized protein	37.21	71.43
group_5829	A0A3A2NRD8	<i>D3B69_11250</i>	SLATT domain-containing protein	2.33	21.43
traD	A0A3A8AEL8	<i>traG</i>	Conjugal transfer protein TraG	2.33	21.43
group_3721	UPI000E75D1DC	<i>AF274_11855</i>	PBSX family phage terminase large subunit	4.3.0	2.33 21.43
group_2744	UPI00086BB360		DUF1642 domain-containing protein	4.3.0	2.33 21.43
group_92	Q8Y4Z9	<i>lmo2280</i>	Protein gp23 [Bacteriophage A118]	4.3.0	2.33 21.43
group_795	A0A394ZJJ3	<i>AF264_07275</i>	VanZ family protein	5.2.0	97.67 78.57

group_5996	UPI0008544E8C	AF973_04920	SAM-dependent methyltransferase		2.33	21.43
group_5201	A0A3A7FNT3	D3C41_12945	Uncharacterized protein		2.33	21.43
group_3829	A0A393T810	AF238_05420	Uncharacterized protein		2.33	21.43
group_4673	A0A2A6A8Y8	CDR86_05485	Uncharacterized protein		2.33	21.43
group_5890	UPI000E6CF39C		siphovirus Gp157 family protein		2.33	21.43
group_3867	A0A393UGI5	DCT05_12735	Uncharacterized protein		2.33	21.43
group_5665	A0A3A7G6E8	sirc	Bifunctional precorrin-2 dehydrogenase/sirohydrochlorin ferrochelata- (Precorrin-2 dehydrogenase) (EC 1.3.1.76)	2.5.0	2.33	21.43
group_122	A0A393VMD8	AF255_13120	Uncharacterized protein	4.3.0	2.33	21.43
group_121	A0A3A2SMD7	D3B75_07210	Uncharacterized protein	4.3.0	2.33	21.43
group_4815	UPI00083E20EE		hypothetical protein		2.33	21.43
group_5662	A0A3A7FE57	AF947_01444	Uncharacterized protein		2.33	21.43
group_3843	UPI0009801844	B0X19_13920	Uncharacterized protein	4.3.0	2.33	21.43
group_5889	A0A3A7GWW5	DYZ36_00768	Uncharacterized protein		2.33	21.43
group_5612	A0A393NK10	AB922_00245	Uncharacterized protein		2.33	21.43
group_962	A0A3A2KTR5	ssb	Single-stranded DNA-binding protein (SSB)	3.1.0	2.33	21.43
group_5241	A0A3A2Y2Q5	AFX76_02491	Uncharacterized protein	6.0.0	2.33	21.43
group_5125	UPI000E70CF52	AF274_11860	Terminase		2.33	21.43
group_379	A0A3A7RE78	inlJ_12	Internalin-J	1.8.0	2.33	21.43
dpnM	A0A394XMY4	AF274_05910	DNA adenine methylase	3.2.0	2.33	21.43
cwlK	A0A3A2RPP5	D3B77_10725	Alkaline phosphatase		2.33	21.43
group_2284	A0A3A2WY97	AF264_07280	Lmo1656 family SNX6-recruiting virulence factor	5.2.0	97.67	78.57
group_6209	A0A0H3GEB7	LMRG_01556	Gp27		2.33	21.43
group_5830	A0A3A2TSA1	D3B69_11245	Nucleotidyltransferase		2.33	21.43
group_3917	A0A0H3G8X1	LMRG_02492	Uncharacterized protein		39.53	7.14
group_2056	A0A3A6WUY8	AF251_14005	Uncharacterized protein		39.53	7.14
group_239	A0A392XPZ3	AF264_04535	Uncharacterized protein	5.1.0	79.07	50.00
group_1335	A0A3A2U4P7	AF236_08115	Phage baseplate upper protein	4.3.0	20.93	50.00
group_688	A0A3A7T3T4	cas1_2	CRISPR-associated endonuclease Cas1 (EC 3.1.-.-)		20.93	50.00
csbB	Q93RN0	mtrA	Dolichol-phosphate mannosyltransferase MtrA (Hypothetical glycosyl transferase)	1.1.0	74.42	100.00
group_1150	A0A394RBJ1	AF239_04485	Uncharacterized protein		25.58	0.00
tagH	UPI000BDFED64		teichoic acids export ABC transporter ATP-binding subunit TagH	1.1.0	74.42	100.00
rmlC	A0A1C7Q2S5	rfbC	dTDP-4-dehydrorhamnose 3,5-epimerase (EC 5.1.3.13) (Thymidine diphospho-4-keto-rhamnose 3,5-epimerase)	1.1.0	74.42	100.00
malP	Q8Y5E3	lmo2121	Lmo2121 protein	2.1.1	74.42	100.00
group_1153	A0A0E0UUS7	pncB	Nicotinate phosphoribosyltransferase (EC 6.3.4.21)	5.2.0	25.58	0.00

‡ Non *L. monocytogenes* species

† Description for each functional category code is presented below

- [1.1.0] Cell envelope and cellular processes > Cell wall
- [1.2.0] Cell envelope and cellular processes > Transport/binding proteins and lipoproteins
- [1.3.0] Cell envelope and cellular processes > Sensors (signal transduction)
- [1.4.0] Cell envelope and cellular processes > Membrane bioenergetics
- [1.5.0] Cell envelope and cellular processes > Mobility and chemotaxis
- [1.6.0] Cell envelope and cellular processes > Protein secretion
- [1.7.0] Cell envelope and cellular processes > Cell division
- [1.8.0] Cell envelope and cellular processes > Cell surface proteins
- [1.9.0] Cell envelope and cellular processes > Soluble internalin
- [1.10.0] Cell envelope and cellular processes > Transformation/competence
- [2.1.0] Intermediary metabolism > Metabolism of carbohydrates and related molecule
- [2.1.1] Intermediary metabolism > Metabolism of carbohydrates and related molecule > Specific pathways
- [2.1.2] Intermediary metabolism > Metabolism of carbohydrates and related molecule > Main glycolytic pathways
- [2.1.3] Intermediary metabolism > Metabolism of carbohydrates and related molecule > TCA cycle
- [2.2.0] Intermediary metabolism > Metabolism of amino acids and related molecules
- [2.3.0] Intermediary metabolism > Metabolism of nucleotides and nucleic acids
- [2.4.0] Intermediary metabolism > Metabolism of lipids
- [2.5.0] Intermediary metabolism > Metabolism of coenzymes and prosthetic groups
- [2.6.0] Intermediary metabolism > Metabolism of phosphate
- [3.1.0] Information pathways > DNA replication
- [3.2.0] Information pathways > DNA restriction/modification and repair
- [3.3.0] Information pathways > DNA recombination
- [3.4.0] Information pathways > DNA packaging and segregation
- [3.5.1] Information pathways > RNA synthesis > Initiation
- [3.5.2] Information pathways > RNA synthesis > Regulation
- [3.5.3] Information pathways > RNA synthesis > Elongation
- [3.5.4] Information pathways > RNA synthesis > Termination
- [3.6.0] Information pathways > RNA modification
- [3.7.1] Information pathways > Protein synthesis > Ribosomal proteins
- [3.7.2] Information pathways > Protein synthesis > Aminoacyl-tRNA synthetases
- [3.7.3] Information pathways > Protein synthesis > Initiation
- [3.7.4] Information pathways > Protein synthesis > Elongation
- [3.7.5] Information pathways > Protein synthesis > Termination
- [3.8.0] Information pathways > Protein modification
- [3.9.0] Information pathways > Protein folding
- [4.1.0] Other functions > Adaptation to atypical conditions
- [4.2.0] Other functions > Detoxification
- [4.3.0] Other functions > Phage-related functions
- [4.4.0] Other functions > Transposon and IS

[4.5.0] Other functions > Miscellaneous

[5.1.0] Similar to unknown proteins > From Listeria

[5.2.0] Similar to unknown proteins > From other organisms

[6.0.0] No similarity

Supplementary Table 2. List of genes associated with biofilm production in dBHI media at 37°C after pan-GWAS (p < 0.05).

GWAS name	Uniprot Entry	Gene name	Protein names	Functional category †	% in weak biofilm formers	% in strong biofilm formers
group_5020	A0A3A8BWY7	<i>CFSAN002345_002255</i>	Uncharacterized protein		2.17	45.45
group_5015	A0A3A2TJS8	<i>AFX42_02310</i>	Uncharacterized protein		0.00	36.36
clpP_1	A0A0B8R8I5	<i>clpP</i>	ATP-dependent Clp protease proteolytic subunit (EC 3.4.21.92) (Endopeptidase Clp)	4.1.0	100.00	63.64
group_5012	A0A3A2KHQ4	<i>AFX42_02307</i>	Uncharacterized protein		0.00	36.36
group_5013	UPI00074D6A4B	<i>DLE78_04650</i>	N-acetyltransferase		0.00	36.36
group_5010	UPI00074D6014	<i>DLE78_04630</i>	ATP-dependent Clp protease proteolytic subunit	4.1.0	0.00	36.36
group_5011	A0A393L9E6	<i>AFX42_02305</i>	Uncharacterized protein	6.0.0	0.00	36.36
group_5016	UPI000BE01261		hypothetical protein	6.0.0	0.00	36.36
group_5014	A0A3A7P6T3	<i>AFX42_02309</i>	Uncharacterized protein		0.00	36.36
group_1298	Q8Y842	<i>lmo1076</i>	Lmo1076 protein	1.1.0	86.96	36.36
group_2102	A0A3A7DM92	<i>AF264_12825</i>	NUDIX pyrophosphatase		13.04	63.64
group_4118	UPI000E6B7FBF		glycerol-3-phosphate cytidyltransferase		8.70	54.55
tagB_2	A0A1D2ISQ5	<i>CDR86_11250</i>	Glycosyl transferase family 2	1.1.0	91.30	45.45
group_477	Q8Y9M5	<i>lmo0501</i>	Lmo0501 protein	3.5.2	91.30	45.45
group_4119	UPI000035D008	<i>APS76_03080</i>	CDP-glycerol glycerophosphotransferase family protein		8.70	54.55
tagD	A0A1C7PZ73	<i>tagD</i>	Glycerol-3-phosphate cytidyltransferase	1.1.0	91.30	45.45
tagF	A0A3A8BW41	<i>tagF</i>	Teichoic acid poly(Glycerol phosphate) polymerase (EC 2.7.8.12)		8.70	54.55
epsJ	A0A3A7GEL8	<i>epsj</i>	Glycosyltransferase family 2 protein (Putative glycosyltransferase EpsJ) (EC 2.4.-.-)		8.70	54.55
lytG_5	A0A3A8BW61	<i>lytG_3</i>	Exo-glucosaminidase LytG (EC 3.2.1.-)		8.70	54.55
pncB2	A0A0D8X9Q4	<i>CDR86_11285</i>	Nicotinate phosphoribosyltransferase (EC 6.3.4.21)	5.2.0	91.30	45.45
group_4426	Q8Y8H1	<i>lmo0933</i>	Lmo0933 protein	1.1.0	91.30	45.45
group_4049	A0A3A8BMB0	<i>blaSE</i>	Serine protease (EC 3.4.21.-)		8.70	54.55
gtaB	UPI000931810D		UTP--glucose-1-phosphate uridylyltransferase GalU	1.1.0	91.30	45.45
ispD2_1	UPI0004D75A86	<i>HT50_11035</i>	2-C-methyl-D-erythritol 4-phosphate cytidyltransferase (Fragment)	2.1.0	91.30	45.45
group_3882	A0A3A6WVM4	<i>AF241_14355</i>	Uncharacterized protein	4.3.0	8.70	54.55
group_4238	A0A394Y3M2	<i>AF264_00535</i>	PH domain-containing protein		8.70	54.55
group_4030	A0A0B8R4F9	<i>LmNIHS28_01899</i>	Teichoic acid biosynthesis protein		8.70	54.55
group_3939	A0A0B8QQZ7	<i>LmNIHS28_00261</i>	Membrane protein		8.70	54.55
group_3938	Q9ZIC5	<i>LmNIHS28_00260</i>	Uncharacterized protein		8.70	54.55
group_4132	A0A3A2P6F9	<i>AF241_04305</i>	DUF5068 domain-containing protein		8.70	54.55
group_4131	A0A3A8BVC9	<i>tagG</i>	Transport permease protein		8.70	54.55
group_1860	Q8YA42	<i>lmo0322</i>	Lmo0322 protein	5.2.0	91.30	45.45
group_4446	Q8Y839	<i>lmo1079</i>	Lmo1079 protein	5.2.0	91.30	45.45

group_1891	Q8Y7T3	<i>lmo1188</i>	Lmo1188 protein	6.0.0	91.30	45.45
group_4454	Q8Y831	<i>tarJ</i>	Ribulose-5-phosphate reductase (Ribulose-5-P reductase) (EC 1.1.1.405) (Ribitol-5-phosphate dehydrogenase)	2.1.0	91.30	45.45
group_3885	A0A393D4V0	<i>AF264_14565</i>	Pyruvyl-transferase		8.70	54.55
group_4672	UPI0009305ABB		GtrA family protein	1.1.0	91.30	45.45
group_4123	A0A0E1R4Q8	<i>ispD2</i>	Ribitol-5-phosphate cytidyltransferase (EC 2.7.7.40)		8.70	54.55
group_2892	UPI0009B09F82		GW domain-containing glycosaminoglycan-binding protein	1.8.0	8.70	54.55
tagB_3	Q8Y830	<i>tagB</i>	TagB protein	1.1.0	91.30	45.45
group_2384	UPI000766C630	<i>ERS409610_00158</i>	Uncharacterized protein		8.70	54.55
ykoT	UPI000035CFFF	<i>NT04LM_1735</i>	Glycosyl transferase, group 2 family protein		8.70	54.55
sdpR	A0A3A8BPZ1	<i>sdpR</i>	Transcriptional repressor SdpR	3.5.2	8.70	54.55
group_965	UPI000D6455E8	<i>DF273_02615</i>	Uncharacterized protein (Fragment)		8.70	54.55
group_4237	A0A394YEX0	<i>AF264_00540</i>	Endonuclease (Endonuclease/exonuclease/phosphatase family protein)	5.2.0	8.70	54.55
gutB	A0A3A7GLG3	<i>tarj</i>	Ribulose-5-phosphate reductase (Ribulose-5-P reductase) (EC 1.1.1.405) (Ribitol-5-phosphate dehydrogenase)		8.70	54.55
group_4125	UPI000D66CEA1	<i>DF274_15095</i>	Uncharacterized protein (Fragment)		8.70	54.55
group_4124	A0A3A8BY01	<i>gtab</i>	UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) (UDP-glucose pyrophosphorylase)		8.70	54.55
group_4126	A0A3A7GN59	<i>tarl</i>	CDP-glycerol:glycerophosphate glycerophosphotransferase (Teichoic acid poly(Ribitol-phosphate) polymerase) (EC 2.7.8.-)		8.70	54.55
group_4130	UPI000D66B0A6	<i>tagH</i>	Teichoic acids export ABC transporter ATP-binding subunit TagH (Fragment)		8.70	54.55
group_3562	Q8Y850	<i>lmo1068</i>	Lmo1068 protein	6.0.0	91.30	45.45
group_3954	UPI000E3C8303		cell wall teichoic acid glycosylation protein GtcA		8.70	54.55
group_3925	A0A3A8BY26	<i>CFSAN002345_001436</i>	Uncharacterized protein		8.70	54.55
group_3454	A0A0B8RAV3	<i>LmNIHS28_01817</i>	Uncharacterized protein		8.70	54.55
rffG	A0A1D2IST6	<i>rfbB</i>	dTDP-glucose 4,6-dehydratase (EC 4.2.1.46)	1.1.0	91.30	45.45
arnT	A0A3A7F315	<i>arnt</i>	Phospholipid carrier-dependent glycosyltransferase (Undecaprenyl phosphate-alpha-4-amino-4-deoxy-L-arabinose arabinosyl transferase) (EC 2.4.2.43)		8.70	54.55
group_4127	A0A3A7GRB2	<i>AF264_04425</i>	Uncharacterized protein		8.70	54.55
rmlD	A0A1D2ISS6	<i>rfbD</i>	dTDP-4-dehydrorhamnose reductase (EC 1.1.1.133)	1.1.0	91.30	45.45
rmlA1	A0A0D8X3Y7	<i>rfbA</i>	Glucose-1-phosphate thymidyltransferase (EC 2.7.7.24)	1.1.0	91.30	45.45
epsJ_3	A0A3A8CCS3	<i>epsJ_2</i>	Putative glycosyltransferase EpsJ (EC 2.4.-.-)	1.1.0	91.30	45.45
epsJ_2	A0A3A7NTY9	<i>epsJ_2</i>	Glycosyltransferase (Putative glycosyltransferase EpsJ) (EC 2.4.-.-)	1.1.0	91.30	45.45
epsJ_1	Q8Y9M9	<i>lmo0497</i>	Lmo0497 protein	1.1.0	91.30	45.45
epsJ_4	A0A3A8BXQ8	<i>epsJ_1</i>	Putative glycosyltransferase EpsJ (EC 2.4.-.-)	1.1.0	91.30	45.45
group_511	A0A3A7GBM6	<i>chia1</i>	Chitinase (Chitinase A1) (EC 3.2.1.14)	2.1.1	15.22	63.64
lacE	A0A3A2WV58	<i>lace</i>	Permease IIC component		2.17	36.36
group_4998	A0A3A7BLW8	<i>licr_6</i>	HTH domain-containing protein (Putative licABCH operon regulator)		2.17	36.36
group_4997	A0A3A7J3I9	<i>chbG</i>	Carbohydrate deacetylase (EC 3.5.1.-)		2.17	36.36
group_3707	UPI00003CAC0A	<i>AF251_12155</i>	Uncharacterized protein		2.17	36.36

pagL	A0A3A7PIR9	<i>pagL</i>	6-phospho-alpha-glucosidase (EC 3.2.1.-)		2.17	36.36
lacF_6	A0A3A7PRS4	<i>lacF_1</i>	PTS lactose/cellobiose transporter subunit IIA (PTS system lactose-specific EIIA component) (EC 2.7.1.207)		2.17	36.36
licB_6	A0A3A7EDF1	<i>cela_3</i>	PTS sugar transporter subunit IIB (PTS system cellobiose-specific EIIB component) (EC 2.7.1.205)		2.17	36.36
csbB	Q93RN0	<i>mtrA</i>	Dolichol-phosphate mannosyltransferase MtrA (Hypothetical glycosyl transferase) (Hypothetical glycosyl transferaseglycosyl transferase)	1.1.0	89.13	45.45
group_2486	A0A3A7PTC4	<i>AF251_01345</i>	DNA double-strand break repair Rad50 ATPase		10.87	54.55
tagH	UPI000BDFED64		teichoic acids export ABC transporter ATP-binding subunit TagH	1.1.0	89.13	45.45
group_4194	A0A3A8BYI6	<i>CFSAN002345_001197</i>	Uncharacterized protein		10.87	54.55
group_4195	A0A0B8RHP3	<i>LmNIHS28_01665</i>	Uncharacterized protein		10.87	54.55
group_1153	A0A0E0UUS7	<i>pncB</i>	Nicotinate phosphoribosyltransferase (EC 6.3.4.21)	5.2.0	10.87	54.55
rmlC	A0A1C7Q2S5	<i>rfbC</i>	dTDP-4-dehydrorhamnose 3,5-epimerase (EC 5.1.3.13) (Thymidine diphospho-4-keto-rhamnose 3,5-epimerase)	1.1.0	89.13	45.45
group_1749	A0A2Z5C202	<i>RK57_12045</i>	Uncharacterized protein	6.0.0	10.87	54.55
malP	Q8Y5E3	<i>lmo2121</i>	Lmo2121 protein	2.1.1	89.13	45.45
chiA1	Q8YAL3	<i>lmo0105</i>	Lmo0105 protein	2.1.1	82.61	36.36
group_4056	A0A393JPV1	<i>AF241_07740</i>	Uncharacterized protein	6.0.0	6.52	45.45
group_2173	Q8Y4R2	<i>lmo2372</i>	Lmo2372 protein	1.2.0	93.48	54.55
group_3924	UPI0009B11300		GW domain-containing glycosaminoglycan-binding protein		6.52	45.45
group_396	UPI00086EB4E1		hypothetical protein		67.39	18.18
pdxT	Q71XR2	<i>pdxT</i>	Pyridoxal 5'-phosphate synthase subunit PdxT (EC 4.3.3.6) (Pdx2) (Pyridoxal 5'-phosphate synthase glutaminase subunit) (EC 3.5.1.2)	5.2.0	41.30	90.91
group_3706	UPI000771B0EF	<i>cas9</i>	Type II CRISPR RNA-guided endonuclease Cas9		0.00	27.27
group_1253	A0A0E1R3M0	<i>BN389_02790</i>	Uncharacterized protein		0.00	27.27
group_2019	A0A0E0URY6	<i>LMM7_0171</i>	Uncharacterized protein	6.0.0	34.78	81.82
group_1374	UPI000990612F		hypothetical protein	6.0.0	65.22	18.18
group_1062	A0A393CV23	<i>AF264_09920</i>	Glycoside hydrolase family 65 protein	2.1.1	13.04	54.55
group_3297	A0A394XZE5	<i>AF264_03740</i>	SMI1/KNR4 family protein	6.0.0	19.57	63.64
group_2913	A0A2Z5BYV4	<i>RK57_05535</i>	Uncharacterized protein	6.0.0	19.57	63.64
group_4150	A0A394XVS5	<i>gata_1</i>	Amidase (EC 3.5.1.4) (Glutamyl-tRNA(Gln) amidotransferase subunit A) (EC 6.3.5.7)	1.1.0	19.57	63.64
group_4142	A0A3A8BVY8	<i>nfrA1_1</i>	FMN reductase (NADPH) (EC 1.5.1.38)	1.4.0	19.57	63.64
group_4141	A0A3A8C3E2	<i>yfkJ</i>	Low molecular weight protein-tyrosine-phosphatase YfkJ (EC 3.1.3.48)		19.57	63.64
tagG	UPI000BE10CE8		ABC transporter permease	1.1.0	80.43	36.36
group_4664	Q8Y4K6	<i>lmo2432</i>	Lmo2432 protein	6.0.0	80.43	36.36
nfrA1_2	A0A3A8BZV6	<i>nfrA1_1</i>	FMN reductase (NADPH) (EC 1.5.1.38)	1.4.0	80.43	36.36
sttH	Q8Y9A3	<i>lmo0629</i>	Lmo0629 protein	5.2.0	80.43	36.36
tagB_1	A0A3A8BZ54	<i>tarL_2</i>	Teichoic acid ribitol-phosphate polymerase TarL (EC 2.7.8.14)	1.1.0	80.43	36.36
group_3621	Q8Y4Q9	<i>lmo2375</i>	Lmo2375 protein	6.0.0	80.43	36.36

yfkJ	Q8Y8G6	<i>lmo0938</i>	Lmo0938 protein	3.8.0	80.43	36.36
group_1295	Q8Y8G5	<i>lmo0939</i>	Lmo0939 protein	6.0.0	80.43	36.36
group_3764	A0A3A2PYQ0	<i>AF255_08255</i>	Uncharacterized protein	6.0.0	54.35	9.09
ytrB_3	A0A0E1R8M1	<i>yhcG</i>	Uncharacterized ABC transporter ATP-binding protein YhcG	1.2.0	8.70	45.45
hrtA_2	A0A0E1RFE7	<i>hrtA</i>	Putative hemin import ATP-binding protein HrtA (EC 3.6.3.-)	1.2.0	8.70	45.45
group_4931	A0A393UJY3	<i>AB922_03066</i>	Dihydroorotate dehydrogenase (Quinone)	5.1.0	8.70	45.45
inlA_13	A0A394XWP9	<i>AF264_05160</i>	Cell surface protein		4.35	36.36
group_194	A0A394YAU8	<i>AF255_15365</i>	Uncharacterized protein		73.91	27.27
group_3355	A0A3A8BXQ6	<i>mhqA_2</i>	Putative ring-cleaving dioxygenase MhqA (EC 1.13.11.-)	5.2.0	21.74	63.64
mhqA_2	Q8Y8Y4	<i>lmo0758</i>	Lmo0758 protein	5.2.0	78.26	36.36
group_745	Q8Y4R3	<i>lmo2371</i>	Lmo2371 protein	1.2.0	78.26	36.36
trxA_3	UPI000BDFC1FB		thioredoxin	1.4.0	78.26	36.36
group_3532	Q8Y9D1	<i>lmo0601</i>	Lmo0601 protein	1.8.0	84.78	45.45
group_3961	A0A0E0UZG3	<i>LMM7_2508</i>	Uncharacterized protein	6.0.0	15.22	54.55
group_3479	A0A3A8BLK1	<i>CFSAN002345_002071</i>	Uncharacterized protein		15.22	54.55
group_4198	W5U092	<i>lntA</i>	Nuclear-targeted protein A	6.0.0	15.22	54.55
group_676	Q8Y496	<i>ami</i>	Autolysin, amidase	1.8.0	84.78	45.45
group_4184	A0A394ZL82	<i>AF264_02035</i>	DUF4097 domain-containing protein	1.8.0	15.22	54.55
group_2446	Q8Y9C6	<i>lmo0606</i>	Lmo0606 protein	3.5.2	84.78	45.45
group_1275	Q8YA41	<i>lmo0323</i>	Lmo0323 protein	5.2.0	71.74	27.27
group_3711	A0A392WYQ6	<i>AB922_00952</i>	Glycosyltransferase		28.26	72.73
mgtB	A0A1D2IRU1	<i>mgtA</i>	Magnesium-translocating P-type ATPase	1.2.0	69.57	27.27
group_2548	UPI000874D6A9		polysaccharide deacetylase		69.57	27.27
group_1624	A0A3A7U6D9	<i>ARK97_06545</i>	ABC transporter permease	5.2.0	69.57	27.27
group_4156	A0A0B8QPW4	<i>LmNIHS28_00567</i>	Uncharacterized protein		10.87	45.45
group_1747	Q8Y8S5	<i>lmo0819</i>	Lmo0819 protein	6.0.0	89.13	54.55
group_1843	A0A1S7FP06	<i>DC57_14095</i>	6-phospho-beta-glucosidase	2.1.1	60.87	18.18
group_620	A0A0E0UTZ8	<i>rarD</i>	Putative chloramphenicol resistance permease	5.2.0	50.00	90.91
group_4408	Q8Y8U3	<i>lmo0800</i>	Lmo0800 protein	5.2.0	50.00	9.09
group_2584	Q8Y8U2	<i>lmo0801</i>	Lmo0801 protein	1.8.0	50.00	9.09
group_4160	A0A0E1RAZ5	<i>yqkB</i>	Uncharacterized protein yqkB	5.2.0	50.00	90.91
group_138	UPI000D733290		hypothetical protein		17.39	54.55
group_3888	A0A0B8RBN9	<i>LmNIHS28_00109</i>	Uncharacterized protein	6.0.0	17.39	54.55
iscS_1	Q8Y713	<i>lmo1513</i>	Lmo1513 protein	2.5.0	82.61	45.45
group_3931	A0A2Z5BZG6	<i>RK57_07490</i>	Uncharacterized protein	6.0.0	17.39	54.55
group_1946	A0A0B8REH4	<i>LmNIHS28_00150</i>	Membrane protein		17.39	54.55
group_4099	UPI000D648E93	<i>DF275_07015</i>	Uncharacterized protein (Fragment)		17.39	54.55
group_1250	A0A1S7FP90	<i>DC57_14415</i>	Uncharacterized protein		17.39	54.55
group_2447	Q8Y9C6	<i>lmo0606</i>	Lmo0606 protein	3.5.2	17.39	54.55
group_5029	A0A3A7M840	<i>wapA_2</i>	tRNA(Glu)-specific nuclease WapA (EC 3.1.-.-)		2.17	27.27

group_5028	A0A3A2S117	<i>AF251_01095</i>	Uncharacterized protein		2.17	27.27
tipA	A0A3A2S5M2	<i>tipa</i>	HTH-type transcriptional activator TipA (MerR family DNA-binding transcriptional regulator) (MerR family transcriptional regulator)	3.5.2	97.83	72.73
group_5054	A0A394X1X5	<i>AF241_10790</i>	RNA-dependent DNA polymerase		2.17	27.27
group_5055	A0A0B8QVQ7	<i>LmNIHS28_01548</i>	Uncharacterized protein	6.0.0	2.17	27.27
group_5053	A0A0B8R0D3	<i>LmNIHS28_01546</i>	Uncharacterized protein		2.17	27.27
gatZ	UPI000436C1E8	<i>HR60_13125</i>	Sugar-phosphate kinase	2.1.1	97.83	72.73
wapA_4	UPI000766B890	<i>DLE78_09465</i>	RHS repeat protein		2.17	27.27
wapA_1	UPI00098DDBEB		RHS repeat protein		2.17	27.27
group_5030	A0A3A7D2C0	<i>AF251_01085</i>	Uncharacterized protein		2.17	27.27
group_5023	A0A3A8BNT5	<i>CFSAN002345_002252</i>	Uncharacterized protein		2.17	27.27
group_1772	A0A3A7DAW7	<i>yjg_1</i>	HAD family hydrolase (Pyrimidine 5'-nucleotidase YjjG) (EC 3.1.3.5)	5.2.0	97.83	72.73
group_5021	A0A3A2JJ17	<i>AF251_01115</i>	Uncharacterized protein		2.17	27.27
group_5119	A0A3A8BVS8	<i>CFSAN002345_001735</i>	Uncharacterized protein		2.17	27.27
group_5022	UPI000BE0260F		hypothetical protein		2.17	27.27
group_5026	A0A3A7LWS8	<i>AFX52_00217</i>	Uncharacterized protein		2.17	27.27
group_5024	A0A3A2RTQ9	<i>AF251_01105</i>	Uncharacterized protein		2.17	27.27
manP_4	UPI000434E433	<i>HR60_13110</i>	PTS fructose transporter subunit IIA	1.2.0	97.83	72.73
manP_3	A0A0E1R4Q4	<i>frwC</i>	Fructose-like permease IIC component 2 (EC 2.7.1.69)	1.2.0	97.83	72.73
manP_2	A0A0E1R3Y0	<i>frwB_2</i>	Fructose-like phosphotransferase enzyme IIB component 2 (EC 2.7.1.69)	1.2.0	97.83	72.73
licR_4	A0A393DPZ5	<i>manR_2</i>	PRD domain-containing protein (Transcriptional regulator ManR)	3.5.2	97.83	72.73
wapA_2	A0A3A7MMB4	<i>wapA_3</i>	tRNA(Glu)-specific nuclease WapA (EC 3.1.-.-)		2.17	27.27
group_728	A0A393CRH4	<i>mgtA</i>	Magnesium-translocating P-type ATPase (Magnesium-transporting ATPase, P-type 1) (EC 3.6.3.2)	1.2.0	32.61	72.73
group_2018	A0A3A7KBU5	<i>AF844_02597</i>	Uncharacterized protein	6.0.0	32.61	72.73
group_4350	P58495	<i>lmo0363</i>	Uncharacterized peptidase Lmo0363 (EC 3.4.21.-)	2.2.0	67.39	27.27
group_4351	Q8YA03	<i>lmo0364</i>	Lmo0364 protein	3.5.2	67.39	27.27
group_1623	A0A0B8QZI6	<i>LmNIHS28_01291</i>	ABC transporter permease	5.2.0	32.61	72.73
group_2675	A0A0H3GDV9	<i>LMRG_01255</i>	Uncharacterized protein		58.70	18.18
group_4816	A0A0E0UXP2	<i>LMM7_2202</i>	Uncharacterized protein		58.70	18.18
group_1963	UPI00098E7CD3		superoxide dismutase	6.0.0	58.70	18.18
group_1845	Q9EXF8	<i>bglA</i>	Beta-glucosidase (EC 3.2.1.21) (Glycoside hydrolase family 1 protein)	2.1.1	41.30	81.82
actA	Q6E9G6	<i>actA</i>	ActA (Actin nucleator protein ActA)	1.8.0	93.48	63.64
group_2832	A0A393FL10	<i>AF264_13375</i>	DUF1310 domain-containing protein (DUF1310 family protein)	5.1.0	6.52	36.36
wapA	A0A0E1R9W5	<i>wapA_2</i>	Wall-associated protein		6.52	36.36
group_925	A0A0E0USB0	<i>prs</i>	Ribose-phosphate pyrophosphokinase (RPPK) (EC 2.7.6.1) (5-phospho-D-ribosyl alpha-1-diphosphate)		93.48	63.64
group_4930	UPI000BE0165D		actin assembly-inducing protein ActA	1.8.0	6.52	36.36
group_3771	A0A2A6A353	<i>CDR86_14020</i>	Uncharacterized protein		36.96	0.00

group_3773	A0A2A6A3R8	<i>CDR86_14045</i>	Uncharacterized protein		36.96	0.00
group_3870	A0A2A6A392	<i>CDR86_14115</i>	RNA polymerase subunit sigma		36.96	0.00
group_3775	A0A2A5ZJU3	<i>CDR86_14055</i>	Head-tail adaptor protein		36.96	0.00
group_3774	A0A2A5ZKW1	<i>CDR86_14050</i>	Uncharacterized protein		36.96	0.00
group_3776	A0A2A5ZK62	<i>CDR86_14085</i>	Terminase large subunit		36.96	0.00
group_5438	A0A2A6A383	<i>CDR86_14065</i>	Phage major capsid protein		36.96	0.00
group_5436	A0A2A6A494	<i>CDR86_14040</i>	Phage tail protein		36.96	0.00
group_5437	A0A2A6A2S9	<i>CDR86_14060</i>	Uncharacterized protein		36.96	0.00
group_2732	A0A393U4Y6	<i>AF255_14330</i>	DUF2974 domain-containing protein	6.0.0	36.96	0.00
group_5515	UPI000BE047C1		DUF1310 family protein	5.1.0	36.96	0.00
group_5452	A0A2A5ZM51	<i>CDR86_09880</i>	DUF771 domain-containing protein		36.96	0.00
group_5450	A0A3A2JSK3	<i>AF847_01777</i>	Uncharacterized protein		36.96	0.00
group_5455	A0A2A6A624	<i>CDR86_09860</i>	Uncharacterized protein		36.96	0.00
group_2724	A0A2A6A2X1	<i>CDR86_14035</i>	Uncharacterized protein		36.96	0.00
group_2723	A0A2A6A314	<i>CDR86_14025</i>	Phage tail protein		36.96	0.00
smc_5	A0A3A2L5G2	<i>AF249_02565</i>	Phage tail tape measure protein		36.96	0.00
group_1980	A0A392WP24	<i>AF255_14340</i>	DUF1310 domain-containing protein (DUF1310 family protein)	5.1.0	36.96	0.00
group_5441	A0A2A6A2T7	<i>CDR86_14110</i>	Site-specific integrase		36.96	0.00
group_5440	A0A3A2Q1E8	<i>AF847_01796</i>	Phage portal protein		36.96	0.00
group_3781	A0A3A7A859	<i>AF847_01778</i>	Uncharacterized protein		36.96	0.00
group_2664	A0A392YE54	<i>AF247_14605</i>	Uncharacterized protein		36.96	0.00
Int-Tn	A0A2A6A695	<i>CDR86_09855</i>	Site-specific integrase		34.78	0.00
group_3777	A0A2A5ZK31	<i>CDR86_14090</i>	Phage terminase small subunit P27 family		34.78	0.00
group_2672	A0A3A7FGJ9	<i>AF239_12510</i>	Uncharacterized protein	4.3.0	34.78	0.00
group_2671	A0A393PJM9	<i>AF828_02772</i>	AP2 domain-containing protein	4.3.0	34.78	0.00
group_5439	A0A2A5ZKF2	<i>CDR86_14070</i>	HK97 family phage prohead protease		34.78	0.00
group_1346	A0A3A7FZC8	<i>AF951_02536</i>	Uncharacterized protein		34.78	0.00
group_746	A0A0B8R487	<i>LmNIHS28_01552</i>	ABC transporter permease	1.2.0	23.91	63.64
group_2646	Q8Y4H5	<i>lmo2466</i>	Lmo2466 protein	6.0.0	76.09	36.36
group_2223	A0A0B8R893	<i>AJL15_12980</i>	Transcriptional regulator	5.2.0	23.91	63.64
group_2786	A0A3A7GA62	<i>AF264_14775</i>	Uncharacterized protein	6.0.0	23.91	63.64
group_1443	Q8Y3Y2	<i>lmo2697</i>	Lmo2697 protein	5.2.0	76.09	36.36
group_1424	A0A1S7FQ19	<i>DC57_01000</i>	Uncharacterized protein	6.0.0	13.04	45.45
group_877	UPI000D65622D	<i>DF271_11275</i>	Uncharacterized protein (Fragment)	6.0.0	13.04	45.45
group_3930	A0A2Z5BZG2	<i>RK57_07500</i>	DUF1310 family protein	5.1.0	13.04	45.45
group_4176	A0A0B8RDT5	<i>LmNIHS28_00904</i>	Uncharacterized protein		13.04	45.45
group_4175	A0A3A6WQ80	<i>AB922_01521</i>	Uncharacterized protein		13.04	45.45
group_143	A0A3A2J7V9	<i>AF247_01180</i>	BspA family leucine-rich repeat surface protein	1.8.0	13.04	45.45
group_4612	Q8Y5J1	<i>lmo2070</i>	Lmo2070 protein	5.2.0	80.43	45.45
group_3197	A0A3A7EY63	<i>AB922_02243</i>	N-acetyltransferase	5.2.0	19.57	54.55
group_3196	Q720B7	<i>LMOF2365_1322</i>	UPF0291 protein LMOF2365_1322	5.2.0	19.57	54.55

group_4614	A0A2A5ZFW1	<i>CDR86_01560</i>	FeoB-associated Cys-rich membrane protein		80.43	45.45
licT_3	Q8Y3P6	<i>bvrA</i>	Transcription antiterminator	3.5.2	80.43	45.45
ulaB_2	A0A3A8BNH7	<i>ulaB_2</i>	Ascorbate-specific PTS system EIIB component (EC 2.7.1.194)	1.2.0	80.43	45.45
inlB_2	Q8Y9H9	<i>lmo0549</i>	Lmo0549 protein	1.9.0	80.43	45.45
manX_4	Q8YAU2	<i>lmo0021</i>	Lmo0021 protein	1.2.0	80.43	45.45
group_4516	Q8Y6P9	<i>lmo1635</i>	Lmo1635 protein	5.2.0	80.43	45.45
group_4517	Q8Y6P4	<i>lmo1640</i>	Lmo1640 protein	6.0.0	80.43	45.45
tpiA_1	Q8YA20	<i>tpiA2</i>	Probable triosephosphate isomerase 2 (TIM 2) (TPI 2) (EC 5.3.1.1) (Triose-phosphate isomerase 2)	2.1.2	80.43	45.45
group_4054	A0A394RA98	<i>AF239_08275</i>	HD domain-containing protein	5.2.0	19.57	54.55
group_4057	A0A3A7ML43	<i>AF251_07735</i>	2-methyl-6-phytyl-1,4-hydroquinone methyltransferase (EC 2.1.1.295) (Class I SAM-dependent methyltransferase)	5.2.0	19.57	54.55
group_4050	A0A3A8BL21	<i>thiN</i>	Thiamine pyrophosphokinase (EC 2.7.6.2)	2.5.0	19.57	54.55
group_4053	A0A0B8R933	<i>LmNIHS28_02291</i>	Uncharacterized protein	6.0.0	19.57	54.55
group_4052	A0A2Z5BX03	<i>RK57_02435</i>	DUF1697 domain-containing protein	5.2.0	19.57	54.55
group_4059	A0A3A8BR73	<i>fosX</i>	Fosfomycin resistance protein FosX	4.1.0	19.57	54.55
group_4058	UPI0004366B26	<i>HR60_00125</i>	UPF0435 protein HR60_00125	5.2.0	19.57	54.55
group_820	A0A393CUI8	<i>AF264_04565</i>	Alpha/beta hydrolase	6.0.0	19.57	54.55
group_2626	Q8Y593	<i>lmo2176</i>	Lmo2176 protein	3.5.2	80.43	45.45
group_2627	Q8Y582	<i>lmo2189</i>	Lmo2189 protein	1.10.0	80.43	45.45
group_2629	Q8Y512	<i>lmo2266</i>	Lmo2266 protein	5.2.0	80.43	45.45
fruA_9	A0A3A8BML0	<i>fruA_3</i>	PTS system fructose-specific EIIBC component	1.2.0	19.57	54.55
glmS_1	A0A3A8C038	<i>glmS_2</i>	Glutamine--fructose-6-phosphate aminotransferase isomerizing (EC 2.6.1.16)	2.1.1	80.43	45.45
group_3537	Q8Y973	<i>lmo0660</i>	Lmo0660 protein	4.4.0	80.43	45.45
group_3535	UPI000EF5BE8A		DUF975 family protein	5.2.0	80.43	45.45
group_3534	A0A3A8CFC5	<i>speG_1</i>	Spermidine N(1)-acetyltransferase (EC 2.3.1.57)	5.2.0	80.43	45.45
group_3539	Q8Y8Z5	<i>lmo0747</i>	Lmo0747 protein	6.0.0	80.43	45.45
ytnP	Q8Y6R9	<i>lmo1614</i>	Lmo1614 protein	5.2.0	80.43	45.45
addB	Q8Y510	<i>addB</i>	ATP-dependent helicase/deoxyribonuclease subunit B (EC 3.1.-.-) (EC 3.6.4.12) (ATP-dependent helicase/nuclease AddB)	3.3.0	80.43	45.45
addA	Q8Y511	<i>addA</i>	ATP-dependent helicase/nuclease subunit A (EC 3.1.-.-) (EC 3.6.4.12) (ATP-dependent helicase/nuclease AddA)	3.3.0	80.43	45.45
group_225	UPI0001D010DE	<i>inlj_14</i>	Internalin-J	1.8.0	19.57	54.55
group_3965	A0A3A7GK80	<i>mggb</i>	Bifunctional metallophosphatase/5'-nucleotidase (Mannosylglucosyl-3-phosphoglycerate phosphatase) (EC 3.1.3.-)	5.2.0	19.57	54.55
group_3966	A0A2Z5BYS6	<i>RK57_05330</i>	Crp/Fnr family transcriptional regulator		19.57	54.55
group_3963	A0A3A7G3T8	<i>AF251_11130</i>	Uncharacterized protein	6.0.0	19.57	54.55
group_3339	A0A393CSM1	<i>AF264_03070</i>	DUF3130 family protein (TIGR04197 family type VII secretion effector)		19.57	54.55
proC_2	A0A3A8C3U2	<i>proC_1</i>	Pyrroline-5-carboxylate reductase (EC 1.5.1.2)	2.2.0	80.43	45.45
sigW	Q8Y9U7	<i>lmo0423</i>	Lmo0423 protein	3.5.1	80.43	45.45

group_1244	A0A393CR87	<i>AF264_00605</i>	Ribonuclease P	5.1.0	19.57	54.55
group_4573	Q8Y6D7	<i>lmo1750</i>	Lmo1750 protein	5.2.0	80.43	45.45
group_4577	Q8Y6B2	<i>lmo1779</i>	Lmo1779 protein	6.0.0	80.43	45.45
group_4575	Q8Y6B4	<i>lmo1777</i>	Lmo1777 protein	5.2.0	80.43	45.45
group_4578	A0A3A8BJ82	<i>azoR_2</i>	FMN-dependent NADH-azoreductase (EC 1.7.-.-)	1.4.0	80.43	45.45
ybjG	Q8Y6R1	<i>lmo1623</i>	Lmo1623 protein	5.2.0	80.43	45.45
cbiE	A0A3A8C045	<i>cbiE</i>	Cobalt-precorrin-7 C(5)-methyltransferase (EC 2.1.1.289)	2.5.0	80.43	45.45
yjaB	A0A3A8BXM4	<i>yjaB</i>	Putative N-acetyltransferase YjaB (EC 2.3.1.-)	5.2.0	80.43	45.45
ulaC_3	A0A3A8BN71	<i>ulaC_3</i>	Ascorbate-specific PTS system EIIA component (EC 2.7.1.194)	1.2.0	80.43	45.45
group_4503	Q8Y760	<i>lmo1443</i>	Lmo1443 protein	5.2.0	80.43	45.45
group_4500	Q8Y785	<i>lmo1410</i>	Lmo1410 protein	6.0.0	80.43	45.45
group_4509	Q8Y6X6	<i>lmo1555</i>	Lmo1555 protein	2.5.0	80.43	45.45
group_4487	Q8Y7L2	<i>lmo1265</i>	Lmo1265 protein	1.2.0	80.43	45.45
group_4489	A0A1D2IPZ2	<i>dprA</i>	DNA-protecting protein DprA	3.8.0	80.43	45.45
group_3470	A0A392X3L4	<i>AF241_00505</i>	Superoxide dismutase	6.0.0	19.57	54.55
group_2916	A0A393D408	<i>trxa_4</i>	Thioredoxin (Thioredoxin 1)	1.4.0	19.57	54.55
group_5648	A0A0B8RAI5	<i>LmNIHS28_01933</i>	Cell surface protein		19.57	54.55
group_4374	Q8Y9B7	<i>lmo0615</i>	Lmo0615 protein	6.0.0	80.43	45.45
group_4375	Q8Y9B5	<i>lmo0617</i>	Lmo0617 protein	5.1.0	80.43	45.45
group_4472	Q8Y7Q8	<i>lmo1214</i>	Lmo1214 protein	6.0.0	80.43	45.45
group_1303	Q8Y7Z1	<i>lmo1128</i>	Lmo1128 protein	6.0.0	80.43	45.45
group_4090	A0A3A7N8T5	<i>bioC</i>	Class I SAM-dependent methyltransferase (Malonyl-[acyl-carrier protein] O-methyltransferase) (EC 2.1.1.197)	3.8.0	19.57	54.55
group_4093	C1L2K1	<i>miaA</i>	tRNA dimethylallyltransferase (EC 2.5.1.75) (Dimethylallyl diphosphate:tRNA dimethylallyltransferase)	3.6.0	19.57	54.55
group_4092	A0A0E1R7G6	<i>ynbB</i>	Uncharacterized protein ynbB	4.2.0	19.57	54.55
group_4095	C1L2I1	<i>rnhB</i>	Ribonuclease HII (RNase HII) (EC 3.1.26.4)	3.1.0	19.57	54.55
group_4094	A0A2Z5C362	<i>dprA</i>	DNA-protecting protein DprA		19.57	54.55
group_4096	A0A2Z5C3E4	<i>RK57_14300</i>	Uncharacterized protein	1.2.0	19.57	54.55
group_4623	Q8Y555	<i>lmo2221</i>	Lmo2221 protein	5.2.0	80.43	45.45
group_4152	A0A0E1R689	<i>ysdA</i>	Uncharacterized protein ysdA	5.2.0	19.57	54.55
group_4621	Q8Y592	<i>lmo2177</i>	Lmo2177 protein	5.2.0	80.43	45.45
group_4154	A0A1T1YQG4	<i>DC57_11460</i>	Transposase	4.4.0	19.57	54.55
sdrF	Q8Y5H7	<i>lmo2085</i>	Putative peptidoglycan bound protein (LPXTG motif)	1.8.0	80.43	45.45
sdrD	Q8Y479	<i>lmo2576</i>	Peptidoglycan anchored protein (LPXTG motif)	1.8.0	80.43	45.45
group_4252	A0A2Z5C1U4	<i>RK57_09025</i>	Uncharacterized protein	6.0.0	19.57	54.55
thiO	A0A3A8BP94	<i>thiO</i>	Glycine oxidase (EC 1.4.3.19)	2.2.0	80.43	45.45
thiN	A0A3A8BXM3	<i>thiN</i>	Thiamine pyrophosphokinase (EC 2.7.6.2)	2.5.0	80.43	45.45
group_4392	A0A3A8CAQ5	<i>rbsR_1</i>	Ribose operon repressor	3.5.2	80.43	45.45
group_4396	A0A3A8C7X5	<i>bglF_2</i>	PTS system beta-glucoside-specific EIIBCA component	1.2.0	80.43	45.45
thiF	Q8Y868	<i>lmo1049</i>	Lmo1049 protein	2.5.0	80.43	45.45

group_2703	A0A393RS60	<i>inlK</i>	Class 1 internalin InlK (LPXTG cell wall anchor domain-containing protein)	1.8.0	19.57	54.55
group_2701	A0A0B8RBH2	<i>LmNIHS28_02243</i>	Uncharacterized protein		19.57	54.55
inla_11	A0A394Y342	<i>inla_4</i>	Internalin (Internalin-A) (LPXTG cell wall anchor domain-containing protein)	1.8.0	19.57	54.55
inla_3	UPI000BDFD377		lmo1136 family class 1 internalin	1.8.0	80.43	45.45
ulaA_2	Q8Y5T4	<i>lmo1971</i>	Lmo1971 protein	1.2.0	80.43	45.45
inla_1	Q8Y7I7	<i>lmo1290</i>	Lmo1290 protein	1.8.0	80.43	45.45
group_4024	UPI000035D3A8	<i>isdE</i>	Heme ABC transporter substrate-binding protein IsdE	1.2.0	19.57	54.55
group_4025	A0A2Z5BZU3	<i>RK57_04520</i>	ABC transporter ATP-binding protein	1.2.0	19.57	54.55
group_4026	A0A0D4CB02	<i>AJL15_12175</i>	Uncharacterized protein	5.2.0	19.57	54.55
group_4027	A0A2Z5BZF4	<i>RK57_04485</i>	TetR/AcrR family transcriptional regulator		19.57	54.55
group_4020	A0A3A7JKS7	<i>yhaO</i>	Exonuclease SbcCD subunit D (Putative metallophosphoesterase YhaO)	5.2.0	19.57	54.55
group_4021	A0A0B8QRP4	<i>LmNIHS28_01575</i>	Uncharacterized protein	5.2.0	19.57	54.55
group_4022	A0A0B8RAU1	<i>LmNIHS28_02204</i>	Membrane protein	6.0.0	19.57	54.55
group_4023	UPI0001EBA5A3	<i>NT04LM_3257</i>	Heme uptake protein IsdC	1.8.0	19.57	54.55
albF	Q8Y797	<i>lmo1393</i>	Lmo1393 protein	2.2.0	80.43	45.45
group_3588	Q8Y7E0	<i>lmo1343</i>	Lmo1343 protein	1.10.0	80.43	45.45
group_2775	A0A393S3L9	<i>AF264_15050</i>	Uncharacterized protein	6.0.0	19.57	54.55
group_5614	A0A3A6XF35	<i>addb</i>	ATP-dependent helicase/deoxyribonuclease subunit B (EC 3.1.-.-) (EC 3.6.4.12) (ATP-dependent helicase/nuclease AddB)	3.3.0	19.57	54.55
group_3927	A0A0B8RBU5	<i>LmNIHS28_00179</i>	RNA-binding protein	5.2.0	19.57	54.55
lutR_1	A0A3A8CF58	<i>lutR_2</i>	HTH-type transcriptional regulator LutR	3.5.2	80.43	45.45
group_3500	Q8Y451	<i>lmo2604</i>	Lmo2604 protein	5.2.0	80.43	45.45
macB_4	A0A3A8BUW4	<i>yknY_2</i>	Putative ABC transporter ATP-binding protein YknY (EC 3.6.3.-)		19.57	54.55
aguA_2	A0A0H3G891	<i>aguA</i>	Putative agmatine deiminase (EC 3.5.3.12) (Agmatine iminohydrolase)	5.2.0	80.43	45.45
group_3306	A0A0B8QYA4	<i>LmNIHS28_00502</i>	Uncharacterized protein		19.57	54.55
group_662	Q8Y7Z0	<i>lmo1129</i>	Lmo1129 protein	5.2.0	80.43	45.45
group_3571	Q8Y7X3	<i>lmo1146</i>	Lmo1146 protein	5.2.0	80.43	45.45
group_4440	Q8Y855	<i>lmo1063</i>	Lmo1063 protein	1.2.0	80.43	45.45
ypdB	Q8Y8C4	<i>lmo0984</i>	Lmo0984 protein	3.5.2	80.43	45.45
group_4087	A0A2Z5BXN3	<i>RK57_00065</i>	Type II secretion system protein	1.10.0	19.57	54.55
IntA	Q8Y9T5	<i>IntA</i>	Listeria nuclear targeted protein A	6.0.0	80.43	45.45
group_2953	UPI0001B4220F	<i>ARJ20_02020</i>	LPXTG cell wall anchor domain-containing protein		19.57	54.55
group_4085	A0A0E0UWI3	<i>LMM7_1468</i>	Uncharacterized protein	5.2.0	19.57	54.55
group_4432	A0A0H3GJ44	<i>LMRG_02074</i>	Uncharacterized protein		80.43	45.45
group_4430	Q8Y8D8	<i>lmo0966</i>	Lmo0966 protein	5.2.0	80.43	45.45
group_2353	Q8VMX1		Putative Gp2		19.57	54.55
group_4088	A0A393RS12	<i>AF264_05675</i>	Competence protein ComG	1.10.0	19.57	54.55
group_4190	A0A3A7GJ00	<i>inla_3</i>	Internalin-A (Leucine-rich repeat domain-containing protein)	1.9.0	19.57	54.55
group_4191	A0A394Y4B3	<i>AF264_01750</i>	Transcriptional regulator	6.0.0	19.57	54.55
group_4219	A0A2Z5C2B1	<i>RK57_09890</i>	GntR family transcriptional regulator		19.57	54.55
group_4218	A0A393CNN4	<i>AF240_00940</i>	Uncharacterized protein		19.57	54.55

group_4216	UPI000035CDC6	<i>BN389_04240</i>	Uncharacterized protein		19.57	54.55
group_4215	A0A0B8R4Y8	<i>LmNIHS28_01937</i>	ATPase	5.2.0	19.57	54.55
group_4214	A0A2Z5C2C0	<i>RK57_09950</i>	Uncharacterized protein	6.0.0	19.57	54.55
group_4668	Q8Y4D7	<i>comFC</i>	ComFC protein	1.10.0	80.43	45.45
group_4669	Q8Y4D6	<i>comFA</i>	ComFA protein	1.10.0	80.43	45.45
pknB	A0A3A8C235	<i>pknB</i>	Serine/threonine-protein kinase PknB (EC 2.7.11.1)	3.8.0	80.43	45.45
hcnC	A0A3A7J837	<i>hcnC</i>	FAD-binding oxidoreductase (Hydrogen cyanide synthase subunit HcnC) (EC 1.4.99.5)	2.2.0	19.57	54.55
group_897	Q8Y7R0	<i>lmo1212</i>	Lmo1212 protein	5.2.0	80.43	45.45
group_3399	A0A0E1R5P0	<i>yesJ</i>	Uncharacterized N-acetyltransferase YesJ (EC 2.3.1.-)	5.2.0	19.57	54.55
adrA	A0A0E1REZ1	<i>yhcK</i>	Uncharacterized protein yhcK	5.2.0	19.57	54.55
group_4322	Q8Y3I4	<i>lmo2852</i>	Lmo2852 protein	5.2.0	80.43	45.45
group_4324	Q8YAT7	<i>cutC</i>	Copper homeostasis protein CutC	4.2.0	80.43	45.45
group_4068	A0A3A7T7A5	<i>ytnP</i>	MBL fold metallo-hydrolase (Putative quorum-quenching lactonase YtnP) (EC 3.1.1.-)	5.2.0	19.57	54.55
group_4069	C1KVN8	<i>argC</i>	N-acetyl-gamma-glutamyl-phosphate reductase (AGPR) (EC 1.2.1.38)	2.2.0	19.57	54.55
ytrA_4	A0A3A8BN52	<i>ytrA_3</i>	HTH-type transcriptional repressor YtrA	3.5.2	80.43	45.45
rnhB	Q8Y7K4	<i>rnhB</i>	Ribonuclease HII (RNase HII) (EC 3.1.26.4)	3.1.0	80.43	45.45
group_4060	A0A3A2X1R4	<i>AF264_07635</i>	Uncharacterized protein	6.0.0	19.57	54.55
group_4061	A0A393RQY0	<i>ybbh_2</i>	MurR/RpiR family transcriptional regulator (Putative HTH-type transcriptional regulator YbbH)		19.57	54.55
group_4063	A0A0B8R8T3	<i>LmNIHS28_01308</i>	Permease		19.57	54.55
group_4064	UPI000035D1DA	<i>SAMD00023519_01157</i>	Cell surface protein		19.57	54.55
group_4065	A0A2Z5BWP2	<i>RK57_01585</i>	Uncharacterized protein	6.0.0	19.57	54.55
group_4066	UPI0004352777	<i>X846_1709</i>	Uncharacterized protein	5.2.0	19.57	54.55
group_4067	A0A0E1R8B1	<i>yodM</i>	Putative lipid phosphate phosphatase yodM (EC 3.1.3.-)	5.2.0	19.57	54.55
group_4103	A0A3A7Z0I1	<i>pduX</i>	L-threonine kinase (EC 2.7.1.177) (Propanediol utilization protein)	5.2.0	19.57	54.55
group_4102	A0A0B8R3Z5	<i>LmNIHS28_00732</i>	DNA topology modulation protein	5.2.0	19.57	54.55
group_4101	A0A0B8QUW8	<i>LmNIHS28_00730</i>	Uncharacterized protein	6.0.0	19.57	54.55
group_4100	A0A1S7FLP7	<i>DC57_09570</i>	ABC transporter permease	5.2.0	19.57	54.55
group_4107	A0A3A8BV76	<i>cobU</i>	Bifunctional adenosylcobalamin biosynthesis protein CobU (EC 2.7.1.156)		19.57	54.55
group_4106	A0A2Z5C4I3	<i>cobC</i>	Alpha-ribazole phosphatase	2.5.0	19.57	54.55
group_4105	A0A0E1R5F1	<i>eutJ</i>	Ethanolamine utilization protein eutJ	2.1.1	19.57	54.55
group_4104	A0A2Z5C4F6	<i>pduM</i>	Microcompartment protein PduM	6.0.0	19.57	54.55
group_4034	A0A2Z5BZ37	<i>RK57_04110</i>	DeoR/GlpR transcriptional regulator	3.5.2	19.57	54.55
group_4108	A0A0B8R7E7	<i>LmNIHS28_00778</i>	Alpha-L-fucosidase	5.2.0	19.57	54.55
group_3612	Q8Y531	<i>lmo2245</i>	Lmo2245 protein	5.2.0	80.43	45.45
nagA_1	A0A3A7N225	<i>nagA_1</i>	N-acetylglucosamine-6-phosphate deacetylase (EC 3.5.1.25)	2.1.1	19.57	54.55
pduX	Q8Y7U9	<i>lmo1170</i>	Lmo1170 protein	5.2.0	80.43	45.45
cpnA	A0A3A8BW91	<i>cpnA</i>	Cyclopentanol dehydrogenase (EC 1.1.1.163)	2.1.1	19.57	54.55

group_3396	A0A392Y5A5	<i>inlj_7</i>	Cell surface protein (Internalin-J) (LPXTG cell wall anchor domain-containing protein)		19.57	54.55
group_3606	Q8Y5F8	<i>lmo2106</i>	Lmo2106 protein	5.2.0	80.43	45.45
group_3541	Q8Y8Z4	<i>lmo0748</i>	Lmo0748 protein	6.0.0	80.43	45.45
mtlR_4	A0A3A8C544	<i>mtlR_1</i>	Transcriptional regulator MtlR	3.5.2	19.57	54.55
group_3977	UPI00043694BE	<i>HR60_08380</i>	Hydrolase	5.2.0	19.57	54.55
group_3979	A0A3A7GK99	<i>adda</i>	ATP-dependent helicase/nuclease subunit A (EC 3.1.-.-) (EC 3.6.4.12) (ATP-dependent helicase/nuclease AddA)	3.3.0	19.57	54.55
group_3978	A0A2Z5BY92	<i>RK57_04995</i>	DUF523 domain-containing protein	5.2.0	19.57	54.55
group_2127	Q8Y482	<i>lmo2573</i>	Zinc-type alcohol dehydrogenase-like protein	2.1.1	80.43	45.45
pleD	A0A3A8BW24	<i>pleD</i>	Response regulator PleD	5.2.0	80.43	45.45
argB	A0A1D2IV64	<i>argB</i>	Acetylglutamate kinase (EC 2.7.2.8) (N-acetyl-L-glutamate 5-phosphotransferase) (NAG kinase) (NAGK)	2.2.0	80.43	45.45
argC	Q8Y6U1	<i>argC</i>	N-acetyl-gamma-glutamyl-phosphate reductase (AGPR) (EC 1.2.1.38)	2.2.0	80.43	45.45
argD	Q8Y6U4	<i>argD</i>	Acetylmornithine aminotransferase (ACOAT) (EC 2.6.1.11)	2.2.0	80.43	45.45
glyS	Q8Y754	<i>glyS</i>	Glycine--tRNA ligase beta subunit (EC 6.1.1.14) (Glycyl-tRNA synthetase beta subunit) (GlyRS)	3.7.2	80.43	45.45
group_1908	A0A1D2IZW1	<i>nagA</i>	N-acetylglucosamine-6-phosphate deacetylase	2.1.1	80.43	45.45
glmS_3	A0A3A8C081	<i>glmS_2</i>	Glutamine--fructose-6-phosphate aminotransferase isomerizing (EC 2.6.1.16)	2.1.1	19.57	54.55
group_4569	Q8Y6H7	<i>lmo1707</i>	UPF0435 protein lmo1707	5.2.0	80.43	45.45
group_3624	Q8Y481	<i>lmo2574</i>	Lmo2574 protein	6.0.0	80.43	45.45
bglH_3	A0A3A8C1L2	<i>bglH_2</i>	Aryl-phospho-beta-D-glucosidase BglH (EC 3.2.1.86)	2.1.1	80.43	45.45
group_4703	A0A394ZKB6	<i>inlj_1</i>	Internalin-J (LPXTG cell wall anchor domain-containing protein) (Peptidoglycan-binding protein)	1.8.0	19.57	54.55
group_4318	Q8Y3P8	<i>bvrC</i>	BvrC protein	5.2.0	80.43	45.45
group_4494	Q8Y7H5	<i>lmo1304</i>	UPF0291 protein lmo1304	5.2.0	80.43	45.45
group_4497	UPI000BDF6015		DUF1033 family protein	5.2.0	80.43	45.45
group_4496	Q8Y7A8	<i>lmo1380</i>	Lmo1380 protein	6.0.0	80.43	45.45
group_4491	Q8Y7I1	<i>lmo1297</i>	Lmo1297 protein	4.2.0	80.43	45.45
group_4492	Q8Y7H8	<i>lmo1301</i>	Lmo1301 protein	5.2.0	80.43	45.45
group_4499	A0A1D2IVP2	<i>fabG</i>	3-oxoacyl-ACP reductase (EC 1.1.1.100)	2.4.0	80.43	45.45
xylF	Q8Y5F5	<i>lmo2109</i>	Lmo2109 protein	2.1.1	80.43	45.45
ydfG	Q8Y5S9	<i>lmo1976</i>	Lmo1976 protein	2.1.1	80.43	45.45
group_2269	A0A393RX26	<i>AF264_07710</i>	Uncharacterized protein	5.2.0	19.57	54.55
group_4402	A0A0E0UTV9	<i>LMM7_0781</i>	Uncharacterized protein	6.0.0	80.43	45.45
group_4369	Q8Y9K2	<i>lmo0525</i>	Lmo0525 protein	5.2.0	80.43	45.45
miaA	Q8Y7I3	<i>miaA</i>	tRNA dimethylallyltransferase (EC 2.5.1.75) (Dimethylallyl diphosphate:tRNA dimethylallyltransferase)	3.6.0	80.43	45.45
pgcA_1	Q8Y8N1	<i>lmo0865</i>	Lmo0865 protein	2.1.1	80.43	45.45
group_4149	A0A393JKC4	<i>AF239_03205</i>	Uncharacterized protein	6.0.0	19.57	54.55

group_4147	A0A2Z5C668	<i>RK57_12295</i>	TetR/AcrR family transcriptional regulator	6.0.0	19.57	54.55
group_4146	A0A393PPX4	<i>AB922_01757</i>	Uncharacterized protein	6.0.0	19.57	54.55
group_4144	A0A3A7GNS4	<i>AF264_03680</i>	Putative 3-methyladenine DNA glycosylase (EC 3.2.2.-)	3.2.0	19.57	54.55
group_1286	Q8Y945	<i>lmo0695</i>	Lmo0695 protein	6.0.0	80.43	45.45
group_4225	A0A1T1YI43	<i>DC57_13835</i>	Uncharacterized protein		19.57	54.55
group_1283	Q8Y9E3	<i>lmo0587</i>	Putative secreted protein	6.0.0	80.43	45.45
group_4223	A0A241SLD8	<i>ltrA</i>	Low temperature requirement protein A	4.1.0	19.57	54.55
group_4221	A0A0E1R4Z6	<i>BN389_04160</i>	Uncharacterized protein		19.57	54.55
group_4382	Q8Y981	<i>lmo0652</i>	Lmo0652 protein	5.2.0	80.43	45.45
group_4384	A0A1C7PWW5	<i>CDR86_13880</i>	Endonuclease III domain-containing protein	5.2.0	80.43	45.45
group_4228	A0A394ZC38	<i>AB922_00937</i>	N-acetyltransferase		19.57	54.55
dasR	Q8Y5T1	<i>lmo1974</i>	Lmo1974 protein	3.5.2	80.43	45.45
group_3083	A0A3A8BST8	<i>gloC</i>	Hydroxyacylglutathione hydrolase GloC (EC 3.1.2.6)	5.2.0	19.57	54.55
group_3461	A0A0E1R2S8	<i>BN389_04180</i>	Uncharacterized protein		19.57	54.55
group_3469	A0A394Y9C8	<i>inJ_15</i>	Cell surface protein (Internalin-J) (LPXTG cell wall anchor domain-containing protein)	1.8.0	19.57	54.55
group_4032	UPI0009A4F8FD		alpha/beta hydrolase	2.1.1	19.57	54.55
group_4031	A0A3A8BNZ3	<i>yvbK</i>	Putative N-acetyltransferase YvbK (EC 2.3.1.-)	5.2.0	19.57	54.55
group_4037	A0A3A7D8F9	<i>AF264_09645</i>	CPBP family intramembrane metalloprotease	5.2.0	19.57	54.55
group_4036	A0A3A7GG31	<i>sdrd</i>	Cell surface protein (LPXTG cell wall anchor domain-containing protein) (Serine-aspartate repeat-containing protein D)	1.8.0	19.57	54.55
group_3936	A0A392WP35	<i>AF251_13240</i>	Bacteriocin-associated integral membrane family protein (DUF1430 domain-containing protein)	1.2.0	19.57	54.55
group_3935	A0A3A7PI73	<i>AF251_13245</i>	Lactococcin 972 family bacteriocin	6.0.0	19.57	54.55
group_4136	A0A3A8C5J2	<i>ypdB</i>	Transcriptional regulatory protein YpdB	3.5.2	19.57	54.55
group_3932	A0A2Z5C1E0	<i>RK57_07485</i>	Uncharacterized protein		19.57	54.55
yhaO	Q8Y554	<i>lmo2222</i>	Lmo2222 protein	5.2.0	80.43	45.45
group_1862	Q8Y9U9	<i>lmo0421</i>	Lmo0421 protein	1.7.0	80.43	45.45
group_1861	Q8YA24	<i>lmo0341</i>	Lmo0341 protein	5.2.0	80.43	45.45
group_3510	Q8YAM4	<i>lmo0094</i>	Lmo0094 protein	6.0.0	80.43	45.45
group_3513	P33383	<i>lmo0206</i>	Uncharacterized protein Lmo0206	6.0.0	80.43	45.45
fmnP	A0A3A8BXM0	<i>fmnP</i>	Riboflavin transporter	5.2.0	80.43	45.45
dnaK_1	Q8Y7V8	<i>lmo1161</i>	Lmo1161 protein	2.1.1	80.43	45.45
group_3948	A0A1T1YKC2	<i>DC57_02040</i>	Uncharacterized protein	5.2.0	19.57	54.55
group_3949	A0A393RP85	<i>AF239_12775</i>	Acetamidase	5.2.0	19.57	54.55
group_3940	A0A3A7GBK9	<i>trpg</i>	Aminodeoxychorismate/anthranilate synthase component II (Anthranilate synthase component 2) (EC 4.1.3.27)	2.2.0	19.57	54.55
group_3947	A0A0B8R180	<i>LmNIHS28_00331</i>	Uncharacterized protein	6.0.0	19.57	54.55
group_1307	Q8Y7E2	<i>lmo1341</i>	Lmo1341 protein	1.10.0	80.43	45.45
group_1305	Q8Y7Y4	<i>lmo1135</i>	Lmo1135 protein	6.0.0	80.43	45.45
group_3587	A0A1D2IQ28	<i>rsgA</i>	Small ribosomal subunit biogenesis GTPase RsgA (EC 3.6.1.-)	5.2.0	80.43	45.45

group_1301	Q8Y7Z4	<i>lmo1125</i>	Lmo1125 protein	5.2.0	80.43	45.45
group_3589	Q8Y784	<i>lmo1411</i>	Lmo1411 protein	5.2.0	80.43	45.45
group_4599	A0A3A8BP41	<i>php_2</i>	Phosphotriesterase homology protein	2.4.0	80.43	45.45
rpe_3	A0A1D2INB4	<i>rpe</i>	Ribulose-phosphate 3-epimerase	2.1.1	80.43	45.45
bag	A0A394ZRE6	<i>AF264_02310</i>	DUF975 domain-containing protein (DUF975 family protein)	5.2.0	19.57	54.55
crnA_2	A0A3A8BU09	<i>crnA_2</i>	Creatinine amidohydrolase (EC 3.5.2.10)	2.2.0	80.43	45.45
group_1942	UPI000CE9721B	<i>LMJF5203_01179</i>	Cell wall surface anchor protein	1.8.0	19.57	54.55
group_3887	A0A2Z5C1D2	<i>RK57_08200</i>	Crp/Fnr family transcriptional regulator	5.1.0	19.57	54.55
group_3886	A0A0B8QU91	<i>LmNIHS28_00102</i>	Uncharacterized protein	6.0.0	19.57	54.55
group_3883	A0A393UMT7	<i>AB922_03025</i>	Uncharacterized protein	6.0.0	19.57	54.55
group_4670	UPI00098E7F8A		hypothetical protein		80.43	45.45
group_3881	A0A3A8BR90	<i>folK</i>	2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase (EC 2.7.6.3)	2.5.0	19.57	54.55
hisK	Q8Y9F8	<i>hisJ</i>	HisJ protein	2.2.0	80.43	45.45
group_4158	A0A3A7GM56	<i>AF264_03080</i>	Ribonuclease (EC 3.1.-.-)	5.1.0	19.57	54.55
group_4227	A0A2Z5C2F1	<i>RK57_09645</i>	LPXTG cell wall anchor domain-containing protein		19.57	54.55
comEA	A0A3A8BUN0	<i>comEA</i>	ComE operon protein 1	1.10.0	80.43	45.45
group_4048	A0A393S206	<i>AB922_00453</i>	Thioredoxin	1.4.0	19.57	54.55
group_4356	UPI00074D66E8	<i>LM7424_90077</i>	Uncharacterized protein	6.0.0	80.43	45.45
group_4355	Q8Y9X1	<i>lmo0397</i>	Lmo0397 protein	5.2.0	80.43	45.45
group_842	Q8Y8S6	<i>lmo0818</i>	Lmo0818 protein	1.2.0	80.43	45.45
group_4079	UPI00003CABCA	<i>BN389_14870</i>	Uncharacterized protein	6.0.0	19.57	54.55
group_4078	A0A3A2NXS6	<i>comea</i>	ComE operon protein 1 (ComEA family DNA-binding protein) (Competence protein ComEA)	1.10.0	19.57	54.55
group_4077	A0A3A8BV07	<i>tylM1</i>	dTDP-3-amino-3,6-dideoxy-alpha-D-glucopyranose N,N-dimethyltransferase (EC 2.1.1.235)	5.2.0	19.57	54.55
group_4076	A0A3A8BU71	<i>iscS_2</i>	Cysteine desulfurase IscS (EC 2.8.1.7)	2.5.0	19.57	54.55
group_4074	A0A3A8BU44	<i>rne</i>	Ribonuclease E (EC 3.1.26.12)	2.3.0	19.57	54.55
group_4073	A0A241SQE4	<i>folC</i>	Folylpolyglutamate synthase	2.5.0	19.57	54.55
group_4072	A0A3A8BUT3	<i>CFSAN002345_000149</i>	Uncharacterized protein	2.5.0	19.57	54.55
group_4071	Q71Z79	<i>argD</i>	Acetylornithine aminotransferase (ACOAT) (EC 2.6.1.11)	2.2.0	19.57	54.55
group_4070	Q71Z78	<i>argB</i>	Acetylglutamate kinase (EC 2.7.2.8) (N-acetyl-L-glutamate 5-phosphotransferase) (NAG kinase) (NAGK)	2.2.0	19.57	54.55
group_703	A0A3A8C0B4	<i>atpG_1</i>	ATP synthase gamma chain, sodium ion specific	1.4.0	80.43	45.45
group_4174	A0A392Y8U3	<i>AF264_02300</i>	GntR family transcriptional regulator	3.5.2	19.57	54.55
group_706	Q8YAN0	<i>lmo0087</i>	Lmo0087 protein	5.1.0	80.43	45.45
group_4170	A0A2Z5C307	<i>RK57_11240</i>	Crp/Fnr family transcriptional regulator		19.57	54.55
group_4171	A0A393D3V6	<i>AF264_02350</i>	Cell surface protein (LPXTG cell wall anchor domain-containing protein)		19.57	54.55
fgs	Q8Y6Y0	<i>folC</i>	FolC protein	2.5.0	80.43	45.45

group_4179	A0A3A7PLI4	<i>pknB</i>	Serine/threonine protein kinase (Serine/threonine-protein kinase PknB) (EC 2.7.11.1)	3.8.0	19.57	54.55
group_1137	Q8Y7E3	<i>lmo1340</i>	Lmo1340 protein	5.2.0	80.43	45.45
group_4189	C1L0J0	<i>hisE</i>	Phosphoribosyl-ATP pyrophosphatase (PRA-PH) (EC 3.6.1.31)	2.2.0	19.57	54.55
group_4188	C1L0J4	<i>hisH</i>	Imidazole glycerol phosphate synthase subunit HisH (EC 4.3.2.10) (IGP synthase glutaminase subunit) (EC 3.5.1.2)	2.2.0	19.57	54.55
group_4400	Q8Y8Z3	<i>lmo0749</i>	Lmo0749 protein		80.43	45.45
group_4183	A0A3A8CAW5	<i>glpE_2</i>	Thiosulfate sulfurtransferase GlpE (EC 2.8.1.1)	4.1.0	19.57	54.55
group_4172	UPI000BE051DD		transposase		19.57	54.55
group_4181	A0A3A7TYK7	<i>speG_1</i>	N-acetyltransferase (Spermidine N(1)-acetyltransferase) (EC 2.3.1.57)	5.2.0	19.57	54.55
group_4180	A0A0B8RG88	<i>LmNIHS28_00920</i>	Uncharacterized protein	5.1.0	19.57	54.55
yxIG	Q8Y550	<i>lmo2226</i>	Lmo2226 protein	5.2.0	80.43	45.45
group_4185	A0A393RUI1	<i>AF264_01965</i>	Uncharacterized protein	6.0.0	19.57	54.55
rpiB_3	G9G5K4	<i>rpiB</i>	Ribose-5-phosphate isomerase B	2.1.1	80.43	45.45
group_3412	A0A393RT87	<i>AF264_02105</i>	Uncharacterized protein	6.0.0	19.57	54.55
polC_2	Q8Y7E7	<i>lmo1336</i>	5-formyltetrahydrofolate cyclo-ligase (EC 6.3.3.2)	2.5.0	80.43	45.45
mngB_1	A0A255C9M1	<i>CDR86_08635</i>	Alpha-mannosidase	2.1.1	80.43	45.45
panC	Q8Y602	<i>panC</i>	Pantothenate synthetase (PS) (EC 6.3.2.1) (Pantoate--beta-alanine ligase) (Pantoate-activating enzyme)	2.5.0	80.43	45.45
group_4148	A0A3A7F1F5	<i>pgca_1</i>	Phospho-sugar mutase (Phosphoglucomutase) (EC 5.4.2.2)	2.1.1	19.57	54.55
group_1736	Q8Y8Q6	<i>lmo0840</i>	Lmo0840 protein	5.2.0	80.43	45.45
group_3709	A0A3A7ZGP4	<i>AF891_02052</i>	Uncharacterized protein		19.57	54.55
group_3319	A0A3A2NVJ1	<i>AB922_01742</i>	Uncharacterized protein		19.57	54.55
group_867	A0A1T1YI19	<i>DC57_13950</i>	Inorganic pyrophosphatase	2.6.0	80.43	45.45
hrtA_3	UPI00067846F2		ATP-binding cassette domain-containing protein		19.57	54.55
ecfA2	A0A0H3GF97	<i>ecfA</i>	Energy-coupling factor transporter ATP-binding protein EcfA (ECF transporter A component EcfA) (EC 3.6.3.-)	1.2.0	80.43	45.45
group_4388	Q8Y917	<i>lmo0725</i>	Putative peptidoglycan bound protein (LPXTG motif)	1.8.0	80.43	45.45
group_2380	A0A0E1R602	<i>yjaB</i>	Uncharacterized N-acetyltransferase YjaB (EC 2.3.1.-)	5.2.0	19.57	54.55
group_5075	A0A3A8B0G1	<i>levS</i>	Cell invasion LPXTG protein Vip (Levansucrase) (EC 2.4.1.10)	1.8.0	19.57	54.55
group_2577	Q8Y905	<i>lmo0737</i>	Lmo0737 protein	5.2.0	80.43	45.45
group_4301	Q8Y452	<i>lmo2603</i>	Lmo2603 protein	5.2.0	80.43	45.45
group_2208	A0A0B8RAD6	<i>LmNIHS28_01888</i>	Serine/threonine protein phosphatase	5.2.0	19.57	54.55
hisE	Q8Y9G7	<i>hisE</i>	Phosphoribosyl-ATP pyrophosphatase (PRA-PH) (EC 3.6.1.31)	2.2.0	80.43	45.45
group_4667	Q8Y4F2	<i>lmo2492</i>	Lmo2492 protein	6.0.0	80.43	45.45
glcR	Q8Y5F7	<i>lmo2107</i>	Lmo2107 protein	3.5.2	80.43	45.45
inIJ_11	A0A393CQT2	<i>inlj_6</i>	Cell surface protein (Internalin-J)	1.8.0	19.57	54.55
group_4192	A0A394ZNT3	<i>mta</i>	HTH-type transcriptional activator mta (MerR family transcriptional regulator)	3.5.2	19.57	54.55
group_4039	A0A3A8BN86	<i>ubiG</i>	Ubiquinone biosynthesis O-methyltransferase (EC 2.1.1.222)		19.57	54.55
group_4504	Q8Y751	<i>lmo1461</i>	Lmo1461 protein	6.0.0	80.43	45.45

group_4419	Q8Y8M8	<i>lmo0868</i>	Lmo0868 protein	6.0.0	80.43	45.45
group_949	A0A0E1R447	<i>manZ_2</i>	Mannose permease IID component	1.2.0	80.43	45.45
group_4415	Q8Y8Q3	<i>lmo0843</i>	Lmo0843 protein	5.2.0	80.43	45.45
group_4417	Q8Y8P6	<i>lmo0850</i>	Lmo0850 protein	6.0.0	80.43	45.45
group_4229	A0A2Z5C0J8	<i>RK57_09605</i>	Triosephosphate isomerase (EC 5.3.1.1)	2.1.2	19.57	54.55
group_4411	Q8Y8R3	<i>lmo0832</i>	Lmo0832 protein	4.4.0	80.43	45.45
group_4213	A0A3A2LR66	<i>inla_6</i>	Internalin (Internalin-A) (LPXTG cell wall anchor domain-containing protein)	1.8.0	19.57	54.55
inIJ_6	Q8Y8R0	<i>lmo0835</i>	Putative peptidoglycan bound protein (LPXTG motif)	1.8.0	80.43	45.45
group_4182	A0A3A8BWT2	<i>inlB_1</i>	Internalin B	1.8.0	19.57	54.55
kdgA	A0A2A6A934	<i>CDR86_00865</i>	Aldolase	2.1.1	80.43	45.45
group_4187	A0A1S7FNB3	<i>DC57_12750</i>	Histidinol-phosphatase	2.2.0	19.57	54.55
group_3171	A0A0E1RCR1	<i>yozG</i>	Uncharacterized HTH-type transcriptional regulator YozG	5.2.0	19.57	54.55
yflN	Q8Y6A5	<i>lmo1790</i>	Lmo1790 protein	5.2.0	80.43	45.45
yneA	Q8Y7H6	<i>yneA</i>	Cell division suppressor protein YneA	5.2.0	80.43	45.45
cca	Q8Y5Z8	<i>cca</i>	CCA tRNA nucleotidyltransferase (EC 2.7.7.72)	3.6.0	80.43	45.45
group_3921	A0A1S7FGU9	<i>DC57_00570</i>	LD-carboxypeptidase	4.5.0	19.57	54.55
nth_2	A0A3A7HTM1	<i>nth_1</i>	Endonuclease III (EC 4.2.99.18) (Endonuclease III domain-containing protein)	5.2.0	19.57	54.55
group_4047	C1KWK5	<i>cca</i>	CCA tRNA nucleotidyltransferase (EC 2.7.7.72)	3.6.0	19.57	54.55
group_4044	A0A393CLM7	<i>AF264_09030</i>	DUF5011 domain-containing protein		19.57	54.55
group_4045	A0A0E0UXG9	<i>aroH</i>	Chorismate mutase AroH (EC 5.4.99.5)	2.2.0	19.57	54.55
group_4042	A0A2Z5BZ76	<i>RK57_03415</i>	Uncharacterized protein	5.2.0	19.57	54.55
group_4043	A0A3A8BVH1	<i>act</i>	Methanol dehydrogenase activator (EC 3.-.-.-)	5.2.0	19.57	54.55
gdh	A0A3A8BLH6	<i>gdh_2</i>	Glucose 1-dehydrogenase (EC 1.1.1.47)	2.1.1	80.43	45.45
group_3922	A0A1S7FH11	<i>cutC</i>	Copper homeostasis protein CutC	4.2.0	19.57	54.55
cssS	Q8Y857	<i>lmo1061</i>	Histidine kinase (EC 2.7.13.3)	1.3.0	80.43	45.45
group_2610	Q8Y6G4	<i>lmo1723</i>	Lmo1723 protein	6.0.0	80.43	45.45
isdC	Q8Y585	<i>hbp1</i>	Hemin/hemoglobin-binding protein 1 (Hn/Hb-binding protein 1) (Cell wall protein Lmo2186)	1.8.0	80.43	45.45
group_3210	A0A393VWD9	<i>AB922_02198</i>	NUDIX domain-containing protein		19.57	54.55
group_3923	A0A2Z5BZQ8	<i>RK57_07860</i>	PTS fructose transporter subunit IIA	1.2.0	19.57	54.55
group_3219	A0A3A2WX84	<i>cbie</i>	Cobalt-precorrin-7 (C(5))-methyltransferase (Cobalt-precorrin-7 C(5)-methyltransferase) (EC 2.1.1.289)	2.5.0	19.57	54.55
nudF	Q8Y5U0	<i>lmo1965</i>	Lmo1965 protein	5.2.0	80.43	45.45
rne	Q8Y6Y8	<i>lmo1543</i>	Lmo1543 protein	2.3.0	80.43	45.45
group_3959	A0A394ZKW3	<i>gbpa</i>	Chitin-binding protein (GlcNAc-binding protein A)	2.1.1	19.57	54.55
group_3958	A0A2Z5BYZ7	<i>RK57_05850</i>	Uncharacterized protein	6.0.0	19.57	54.55
group_3951	A0A1T1YDG1	<i>DC57_02225</i>	Uncharacterized protein	6.0.0	19.57	54.55
group_3952	A0A3A2JZK0	<i>AF239_12415</i>	Zinc-type alcohol dehydrogenase-like protein	2.1.1	19.57	54.55
group_3957	A0A3A6WIB6	<i>AF239_12100</i>	Amidophosphoribosyltransferase (ComF family protein)	1.10.0	19.57	54.55
group_3956	A0A3A8BKJ7	<i>comFA</i>	ComF operon protein 1 (EC 3.6.4.12)	1.10.0	19.57	54.55

group_3593	Q8Y6N1	<i>lmo1653</i>	Putative cell surface protein	6.0.0	80.43	45.45
group_4466	A0A3A7HYF6	<i>DYZ90_00006</i>	Uncharacterized protein	6.0.0	80.43	45.45
group_4584	Q8Y600	<i>lmo1903</i>	Lmo1903 protein	1.4.0	80.43	45.45
phnA	Q8Y778	<i>lmo1418</i>	Lmo1418 protein	2.6.0	80.43	45.45
murQ	C1KVV7	<i>murQ</i>	N-acetylmuramic acid 6-phosphate etherase (MurNAc-6-P etherase) (EC 4.2.1.126)		19.57	54.55
group_3328	A0A394Y0E1	<i>AF264_03215</i>	Cell surface protein (LPXTG cell wall anchor domain-containing protein)	1.8.0	19.57	54.55
group_4386	A0A3A7EMK5	<i>AE233_02029</i>	Uncharacterized protein	1.8.0	80.43	45.45
rsgA_2	A0A0B8R6Z0	<i>rsgA</i>	Small ribosomal subunit biogenesis GTPase RsgA (EC 3.6.1.-)	5.2.0	19.57	54.55
azoR1_1	A0A3A8BPK0	<i>azoR1</i>	FMN-dependent NADH-azoreductase 1 (EC 1.7.-.-)	1.4.0	19.57	54.55
group_4438	Q8Y856	<i>lmo1062</i>	Lmo1062 protein	1.2.0	80.43	45.45
group_3028	A0A2Z5BXF4	<i>RK57_03270</i>	Riboflavin transporter	5.2.0	19.57	54.55
group_3135	A0A0E1R796	<i>yteJ</i>	Uncharacterized membrane protein yteJ	5.2.0	19.57	54.55
group_4138	A0A1S7FMA8	<i>DC57_10750</i>	Uncharacterized protein	5.2.0	19.57	54.55
group_4347	Q8YA09	<i>lmo0357</i>	Lmo0357 protein	1.2.0	80.43	45.45
group_4346	Q8YA13	<i>lmo0353</i>	Lmo0353 protein	5.2.0	80.43	45.45
inlA_8	UPI00073B62EC	<i>AOB47_624c</i>	Internalin-like protein	1.8.0	80.43	45.45
group_4082	A0A2Z5C055	<i>RK57_00410</i>	DUF2975 domain-containing protein		19.57	54.55
group_4080	A0A3A2XB09	<i>glys</i>	Glycine--tRNA ligase beta subunit (EC 6.1.1.14) (Glycyl-tRNA synthetase beta subunit) (GlyRS)	3.7.2	19.57	54.55
group_4081	A0A0E0UW34	<i>LMM7_1529</i>	Putative branched-chain amino acid export protein (BAAC homeostasis)	5.2.0	19.57	54.55
group_4086	A0A0B8R1M7	<i>LmNIHS28_01991</i>	Uncharacterized protein	6.0.0	19.57	54.55
group_4035	A0A2Z5C1Q5	<i>RK57_04100</i>	FeoB-associated Cys-rich membrane protein		19.57	54.55
group_4084	A0A3A7KDD8	<i>proC_1</i>	Pyrroline-5-carboxylate reductase (EC 1.5.1.2)	2.2.0	19.57	54.55
cobU	A0A3A8BXJ5	<i>cobU</i>	Bifunctional adenosylcobalamin biosynthesis protein CobU (EC 2.7.1.156)	2.5.0	80.43	45.45
group_3987	A0A3A8BPP2	<i>yxIG</i>	Putative transmembrane protein YxIG	5.2.0	19.57	54.55
group_3984	A0A3A8BNU1	<i>adaB</i>	Methylated-DNA--protein-cysteine methyltransferase, inducible (EC 2.1.1.63)	3.2.0	19.57	54.55
group_3985	UPI00086E8416		GntR family transcriptional regulator	3.5.2	19.57	54.55
group_3983	A0A0E1RA49	<i>yqjT</i>	Uncharacterized protein yqjT	5.2.0	19.57	54.55
group_3980	A0A0E1RA70	<i>yisK</i>	Uncharacterized protein yisK	5.2.0	19.57	54.55
group_3981	UPI0000F53EDE	<i>ARJ20_15280</i>	GNAT family N-acetyltransferase	5.2.0	19.57	54.55
group_4165	G9G5K0		Internalin protein	1.8.0	19.57	54.55
group_4167	A0A241SMW0	<i>A410_0767</i>	Uncharacterized protein	1.8.0	19.57	54.55
group_4166	UPI00003CA86A	<i>ARJ20_09330</i>	LPXTG cell wall anchor domain-containing protein	1.8.0	19.57	54.55
group_4161	A0A3A6WTN7	<i>ydde</i>	PhzF family phenazine biosynthesis protein (Putative isomerase Ydde) (EC 5.1.-.-)	5.2.0	19.57	54.55
group_4133	A0A0E1R4P0	<i>BN389_10880</i>	Uncharacterized protein		19.57	54.55
czcR	A0A3A8CCY3	<i>czcR</i>	Transcriptional activator protein CzcR	3.5.2	80.43	45.45
group_4169	A0A1T1YRJ7	<i>DC57_12265</i>	Carboxymuconolactone decarboxylase	5.2.0	19.57	54.55
group_4168	A0A0B8R2G1	<i>LmNIHS28_00854</i>	Flagellar hook protein	6.0.0	19.57	54.55

group_4038	A0A0B8R0U3	<i>LmNIHS28_01736</i>	TetR family transcriptional regulator		19.57	54.55
group_2864	A0A394XIB0	<i>inlj_9</i>	Cell wall anchor protein (Internalin-J) (LPXTG cell wall anchor domain-containing protein)		19.57	54.55
group_4371	Q8Y9I3	<i>lmo0545</i>	Lmo0545 protein	6.0.0	80.43	45.45
group_4137	A0A2Z5C2J4	<i>RK57_12860</i>	Teichoic acid D-Ala incorporation-associated protein DltX		19.57	54.55
group_4134	A0A3A7GGN8	<i>thif</i>	Molybdopterin biosynthesis protein MoeB (Sulfur carrier protein ThiS adenylyltransferase) (EC 2.7.7.73)	2.5.0	19.57	54.55
group_3408	A0A3A7C5V3	<i>stth</i>	Cysteine hydrolase (Streptothricin hydrolase) (EC 3.5.2.19)	5.2.0	19.57	54.55
hprA	Q8Y6K0	<i>lmo1684</i>	Lmo1684 protein	2.1.1	80.43	45.45
group_1192	A0A3A8C9D9	<i>artQ_1</i>	Arginine transport system permease protein ArtQ	1.2.0	19.57	54.55
yknZ_2	A0A393R639	<i>yknZ_1</i>	ABC transporter permease (FtsX-like permease family protein) (Putative ABC transporter permease YknZ)		19.57	54.55
mta	A0A3A8CEM4	<i>mta</i>	HTH-type transcriptional activator mta	3.5.2	80.43	45.45
yusV_2	Q8Y587	<i>lmo2182</i>	Lmo2182 protein	1.2.0	80.43	45.45
group_3710	UPI00074D523C	<i>DLE78_10480</i>	Uncharacterized protein		19.57	54.55
group_4091	B8DG24	<i>yneA</i>	Cell division suppressor protein YneA	5.2.0	19.57	54.55
group_4159	A0A3A7G936	<i>AF264_03075</i>	Ribonuclease P		19.57	54.55
cobC	A0A1D2IT42	<i>cobC</i>	Alpha-ribazole phosphatase	2.5.0	80.43	45.45
group_4628	Q8Y518	<i>lmo2260</i>	Lmo2260 protein	5.2.0	80.43	45.45
yvbK	Q8Y5E7	<i>lmo2117</i>	Lmo2117 protein	5.2.0	80.43	45.45
inlJ_4	A0A1D2IXY9	<i>CDR86_09540</i>	Cell surface protein	1.8.0	80.43	45.45
mgIA	A0A3A8C417	<i>mgIA</i>	Galactose/methyl galactoside import ATP-binding protein MglA (EC 3.6.3.17)	1.2.0	80.43	45.45
fabG_3	A0A3A8BVY0	<i>fabG_1</i>	3-oxoacyl-[acyl-carrier-protein] reductase FabG (EC 1.1.1.100)	2.4.0	19.57	54.55
inlJ_7	UPI000BDF441A		LPXTG cell wall anchor domain-containing protein	1.8.0	80.43	45.45
inlJ_1	Q8YAF4	<i>lmo0175</i>	Putative peptidoglycan bound protein (LPXTG motif)	1.8.0	80.43	45.45
group_4055	A0A2Z5BWW4	<i>RK57_02265</i>	Molybdate metabolism regulator	5.2.0	19.57	54.55
inlJ_8	UPI00043541E8	<i>HR60_04430</i>	Cell surface protein		19.57	54.55
group_4622	Q8Y578	<i>lmo2197</i>	Lmo2197 protein	6.0.0	80.43	45.45
group_2561	UPI000D72CB8D		IS3 family transposase	4.4.0	80.43	45.45
group_4151	A0A3A8BXI7	<i>yabJ</i>	2-iminobutanoate/2-iminopropanoate deaminase (EC 3.5.99.10)	5.2.0	19.57	54.55
group_2568	Q8Y9X8	<i>ltrA</i>	Low temperature requirement protein A	4.1.0	80.43	45.45
group_3567	Q8Y7Y2	<i>lmo1137</i>	Lmo1137 protein	6.0.0	80.43	45.45
argJ_1	Q8Y6U7	<i>lmo1584</i>	Lmo1584 protein	5.2.0	80.43	45.45
group_4335	A0A1D2J1W2	<i>CDR86_05500</i>	Internalin	1.8.0	80.43	45.45
group_4153	A0A3A7KR34	<i>inlJ_12</i>	Internalin-J (Peptidoglycan-binding protein)	1.8.0	19.57	54.55
group_4330	Q8YAN2	<i>lmo0085</i>	Lmo0085 protein	5.1.0	80.43	45.45
group_4331	Q8YAL4	<i>lmo0104</i>	Lmo0104 protein	6.0.0	80.43	45.45
uvrA_2	Q8Y4F6	<i>uvrA</i>	UvrABC system protein A (UvrA protein) (Excinuclease ABC subunit A)	3.2.0	80.43	45.45
adaB	Q8Y534	<i>lmo2242</i>	Lmo2242 protein	3.2.0	80.43	45.45
group_4157	UPI000939B687		hypothetical protein		19.57	54.55

glpE	A0A3A8C167	<i>glpE_1</i>	Thiosulfate sulfurtransferase GlpE (EC 2.8.1.1)	4.1.0	80.43	45.45
group_4424	A0A1D2IWW8	<i>CDR86_10445</i>	Putative 3-methyladenine DNA glycosylase (EC 3.2.2.-)	3.2.0	80.43	45.45
group_3478	A0A0E1R3M5	<i>inlA_2</i>	Internalin-A	1.8.0	19.57	54.55
tylM1	A0A3A8BVR5	<i>tylM1</i>	dTDP-3-amino-3,6-dideoxy-alpha-D-glucopyranose N,N-dimethyltransferase (EC 2.1.1.235)	5.2.0	80.43	45.45
lolD	UPI000EF63221		ATP-binding cassette domain-containing protein	1.2.0	26.09	63.64
group_1261	Q8Y3N2	<i>lmo2803</i>	Lmo2803 protein	6.0.0	73.91	36.36
aroH	A0A1D2J080	<i>aroH</i>	Chorismate mutase AroH (EC 5.4.99.5)	2.2.0	73.91	36.36
dhaM_1	A0A0E1R9L3	<i>dhaM</i>	PTS-dependent dihydroxyacetone kinase,phosphotransferase subunit dhaM (EC 2.7.1.-)	5.2.0	26.09	63.64
group_689	A0A3A7UBE8	<i>AF876_02227</i>	Uncharacterized protein	1.2.0	73.91	36.36
group_5175	A0A3A7PGJ7	<i>AFX42_00809</i>	Uncharacterized protein		0.00	18.18
group_5177	UPI000BDF1D90		BspA family leucine-rich repeat surface protein	1.8.0	0.00	18.18
group_5009	A0A3A6XXK8	<i>sirc</i>	Precorrin-2 dehydrogenase (EC 1.3.1.76)	2.5.0	0.00	18.18
group_4992	A0A393IY47	<i>D3B20_13165</i>	Uncharacterized protein	5.2.0	0.00	18.18
group_4993	A0A3A7CLP1	<i>D3B20_13150</i>	Uncharacterized protein	6.0.0	0.00	18.18
group_3731	UPI000E6CAEA9		BspA family leucine-rich repeat surface protein	1.8.0	0.00	18.18
ppnK1_2	UPI000D738E8C		NAD kinase	5.2.0	0.00	18.18
group_5190	A0A3A7PES7	<i>mshD</i>	Mycothiol acetyltransferase (EC 2.3.1.189) (N-acetyltransferase)	5.2.0	0.00	18.18
group_5182	UPI000BE06427		DNA cytosine methyltransferase		0.00	18.18
group_5183	A0A3A2TIQ6	<i>AFX42_02769</i>	ATP-binding protein		0.00	18.18
group_5184	A0A3A7D5I0	<i>AFX42_02768</i>	Uncharacterized protein		0.00	18.18
group_5185	A0A3A7D4F3	<i>AFX42_02327</i>	DUF4435 domain-containing protein		0.00	18.18
group_5186	A0A3A2T1D5	<i>recF_2</i>	ABC transporter ATP-binding protein (DNA replication and repair protein RecF)		0.00	18.18
group_5187	A0A0E0UUJ4	<i>LMM7_1122</i>	Uncharacterized protein		0.00	18.18
group_5188	A0A3A7P6J7	<i>AFX42_02324</i>	Uncharacterized protein		0.00	18.18
group_5176	A0A393IIP4	<i>AFX42_00806</i>	Uncharacterized protein		0.00	18.18
glnQ_2	UPI000E71158B	<i>AF253_04480</i>	ABC transporter ATP-binding protein		8.70	36.36
group_4693	A0A3A7SXN9	<i>AF247_04435</i>	Streptolysin associated protein SagD		8.70	36.36
group_3641	A0A3A7DQS9	<i>AF247_04430</i>	Bacteriocin biosynthesis cyclodehydratase		8.70	36.36
group_3640	A0A394XKL8	<i>AF241_04465</i>	SagB/ThcOx family dehydrogenase		8.70	36.36
group_3639	A0A0B8QY40	<i>LmNIHS28_00811</i>	ABC transporter permease		8.70	36.36
licH_1	UPI000EFDE50F		6-phospho-beta-glucosidase	2.1.1	91.30	63.64
group_1798	UPI000EFDE50F		6-phospho-beta-glucosidase	2.1.1	8.70	36.36
group_4692	A0A0B8RFY9	<i>LmNIHS28_00810</i>	Uncharacterized protein		8.70	36.36
group_51	A0A393IDA4	<i>DN830_06205</i>	LPXTG cell wall anchor domain-containing protein	6.0.0	8.70	36.36
group_3499	UPI000D0B11C5	<i>C7K50_14635</i>	Uncharacterized protein		45.65	9.09
group_3501	Q8Y3Z3	<i>lmo2686</i>	Lmo2686 protein	6.0.0	71.74	36.36
bioC	Q8Y7H2	<i>lmo1308</i>	Lmo1308 protein	3.8.0	71.74	36.36
group_44	UPI00098E51FB		transcriptional regulator	3.5.2	28.26	63.64

group_876	A0A1D2IYH2	<i>CDR86_08530</i>	Uncharacterized protein	6.0.0	28.26	63.64
group_1323	A0A393NY83	<i>AF252_05645</i>	Terminase large subunit		65.22	27.27
group_1930	UPI000987417B	<i>C7K67_12540</i>	Uncharacterized protein		65.22	27.27
group_1936	UPI0001E38E7D	<i>lmo4a_1264</i>	hypothetical protein		65.22	27.27
group_911	A0A394UBA6	<i>AF237_14510</i>	Phage portal protein		65.22	27.27
group_2560	UPI000BE05954		hypothetical protein	5.1.0	34.78	72.73
group_1329	A0A393DYM6	<i>AF840_02541</i>	Uncharacterized protein		56.52	18.18
group_661	UPI00025485A0	<i>AJZ74_02635</i>	Uncharacterized protein	5.2.0	56.52	18.18
group_1955	UPI000BE0056E		pyridoxal 5'-phosphate synthase glutaminase subunit PdxT	5.2.0	56.52	18.18
tsf_2	D7PCG5		Uncharacterized protein		43.48	9.09
clpP1	A0A3A7GTR6	<i>clpp1</i>	ATP-dependent Clp protease proteolytic subunit		43.48	9.09
group_4295	D7PCG6	<i>CDR86_14670</i>	DUF2786 domain-containing protein		43.48	9.09
group_4294	UPI000E7385DC		hypothetical protein		43.48	9.09
chpS	D7PCG9	<i>CDR86_14685</i>	AbrB/MazE/SpoVT family DNA-binding domain-containing protein (Putative PemI-like inhibitor)		43.48	9.09
mazF	D7PCH0	<i>CDR86_14690</i>	Putative PemK-like protein (Type II toxin-antitoxin system PemK/MazF family toxin)		43.48	9.09
group_4683	A0A393SKA6	<i>AF239_00415</i>	Uncharacterized protein	6.0.0	15.22	45.45
inlA_9	A0A3A2X399	<i>D3B21_09430</i>	LPXTG cell wall anchor domain-containing protein		15.22	45.45
group_366	A0A393SJQ0	<i>AF264_04585</i>	ABC transporter ATP-binding protein (Putative ABC transporter ATP-binding protein)	1.2.0	84.78	54.55
group_4041	A0A0E1R7D2	<i>BN389_20230</i>	Uncharacterized protein		15.22	45.45
group_1849	A0A3A7G8Z3	<i>AF264_00205</i>	ABC transporter ATP-binding protein (Putative ABC transporter ATP-binding protein)		15.22	45.45
group_197	A0A0H3G937	<i>LMRG_02391</i>	Uncharacterized protein	5.1.0	54.35	18.18
yjg_2	A0A3A7DAW7	<i>yjg_1</i>	HAD family hydrolase (Pyrimidine 5'-nucleotidase YjgG) (EC 3.1.3.5)	5.2.0	4.35	27.27
isfD	A0A3A7N465	<i>AF239_02990</i>	Putative oxidoreductase (EC 1.-.-.-) (SDR family NAD(P)-dependent oxidoreductase)		4.35	27.27
group_3708	A0A394R480	<i>AF239_02995</i>	MerR family transcriptional regulator (Putative HTH-type transcriptional regulator)		4.35	27.27
group_1939	A0A2A6A897	<i>CDR86_05340</i>	Phage tail protein		63.04	27.27
group_501	A0A394UQL1	<i>AF258_00550</i>	Internalin	1.8.0	63.04	27.27
nicS	A0A3A2WM62	<i>AF239_07990</i>	HTH-type transcriptional repressor (TetR/AcrR family transcriptional regulator)	3.5.2	36.96	72.73
group_2805	A0A3A7LSN2	<i>AF818_02838</i>	Uncharacterized protein		30.43	0.00
group_1355	UPI00083DFC0A		VRR-NUC domain-containing protein		30.43	0.00
group_684	UPI00070F78E1	<i>ARD00_01562</i>	Uncharacterized protein		30.43	0.00

† Description for each functional category code is presented below

[1.1.0] Cell envelope and cellular processes > Cell wall

[1.2.0] Cell envelope and cellular processes > Transport/binding proteins and lipoproteins

[1.3.0] Cell envelope and cellular processes > Sensors (signal transduction)

- [1.4.0] Cell envelope and cellular processes > Membrane bioenergetics
- [1.5.0] Cell envelope and cellular processes > Mobility and chemotaxis
- [1.6.0] Cell envelope and cellular processes > Protein secretion
- [1.7.0] Cell envelope and cellular processes > Cell division
- [1.8.0] Cell envelope and cellular processes > Cell surface proteins
- [1.9.0] Cell envelope and cellular processes > Soluble internalin
- [1.10.0] Cell envelope and cellular processes > Transformation/competence
- [2.1.0] Intermediary metabolism > Metabolism of carbohydrates and related molecule
- [2.1.1] Intermediary metabolism > Metabolism of carbohydrates and related molecule > Specific pathways
- [2.1.2] Intermediary metabolism > Metabolism of carbohydrates and related molecule > Main glycolytic pathways
- [2.1.3] Intermediary metabolism > Metabolism of carbohydrates and related molecule > TCA cycle
- [2.2.0] Intermediary metabolism > Metabolism of amino acids and related molecules
- [2.3.0] Intermediary metabolism > Metabolism of nucleotides and nucleic acids
- [2.4.0] Intermediary metabolism > Metabolism of lipids
- [2.5.0] Intermediary metabolism > Metabolism of coenzymes and prosthetic groups
- [2.6.0] Intermediary metabolism > Metabolism of phosphate
- [3.1.0] Information pathways > DNA replication
- [3.2.0] Information pathways > DNA restriction/modification and repair
- [3.3.0] Information pathways > DNA recombination
- [3.4.0] Information pathways > DNA packaging and segregation
- [3.5.1] Information pathways > RNA synthesis > Initiation
- [3.5.2] Information pathways > RNA synthesis > Regulation
- [3.5.3] Information pathways > RNA synthesis > Elongation
- [3.5.4] Information pathways > RNA synthesis > Termination
- [3.6.0] Information pathways > RNA modification
- [3.7.1] Information pathways > Protein synthesis > Ribosomal proteins
- [3.7.2] Information pathways > Protein synthesis > Aminoacyl-tRNA synthetases
- [3.7.3] Information pathways > Protein synthesis > Initiation
- [3.7.4] Information pathways > Protein synthesis > Elongation
- [3.7.5] Information pathways > Protein synthesis > Termination
- [3.8.0] Information pathways > Protein modification
- [3.9.0] Information pathways > Protein folding
- [4.1.0] Other functions > Adaptation to atypical conditions
- [4.2.0] Other functions > Detoxification
- [4.3.0] Other functions > Phage-related functions
- [4.4.0] Other functions > Transposon and IS
- [4.5.0] Other functions > Miscellaneous
- [5.1.0] Similar to unknown proteins > From *Listeria*
- [5.2.0] Similar to unknown proteins > From other organisms
- [6.0.0] No similarity

Supplementary Table 3. List of genes associated with biofilm production in BHI media supplemented with 0.85% NaCl at 37°C after pan-GWAS ($p < 0.05$).

GWAS name	Uniprot Entry	Organism ¥	Gene name	Protein names	Function al category †	% in weak biofilm formers	% in strong biofilm formers
group_3614	UPI000BDFAB31			hypothetical protein		9.09	66.67
eccCa1	A0A393D7A8		<i>essC</i>	ESAT-6 secretion machinery protein EssC (Type VII secretion protein EssC)	5.2.0	63.64	8.33
group_474	A0A393CRL8		<i>AF264_01650</i>	Putative sulfate transporter (SulP family inorganic anion transporter)	1.2.0	54.55	4.17
group_4197	UPI00098E3EF0			hypothetical protein		60.61	8.33
group_3636	A0A3A2YAK1		<i>cas5b</i>	Type I-B CRISPR-associated protein Cas5		27.27	79.17
cas1	UPI00092E4084		<i>B0X19_02870</i>	CRISPR-associated endonuclease Cas1		27.27	79.17
cas2	A0A0E0UTU7		<i>cas2</i>	CRISPR-associated endoribonuclease Cas2 (EC 3.1.-.-)		27.27	79.17
group_2659	A0A3A7SZG9		<i>cas6</i>	CRISPR-associated endoribonuclease Cas6		27.27	79.17
cas3	UPI00083D7946			CRISPR-associated helicase/endonuclease Cas3		27.27	79.17
group_311	A0A3A7W0T2		<i>AF947_01398</i>	Uncharacterized protein		24.24	75.00
group_1331	A0A394UA13		<i>AF237_14675</i>	Uncharacterized protein		24.24	75.00
group_1298	Q8Y842		<i>lmo1076</i>	Lmo1076 protein	1.1.0	60.61	100.00
group_1807	UPI000BE00DE2			hypothetical protein		54.55	8.33
group_2195	A0A393SL84		<i>coia</i>	Competence protein CoiA	1.10.0	60.61	12.50
group_2547	Q8Y403		<i>lmo2675</i>	Lmo2675 protein	6.0.0	39.39	87.50
group_4631	UPI00074D6448		<i>LM901004_160002</i>	Uncharacterized protein		21.21	70.83
group_673	A0A394V0T8		<i>AF237_14690</i>	Uncharacterized protein		21.21	70.83
group_4145	A0A3A7PI72		<i>AF239_03595</i>	Permease (Putative two-component membrane permease complex subunit)	5.2.0	66.67	16.67
group_4422	Q8Y8I2		<i>lmo0920</i>	Lmo0920 protein	5.2.0	33.33	83.33
group_4655	UPI0001698DDC		<i>LMJG_02653</i>	Uncharacterized protein		3.03	41.67
group_2733	A0A3A7T550		<i>clpP1</i>	ATP-dependent Clp protease proteolytic subunit		3.03	41.67
group_2710	UPI00003CA3EB		<i>AE052_00030</i>	DUF3954 domain-containing protein		3.03	41.67
group_2474	UPI000D72D1E5			DHA2 family efflux MFS transporter permease subunit	1.2.0	69.70	20.83
qacC	I7A797		<i>bcrB</i>	BcrB		0.00	33.33
slmA	I7B1B9		<i>bcrA</i>	BcrA		0.00	33.33
group_4280	S5XPK5			Glyoxalase family protein		0.00	33.33
group_4281	UPI00003CAA5B		<i>M643_p00795</i>	Transposon tn1546 resolvase		0.00	33.33
group_4282	UPI00003CAA5C			Putative resolvase		0.00	33.33
ebrB	I6ZWM1		<i>bcrC</i>	BcrC		0.00	33.33
marA	Q8Y803		<i>lmo1116</i>	Lmo1116 protein	3.5.2	63.64	16.67
group_4686	A0A393MBE2		<i>cas7i</i>	Type I-B CRISPR-associated protein Cas7/Cst2/DevR		27.27	75.00
group_2660	A0A3A7IMJ8		<i>cas8a1</i>	Type I-B CRISPR-associated protein Cas8b1/Cst1		27.27	75.00

group_1062	A0A393CV23	<i>AF264_09920</i>	Glycoside hydrolase family 65 protein	2.1.1	36.36	0.00
group_3613	A0A3A7UAN8	<i>AF252_15405</i>	Uncharacterized protein		6.06	45.83
group_672	A0A1B2LR20	<i>pLM-C-273_00081</i>	Uncharacterized protein		21.21	66.67
group_494	A0A3A7W452	<i>AF947_01400</i>	Uncharacterized protein		24.24	70.83
group_5508	A0A3A7W759	<i>AF951_01101</i>	Uncharacterized protein		24.24	70.83
group_1914	A0A1B2LR10	<i>pLM-C-273_00079</i>	Uncharacterized protein		24.24	70.83
group_1317	A0A1B2LR19	<i>pLM-C-273_00082</i>	Uncharacterized protein		24.24	70.83
group_1318	A0A1B2LR12	<i>pLM-C-273_00075</i>	Phage minor capsid protein 2		24.24	70.83
group_4796	A0A3A2TCH8	<i>AF255_15040</i>	IcLR family transcriptional regulator		12.12	54.17
group_3620	A0A2A6AA80	<i>CDR86_02685</i>	Uncharacterized protein	4.3.0	12.12	54.17
group_3665	UPI000C84336F		DUF1829 domain-containing protein		3.03	37.50
group_2674	A0A2A6AA36	<i>CDR86_02700</i>	Uncharacterized protein		3.03	37.50
group_4632	A0A1B2LR07	<i>pLM-C-273_00077</i>	Uncharacterized protein		3.03	37.50
emrY	A0A3A8BX24	<i>emrY</i>	Putative multidrug resistance protein EmrY	1.2.0	33.33	79.17
group_893	Q8Y802	<i>lmo1117</i>	Lmo1117 protein	6.0.0	66.67	20.83
group_6123	A0A3A2UAF9	<i>D3B62_10355</i>	XRE family transcriptional regulator		0.00	29.17
group_6122	UPI000BE0AF1F		site-specific integrase		0.00	29.17
group_6121	A0A393IBI0	<i>AF272_04760</i>	Uncharacterized protein		0.00	29.17
group_6120	A0A3A7S6F1	<i>AF272_04755</i>	Uncharacterized protein		0.00	29.17
clpB_1	UPI000BE11C1D		ATP-dependent Clp protease ATP-binding subunit		0.00	29.17
group_6112	A0A3A6XLA1	<i>AF856_02019</i>	Uncharacterized protein	6.0.0	0.00	29.17
group_6119	A0A3A7SLG2	<i>AF272_04750</i>	Uncharacterized protein		0.00	29.17
traC	UPI000EF5BB8B		DUF1738 domain-containing protein		0.00	29.17
group_5610	S5XI77		Uncharacterized protein		0.00	29.17
group_5607	A0A393MDT4	<i>AF862_02995</i>	IS30 family transposase		0.00	29.17
group_5606	S5XPL2		Uncharacterized protein		0.00	29.17
group_5609	A0A393Q5K9	<i>AB922_00255</i>	Uncharacterized protein		0.00	29.17
qorB_1	S5Y6N6		Uncharacterized protein		0.00	29.17
ravA_1	UPI000EF57D53		AAA family ATPase		0.00	29.17
group_5845	UPI000CDB4CAA		hypothetical protein		0.00	29.17
group_5846	A0A3A6X0N4	<i>AF856_03033</i>	Uncharacterized protein		0.00	29.17
group_5834	UPI0005447E48	<i>AF856_00972</i>	Uncharacterized protein	2.5.0	0.00	29.17
csbB	Q93RN0	<i>mtrA</i>	Dolichol-phosphate mannosyltransferase MtrA (Hypothetical glycosyl transferase)	1.1.0	66.67	100.00
tagH	UPI000BDFED64		teichoic acids export ABC transporter ATP-binding subunit TagH	1.1.0	66.67	100.00
malP	Q8Y5E3	<i>lmo2121</i>	Lmo2121 protein	2.1.1	66.67	100.00
group_1153	A0A0E0UUS7	<i>pncB</i>	Nicotinate phosphoribosyltransferase (EC 6.3.4.21)	5.2.0	33.33	0.00
rmlC	A0A1C7Q2S5	<i>rfbC</i>	dTDP-4-dehydrorhamnose 3,5-epimerase (EC 5.1.3.13) (Thymidine diphospho-4-keto-rhamnose 3,5-epimerase)	1.1.0	66.67	100.00
group_2636	A0A1B2LR21	<i>pLM-C-273_00076</i>	Uncharacterized protein		27.27	70.83
group_3520	Q8YA27	<i>lmo0338</i>	Lmo0338 protein	6.0.0	27.27	70.83

group_2567	Q7AP83	<i>lmo0320</i>	Lmo0320 protein	1.8.0	27.27	70.83
mtlR_4	A0A3A8C544	<i>mtlR_1</i>	Transcriptional regulator MtlR	3.5.2	42.42	4.17
group_904	A0A3A7P9G8	<i>inlJ_10</i>	Class 1 internalin InlL (Internalin-J)	1.8.0	42.42	4.17
group_2730	A0A392X2X8	<i>AF238_14485</i>	Uncharacterized protein		6.06	41.67
group_1319	UPI0008692819		sugar-phosphate nucleotidyltransferase		6.06	41.67
ssb_4	UPI000BE1101C		hypothetical protein		24.24	66.67
group_2597	A0A393F8Q4	<i>D3B62_10335</i>	Uncharacterized protein		12.12	50.00
group_1979	A0A0H3GEH2	<i>LMRG_00323</i>	Uncharacterized protein	6.0.0	36.36	79.17
group_473	A0A3A2JGS5	<i>AF247_01515</i>	Putative sulfate transporter (SulP family inorganic anion transporter)	1.2.0	36.36	79.17
group_3986	A0A3A8BQ69	<i>yxIE</i>	Negative regulatory protein YxIE		63.64	20.83
group_5451	A0A2A6A6P5	<i>CDR86_09885</i>	Uncharacterized protein		3.03	33.33
group_3780	A0A3A7G6J0	<i>AF847_01785</i>	DUF3850 domain-containing protein		3.03	33.33
group_903	A0A3A2NUT3	<i>inlJ_11</i>	Internalin-J (Peptidoglycan-binding protein)	1.8.0	3.03	33.33
group_5453	A0A2A6A785	<i>CDR86_09870</i>	XRE family transcriptional regulator		3.03	33.33
group_5454	A0A2A6A617	<i>CDR86_09865</i>	Uncharacterized protein		3.03	33.33
group_5445	UPI00083E1BDA		hypothetical protein	6.0.0	3.03	33.33
group_3782	A0A2A6A6S9	<i>CDR86_09890</i>	MerR family transcriptional regulator		3.03	33.33
group_3783	A0A2A6A5V6	<i>CDR86_09875</i>	XRE family transcriptional regulator		3.03	33.33
group_3454	A0A0B8RAV3	<i>LmNIHS28_01817</i>	Uncharacterized protein		30.30	0.00
group_4119	UPI000035D008	<i>APS76_03080</i>	CDP-glycerol glycerophosphotransferase family protein		30.30	0.00
tagB_2	A0A1D2ISQ5	<i>CDR86_11250</i>	Glycosyl transferase family 2	1.1.0	69.70	100.00
group_1891	Q8Y7T3	<i>lmo1188</i>	Lmo1188 protein	6.0.0	69.70	100.00
tagD	A0A1C7PZ73	<i>tagD</i>	Glycerol-3-phosphate cytidyltransferase	1.1.0	69.70	100.00
tagF	A0A3A8BW41	<i>tagF</i>	Teichoic acid poly(Glycerol phosphate) polymerase (EC 2.7.8.12)		30.30	0.00
epsJ	A0A3A7GEL8	<i>epsj</i>	Glycosyltransferase family 2 protein (Putative glycosyltransferase EpsJ) (EC 2.4.-.-)		30.30	0.00
lytG_5	A0A3A8BW61	<i>lytG_3</i>	Exo-glucosaminidase LytG (EC 3.2.1.-)		30.30	0.00
group_3925	A0A3A8BY26	<i>CFSAN002345_001436</i>	Uncharacterized protein		30.30	0.00
group_4118	UPI000E6B7FBF		glycerol-3-phosphate cytidyltransferase		30.30	0.00
pncB2	A0A0D8X9Q4	<i>CDR86_11285</i>	Nicotinate phosphoribosyltransferase (EC 6.3.4.21)	5.2.0	69.70	100.00
gtaB	UPI000931810D		UTP--glucose-1-phosphate uridylyltransferase GalU	1.1.0	69.70	100.00
nfrA1_1	A0A3A7H264	<i>nfra1_2</i>	FMN reductase (NADPH) (EC 1.5.1.38) (NADPH-dependent oxidoreductase)	1.4.0	69.70	100.00
ispD2_1	UPI0004D75A86	<i>HT50_11035</i>	2-C-methyl-D-erythritol 4-phosphate cytidyltransferase (Fragment)	2.1.0	69.70	100.00
group_965	UPI000D6455E8	<i>DF273_02615</i>	Uncharacterized protein (Fragment)		30.30	0.00
group_4030	A0A0B8R4F9	<i>LmNIHS28_01899</i>	Teichoic acid biosynthesis protein		30.30	0.00
group_6291	UPI000BDFECA9		DUF262 domain-containing protein	5.2.0	30.30	0.00
group_3939	A0A0B8QQZ7	<i>LmNIHS28_00261</i>	Membrane protein		30.30	0.00

group_3938	Q9ZIC5	<i>LmNIHS28_00260</i>	Uncharacterized protein		30.30	0.00
group_4132	A0A3A2P6F9	<i>AF241_04305</i>	DUF5068 domain-containing protein		30.30	0.00
group_4130	UPI000D66B0A6	<i>tagH</i>	Teichoic acids export ABC transporter ATP-binding subunit TagH (Fragment)		30.30	0.00
group_4131	A0A3A8BVC9	<i>tagG</i>	Transport permease protein		30.30	0.00
group_1860	Q8YA42	<i>lmo0322</i>	Lmo0322 protein	5.2.0	69.70	100.00
group_4446	Q8Y839	<i>lmo1079</i>	Lmo1079 protein	5.2.0	69.70	100.00
group_477	Q8Y9M5	<i>lmo0501</i>	Lmo0501 protein	3.5.2	69.70	100.00
group_4454	Q8Y831	<i>tarJ</i>	Ribulose-5-phosphate reductase (Ribulose-5-P reductase) (EC 1.1.1.405) (Ribitol-5-phosphate dehydrogenase)	2.1.0	69.70	100.00
group_5994	A0A0H3GDM5	<i>LMRG_00003</i>	Uncharacterized protein	6.0.0	30.30	0.00
group_3885	A0A393D4V0	<i>AF264_14565</i>	Pyruvyl-transferase		30.30	0.00
group_3882	A0A3A6WVM4	<i>AF241_14355</i>	Uncharacterized protein	4.3.0	30.30	0.00
group_4672	UPI0009305ABB		GtrA family protein	1.1.0	69.70	100.00
group_4126	A0A3A7GN59	<i>tarI</i>	CDP-glycerol:glycerophosphate glycerophosphotransferase (Teichoic acid poly(Ribitol-phosphate) polymerase) (EC 2.7.8.-)		30.30	0.00
group_2892	UPI0009B09F82		GW domain-containing glycosaminoglycan-binding protein	1.8.0	30.30	0.00
group_3705	A0A3A7DYA1	<i>AF249_03765</i>	DUF1541 domain-containing protein		30.30	0.00
tagB_3	Q8Y830	<i>tagB</i>	TagB protein	1.1.0	69.70	100.00
group_2384	UPI000766C630	<i>ERS409610_00158</i>	Uncharacterized protein		30.30	0.00
ykoT	UPI000035CFFF	<i>NT04LM_1735</i>	Glycosyl transferase, group 2 family protein		30.30	0.00
sdpR	A0A3A8BPZ1	<i>sdpR</i>	Transcriptional repressor SdpR	3.5.2	30.30	0.00
group_4237	A0A394YEX0	<i>AF264_00540</i>	Endonuclease (Endonuclease/exonuclease/phosphatase family protein)	5.2.0	30.30	0.00
group_4238	A0A394Y3M2	<i>AF264_00535</i>	PH domain-containing protein		30.30	0.00
group_4123	A0A0E1R4Q8	<i>ispD2</i>	Ribitol-5-phosphate cytidyltransferase (EC 2.7.7.40)		30.30	0.00
gutB	A0A3A7GLG3	<i>tarj</i>	Ribulose-5-phosphate reductase (Ribulose-5-P reductase) (EC 1.1.1.405) (Ribitol-5-phosphate dehydrogenase)		30.30	0.00
group_4125	UPI000D66CEA1	<i>DF274_15095</i>	Uncharacterized protein (Fragment)		30.30	0.00
group_4124	A0A3A8BY01	<i>gtab</i>	UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) (UDP-glucose pyrophosphorylase)		30.30	0.00
group_4127	A0A3A7GRB2	<i>AF264_04425</i>	Uncharacterized protein		30.30	0.00
group_4049	A0A3A8BMB0	<i>blaSE</i>	Serine protease (EC 3.4.21.-)		30.30	0.00
group_2752	A0A0H3GD86	<i>LMRG_02933</i>	Uncharacterized protein		30.30	0.00
group_3954	UPI000E3C8303		cell wall teichoic acid glycosylation protein GtcA		30.30	0.00
rffG	A0A1D2IST6	<i>rffB</i>	dTDP-glucose 4,6-dehydratase (EC 4.2.1.46)	1.1.0	69.70	100.00
gltR_1	A0A0B8QZ17	<i>LmNIHS28_01096</i>	LysR family transcriptional regulator	3.5.2	69.70	100.00
arnT	A0A3A7F315	<i>arnt</i>	Phospholipid carrier-dependent glycosyltransferase (Undecaprenyl phosphate-alpha-4-amino-4-deoxy-L-arabinose arabinosyl transferase) (EC 2.4.2.43)		30.30	0.00
group_3762	A0A142EC64	<i>pA144_0007</i>	Uncharacterized protein		30.30	0.00

rmlD	A0A1D2ISS6	<i>rfbD</i>	dTDP-4-dehydrorhamnose reductase (EC 1.1.1.133)	1.1.0	69.70	100.00
rmlA1	A0A0D8X3Y7	<i>rfbA</i>	Glucose-1-phosphate thymidyltransferase (EC 2.7.7.24)	1.1.0	69.70	100.00
group_3562	Q8Y850	<i>lmo1068</i>	Lmo1068 protein	6.0.0	69.70	100.00
epsJ_3	A0A3A8CCS3	<i>epsJ_2</i>	Putative glycosyltransferase EpsJ (EC 2.4.-.-)	1.1.0	69.70	100.00
epsJ_2	A0A3A7NTY9	<i>epsJ_2</i>	Glycosyltransferase (Putative glycosyltransferase EpsJ) (EC 2.4.-.-)	1.1.0	69.70	100.00
epsJ_1	Q8Y9M9	<i>lmo0497</i>	Lmo0497 protein	1.1.0	69.70	100.00
epsJ_4	A0A3A8BXQ8	<i>epsJ_1</i>	Putative glycosyltransferase EpsJ (EC 2.4.-.-)	1.1.0	69.70	100.00
group_4426	Q8Y8H1	<i>lmo0933</i>	Lmo0933 protein	1.1.0	69.70	100.00
group_749	Q8Y4S3	<i>lmo2359</i>	Lmo2359 protein	5.2.0	15.15	54.17
group_3667	UPI00074D6208	<i>LM83088_160259</i>	Uncharacterized protein		0.00	25.00
cwlO_1	A0A3A7JTC0	<i>cwlO_2</i>	Peptidoglycan DL-endopeptidase CwlO (EC 3.4.-.-)		0.00	25.00
group_3799	A0A3A7AUB6	<i>AB922_00627</i>	Uncharacterized protein		0.00	25.00
group_5575	A0A393NXT1	<i>AB922_00593</i>	Uncharacterized protein		0.00	25.00
group_5574	UPI000EF5AA7F		ImmA/IrrE family metallo-endopeptidase		0.00	25.00
group_5571	A0A3A7JXP8	<i>AB922_00597</i>	Restriction endonuclease		0.00	25.00
group_5570	A0A393QNC4	<i>AB922_00598</i>	Riboflavin synthase subunit alpha		0.00	25.00
group_5573	A0A3A7W8P2	<i>AB922_00595</i>	Uncharacterized protein		0.00	25.00
group_5572	A0A393SKE9	<i>AF236_15490</i>	Uncharacterized protein		0.00	25.00
group_5579	A0A3A7ST51	<i>AB922_00589</i>	Uncharacterized protein		0.00	25.00
nucH	A0A3A7QU08	<i>nucH</i>	Thermonuclease (EC 3.1.31.1)		0.00	25.00
group_6021	A0A2A6AA27	<i>CDR86_02650</i>	Uncharacterized protein	4.3.0	0.00	25.00
group_5550	UPI000D726E6E		hypothetical protein		0.00	25.00
group_5589	UPI000BE0B2D8		plasmid replication protein		0.00	25.00
rsrIM	UPI00003CAA42	<i>pLIS100090</i>	DNA modification methylase		0.00	25.00
group_5548	A0A393I3M4	<i>AB922_00620</i>	Uncharacterized protein		0.00	25.00
group_5549	A0A393VTF5	<i>AF236_15595</i>	Uncharacterized protein		0.00	25.00
group_5540	A0A393VTE6	<i>AB922_00629</i>	Uncharacterized protein		0.00	25.00
group_5541	A0A3A7TQJ4	<i>AB922_00628</i>	Uncharacterized protein		0.00	25.00
group_5542	UPI000EF5635A		DUF3324 domain-containing protein		0.00	25.00
group_5543	A0A393N4Q5	<i>AB922_00625</i>	Uncharacterized protein		0.00	25.00
group_5544	A0A3A7WL76	<i>AB922_00624</i>	Uncharacterized protein		0.00	25.00
group_5545	A0A3A7TAI8	<i>AB922_00623</i>	Uncharacterized protein		0.00	25.00
group_5546	A0A393QVS4	<i>AB922_00622</i>	Putative conjugal transfer protein (Type IV secretion protein)		0.00	25.00
group_5547	A0A3A7NVN4	<i>AB922_00621</i>	Uncharacterized protein		0.00	25.00
group_5584	UPI000E73B5A8		hypothetical protein		0.00	25.00
group_5585	A0A3A7M9C2	<i>AB922_00583</i>	XRE family transcriptional regulator		0.00	25.00
group_5586	A0A392WM50	<i>AB922_00582</i>	Uncharacterized protein		0.00	25.00
group_5587	UPI000EF5BA74		IS3 family transposase		0.00	25.00
group_5580	UPI00003CAA45	<i>AJN46_07220</i>	Uncharacterized protein		0.00	25.00
group_5581	D7V1H8	<i>HMPREF0556_plasmid12603</i>	Uncharacterized protein		0.00	25.00

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group_5582	A0A393RIL7		AB922_00586	Uncharacterized protein	0.00	25.00
group_5583	A0A3A7W8N1		AB922_00585	Uncharacterized protein	0.00	25.00
group_5588	A0A3A7P0S6		AB922_00580	Uncharacterized protein	0.00	25.00
group_5578	A0A3A7K0H3		AB922_00590	Uncharacterized protein	0.00	25.00
copY	A0A392WH77		copy	CopY/TcrY family copper transport repressor (Transcriptional repressor CopY)	0.00	25.00
rhIE	UPI000869703C			hypothetical protein	0.00	25.00
group_5559	A0A3A7MIR8		AB922_00609	Conjugal transfer protein TraG	0.00	25.00
group_5558	A0A393T254		AB922_00610	Uncharacterized protein	0.00	25.00
group_5557	A0A3A7NVP5		AB922_00611	Uncharacterized protein	0.00	25.00
group_5556	A0A393QNZ5		AB922_00612	Uncharacterized protein	0.00	25.00
group_5555	A0A3A7M9E3		AB922_00613	Uncharacterized protein	0.00	25.00
group_5554	A0A393N712		AB922_00614	Uncharacterized protein	0.00	25.00
group_5553	UPI000C86C85D		C1118_15230	Uncharacterized protein (Fragment)	0.00	25.00
group_5552	A0A393QP37		AB922_00616	Sodium:dicarboxylate symporter family protein	0.00	25.00
group_5551	D7V1E8	<i>Listeria grayi</i>	HMPREF0556_plasmid12573	Uncharacterized protein	0.00	25.00
group_5564	A0A3A7VTB4		AB922_00604	Uncharacterized protein	0.00	25.00
group_5562	A0A394RJT3		AB922_00606	Uncharacterized protein	0.00	25.00
group_5563	A0A393TGS3		AB922_00605	DUF87 domain-containing protein	0.00	25.00
group_5560	A0A393PMD5		AB922_00608	Uncharacterized protein	0.00	25.00
group_5561	A0A393VTG5		AB922_00607	Uncharacterized protein	0.00	25.00
group_5569	A0A392WH96		AB922_00599	Uncharacterized protein	0.00	25.00
group_5593	A0A393W756		AB922_00575	Restriction endonuclease	0.00	25.00
group_5592	A0A3A7AMA0		AB922_00576	Site-specific DNA-methyltransferase	0.00	25.00
group_5591	A0A393QQU6		AB922_00577	Uncharacterized protein	0.00	25.00
group_5596	UPI000D729918			IS6 family transposase	0.00	25.00
group_5594	A0A1X9VTW9	<i>Leuconostoc mesenteroides</i>	BSR26_10010	DNA methyltransferase	0.00	25.00
group_5566	A0A393QP03		AF236_15520	Uncharacterized protein	0.00	25.00
group_5567	A0A393SB73		AB922_00601	Fructose 1,6-bisphosphatase	0.00	25.00
tnsB	S5XPZ4			Putative transposase	0.00	25.00
group_5568	A0A393QVU4		AB922_00600	Uncharacterized protein	0.00	25.00
group_5539	UPI0001B4211E		AB922_00630	Uncharacterized protein	0.00	25.00
group_5538	A0A393NZ28		AF236_15655	Uncharacterized protein	0.00	25.00
group_5531	Q2V4W5		pCT0006	Site-specific recombinase, resolvase family	0.00	25.00
group_5533	Q2V4W3		pCT0008	Cation-transporting ATPase E1-E2 family	0.00	25.00
group_5532	Q2V4W4		pCT0007	Cadmium efflux system accessory protein	0.00	25.00
group_5535	UPI000D73450A			DNA recombinase	0.00	25.00
group_5534	UPI000931B2A1			transporter	0.00	25.00

group_5537	S5XI53		Pli0065		0.00	25.00
group_5536	UPI000C86D6AB		IS6 family transposase		0.00	25.00
group_2447	Q8Y9C6	<i>lmo0606</i>	Lmo0606 protein	3.5.2	39.39	4.17
group_3532	Q8Y9D1	<i>lmo0601</i>	Lmo0601 protein	1.8.0	63.64	95.83
group_3961	A0A0E0UZG3	<i>LMM7_2508</i>	Uncharacterized protein	6.0.0	36.36	4.17
group_4198	W5U092	<i>lntA</i>	Nuclear-targeted protein A	6.0.0	36.36	4.17
group_4184	A0A394ZL82	<i>AF264_02035</i>	DUF4097 domain-containing protein	1.8.0	36.36	4.17
group_2446	Q8Y9C6	<i>lmo0606</i>	Lmo0606 protein	3.5.2	63.64	95.83
group_2040	A0A3A7F101	<i>AF264_14455</i>	Ribonuclease (EC 3.1.-.-)	5.2.0	51.52	87.50
manZ_2	Q8YAT9	<i>lmo0024</i>	Lmo0024 protein	1.2.0	93.94	62.50
group_2709	A0A394THM9	<i>AF251_11415</i>	RNA polymerase subunit sigma-70 (Sigma-70 family RNA polymerase sigma factor)		6.06	37.50
group_1945	A0A3A2LWG0	<i>AF238_14270</i>	DUF2705 domain-containing protein		6.06	37.50
group_5797	A0A3A7RAL1	<i>ykfA</i>	LD-carboxypeptidase (Putative murein peptide carboxypeptidase) (EC 3.4.16.-)	4.5.0	6.06	37.50
group_671	UPI00098E2822		hypothetical protein		24.24	62.50
nifS	Q8Y5N5	<i>lmo2022</i>	Lmo2022 protein	2.5.0	24.24	62.50
group_3664	A0A3A2V097	<i>AF255_15050</i>	Uncharacterized protein	6.0.0	27.27	66.67
group_3618	A0A3A7RSE5	<i>AF249_11800</i>	Single-stranded DNA-binding protein		12.12	45.83
group_1898	A0A3A6XF63	<i>AF847_02154</i>	Uncharacterized protein		12.12	45.83
group_5501	A0A392ZMB7	<i>inlA_5</i>	Internalin-A (LPXTG cell wall anchor domain-containing protein)		12.12	45.83
yxIE	UPI000E759913	<i>yxle</i>	Negative regulatory protein YxIE	5.2.0	36.36	75.00
group_639	A0A3A7GLC4	<i>zosa_1</i>	Heavy metal translocating P-type ATPase (Zinc-transporting ATPase) (EC 3.6.3.-)	1.2.0	57.58	20.83
ytrB_3	A0A0E1R8M1	<i>yhcG</i>	Uncharacterized ABC transporter ATP-binding protein YhcG	1.2.0	27.27	0.00
group_3841	UPI000E6B9871		hypothetical protein		27.27	0.00
group_5915	A0A0H3G8Y5	<i>LMRG_02330</i>	Uncharacterized protein	6.0.0	27.27	0.00
group_397	A0A0B8R5D0	<i>LmNIHS28_00068</i>	Uncharacterized protein	5.1.0	72.73	100.00
group_5722	UPI0009853537		hypothetical protein		27.27	0.00
fosB	A0A0B8R4C4	<i>LmNIHS28_00813</i>	Glyoxalase	6.0.0	27.27	0.00
hrtA_2	A0A0E1RFE7	<i>hrtA</i>	Putative heme import ATP-binding protein HrtA (EC 3.6.3.-)	1.2.0	27.27	0.00
group_2750	A0A0H3GCJ6	<i>LMRG_02892</i>	Uncharacterized protein		27.27	0.00
group_488	A0A3A7U2K0	<i>AF856_02018</i>	Carbohydrate deacetylase (EC 3.5.1.-) (ChbG/HpnK family deacetylase)	5.2.0	27.27	0.00
group_5916	A0A0H3GCY0	<i>LMRG_02891</i>	Uncharacterized protein		27.27	0.00
group_3668	A0A3A2JQP2	<i>D3B79_08735</i>	PBSX family phage terminase large subunit		3.03	29.17
group_445	Q8Y698	<i>lmo1798</i>	Lmo1798 protein	5.2.0	3.03	29.17
group_1986	UPI00047C87C6		hypothetical protein	4.3.0	3.03	29.17
group_5444	A0A3A2L9Q7	<i>AF847_01784</i>	Preprotein translocase subunit YajC		3.03	29.17
yfkN	UPI0000F3E6A2	<i>LMRG_01845</i>	Uncharacterized protein	5.2.0	30.30	66.67
group_3700	UPI000984B87F		hypothetical protein		33.33	4.17

group_401	A0A394XJ12	<i>AF264_14015</i>	Uncharacterized protein		33.33	4.17
group_5799	UPI00092FB1F5		arsenic metallochaperone ArsD family protein		33.33	4.17
group_5471	A0A3A7D900	<i>AF847_03067</i>	DUF3850 domain-containing protein		9.09	41.67
group_5473	A0A3A7YSL8	<i>AF844_01551</i>	Uncharacterized protein		9.09	41.67
group_5431	A0A2A6A227	<i>CDR86_14950</i>	Uncharacterized protein		9.09	41.67
group_5432	UPI0000CCA78	<i>pLIS100300</i>	ParA family protein		9.09	41.67
group_162	A0A394V460	<i>essC</i>	ESAT-6 secretion machinery protein EssC (Type VII secretion protein EssC)	5.2.0	9.09	41.67
group_5796	UPI0009301249		cytadherence accessory protein		9.09	41.67
group_3825	A0A393Q993	<i>AF238_14460</i>	Uncharacterized protein		9.09	41.67
group_3824	A0A3A2QTE1	<i>AF238_14465</i>	Uncharacterized protein		9.09	41.67
group_5831	UPI000E7682E3		Dna2/Cas4 domain-containing protein		9.09	41.67
group_68	Q8YA28	<i>lmo0337</i>	Lmo0337 protein	5.1.0	18.18	54.17
inlA_7	L7X106	<i>inlA</i>	Internalin A	1.8.0	54.55	87.50
group_2056	A0A3A6WUY8	<i>AF251_14005</i>	Uncharacterized protein		45.45	12.50
group_1699	A0A2Z5C4D1	<i>RK57_13295</i>	UPF0637 protein RK57_13295	5.2.0	45.45	12.50
group_3917	A0A0H3G8X1	<i>LMRG_02492</i>	Uncharacterized protein		45.45	12.50
group_178	UPI000BDFE765	<i>AWK33_07760</i>	hypothetical protein		0.00	20.83
group_6033	A0A3A7UW75	<i>secB</i>	Protein-export protein SecB		0.00	20.83
group_6032	A0A3A6X357	<i>AF856_01589</i>	Uncharacterized protein		0.00	20.83
group_318	A0A393P2S7	<i>AF856_01561</i>	DUF1064 domain-containing protein	4.3.0	0.00	20.83
group_6019	A0A2A6AAG8	<i>CDR86_02670</i>	XRE family transcriptional regulator		0.00	20.83
group_6018	A0A0B8RGQ4	<i>CDR86_02675</i>	Gp33 protein (XRE family transcriptional regulator)		0.00	20.83
group_4801	A0A3A2R9E5	<i>D3B46_07385</i>	Uncharacterized protein		0.00	20.83
group_6020	A0A2A6AAX3	<i>CDR86_02665</i>	Uncharacterized protein		0.00	20.83
group_66	UPI000930FC04		hypothetical protein	6.0.0	0.00	20.83
group_6051	A0A3A7TMP1	<i>AF856_01566</i>	Uncharacterized protein		0.00	20.83
group_6031	UPI00086B6770		hypothetical protein		0.00	20.83
group_1322	A0A1D2IMX9	<i>CDR86_05480</i>	Uncharacterized protein		6.06	33.33
group_693	UPI000479B88B		hypothetical protein		6.06	33.33
group_2657	A0A2Z5C560	<i>RK57_09450</i>	Endonuclease	5.2.0	6.06	33.33
gadB_2	A0A241SSP1	<i>gadB</i>	Glutamate decarboxylase (EC 4.1.1.15)	2.2.0	93.94	66.67
group_2635	A0A1B2LR14	<i>pLM-C-273_00080</i>	Uncharacterized protein		6.06	33.33
group_1951	A0A3A2UIX5	<i>AF252_11530</i>	Uncharacterized protein		6.06	33.33
group_2741	A0A3A2SDU8	<i>D3B73_13335</i>	SMI1/KNR4 family protein	6.0.0	39.39	8.33
chiA1	Q8YAL3	<i>lmo0105</i>	Lmo0105 protein	2.1.1	60.61	91.67
copB	UPI000E76FAAA		copper-translocating P-type ATPase		39.39	8.33
group_489	A0A393SSR6	<i>AF245_00250</i>	SMI1/KNR4 family protein	6.0.0	60.61	91.67
group_4056	A0A393JPV1	<i>AF241_07740</i>	Uncharacterized protein	6.0.0	24.24	0.00
group_4114	A0A2Z5C2X9	<i>RK57_13530</i>	Uncharacterized protein	5.1.0	24.24	0.00

group_6284	A0A0H3GFH8	<i>LMRG_02220</i>	Uncharacterized protein	6.0.0	24.24	0.00
group_6280	A0A3A7NSF4		Uncharacterized protein		24.24	0.00
group_6281	A0A3A7NH96		Uncharacterized protein		24.24	0.00
group_3875	A0A3A7Q520		Uncharacterized protein		24.24	0.00
group_3924	UPI0009B11300		GW domain-containing glycosaminoglycan-binding protein		24.24	0.00
group_2173	Q8Y4R2		Lmo2372 protein	1.2.0	75.76	100.00
group_6273	A0A3A7UXE8		Uncharacterized protein		24.24	0.00
group_6272	A0A3A7V8A6		Sugar-phosphate nucleotidyltransferase		24.24	0.00
group_6271	UPI00053BE8EB		Uncharacterized protein		24.24	0.00
group_6270	UPI000678F014		Uncharacterized protein		24.24	0.00
group_6277	A0A393A7N5	<i>DOZ93_04605</i>	Phage antirepressor		24.24	0.00
glnQ_2	UPI000E71158B		ABC transporter ATP-binding protein		24.24	0.00
group_6265	UPI00076722D3		Uncharacterized protein		24.24	0.00
group_6263	UPI000507E686		Uncharacterized protein		24.24	0.00
group_6279	A0A3A7NV98		Uncharacterized protein	4.3.0	24.24	0.00
group_4693	A0A3A7SXN9		Streptolysin associated protein SagD		24.24	0.00
group_294	UPI000BE003A6		helicase SNF2		24.24	0.00
group_6276	A0A3A7EN18		XRE family transcriptional regulator		24.24	0.00
group_3878	A0A393A2Z5		XRE family transcriptional regulator		24.24	0.00
group_3873	UPI0004D8BD21		Uncharacterized protein		24.24	0.00
group_3876	UPI00074D51A1	<i>LM800396_140057</i>	Uncharacterized protein		24.24	0.00
group_3877	A0A3A7UV92		Uncharacterized protein		24.24	0.00
group_3874	A0A0V7YCU8		Uncharacterized protein		24.24	0.00
group_1839	UPI000E75DD0C		Uncharacterized protein	5.1.0	24.24	0.00
group_3641	A0A3A7DQS9		Bacteriocin biosynthesis cyclodehydratase		24.24	0.00
group_3640	A0A394XKL8		SagB/ThcOx family dehydrogenase		24.24	0.00
group_2760	UPI00086F2DD0		DUF1738 domain-containing protein		24.24	0.00
bcgIB	UPI0009850DB7		Uncharacterized protein		24.24	0.00
bcgIA	UPI00074D58A5		Adenine methyltransferase		24.24	0.00
group_938	Q8YAG9		Lmo0157 protein	3.2.0	24.24	0.00
group_6253	UPI000BE1046E	<i>lmo0157</i>	relaxase		24.24	0.00
group_6255	E6EXY6		Uncharacterized protein		24.24	0.00
group_6254	UPI00098E5223		plasmid mobilization relaxosome protein MobC		24.24	0.00
group_6256	UPI0004D69275		LPXTG cell wall anchor domain-containing protein		24.24	0.00
group_6258	UPI000BE07A8C		CHAP domain-containing protein		24.24	0.00
group_3639	A0A0B8QY40		ABC transporter permease		24.24	0.00

yofA	A0A393QJ60	<i>yofA</i>	HTH-type transcriptional regulator YofA (LysR family transcriptional regulator)		24.24	0.00
licH_1	UPI000EFDE50F		6-phospho-beta-glucosidase	2.1.1	75.76	100.00
group_1798	UPI000EFDE50F		6-phospho-beta-glucosidase	2.1.1	24.24	0.00
group_487	A0A3A7GDL7	<i>AF264_00475</i>	Carbohydrate deacetylase (EC 3.5.1.-) (ChbG/HpnK family deacetylase)	5.2.0	75.76	100.00
group_4692	A0A0B8RFY9	<i>LmNIHS28_00810</i>	Uncharacterized protein		24.24	0.00
group_6264	A0A0H3GD71	<i>LMRG_02934</i>	Uncharacterized protein		24.24	0.00
group_6266	A0A3A7MCD0	<i>AF821_01506</i>	Uncharacterized protein		24.24	0.00
group_6267	A0A0H3G912	<i>LMRG_02574</i>	GNAT family acetyltransferase		24.24	0.00
group_6260	Q2V4W9	<i>pCT0002</i>	Uncharacterized protein		24.24	0.00
group_6261	UPI00074D5B8B	<i>LM800396_140058</i>	Uncharacterized protein		24.24	0.00
group_6262	A0A3A7YC45	<i>AF821_01500</i>	Uncharacterized protein		24.24	0.00
group_6268	A0A3A7URE0	<i>ID87_02064</i>	Uncharacterized protein		24.24	0.00
mco	UPI000A1FFD33		copper oxidase		24.24	0.00
hsdM	A0A3A7RFF8	<i>hsdM</i>	SAM-dependent DNA methyltransferase (Type I restriction enzyme EcoKI M protein) (EC 2.1.1.72)		24.24	0.00
hsdR	A0A3A7Y0A7	<i>hsdR</i>	Type I restriction endonuclease subunit R (Type-I restriction enzyme R protein) (EC 3.1.21.3)		24.24	0.00
group_4899	A0A393JAZ3	<i>inlA_6</i>	DUF5011 domain-containing protein (Internalin-A)		15.15	45.83
group_3797	A0A3A2L4U9	<i>AF238_14470</i>	Uncharacterized protein		15.15	45.83
group_5509	A0A3A2KDS0	<i>AF273_15200</i>	Uncharacterized protein		15.15	45.83
group_388	UPI0009870563		DnaD domain protein		15.15	45.83
group_4112	A0A0B8RBG4	<i>LmNIHS28_00797</i>	Uncharacterized protein	6.0.0	30.30	4.17
group_2486	A0A3A7PTC4	<i>AF251_01345</i>	DNA double-strand break repair Rad50 ATPase		30.30	4.17
group_4113	UPI0004311060	<i>HR60_02825</i>	Membrane protein		30.30	4.17
group_4194	A0A3A8BYI6	<i>CFSAN002345_001197</i>	Uncharacterized protein		30.30	4.17
group_4195	A0A0B8RHP3	<i>LmNIHS28_01665</i>	Uncharacterized protein		30.30	4.17
group_1150	A0A394RBJ1	<i>AF239_04485</i>	Uncharacterized protein		30.30	4.17
group_3850	A0A0H3GHG8	<i>LMRG_00005</i>	Uncharacterized protein		30.30	4.17
group_4224	A0A3A7A655	<i>AF241_00720</i>	Peptidase (Putative peptidase) (EC 3.4.21.-)	2.2.0	30.30	4.17
group_2501	A0A394ZN44	<i>AF264_00790</i>	YafY family transcriptional regulator	3.5.2	30.30	4.17
tatAy	Q8YA04	<i>tatA</i>	Sec-independent protein translocase protein TatA	5.2.0	69.70	95.83
group_5404	A0A142EC67	<i>pA144_0010</i>	Uncharacterized protein		30.30	4.17
group_2381	A0A394ZTP0	<i>AF264_04540</i>	Uncharacterized protein	5.1.0	30.30	4.17
group_2751	UPI0000F3E668	<i>LMRG_00004</i>	Uncharacterized protein	6.0.0	30.30	4.17
efeU	Q8YA02	<i>lmo0365</i>	Lmo0365 protein	5.2.0	69.70	95.83
efeM	Q8YA01	<i>lmo0366</i>	Lmo0366 protein	1.2.0	69.70	95.83
group_3761	A0A142EC65	<i>pA144_0008</i>	Uncharacterized protein		30.30	4.17

group_5405	A0A142EC66	<i>pA144_0009</i>	Uncharacterized protein		30.30	4.17
tatC2	Q8YA05	<i>tatC</i>	Sec-independent protein translocase protein TatC	5.2.0	69.70	95.83
group_6278	A0A393AES1	<i>DOZ93_04600</i>	Uncharacterized protein		21.21	0.00
group_295	UPI00042E7F14	<i>ARK89_15370</i>	Uncharacterized protein		21.21	0.00
wapA	A0A0E1R9W5	<i>wapA_2</i>	Wall-associated protein		21.21	0.00
group_6269	A0A3A7V3E1	<i>immR_3</i>	HTH-type transcriptional regulator ImmR		21.21	0.00
group_2069	A0A0H3GGP2	<i>LMRG_02453</i>	Mannose-specific PTS system IID component	1.2.0	9.09	37.50
group_5469	UPI00074D5C6E	<i>DB955_12755</i>	Uncharacterized protein		9.09	37.50
group_2747	A0A3A7GK30	<i>dnax_1</i>	DNA polymerase III subunit gamma/tau (EC 2.7.7.7)	3.1.0	42.42	12.50
cshA_1	UPI000E748D91	<i>yfmI</i>	Putative ATP-dependent RNA helicase YfmL	3.6.0	42.42	12.50
group_590	A0A0B8R1T6	<i>topA</i>	DNA topoisomerase I (EC 5.99.1.2) (DNA topoisomerase I)	3.4.0	42.42	12.50
group_343	A0A393RXH2	<i>uvrA_1</i>	UvrABC system protein A (UvrA protein) (Excinuclease ABC subunit A)	3.2.0	42.42	12.50
group_464	A0A393AUV1	<i>ddrA</i>	Diol dehydratase reactivase subunit alpha (Diol dehydratase-reactivating factor alpha subunit)	2.1.1	42.42	12.50
group_948	A0A3A8BZW0	<i>manZ_2</i>	PTS system mannose-specific EIID component	1.2.0	42.42	12.50
group_1046	A0A241ST46	<i>arpJ</i>	Amino acid ABC transporter, permease protein	1.2.0	42.42	12.50
bglF_4	Q8Y3P7	<i>bvrB</i>	Beta-glucoside-specific phosphotransferase enzyme II ABC component	1.2.0	57.58	87.50
group_276	A0A393UU69	<i>inlJ_12</i>	Cell surface protein (Internalin-J) (LPXTG cell wall anchor domain-containing protein)	1.8.0	42.42	12.50
group_3512	Q8XFU0	<i>lmo0174 lmo0329 lmo0827</i>	Lmo0174 protein (Lmo0329 protein) (Lmo0827 protein)		57.58	87.50
group_2141	A0A3A8BU08	<i>ywtF</i>	Putative transcriptional regulator YwtF	3.5.2	42.42	12.50
group_762	A0A0B8RIH2	<i>LmNIHS28_02100</i>	2-nitropropane dioxygenase	5.2.0	42.42	12.50
group_2444	A0A394ZP22	<i>AF264_02070</i>	ABC transporter ATP-binding protein (Putative ABC transporter ATP-binding protein)	1.2.0	42.42	12.50
group_1633	A0A3A8BTZ2	<i>iscS_1</i>	Cysteine desulfurase IscS (EC 2.8.1.7)	2.5.0	42.42	12.50
group_1698	Q8Y853	<i>lmo1065</i>	UPF0637 protein lmo1065	5.2.0	57.58	87.50
group_2638	A0A1D2J2T1	<i>CDR86_02640</i>	Uncharacterized protein	6.0.0	18.18	50.00
group_1919	A0A393FFS4	<i>AF249_11805</i>	Uncharacterized protein	4.3.0	18.18	50.00
group_271	A0A393EUH1	<i>AF249_11760</i>	Uncharacterized protein	6.0.0	18.18	50.00
lolD	UPI000EF63221		ATP-binding cassette domain-containing protein	1.2.0	45.45	16.67
group_3916	A0A3A7D3S5	<i>AF251_14010</i>	Uncharacterized protein		45.45	16.67
group_689	A0A3A7UBE8	<i>AF876_02227</i>	Uncharacterized protein	1.2.0	54.55	83.33
group_179	A0A3A6XDK1	<i>cwlK_1</i>	M15 family peptidase (Peptidoglycan L-alanyl-D-glutamate endopeptidase CwlK) (EC 3.4.-.-)		0.00	16.67
group_6128	A0A3A7DT48	<i>ydag</i>	General stress protein (General stress protein 26)	5.2.0	0.00	16.67
group_6127	A0A393PKW4	<i>AF856_02681</i>	Uncharacterized protein		0.00	16.67
group_6126	UPI000C184228	<i>P734_13635</i>	Uncharacterized protein		0.00	16.67
group_6125	A0A3A7YXF2	<i>aroH_3</i>	Chorismate mutase AroH (EC 5.4.99.5)	2.2.0	0.00	16.67

group_6124	A0A3A7Z5T3	<i>rsbRD_1</i>	RsbT co-antagonist protein RsbRD (STAS domain-containing protein)	3.5.2	0.00	16.67
dacA_1	A0A3A8C0D1	<i>dacA_1</i>	D-alanyl-D-alanine carboxypeptidase DacA (EC 3.4.16.4)	1.1.0	100.00	83.33
group_6116	A0A3A6X160	<i>AF856_00673</i>	Uncharacterized protein		0.00	16.67
group_6114	UPI0001975C76	<i>AF856_01874</i>	Uncharacterized protein	5.1.0	0.00	16.67
group_6115	A0A3A2QZK9	<i>AF856_00674</i>	Uncharacterized protein		0.00	16.67
group_6113	A0A3A7SN42	<i>AF856_01875</i>	Uncharacterized protein		0.00	16.67
group_6110	UPI00083D8768		DEAD/DEAH box helicase		0.00	16.67
group_6111	UPI000C86987A	<i>DB955_06525</i>	DUF3310 domain-containing protein		0.00	16.67
group_6118	A0A3A2R9S0	<i>AF856_00671</i>	Subtilase		0.00	16.67
rsbRD_2	A0A3A8C0Q6	<i>rsbRD_1</i>	RsbT co-antagonist protein RsbRD	3.5.2	100.00	83.33
group_3849	UPI000C82ECAA	<i>AE052_00662</i>	Uncharacterized protein		0.00	16.67
group_60	UPI000BE0D727	<i>DSD41_15835</i>	Pentapeptide repeat-containing protein		0.00	16.67
pabB	A0A393CPU5	<i>pabB</i>	Aminodeoxychorismate synthase component 1 (Aminodeoxychorismate synthase component I) (EC 2.6.1.85)	2.2.0	100.00	83.33
group_3804	UPI0005DF0EE0	<i>UF18_04880</i>	Uncharacterized protein		0.00	16.67
group_5612	A0A393NK10	<i>AB922_00245</i>	Uncharacterized protein		0.00	16.67
bepR	A0A3A7D1L4	<i>AF264_13415</i>	TetR/AcrR family transcriptional regulator	3.5.2	100.00	83.33
group_6109	A0A3A7IZB5	<i>AF856_03129</i>	Uncharacterized protein		0.00	16.67
feaR	A0A3A8C0I4	<i>feaR</i>	Transcriptional activator FeaR	3.5.2	100.00	83.33
sauU	A0A3A2S3I3	<i>sauu</i>	MFS transporter (Putative sulfoacetate transporter SauU)	1.2.0	100.00	83.33
group_4673	A0A2A6A8Y8	<i>CDR86_05485</i>	Uncharacterized protein		0.00	16.67
ftsH_2	A0A3A7DV86	<i>ftsH_1</i>	ATP-binding protein (ATP-dependent zinc metalloprotease FtsH) (EC 3.4.24.-)		0.00	16.67
ydaG	A0A394XK17	<i>ydag</i>	General stress protein (General stress protein 26)	5.2.0	100.00	83.33
group_3867	A0A393UGI5	<i>DCT05_12735</i>	Uncharacterized protein		0.00	16.67
group_5979	A0A393TCN4	<i>AF828_02778</i>	Uncharacterized protein		0.00	16.67
group_1984	UPI000771AA2D		hypothetical protein	6.0.0	0.00	16.67
traD	A0A3A8AEL8	<i>traG</i>	Conjugal transfer protein TraG		0.00	16.67
pabA_2	A0A3A7DMV1	<i>paba_2</i>	Aminodeoxychorismate synthase component 2 (EC 2.6.1.85) (Aminodeoxychorismate/anthranilate synthase component II)	2.2.0	0.00	16.67
group_5935	UPI0005C68DD0		hypothetical protein	4.3.0	0.00	16.67
group_6217	UPI00076181B6		hypothetical protein	6.0.0	0.00	16.67
group_6130	UPI00083CAFD8		aminodeoxychorismate synthase component I	2.2.0	0.00	16.67
group_6131	A0A3A6XIE2	<i>daca_2</i>	D-alanyl-D-alanine carboxypeptidase (D-alanyl-D-alanine carboxypeptidase DacA) (EC 3.4.16.4)		0.00	16.67
group_6133	A0A3A7DM63	<i>fabg_3</i>	3-oxoacyl-[acyl-carrier-protein] reductase FabG (EC 1.1.1.100) (SDR family NAD(P)-dependent oxidoreductase)	2.1.1	0.00	16.67
group_6134	A0A3A2QX50	<i>sauu</i>	MFS transporter (Putative sulfoacetate transporter SauU)	1.2.0	0.00	16.67
group_6136	A0A3A6WQT3	<i>AF856_02180</i>	Uncharacterized protein		0.00	16.67
group_6137	A0A393IRF0	<i>D3B86_12220</i>	Uncharacterized protein		0.00	16.67

group_6135	A0A3A7YZM5	<i>feaR</i>	Helix-turn-helix domain-containing protein (Transcriptional activator FeaR)	3.5.2	0.00	16.67
mtrR	A0A393NQA7	<i>mtrr</i>	HTH-type transcriptional regulator MtrR (TetR/AcrR family transcriptional regulator)	3.5.2	0.00	16.67
fabG_1	A0A3A7DKS1	<i>fabg_2</i>	3-oxoacyl-[acyl-carrier-protein] reductase FabG (EC 1.1.1.100) (KR domain-containing protein) (SDR family NAD(P)-dependent oxidoreductase)	2.1.1	100.00	83.33
group_513	A0A393M724	<i>DN831_08165</i>	Uncharacterized protein	6.0.0	0.00	16.67
group_4099	UPI000D648E93	<i>DF275_07015</i>	Uncharacterized protein (Fragment)		36.36	8.33
iscS_1	Q8Y713	<i>lmo1513</i>	Lmo1513 protein	2.5.0	63.64	91.67
group_3931	A0A2Z5BZG6	<i>RK57_07490</i>	Uncharacterized protein	6.0.0	36.36	8.33
group_3888	A0A0B8RBN9	<i>LmNIHS28_00109</i>	Uncharacterized protein	6.0.0	36.36	8.33
efeN	Q8YA00	<i>lmo0367</i>	Deferrochelataase/peroxidase (EC 1.11.1.-)	5.2.0	63.64	91.67
group_511	A0A3A7GBM6	<i>chia1</i>	Chitinase (Chitinase A1) (EC 3.2.1.14)	2.1.1	36.36	8.33
group_4477	A0A3A6ZKA9	<i>AF947_02068</i>	Uncharacterized protein		6.06	29.17
group_3741	A0A393MUK4	<i>D3B04_11680</i>	DUF3310 domain-containing protein		6.06	29.17
group_180	UPI000BDFE765		hypothetical protein		6.06	29.17
group_4649	A0A3A7T6Q6	<i>AF249_11825</i>	Uncharacterized protein	4.3.0	6.06	29.17
zosA	A0A3A7WV50	<i>zosA</i>	Heavy metal translocating P-type ATPase (Zinc-transporting ATPase) (EC 3.6.3.-)	1.2.0	48.48	79.17
group_4803	A0A3A7BSB1	<i>AE233_02875</i>	Peptide ABC transporter permease		24.24	54.17
ybiA	A0A0B8R4G2	<i>LmNIHS28_00503</i>	Swarming motility protein YbiA		72.73	41.67
comK_1	UPI000BE018FA		competence protein ComK		30.30	62.50
group_155	A0A394UFW5	<i>inlD</i>	Class 1 internalin InlD (Internalin-A)	1.8.0	30.30	62.50
group_131	A0A393RNT2	<i>AF264_14030</i>	Uncharacterized protein	6.0.0	33.33	8.33
group_2647	A0A3A2YHL0	<i>AF252_05590</i>	ATP-dependent helicase (DEAD/DEAH box helicase)		33.33	8.33
group_2522	A0A3A2PCV4	<i>comEC_1</i>	ComE operon protein 3 (MBL fold metallo-hydrolase)	1.10.0	33.33	8.33
group_676	Q8Y496	<i>ami</i>	Autolysin, amidase	1.8.0	66.67	91.67
group_1332	UPI00057F741C	<i>OJ14_05160</i>	Uncharacterized protein		33.33	8.33
group_2102	A0A3A7DM92	<i>AF264_12825</i>	NUDIX pyrophosphatase		33.33	8.33
group_661	UPI00025485A0	<i>AJZ74_02635</i>	Uncharacterized protein	5.2.0	36.36	66.67
group_2488	UPI000869A2AF		HEAT repeat domain-containing protein		18.18	0.00
inlA_13	A0A394XWP9	<i>AF264_05160</i>	Cell surface protein		18.18	0.00
tkf_3	A0A0D8X574	<i>CDR86_05070</i>	Uncharacterized protein	5.2.0	18.18	0.00
group_4212	A0A0E1R3F0	<i>BN389_04600</i>	Uncharacterized protein		18.18	0.00
parC	A0A3A7I7R9	<i>parc</i>	DNA topoisomerase 4 subunit A (EC 5.99.1.3) (Topoisomerase IV subunit A)	3.4.0	81.82	100.00
group_846	A0A0B8R577	<i>hflX</i>	GTPase HflX (GTP-binding protein HflX)	4.5.0	18.18	0.00
group_966	A0A0B8QWB8	<i>LmNIHS28_00166</i>	Cell surface protein		18.18	0.00
group_1672	A0A0H3GJX6	<i>parC</i>	DNA topoisomerase 4 subunit A (EC 5.99.1.3) (Topoisomerase IV subunit A)	3.4.0	18.18	0.00

group_3452	A0A0B8RG05	<i>LmNIHS28_01809</i>	Uncharacterized protein		18.18	0.00
group_5020	A0A3A8BWY7	<i>CFSAN002345_002255</i>	Uncharacterized protein		18.18	0.00
group_2662	A0A3A2JSN0	<i>AF247_04460</i>	Uncharacterized protein		18.18	0.00
group_3817	UPI00092E980C		uridine kinase		3.03	25.00
group_5820	A0A3A7GWE9	<i>AF238_11110</i>	Ig domain-containing protein		3.03	25.00
group_5891	A0A3A2WIZ3	<i>AF944_02807</i>	Uncharacterized protein		3.03	25.00
group_443	A0A3A6WGG5	<i>AF264_08290</i>	Poly(Glycerol-phosphate) alpha-glucosyltransferase	5.2.0	96.97	75.00
group_5449	A0A2A6A5P4	<i>CDR86_09900</i>	DUF2786 domain-containing protein		3.03	25.00
group_5448	UPI00092FD6C1		hypothetical protein		3.03	25.00
group_5447	UPI0003591FC5	<i>DB944_02160</i>	Uncharacterized protein	4.3.0	3.03	25.00
group_3655	A0A3A7VDZ7	<i>AF239_11030</i>	Phage repressor protein/antirepressor Ant		15.15	41.67
hin	A0A3A2JMV4	<i>hin_1</i>	DNA-invertase hin (Recombinase family protein)	4.3.0	15.15	41.67
group_3751	UPI000BE0CC15		plasmid replication protein		15.15	41.67
group_4521	Q8Y6I3	<i>lmo1701</i>	Lmo1701 protein	6.0.0	15.15	41.67
group_3784	A0A3A2KAA0	<i>AF255_02365</i>	DUF1398 domain-containing protein	6.0.0	15.15	41.67
group_1780	A0A0B8R2H7	<i>LmNIHS28_00917</i>	Phage envelope protein	6.0.0	84.85	58.33
group_1660	A0A3A8C6B9	<i>mgIA</i>	Galactose/methyl galactoside import ATP-binding protein MglA (EC 3.6.3.17)	1.2.0	39.39	12.50
group_860	Q8Y9U8	<i>lmo0422</i>	Lmo0422 protein	5.2.0	60.61	87.50
group_4658	Q8Y4U3	<i>lmo2339</i>	Lmo2339 protein	5.2.0	60.61	87.50
group_261	A0A393F884	<i>AF249_03970</i>	Cell surface protein (LPXTG cell wall anchor domain-containing protein)	1.8.0	60.61	87.50
group_1613	UPI000986F629	<i>D3C41_14375</i>	DEAD/DEAH box helicase	3.6.0	60.61	87.50
atpG_1	A0A3A7I128	<i>atpg_1</i>	ATP synthase gamma chain, sodium ion specific (F0F1 ATP synthase subunit gamma)	1.4.0	39.39	12.50
group_1398	A0A393D0P2	<i>aguA</i>	Putative agmatine deiminase (EC 3.5.3.12) (Agmatine iminohydrolase)	5.2.0	39.39	12.50
isdE_1	Q9EXG4	<i>fufA</i>	Heme ABC transporter substrate-binding protein IsdE (Lipoprotein)	1.2.0	60.61	87.50
group_761	Q8Y599	<i>lmo2170</i>	Lmo2170 protein	5.2.0	60.61	87.50
ogt_2	Q8Y8B2	<i>lmo0996</i>	Methylated-DNA--protein-cysteine methyltransferase (EC 2.1.1.63) (O-6-methylguanine-DNA-alkyltransferase)	3.2.0	60.61	87.50
group_4262	UPI000C8207CA		replication and copy control-associated protein		39.39	12.50
group_4266	D7PCE1		Uncharacterized protein		39.39	12.50
group_1653	A0A1S7FKW2	<i>DC57_08295</i>	Alkaline phosphatase family protein	2.6.0	39.39	12.50
group_1657	A0A3A8BUI8	<i>albF</i>	Putative zinc protease AlbF (EC 3.4.24.-)	2.2.0	39.39	12.50
group_1837	A0A241SLH2	<i>tkt</i>	Transketolase (EC 2.2.1.1)	2.1.2	39.39	12.50
ywtF	A0A3A8BV30	<i>ywtF</i>	Putative transcriptional regulator YwtF	3.5.2	60.61	87.50
artQ_2	Q8Y527	<i>arpJ</i>	ArpJ protein	1.2.0	60.61	87.50
iscS_2	A0A3A8BUZ1	<i>iscS_2</i>	Cysteine desulfurase IscS (EC 2.8.1.7)	2.5.0	60.61	87.50

group_3165	A0A3A7MIL3	<i>garB</i>	Glutathione amide reductase (EC 1.8.1.16) (NAD(P)/FAD-dependent oxidoreductase)	4.1.0	39.39	12.50
group_2697	A0A3A7Q910	<i>AF818_02415</i>	Uncharacterized protein		39.39	12.50
group_4135	A0A3A2VNJ8	<i>ogt</i>	Methylated-DNA--protein-cysteine methyltransferase (EC 2.1.1.63) (O-6-methylguanine-DNA-alkyltransferase)	3.2.0	39.39	12.50
group_1560	A0A3A8BMS5	<i>ydfG</i>	NADP-dependent 3-hydroxy acid dehydrogenase YdfG (EC 1.1.1.381)	2.1.1	39.39	12.50
group_2769	A0A1D2IW42	<i>CDR86_11860</i>	ABC transporter permease	5.2.0	60.61	87.50
group_2119	A0A241STG7	<i>cbiO</i>	Energy-coupling factor transporter ATP-binding protein EcfA (ECF transporter A component EcfA) (EC 3.6.3.-)	1.2.0	39.39	12.50
group_4593	Q8Y5W2	<i>lmo1943</i>	Lmo1943 protein	5.2.0	60.61	87.50
group_1000	A0A3A7RII6	<i>AE233_00940</i>	SMI1/KNR4 family protein	5.2.0	60.61	87.50
fosX	Q8Y6I2	<i>fosX</i>	Fosfomycin resistance protein FosX	4.1.0	60.61	87.50
group_705	A0A2Z5C4I1	<i>RK57_08210</i>	Uncharacterized protein	5.1.0	39.39	12.50
group_1138	A0A394ZK64	<i>AF264_05670</i>	Uncharacterized protein	5.2.0	39.39	12.50
ddrA	A0A0E0UUN7	<i>pduG</i>	Putative diol dehydratase-reactivating factor large subunit	2.1.1	60.61	87.50
group_2575	Q8Y972	<i>lmo0661</i>	Lmo0661 protein	5.2.0	60.61	87.50
group_4665	Q8Y4J5	<i>lmo2443</i>	Lmo2443 protein	6.0.0	60.61	87.50
soj_1	UPI00093201BA		chromosome partitioning protein ParA		39.39	12.50
dnaX_1	A0A1D2IRD3	<i>dnaX</i>	DNA polymerase III subunit gamma/tau (EC 2.7.7.7)	3.1.0	60.61	87.50
group_4609	Q8Y5S4	<i>lmo1981</i>	Lmo1981 protein	5.2.0	60.61	87.50
group_4230	A0A1S7FP22	<i>DC57_13960</i>	Uncharacterized protein		39.39	12.50
topA	A0A1D2IVT6	<i>topA</i>	DNA topoisomerase I (EC 5.99.1.2) (DNA topoisomerase I)	3.4.0	60.61	87.50
group_2445	Q8Y9C4	<i>lmo0608</i>	Lmo0608 protein	1.2.0	60.61	87.50
group_649	A0A393CN22	<i>AF264_00975</i>	Mannosylglycerate hydrolase (EC 3.2.1.170)	2.1.1	39.39	12.50
inlA_4	A0A1D2IYS1	<i>CDR86_07930</i>	Internalin	1.8.0	60.61	87.50
skfE	A0A3A8BUB3	<i>skfE</i>	SkfA peptide export ATP-binding protein SkfE (EC 3.6.3.25)	1.2.0	60.61	87.50
group_4348	A0A0H3GDS2	<i>LMRG_00052</i>	Uncharacterized protein		60.61	87.50
group_1735	A0A0E0UV76	<i>LMM7_0870</i>	Putative transcriptional regulator, MarR family	5.2.0	39.39	12.50
garB	A0A3A7P5T5	<i>garB</i>	Glutathione amide reductase (EC 1.8.1.16) (NAD(P)/FAD-dependent oxidoreductase)	4.1.0	60.61	87.50
xseA_2	A0A0E1R607	<i>yqgN</i>	5-formyltetrahydrofolate cyclo-ligase (EC 6.3.3.2)	2.5.0	39.39	12.50
group_3491	D7PCE0		Transposase		39.39	12.50
inlJ_5	A0A3A8C0G4	<i>inlJ_2</i>	Internalin-J	1.8.0	60.61	87.50
inlJ_9	Q8Y591	<i>lmo2178</i>	Putative peptidoglycan bound protein (LPXTG motif)	1.8.0	60.61	87.50
group_4336	Q8YAA5	<i>lmo0247</i>	Lmo0247 protein	6.0.0	60.61	87.50
group_4570	Q8Y6H1	<i>lmo1715</i>	Lmo1715 protein	5.2.0	9.09	33.33
group_1934	A0A392XCY7	<i>AF828_00150</i>	Phage tail protein		9.09	33.33
group_2178	A0A3A7KNB4	<i>gadB_1</i>	Glutamate decarboxylase (EC 4.1.1.15)	2.2.0	9.09	33.33
group_5624	UPI000BE07ECD		hypothetical protein		9.09	33.33
group_5457	A0A393UJV3	<i>AF828_00146</i>	Phage gp6-like head-tail connector protein		9.09	33.33

group_5416	A0A394VX67	<i>AF239_12505</i>	Uncharacterized protein		9.09	33.33
group_5418	A0A393W8P8	<i>AF847_02885</i>	Uncharacterized protein	4.3.0	9.09	33.33
group_3699	Q8Y4W9	<i>lmo2310</i>	Lmo2310 protein	6.0.0	9.09	33.33
group_3597	Q8Y6H2	<i>lmo1714</i>	Lmo1714 protein	5.2.0	9.09	33.33
group_4888	A0A393CGK6	<i>AF876_00589</i>	Uncharacterized protein	5.1.0	9.09	33.33
group_5415	A0A394VMA7	<i>AF239_12500</i>	Uncharacterized protein		9.09	33.33
group_2559	UPI000B54942D		DUF3130 family protein	5.1.0	18.18	45.83
group_697	A0A1T1YBY4	<i>DC57_15090</i>	Type VII secretion effector	5.1.0	81.82	54.17
group_770	A0A3A2WV59	<i>feoB</i>	Ferrous iron transport protein B	1.2.0	42.42	16.67
group_492	Q8Y7H3	<i>lmo1307</i>	Lmo1307 protein	6.0.0	57.58	83.33
blaSE	UPI0000F53A3E	<i>HR75_01490</i>	Peptidase		57.58	83.33
group_1421	A0A3A7HNU0	<i>AB922_02876</i>	DUF4918 domain-containing protein (DUF4918 family protein) (SMUG2 DNA glycosylase family protein)	6.0.0	42.42	16.67
group_746	A0A0B8R487	<i>LmNIHS28_01552</i>	ABC transporter permease	1.2.0	42.42	16.67
group_2612	A0A0H3GHY8	<i>LMRG_02831</i>	Uncharacterized protein	5.2.0	57.58	83.33

¥ Non *L. monocytogenes* species

† Description for each functional category code is presented below

- [1.1.0] Cell envelope and cellular processes > Cell wall
- [1.2.0] Cell envelope and cellular processes > Transport/binding proteins and lipoproteins
- [1.3.0] Cell envelope and cellular processes > Sensors (signal transduction)
- [1.4.0] Cell envelope and cellular processes > Membrane bioenergetics
- [1.5.0] Cell envelope and cellular processes > Mobility and chemotaxis
- [1.6.0] Cell envelope and cellular processes > Protein secretion
- [1.7.0] Cell envelope and cellular processes > Cell division
- [1.8.0] Cell envelope and cellular processes > Cell surface proteins
- [1.9.0] Cell envelope and cellular processes > Soluble internalin
- [1.10.0] Cell envelope and cellular processes > Transformation/competence
- [2.1.0] Intermediary metabolism > Metabolism of carbohydrates and related molecule
- [2.1.1] Intermediary metabolism > Metabolism of carbohydrates and related molecule > Specific pathways
- [2.1.2] Intermediary metabolism > Metabolism of carbohydrates and related molecule > Main glycolytic pathways
- [2.1.3] Intermediary metabolism > Metabolism of carbohydrates and related molecule > TCA cycle
- [2.2.0] Intermediary metabolism > Metabolism of amino acids and related molecules
- [2.3.0] Intermediary metabolism > Metabolism of nucleotides and nucleic acids
- [2.4.0] Intermediary metabolism > Metabolism of lipids
- [2.5.0] Intermediary metabolism > Metabolism of coenzymes and prosthetic groups
- [2.6.0] Intermediary metabolism > Metabolism of phosphate
- [3.1.0] Information pathways > DNA replication
- [3.2.0] Information pathways > DNA restriction/modification and repair
- [3.3.0] Information pathways > DNA recombination
- [3.4.0] Information pathways > DNA packaging and segregation
- [3.5.1] Information pathways > RNA synthesis > Initiation

- [3.5.2] Information pathways > RNA synthesis > Regulation
- [3.5.3] Information pathways > RNA synthesis > Elongation
- [3.5.4] Information pathways > RNA synthesis > Termination
- [3.6.0] Information pathways > RNA modification
- [3.7.1] Information pathways > Protein synthesis > Ribosomal proteins
- [3.7.2] Information pathways > Protein synthesis > Aminoacyl-tRNA synthetases
- [3.7.3] Information pathways > Protein synthesis > Initiation
- [3.7.4] Information pathways > Protein synthesis > Elongation
- [3.7.5] Information pathways > Protein synthesis > Termination
- [3.8.0] Information pathways > Protein modification
- [3.9.0] Information pathways > Protein folding
- [4.1.0] Other functions > Adaptation to atypical conditions
- [4.2.0] Other functions > Detoxification
- [4.3.0] Other functions > Phage-related functions
- [4.4.0] Other functions > Transposon and IS
- [4.5.0] Other functions > Miscellaneous
- [5.1.0] Similar to unknown proteins > From *Listeria*
- [5.2.0] Similar to unknown proteins > From other organisms
- [6.0.0] No similarity

Supplementary Table 4. List of genes associated with biofilm production in dBHI media supplemented with 0.85% NaCl at 37°C after pan-GWAS ($p < 0.05$).

GWAS name	Uniprot Entry	Organism ¥	Gene name	Protein names	Function al category †	% in weak biofilm formers	% in strong biofilm formers
group_1262	UPI000873C4F1	<i>Lactococcus lactis</i>		DUF1310 family protein	5.1.0	8.57	63.64
group_3691	A0A3A2TPS8		<i>D3B72_03010</i>	DUF4274 domain-containing protein		2.86	45.45
trmK	A0A3A8BUD5		<i>trmK</i>	tRNA (Adenine(22)-N(1))-methyltransferase (EC 2.1.1.217)	5.2.0	97.14	59.09
group_2681	A0A3A2N2S0		<i>D3B30_04480</i>	DUF4274 domain-containing protein		2.86	40.91
group_5815	A0A3A6YNM7		<i>trmk</i>	tRNA (Adenine(22)-N(1))-methyltransferase (EC 2.1.1.217) (tRNA (Adenine(22)-N(1))-methyltransferase TrmK)	5.2.0	2.86	40.91
group_3690	A0A393TFG3		<i>AF876_00592</i>	Uncharacterized protein		2.86	40.91
group_4887	A0A392Z6S3		<i>ABY94_00615</i>	Uncharacterized protein		2.86	40.91
group_3505	Q8Y3M7		<i>lmo2808</i>	Lmo2808 protein	5.1.0	5.71	45.45
folK	A0A3A7Q0D0		<i>folK</i>	2-amino-4-hydroxy-6-hydroxymethyldihydropteridine diphosphokinase (EC 2.7.6.3)	2.5.0	20.00	68.18
group_5820	A0A3A7GWE9		<i>AF238_11110</i>	Ig domain-containing protein		0.00	31.82
group_7000	A0A2Z5Z219		<i>E05_32090</i>	Uncharacterized protein		11.43	54.55
group_1855	UPI000BDFDF92			DUF1310 family protein	5.1.0	11.43	54.55
ccpB_2	A0A3A8BWU9		<i>ccpB_1</i>	Catabolite control protein B	3.5.2	60.00	13.64
group_3504	Q8Y3N1		<i>lmo2804</i>	Lmo2804 protein	6.0.0	5.71	40.91
group_2195	A0A393SL84		<i>coia</i>	Competence protein CoiA	1.10.0	57.14	13.64
group_2547	Q8Y403		<i>lmo2675</i>	Lmo2675 protein	6.0.0	42.86	86.36
group_1222	Q8Y9J2		<i>lmo0535</i>	Lmo0535 protein	3.5.2	42.86	86.36
group_25	UPI000775813C			peptidase M15		0.00	27.27
group_3432	A0A3A2PDH0		<i>hyuC</i>	Hydantoin utilization protein C (Zn-dependent hydrolase)	2.2.0	54.29	13.64
group_4197	UPI00098E3EF0			hypothetical protein		54.29	13.64
hyuC	A0A3A8C8X7		<i>hyuC</i>	Hydantoin utilization protein C	2.2.0	45.71	86.36
group_3503	Q8Y3S8		<i>lmo2753</i>	Lmo2753 protein	6.0.0	45.71	86.36
group_4421	Q8Y8L6		<i>lmo0881</i>	Lmo0881 protein	6.0.0	45.71	86.36
group_3668	A0A3A2JQP2		<i>D3B79_08735</i>	PBSX family phage terminase large subunit		2.86	31.82
group_1699	A0A2Z5C4D1		<i>RK57_13295</i>	UPF0637 protein RK57_13295	5.2.0	45.71	9.09
group_2305	Q8Y718		<i>lmo1508</i>	Lmo1508 protein	1.3.0	48.57	86.36
iscS_1	Q8Y713		<i>lmo1513</i>	Lmo1513 protein	2.5.0	62.86	95.45
group_3931	A0A2Z5BZG6		<i>RK57_07490</i>	Uncharacterized protein	6.0.0	37.14	4.55
inlJ_10	UPI000987BEBE			LPXTG cell wall anchor domain-containing protein		37.14	4.55
group_2447	Q8Y9C6		<i>lmo0606</i>	Lmo0606 protein	3.5.2	37.14	4.55
group_5508	A0A3A7W759		<i>AF951_01101</i>	Uncharacterized protein		28.57	68.18
group_239	A0A392XPZ3		<i>AF264_04535</i>	Uncharacterized protein	5.1.0	85.71	50.00
sbcC	A0A3A7GZ22		<i>sbcC</i>	Nuclease SbcCD subunit C (SMC family ATPase)	3.3.0	74.29	36.36

group_3592	Q8Y6N6	<i>lmo1648</i>	Lmo1648 protein	6.0.0	25.71	63.64
group_4801	A0A3A2R9E5	<i>D3B46_07385</i>	Uncharacterized protein		0.00	22.73
group_129	UPI00098CF0C0	<i>D3B30_10910</i>	Uncharacterized protein	6.0.0	0.00	22.73
group_1228	A0A2Z5C2Q2	<i>RK57_10170</i>	DUF917 domain-containing protein	5.2.0	100.00	77.27
dacA_2	A0A0B8QZU7	<i>LmNIHS28_00259</i>	D-alanyl-D-alanine carboxypeptidase	1.1.0	65.71	27.27
trpG	Q8Y3T2	<i>lmo2749</i>	Lmo2749 protein	2.2.0	34.29	72.73
group_2747	A0A3A7GK30	<i>dnax_1</i>	DNA polymerase III subunit gamma/tau (EC 2.7.7.7)	3.1.0	42.86	9.09
cshA_1	UPI000E748D91	<i>yfmL</i>	Putative ATP-dependent RNA helicase YfmL	3.6.0	42.86	9.09
group_590	A0A0B8R1T6	<i>topA</i>	DNA topoisomerase I (EC 5.99.1.2) (DNA topoisomerase I)	3.4.0	42.86	9.09
group_343	A0A393RXH2	<i>uvra_1</i>	UvrABC system protein A (UvrA protein) (Excinuclease ABC subunit A)	3.2.0	42.86	9.09
group_464	A0A393AUV1	<i>ddrA</i>	Diol dehydratase reactivase subunit alpha (Diol dehydratase-activating factor alpha subunit)	2.1.1	42.86	9.09
group_762	A0A0B8RIH2	<i>LmNIHS28_02100</i>	2-nitropropane dioxygenase	5.2.0	42.86	9.09
group_948	A0A3A8BZW0	<i>manZ_2</i>	PTS system mannose-specific EIID component	1.2.0	42.86	9.09
group_2444	A0A394ZP22	<i>AF264_02070</i>	ABC transporter ATP-binding protein (Putative ABC transporter ATP-binding protein)	1.2.0	42.86	9.09
group_1046	A0A241ST46	<i>arpJ</i>	Amino acid ABC transporter, permease protein	1.2.0	42.86	9.09
bglF_4	Q8Y3P7	<i>bvrB</i>	Beta-glucoside-specific phosphotransferase enzyme II ABC component	1.2.0	57.14	90.91
group_276	A0A393UU69	<i>inlJ_12</i>	Cell surface protein (Internalin-J) (LPXTG cell wall anchor domain-containing protein)	1.8.0	42.86	9.09
group_3512	Q8XFU0	<i>lmo0174 lmo0329 lmo0827</i>	Lmo0174 protein (Lmo0329 protein) (Lmo0827 protein)		57.14	90.91
group_1633	A0A3A8BTZ2	<i>iscS_1</i>	Cysteine desulfurase IscS (EC 2.8.1.7)	2.5.0	42.86	9.09
group_1698	Q8Y853	<i>lmo1065</i>	UPF0637 protein lmo1065	5.2.0	57.14	90.91
group_2141	A0A3A8BU08	<i>ywtF</i>	Putative transcriptional regulator YwtF	3.5.2	42.86	9.09
inlJ_3	UPI000BE06EFB		LPXTG cell wall anchor domain-containing protein	1.8.0	57.14	90.91
fusA_1	A0A0B8R0X1	<i>LmNIHS28_00357</i>	Phosphotriesterase	2.4.0	25.71	0.00
fosB	A0A0B8R4C4	<i>LmNIHS28_00813</i>	Glyoxalase	6.0.0	25.71	0.00
group_1807	UPI000BE00DE2		hypothetical protein		48.57	13.64
group_2910	A0A394XQ43	<i>AF264_11505</i>	Uncharacterized protein		48.57	13.64
group_1969	A0A0E0V124	<i>gidA</i>	tRNA uridine 5-carboxymethylaminomethyl modification enzyme MnmG (Glucose-inhibited division protein A)	1.7.0	48.57	13.64
inlJ_2	Q8Y3L4	<i>inlJ</i>	Internalin J	1.8.0	51.43	86.36
group_1298	Q8Y842	<i>lmo1076</i>	Lmo1076 protein	1.1.0	65.71	95.45
group_3961	A0A0E0UZG3	<i>LMM7_2508</i>	Uncharacterized protein	6.0.0	34.29	4.55
group_4198	W5U092	<i>IntA</i>	Nuclear-targeted protein A	6.0.0	34.29	4.55
group_4109	A0A3A2WY61	<i>AF264_04635</i>	Bifunctional precorrin-2 dehydrogenase/sirohydrochlorin ferrochelatase		34.29	4.55
group_676	Q8Y496	<i>ami</i>	Autolysin, amidase	1.8.0	65.71	95.45

group_4184	A0A394ZL82	<i>AF264_02035</i>	DUF4097 domain-containing protein	1.8.0	34.29	4.55
group_2446	Q8Y9C6	<i>lmo0606</i>	Lmo0606 protein	3.5.2	65.71	95.45
group_3532	Q8Y9D1	<i>lmo0601</i>	Lmo0601 protein	1.8.0	65.71	95.45
group_2813	A0A0H3GCX1	<i>LMRG_02847</i>	Uncharacterized protein		77.14	40.91
group_3807	UPI0005ECD83E	<i>VE88_14755</i>	DNA-binding protein (Fragment)		2.86	27.27
group_3817	UPI00092E980C		uridine kinase		2.86	27.27
yicI_4	Q8Y4J2	<i>lmo2446</i>	Lmo2446 protein	2.1.1	45.71	81.82
eccCa1	A0A393D7A8	<i>essC</i>	ESAT-6 secretion machinery protein EssC (Type VII secretion protein EssC)	5.2.0	54.29	18.18
group_1623	A0A0B8QZI6	<i>LmNIHS28_01291</i>	ABC transporter permease	5.2.0	54.29	18.18
group_4631	UPI00074D6448	<i>LM901004_160002</i>	Uncharacterized protein		28.57	63.64
ssb_4	UPI000BE1101C		hypothetical protein		28.57	63.64
group_458	Q8Y6N9	<i>lmo1645</i>	Lmo1645 protein	3.3.0	28.57	63.64
group_1433	Q8Y3S7	<i>lmo2754</i>	Lmo2754 protein	1.1.0	37.14	72.73
ezrA	Q8Y6T8	<i>ezrA</i>	Septation ring formation regulator EzrA	1.7.0	37.14	72.73
inlA_10	Q723K6	<i>inlA</i>	Internalin A	1.8.0	51.43	18.18
phoR_2	A0A0E1R5Y8	<i>yclK</i>	Sensor histidine kinase yclK (EC 2.7.13.3)	1.3.0	51.43	18.18
yicI_3	A0A0B8RA88	<i>LmNIHS28_01488</i>	Glycosyl hydrolase family 31	2.1.1	51.43	18.18
group_1624	A0A3A7U6D9	<i>ARK97_06545</i>	ABC transporter permease	5.2.0	48.57	81.82
marA	Q8Y803	<i>lmo1116</i>	Lmo1116 protein	3.5.2	57.14	22.73
group_1398	A0A393D0P2	<i>aguA</i>	Putative agmatine deiminase (EC 3.5.3.12) (Agmatine iminohydrolase)	5.2.0	40.00	9.09
group_1660	A0A3A8C6B9	<i>mglA</i>	Galactose/methyl galactoside import ATP-binding protein MglA (EC 3.6.3.17)	1.2.0	40.00	9.09
group_4390	Q8Y916	<i>lmo0726</i>	Hypothetical CDS	6.0.0	60.00	90.91
group_4658	Q8Y4U3	<i>lmo2339</i>	Lmo2339 protein	5.2.0	60.00	90.91
group_261	A0A393F884	<i>AF249_03970</i>	Cell surface protein (LPXTG cell wall anchor domain-containing protein)	1.8.0	60.00	90.91
atpG_1	A0A3A7I128	<i>atpg_1</i>	ATP synthase gamma chain, sodium ion specific (F0F1 ATP synthase subunit gamma)	1.4.0	40.00	9.09
isdE_1	Q9EXG4	<i>fufA</i>	Heme ABC transporter substrate-binding protein IsdE (Lipoprotein)	1.2.0	60.00	90.91
ddrA	A0A0E0UUN7	<i>pduG</i>	Putative diol dehydratase-reactivating factor large subunit	2.1.1	60.00	90.91
group_761	Q8Y599	<i>lmo2170</i>	Lmo2170 protein	5.2.0	60.00	90.91
group_1613	UPI000986F629	<i>D3C41_14375</i>	DEAD/DEAH box helicase	3.6.0	60.00	90.91
group_1653	A0A1S7FKW2	<i>DC57_08295</i>	Alkaline phosphatase family protein	2.6.0	40.00	9.09
group_1657	A0A3A8BUI8	<i>albF</i>	Putative zinc protease AlbF (EC 3.4.24.-)	2.2.0	40.00	9.09
ywtF	A0A3A8BV30	<i>ywtF</i>	Putative transcriptional regulator YwtF	3.5.2	60.00	90.91
artQ_2	Q8Y527	<i>arpJ</i>	ArpJ protein	1.2.0	60.00	90.91
iscS_2	A0A3A8BUZ1	<i>iscS_2</i>	Cysteine desulfurase IscS (EC 2.8.1.7)	2.5.0	60.00	90.91

group_1560	A0A3A8BMS5	<i>ydfG</i>	NADP-dependent 3-hydroxy acid dehydrogenase YdfG (EC 1.1.1.381)	2.1.1	40.00	9.09
group_2769	A0A1D2IW42	<i>CDR86_11860</i>	ABC transporter permease	5.2.0	60.00	90.91
group_2119	A0A241STG7	<i>cbiO</i>	Energy-coupling factor transporter ATP-binding protein EcfA (ECF transporter A component EcfA) (EC 3.6.3.-)	1.2.0	40.00	9.09
xseA_2	A0A0E1R607	<i>yqgN</i>	5-formyltetrahydrofolate cyclo-ligase (EC 6.3.3.2)	2.5.0	40.00	9.09
group_1000	A0A3A7RII6	<i>AE233_00940</i>	SMI1/KNR4 family protein	5.2.0	60.00	90.91
group_3048	Q71YB4	<i>panC</i>	Pantothenate synthetase (PS) (EC 6.3.2.1) (Pantoate--beta-alanine ligase) (Pantoate-activating enzyme)	2.5.0	40.00	9.09
fosX	Q8Y6I2	<i>fosX</i>	Fosfomycin resistance protein FosX	4.1.0	60.00	90.91
group_705	A0A2Z5C4I1	<i>RK57_08210</i>	Uncharacterized protein	5.1.0	40.00	9.09
group_1138	A0A394ZK64	<i>AF264_05670</i>	Uncharacterized protein	5.2.0	40.00	9.09
tagB_1	A0A3A8BZ54	<i>tarL_2</i>	Teichoic acid ribitol-phosphate polymerase TarL (EC 2.7.8.14)	1.1.0	60.00	90.91
group_2575	Q8Y972	<i>lmo0661</i>	Lmo0661 protein	5.2.0	60.00	90.91
tagG	UPI000BE10CE8		ABC transporter permease	1.1.0	60.00	90.91
dnaX_1	A0A1D2IRD3	<i>dnaX</i>	DNA polymerase III subunit gamma/tau (EC 2.7.7.7)	3.1.0	60.00	90.91
group_4609	Q8Y5S4	<i>lmo1981</i>	Lmo1981 protein	5.2.0	60.00	90.91
inIJ_5	A0A3A8C0G4	<i>inIJ_2</i>	Internalin-J	1.8.0	60.00	90.91
topA	A0A1D2IVT6	<i>topA</i>	DNA topoisomerase 1 (EC 5.99.1.2) (DNA topoisomerase I)	3.4.0	60.00	90.91
group_649	A0A393CN22	<i>AF264_00975</i>	Mannosylglycerate hydrolase (EC 3.2.1.170)	2.1.1	40.00	9.09
group_2445	Q8Y9C4	<i>lmo0608</i>	Lmo0608 protein	1.2.0	60.00	90.91
skfE	A0A3A8BUB3	<i>skfE</i>	SkfA peptide export ATP-binding protein SkfE (EC 3.6.3.25)	1.2.0	60.00	90.91
group_4348	A0A0H3GDS2	<i>LMRG_00052</i>	Uncharacterized protein		60.00	90.91
group_1735	A0A0E0UV76	<i>LMM7_0870</i>	Putative transcriptional regulator, MarR family	5.2.0	40.00	9.09
inIJ_9	Q8Y591	<i>lmo2178</i>	Putative peptidoglycan bound protein (LPXTG motif)	1.8.0	60.00	90.91
group_4336	Q8YAA5	<i>lmo0247</i>	Lmo0247 protein	6.0.0	60.00	90.91
group_860	Q8Y9U8	<i>lmo0422</i>	Lmo0422 protein	5.2.0	60.00	90.91
manZ_2	Q8YAT9	<i>lmo0024</i>	Lmo0024 protein	1.2.0	91.43	63.64
group_1945	A0A3A2LWG0	<i>AF238_14270</i>	DUF2705 domain-containing protein		8.57	36.36
group_4641	A0A1D2J0K6	<i>CDR86_15835</i>	Uncharacterized protein		8.57	36.36
group_5797	A0A3A7RAL1	<i>ykfA</i>	LD-carboxypeptidase (Putative murein peptide carboxypeptidase) (EC 3.4.16.-)	4.5.0	8.57	36.36
group_4590	Q8Y5Z0	<i>lmo1913</i>	Lmo1913 protein	5.2.0	17.14	50.00
group_3040	A0A3A7GE33	<i>AF264_08870</i>	Glycoside transferase	5.2.0	82.86	50.00
group_4114	A0A2Z5C2X9	<i>RK57_13530</i>	Uncharacterized protein	5.1.0	22.86	0.00
glnQ_2	UPI000E71158B	<i>AF253_04480</i>	ABC transporter ATP-binding protein		22.86	0.00
group_4196	A0A1T1YRH0	<i>DC57_13240</i>	Uncharacterized protein		22.86	0.00
group_4693	A0A3A7SXN9	<i>AF247_04435</i>	Streptolysin associated protein SagD		22.86	0.00
group_4692	A0A0B8RFY9	<i>LmNIHS28_00810</i>	Uncharacterized protein		22.86	0.00
group_1839	UPI000E75DD0C	<i>DYZ86_01994</i>	Uncharacterized protein	5.1.0	22.86	0.00
group_3641	A0A3A7DQS9	<i>AF247_04430</i>	Bacteriocin biosynthesis cyclodehydratase		22.86	0.00

group_3640	A0A394XKL8	<i>AF241_04465</i>	SagB/ThcOx family dehydrogenase		22.86	0.00
group_3639	A0A0B8QY40	<i>LmNIHS28_00811</i>	ABC transporter permease		22.86	0.00
group_2744	UPI00086BB360		DUF1642 domain-containing protein	4.3.0	0.00	18.18
fbp	C1L199	<i>fbp</i>	Fructose-1,6-bisphosphatase class 3 (FBPase class 3) (EC 3.1.3.11) (D-fructose-1,6-bisphosphate 1-phosphohydrolase class 3)	2.1.2	100.00	81.82
group_3843	UPI0009801844	<i>B0X19_13920</i>	Uncharacterized protein	4.3.0	0.00	18.18
group_1196	A0A0B8R4M8	<i>LmNIHS28_00555</i>	Membrane protein	5.2.0	100.00	81.82
group_3867	A0A393UGI5	<i>DCT05_12735</i>	Uncharacterized protein		0.00	18.18
group_513	A0A393M724	<i>DN831_08165</i>	Uncharacterized protein	6.0.0	0.00	18.18
group_5935	UPI0005C68DD0		hypothetical protein	4.3.0	0.00	18.18
group_6217	UPI00076181B6		hypothetical protein	6.0.0	0.00	18.18
group_1062	A0A393CV23	<i>AF264_09920</i>	Glycoside hydrolase family 65 protein	2.1.1	31.43	4.55
group_4111	A0A3A8BWT7	<i>mshD</i>	Mycothiol acetyltransferase (EC 2.3.1.189)	5.2.0	31.43	4.55
inlA_9	A0A3A2X399	<i>D3B21_09430</i>	LPXTG cell wall anchor domain-containing protein		31.43	4.55
group_4702	A0A0E1R797	<i>BN389_12760</i>	Uncharacterized protein		31.43	4.55
group_4041	A0A0E1R7D2	<i>BN389_20230</i>	Uncharacterized protein		31.43	4.55
group_689	A0A3A7UBE8	<i>AF876_02227</i>	Uncharacterized protein	1.2.0	54.29	86.36
mnmG	A0A0E0V124	<i>gidA</i>	tRNA uridine 5-carboxymethylaminomethyl modification enzyme MnmG (Glucose-inhibited division protein A)	1.7.0	54.29	86.36
group_1261	Q8Y3N2	<i>lmo2803</i>	Lmo2803 protein	6.0.0	54.29	86.36
aroH	A0A1D2J080	<i>aroH</i>	Chorismate mutase AroH (EC 5.4.99.5)	2.2.0	54.29	86.36
lolD	UPI000EF63221		ATP-binding cassette domain-containing protein	1.2.0	45.71	13.64
group_162	A0A394V460	<i>essC</i>	ESAT-6 secretion machinery protein EssC (Type VII secretion protein EssC)	5.2.0	11.43	40.91
group_3825	A0A393Q993	<i>AF238_14460</i>	Uncharacterized protein		11.43	40.91
group_3824	A0A3A2QTE1	<i>AF238_14465</i>	Uncharacterized protein		11.43	40.91
group_5796	UPI0009301249		cytadherence accessory protein		11.43	40.91
tsf_2	D7PCG5		Uncharacterized protein		48.57	18.18
clpP1	A0A3A7GTR6	<i>clpp1</i>	ATP-dependent Clp protease proteolytic subunit		48.57	18.18
group_4295	D7PCG6	<i>CDR86_14670</i>	DUF2786 domain-containing protein		48.57	18.18
group_4294	UPI000E7385DC		hypothetical protein		48.57	18.18
chpS	D7PCG9	<i>CDR86_14685</i>	AbrB/MazE/SpoVT family DNA-binding domain-containing protein (Putative PemI-like inhibitor)		48.57	18.18
mazF	D7PCH0	<i>CDR86_14690</i>	Putative PemK-like protein (Type II toxin-antitoxin system PemK/MazF family toxin)		48.57	18.18
group_3818	A0A3A7FAB2	<i>inlb_6</i>	Internalin B (LPXTG cell wall anchor domain-containing protein)		2.86	22.73
group_3816	A0A393UXZ0	<i>ARL28_13835</i>	MFS transporter		2.86	22.73
group_2745	A0A3A2QVJ3	<i>AF238_09760</i>	Uncharacterized protein		2.86	22.73
group_5750	A0A3A2YHC2	<i>D3B05_03300</i>	Uncharacterized protein		2.86	22.73
group_5697	A0A393V6K3	<i>AF840_02454</i>	DUF4127 family protein		2.86	22.73

gpmA_7	A0A3A7X7L3	<i>pspB</i>	Histidine phosphatase family protein (Putative phosphoserine phosphatase 2) (EC 3.1.3.3)	2.86	22.73
ybbH_3	A0A393LHT2	<i>ybbH_3</i>	MurR/RpiR family transcriptional regulator (Putative HTH-type transcriptional regulator YbbH)	2.86	22.73
group_3844	A0A0H3GMQ7	<i>LMRG_01523</i>	Gp45	2.86	22.73
bin3	A0A3A7R6E9	<i>bin3</i>	DNA-invertase (Recombinase family protein)	2.86	22.73
group_6055	A0A3A7V312	<i>AF951_00084</i>	Uncharacterized protein	2.86	22.73
group_2736	A0A3A7VMA9	<i>rizA</i>	ATP-grasp domain-containing protein (L-arginine-specific L-amino acid ligase) (EC 6.3.2.48)	2.86	22.73
group_2737	A0A393FQK7	<i>AF840_02461</i>	Uncharacterized protein	2.86	22.73
hhaIM	A0A3A2V7Q5	<i>dcm</i>	Cytosine-specific methyltransferase (EC 2.1.1.37)	2.86	22.73
nanE_2	A0A3A7NDZ8	<i>nanE_1</i>	Putative N-acetylmannosamine-6-phosphate 2-epimerase (EC 5.1.3.9) (ManNAc-6-P epimerase)	2.86	22.73
group_5924	A0A3A2Y1W1	<i>AF828_02779</i>	Uncharacterized protein	2.86	22.73
yigL	UPI00074D5656	<i>LM701345_50019</i>	Uncharacterized protein	2.86	22.73
group_700	A0A3A7G652	<i>AF264_14680</i>	Uncharacterized protein	4.3.0	97.14 77.27
sau3AIR	A0A3A7FE85	<i>sau3air</i>	Restriction endonuclease (Type-2 restriction enzyme Sau3AI) (EC 3.1.21.4)	2.86	22.73
group_5934	A0A394R6E5	<i>AF238_05605</i>	Phage holin	2.86	22.73
group_5748	A0A392X8J1	<i>DNH64_05215</i>	Uncharacterized protein	5.1.0	2.86 22.73
group_5749	A0A3A2N1D3	<i>D3B05_03305</i>	Glyoxalase/bleomycin resistance/dioxygenase family protein	6.0.0	2.86 22.73
group_1362	UPI000A61B5F8	<i>AE233_00433</i>	Uncharacterized protein	2.86	22.73
licA_5	A0A3A6X849	<i>lica_3</i>	Lichenan-specific phosphotransferase enzyme IIA component (EC 2.7.1.-) (PTS lactose/cellobiose transporter subunit IIA)	2.86	22.73
bacD	A0A3A6XBZ3	<i>ddaf</i>	ATP-grasp domain-containing protein (Dapdiamide A synthase) (EC 6.3.2.47)	2.86	22.73
group_217	A0A3A7KP06	<i>AE052_02425</i>	Uncharacterized protein	2.86	22.73
group_3854	A0A3A7V0R5	<i>AF951_02096</i>	Uncharacterized protein	3.5.2	2.86 22.73
licB_7	A0A3A7FKG5	<i>cela_5</i>	PTS sugar transporter subunit IIB (PTS system cellobiose-specific EIIB component) (EC 2.7.1.205)	2.86	22.73
group_5704	UPI000E74C0A2		hypothetical protein	5.1.0	2.86 22.73
group_5702	A0A393BLD4	<i>AF840_02465</i>	Cupin domain-containing protein	2.86	22.73
group_5700	A0A393I885	<i>AFT78_13605</i>	Uncharacterized protein	2.86	22.73
group_2739	A0A3A2S9A2	<i>D3B73_14375</i>	Uncharacterized protein	2.86	22.73
group_872	Q8YA59	<i>lmo0302</i>	Lmo0302 protein	6.0.0	45.71 77.27
group_494	A0A3A7W452	<i>AF947_01400</i>	Uncharacterized protein	31.43	63.64
group_1914	A0A1B2LR10	<i>pLM-C-273_00079</i>	Uncharacterized protein	31.43	63.64
group_1318	A0A1B2LR12	<i>pLM-C-273_00075</i>	Phage minor capsid protein 2	31.43	63.64
group_1317	A0A1B2LR19	<i>pLM-C-273_00082</i>	Uncharacterized protein	31.43	63.64
group_816	A0A1T1YP67	<i>dbpA</i>	ATP-dependent RNA helicase DbpA (EC 3.6.4.13)	3.5.3	60.00 27.27
group_1120	A0A393CTH8	<i>ezrA</i>	Septation ring formation regulator EzrA	1.7.0	60.00 27.27

yxIE	UPI000E759913	<i>yxIE</i>	Negative regulatory protein YxIE	5.2.0	40.00	72.73
ybiA	A0A0B8R4G2	<i>LmNIHS28_00503</i>	Swarming motility protein YbiA		71.43	40.91
group_4612	Q8Y5J1	<i>lmo2070</i>	Lmo2070 protein	5.2.0	62.86	90.91
group_3197	A0A3A7EY63	<i>AB922_02243</i>	N-acetyltransferase	5.2.0	37.14	9.09
group_3196	Q720B7	<i>LMOJ2365_1322</i>	UPF0291 protein LMOJ2365_1322	5.2.0	37.14	9.09
group_4614	A0A2A5ZFW1	<i>CDR86_01560</i>	FeoB-associated Cys-rich membrane protein		62.86	90.91
licT_3	Q8Y3P6	<i>bvrA</i>	Transcription antiterminator	3.5.2	62.86	90.91
ulaB_2	A0A3A8BNH7	<i>ulaB_2</i>	Ascorbate-specific PTS system EIIB component (EC 2.7.1.194)	1.2.0	62.86	90.91
inlB_2	Q8Y9H9	<i>lmo0549</i>	Lmo0549 protein	1.9.0	62.86	90.91
manX_4	Q8YAU2	<i>lmo0021</i>	Lmo0021 protein	1.2.0	62.86	90.91
group_4054	A0A394RA98	<i>AF239_08275</i>	HD domain-containing protein	5.2.0	37.14	9.09
group_4057	A0A3A7ML43	<i>AF251_07735</i>	2-methyl-6-phytyl-1,4-hydroquinone methyltransferase (EC 2.1.1.295) (Class I SAM-dependent methyltransferase)	5.2.0	37.14	9.09
group_4053	A0A0B8R933	<i>LmNIHS28_02291</i>	Uncharacterized protein	6.0.0	37.14	9.09
group_4052	A0A2Z5BX03	<i>RK57_02435</i>	DUF1697 domain-containing protein	5.2.0	37.14	9.09
group_2626	Q8Y593	<i>lmo2176</i>	Lmo2176 protein	3.5.2	62.86	90.91
group_2627	Q8Y582	<i>lmo2189</i>	Lmo2189 protein	1.10.0	62.86	90.91
group_2629	Q8Y512	<i>lmo2266</i>	Lmo2266 protein	5.2.0	62.86	90.91
group_3612	Q8Y531	<i>lmo2245</i>	Lmo2245 protein	5.2.0	62.86	90.91
group_4021	A0A0B8QRP4	<i>LmNIHS28_01575</i>	Uncharacterized protein	5.2.0	37.14	9.09
group_4219	A0A2Z5C2B1	<i>RK57_09890</i>	GntR family transcriptional regulator		37.14	9.09
glmS_1	A0A3A8C038	<i>glmS_2</i>	Glutamine--fructose-6-phosphate aminotransferase isomerizing (EC 2.6.1.16)	2.1.1	62.86	90.91
group_3537	Q8Y973	<i>lmo0660</i>	Lmo0660 protein	4.4.0	62.86	90.91
group_3535	UPI000EF5BE8A		DUF975 family protein	5.2.0	62.86	90.91
group_3534	A0A3A8CFC5	<i>speG_1</i>	Spermidine N(1)-acetyltransferase (EC 2.3.1.57)	5.2.0	62.86	90.91
group_3539	Q8Y8Z5	<i>lmo0747</i>	Lmo0747 protein	6.0.0	62.86	90.91
ytnP	Q8Y6R9	<i>lmo1614</i>	Lmo1614 protein	5.2.0	62.86	90.91
addB	Q8Y510	<i>addB</i>	ATP-dependent helicase/deoxyribonuclease subunit B (EC 3.1.-.-) (EC 3.6.4.12) (ATP-dependent helicase/nuclease AddB)	3.3.0	62.86	90.91
group_225	UPI0001D010DE	<i>inlJ_14</i>	Internalin-J	1.8.0	37.14	9.09
group_3965	A0A3A7GK80	<i>mggB</i>	Bifunctional metallophosphatase/5'-nucleotidase (Mannosylglucosyl-3-phosphoglycerate phosphatase) (EC 3.1.3.-)	5.2.0	37.14	9.09
group_3966	A0A2Z5BYS6	<i>RK57_05330</i>	Crp/Fnr family transcriptional regulator		37.14	9.09
group_3963	A0A3A7G3T8	<i>AF251_11130</i>	Uncharacterized protein	6.0.0	37.14	9.09
proC_2	A0A3A8C3U2	<i>proC_1</i>	Pyrroline-5-carboxylate reductase (EC 1.5.1.2)	2.2.0	62.86	90.91
sigW	Q8Y9U7	<i>lmo0423</i>	Lmo0423 protein	3.5.1	62.86	90.91
group_1244	A0A393CR87	<i>AF264_00605</i>	Ribonuclease P	5.1.0	37.14	9.09
group_4573	Q8Y6D7	<i>lmo1750</i>	Lmo1750 protein	5.2.0	62.86	90.91
group_4577	Q8Y6B2	<i>lmo1779</i>	Lmo1779 protein	6.0.0	62.86	90.91
group_4575	Q8Y6B4	<i>lmo1777</i>	Lmo1777 protein	5.2.0	62.86	90.91

group_4578	A0A3A8BJ82	<i>azoR_2</i>	FMN-dependent NADH-azoreductase (EC 1.7.-.-)	1.4.0	62.86	90.91
ybjG	Q8Y6R1	<i>lmo1623</i>	Lmo1623 protein	5.2.0	62.86	90.91
cbiE	A0A3A8C045	<i>cbiE</i>	Cobalt-precorrin-7 C(5)-methyltransferase (EC 2.1.1.289)	2.5.0	62.86	90.91
yjaB	A0A3A8BXM4	<i>yjaB</i>	Putative N-acetyltransferase YjaB (EC 2.3.1.-)	5.2.0	62.86	90.91
ulaC_3	A0A3A8BN71	<i>ulaC_3</i>	Ascorbate-specific PTS system EIIA component (EC 2.7.1.194)	1.2.0	62.86	90.91
group_4504	Q8Y751	<i>lmo1461</i>	Lmo1461 protein	6.0.0	62.86	90.91
group_4503	Q8Y760	<i>lmo1443</i>	Lmo1443 protein	5.2.0	62.86	90.91
group_4500	Q8Y785	<i>lmo1410</i>	Lmo1410 protein	6.0.0	62.86	90.91
group_4509	Q8Y6X6	<i>lmo1555</i>	Lmo1555 protein	2.5.0	62.86	90.91
group_4487	Q8Y7L2	<i>lmo1265</i>	Lmo1265 protein	1.2.0	62.86	90.91
mtlR_4	A0A3A8C544	<i>mtlR_1</i>	Transcriptional regulator MtlR	3.5.2	37.14	9.09
group_4489	A0A1D2IPZ2	<i>dprA</i>	DNA-protecting protein DprA	3.8.0	62.86	90.91
group_3028	A0A2Z5BXF4	<i>RK57_03270</i>	Riboflavin transporter	5.2.0	37.14	9.09
group_2916	A0A393D408	<i>trxa_4</i>	Thioredoxin (Thioredoxin 1)	1.4.0	37.14	9.09
group_4371	Q8Y9I3	<i>lmo0545</i>	Lmo0545 protein	6.0.0	62.86	90.91
group_4374	Q8Y9B7	<i>lmo0615</i>	Lmo0615 protein	6.0.0	62.86	90.91
group_4375	Q8Y9B5	<i>lmo0617</i>	Lmo0617 protein	5.1.0	62.86	90.91
group_4472	Q8Y7Q8	<i>lmo1214</i>	Lmo1214 protein	6.0.0	62.86	90.91
group_1303	Q8Y7Z1	<i>lmo1128</i>	Lmo1128 protein	6.0.0	62.86	90.91
group_4091	B8DG24	<i>yneA</i>	Cell division suppressor protein YneA	5.2.0	37.14	9.09
group_4090	A0A3A7N8T5	<i>bioC</i>	Class I SAM-dependent methyltransferase (Malonyl-[acyl-carrier protein] O-methyltransferase) (EC 2.1.1.197)	3.8.0	37.14	9.09
group_4093	C1L2K1	<i>miaA</i>	tRNA dimethylallyltransferase (EC 2.5.1.75) (Dimethylallyl diphosphate:tRNA dimethylallyltransferase)	3.6.0	37.14	9.09
group_4092	A0A0E1R7G6	<i>ynbB</i>	Uncharacterized protein ynbB	4.2.0	37.14	9.09
group_4095	C1L2I1	<i>rnhB</i>	Ribonuclease HII (RNase HII) (EC 3.1.26.4)	3.1.0	37.14	9.09
group_4094	A0A2Z5C362	<i>dprA</i>	DNA-protecting protein DprA		37.14	9.09
group_4096	A0A2Z5C3E4	<i>RK57_14300</i>	Uncharacterized protein	1.2.0	37.14	9.09
group_4622	Q8Y578	<i>lmo2197</i>	Lmo2197 protein	6.0.0	62.86	90.91
group_4623	Q8Y555	<i>lmo2221</i>	Lmo2221 protein	5.2.0	62.86	90.91
group_4621	Q8Y592	<i>lmo2177</i>	Lmo2177 protein	5.2.0	62.86	90.91
group_4154	A0A1T1YQG4	<i>DC57_11460</i>	Transposase	4.4.0	37.14	9.09
sdrF	Q8Y5H7	<i>lmo2085</i>	Putative peptidoglycan bound protein (LPXTG motif)	1.8.0	62.86	90.91
sdrD	Q8Y479	<i>lmo2576</i>	Peptidoglycan anchored protein (LPXTG motif)	1.8.0	62.86	90.91
group_4252	A0A2Z5C1U4	<i>RK57_09025</i>	Uncharacterized protein	6.0.0	37.14	9.09
thiO	A0A3A8BP94	<i>thiO</i>	Glycine oxidase (EC 1.4.3.19)	2.2.0	62.86	90.91
thiN	A0A3A8BXM3	<i>thiN</i>	Thiamine pyrophosphokinase (EC 2.7.6.2)	2.5.0	62.86	90.91
group_4392	A0A3A8CAQ5	<i>rbsR_1</i>	Ribose operon repressor	3.5.2	62.86	90.91
group_4396	A0A3A8C7X5	<i>bglF_2</i>	PTS system beta-glucoside-specific EIIBCA component	1.2.0	62.86	90.91
thiF	Q8Y868	<i>lmo1049</i>	Lmo1049 protein	2.5.0	62.86	90.91
group_3589	Q8Y784	<i>lmo1411</i>	Lmo1411 protein	5.2.0	62.86	90.91

group_2703	A0A393RS60	<i>inlK</i>	Class 1 internalin InlK (LPXTG cell wall anchor domain-containing protein)	1.8.0	37.14	9.09
group_4055	A0A2Z5BWW4	<i>RK57_02265</i>	Molybdate metabolism regulator	5.2.0	37.14	9.09
group_3470	A0A392X3L4	<i>AF241_00505</i>	Superoxide dismutase	6.0.0	37.14	9.09
inlA_11	A0A394Y342	<i>inla_4</i>	Internalin (Internalin-A) (LPXTG cell wall anchor domain-containing protein)	1.8.0	37.14	9.09
group_3478	A0A0E1R3M5	<i>inla_2</i>	Internalin-A	1.8.0	37.14	9.09
inlA_3	UPI000BDFD377		lmo1136 family class 1 internalin	1.8.0	62.86	90.91
ulaA_2	Q8Y5T4	<i>lmo1971</i>	Lmo1971 protein	1.2.0	62.86	90.91
inlA_1	Q8Y7I7	<i>lmo1290</i>	Lmo1290 protein	1.8.0	62.86	90.91
group_4024	UPI000035D3A8	<i>isdE</i>	Heme ABC transporter substrate-binding protein IsdE	1.2.0	37.14	9.09
group_4026	A0A0D4CB02	<i>AJL15_12175</i>	Uncharacterized protein	5.2.0	37.14	9.09
group_4027	A0A2Z5BZF4	<i>RK57_04485</i>	TetR/AcrR family transcriptional regulator		37.14	9.09
group_4020	A0A3A7JKS7	<i>yhaO</i>	Exonuclease SbcCD subunit D (Putative metallophosphoesterase YhaO)	5.2.0	37.14	9.09
group_4022	A0A0B8RAU1	<i>LmNIHS28_02204</i>	Membrane protein	6.0.0	37.14	9.09
group_4023	UPI0001EBA5A3	<i>NT04LM_3257</i>	Heme uptake protein IsdC	1.8.0	37.14	9.09
group_3923	A0A2Z5BZQ8	<i>RK57_07860</i>	PTS fructose transporter subunit IIA	1.2.0	37.14	9.09
albF	Q8Y797	<i>lmo1393</i>	Lmo1393 protein	2.2.0	62.86	90.91
group_2775	A0A393S3L9	<i>AF264_15050</i>	Uncharacterized protein	6.0.0	37.14	9.09
group_3927	A0A0B8RBU5	<i>LmNIHS28_00179</i>	RNA-binding protein	5.2.0	37.14	9.09
lutR_1	A0A3A8CF58	<i>lutR_2</i>	HTH-type transcriptional regulator LutR	3.5.2	62.86	90.91
group_3500	Q8Y451	<i>lmo2604</i>	Lmo2604 protein	5.2.0	62.86	90.91
macB_4	A0A3A8BUW4	<i>yknY_2</i>	Putative ABC transporter ATP-binding protein YknY (EC 3.6.3.-)		37.14	9.09
aguA_2	A0A0H3G891	<i>aguA</i>	Putative agmatine deiminase (EC 3.5.3.12) (Agmatine iminohydrolase)	5.2.0	62.86	90.91
argB	A0A1D2IV64	<i>argB</i>	Acetylglutamate kinase (EC 2.7.2.8) (N-acetyl-L-glutamate 5-phosphotransferase) (NAG kinase) (NAGK)	2.2.0	62.86	90.91
tpiA_1	Q8YA20	<i>tpiA2</i>	Probable triosephosphate isomerase 2 (TIM 2) (TPI 2) (EC 5.3.1.1) (Triose-phosphate isomerase 2)	2.1.2	62.86	90.91
group_662	Q8Y7Z0	<i>lmo1129</i>	Lmo1129 protein	5.2.0	62.86	90.91
group_3571	Q8Y7X3	<i>lmo1146</i>	Lmo1146 protein	5.2.0	62.86	90.91
group_4050	A0A3A8BL21	<i>thiN</i>	Thiamine pyrophosphokinase (EC 2.7.6.2)	2.5.0	37.14	9.09
group_4440	Q8Y855	<i>lmo1063</i>	Lmo1063 protein	1.2.0	62.86	90.91
ypdB	Q8Y8C4	<i>lmo0984</i>	Lmo0984 protein	3.5.2	62.86	90.91
group_2953	UPI0001B4220F	<i>ARJ20_02020</i>	LPXTG cell wall anchor domain-containing protein		37.14	9.09
group_4059	A0A3A8BR73	<i>fosX</i>	Fosfomycin resistance protein FosX	4.1.0	37.14	9.09
group_4085	A0A0E0UWI3	<i>LMM7_1468</i>	Uncharacterized protein	5.2.0	37.14	9.09
group_4058	UPI0004366B26	<i>HR60_00125</i>	UPF0435 protein HR60_00125	5.2.0	37.14	9.09
panC	Q8Y602	<i>panC</i>	Pantothenate synthetase (PS) (EC 6.3.2.1) (Pantoate--beta-alanine ligase) (Pantoate-activating enzyme)	2.5.0	62.86	90.91

group_4432	A0A0H3GJ44	<i>LMRG_02074</i>	Uncharacterized protein		62.86	90.91
group_4430	Q8Y8D8	<i>lmo0966</i>	Lmo0966 protein	5.2.0	62.86	90.91
group_5435	A0A3A2KJM7	<i>AF255_07855</i>	Uncharacterized protein		37.14	9.09
group_4438	Q8Y856	<i>lmo1062</i>	Lmo1062 protein	1.2.0	62.86	90.91
group_4667	Q8Y4F2	<i>lmo2492</i>	Lmo2492 protein	6.0.0	62.86	90.91
group_4190	A0A3A7GJ00	<i>inla_3</i>	Internalin-A (Leucine-rich repeat domain-containing protein)	1.9.0	37.14	9.09
group_4218	A0A393CNN4	<i>AF240_00940</i>	Uncharacterized protein		37.14	9.09
group_4216	UPI000035CDC6	<i>BN389_04240</i>	Uncharacterized protein		37.14	9.09
group_4215	A0A0B8R4Y8	<i>LmNIHS28_01937</i>	ATPase	5.2.0	37.14	9.09
group_4668	Q8Y4D7	<i>comFC</i>	ComFC protein	1.10.0	62.86	90.91
group_4669	Q8Y4D6	<i>comFA</i>	ComFA protein	1.10.0	62.86	90.91
pknB	A0A3A8C235	<i>pknB</i>	Serine/threonine-protein kinase PknB (EC 2.7.11.1)	3.8.0	62.86	90.91
hcnC	A0A3A7J837	<i>hcnC</i>	FAD-binding oxidoreductase (Hydrogen cyanide synthase subunit HcnC) (EC 1.4.99.5)	2.2.0	37.14	9.09
group_3399	A0A0E1R5P0	<i>yesJ</i>	Uncharacterized N-acetyltransferase YesJ (EC 2.3.1.-)	5.2.0	37.14	9.09
adrA	A0A0E1REZ1	<i>yhcK</i>	Uncharacterized protein yhcK	5.2.0	37.14	9.09
group_4322	Q8Y3I4	<i>lmo2852</i>	Lmo2852 protein	5.2.0	62.86	90.91
group_4324	Q8YAT7	<i>cutC</i>	Copper homeostasis protein CutC	4.2.0	62.86	90.91
group_4068	A0A3A7T7A5	<i>ytnP</i>	MBL fold metallo-hydrolase (Putative quorum-quenching lactonase YtnP) (EC 3.1.1.-)	5.2.0	37.14	9.09
cobU	A0A3A8BXJ5	<i>cobU</i>	Bifunctional adenosylcobalamin biosynthesis protein CobU (EC 2.7.1.156)	2.5.0	62.86	90.91
ytrA_4	A0A3A8BN52	<i>ytrA_3</i>	HTH-type transcriptional repressor YtrA	3.5.2	62.86	90.91
rnhB	Q8Y7K4	<i>rnhB</i>	Ribonuclease HII (RNase HII) (EC 3.1.26.4)	3.1.0	62.86	90.91
group_4060	A0A3A2X1R4	<i>AF264_07635</i>	Uncharacterized protein	6.0.0	37.14	9.09
group_4061	A0A393RQY0	<i>ybbh_2</i>	MurR/RpiR family transcriptional regulator (Putative HTH-type transcriptional regulator YbbH)		37.14	9.09
group_4063	A0A0B8R8T3	<i>LmNIHS28_01308</i>	Permease		37.14	9.09
group_4064	UPI000035D1DA	<i>SAMD00023519_01157</i>	Cell surface protein		37.14	9.09
group_4065	A0A2Z5BWP2	<i>RK57_01585</i>	Uncharacterized protein	6.0.0	37.14	9.09
group_4066	UPI0004352777	<i>X846_1709</i>	Uncharacterized protein	5.2.0	37.14	9.09
group_4067	A0A0E1R8B1	<i>yodM</i>	Putative lipid phosphate phosphatase yodM (EC 3.1.3.-)	5.2.0	37.14	9.09
group_4103	A0A3A7Z0I1	<i>pduX</i>	L-threonine kinase (EC 2.7.1.177) (Propanediol utilization protein)	5.2.0	37.14	9.09
group_4102	A0A0B8R3Z5	<i>LmNIHS28_00732</i>	DNA topology modulation protein	5.2.0	37.14	9.09
group_4101	A0A0B8QUW8	<i>LmNIHS28_00730</i>	Uncharacterized protein	6.0.0	37.14	9.09
group_4107	A0A3A8BV76	<i>cobU</i>	Bifunctional adenosylcobalamin biosynthesis protein CobU (EC 2.7.1.156)		37.14	9.09
group_4106	A0A2Z5C4I3	<i>cobC</i>	Alpha-ribazole phosphatase	2.5.0	37.14	9.09
group_4105	A0A0E1R5F1	<i>eutJ</i>	Ethanolamine utilization protein eutJ	2.1.1	37.14	9.09
group_4104	A0A2Z5C4F6	<i>pduM</i>	Microcompartment protein PduM	6.0.0	37.14	9.09

group_4108	A0A0B8R7E7	<i>LmNIHS28_00778</i>	Alpha-L-fucosidase	5.2.0	37.14	9.09
fruA_9	A0A3A8BML0	<i>fruA_3</i>	PTS system fructose-specific EIIABC component	1.2.0	37.14	9.09
nagA_1	A0A3A7N225	<i>nagA_1</i>	N-acetylglucosamine-6-phosphate deacetylase (EC 3.5.1.25)	2.1.1	37.14	9.09
cpnA	A0A3A8BW91	<i>cpnA</i>	Cyclopentanol dehydrogenase (EC 1.1.1.163)	2.1.1	37.14	9.09
group_4168	A0A0B8R2G1	<i>LmNIHS28_00854</i>	Flagellar hook protein	6.0.0	37.14	9.09
group_3606	Q8Y5F8	<i>lmo2106</i>	Lmo2106 protein	5.2.0	62.86	90.91
group_820	A0A393CUI8	<i>AF264_04565</i>	Alpha/beta hydrolase	6.0.0	37.14	9.09
group_3541	Q8Y8Z4	<i>lmo0748</i>	Lmo0748 protein	6.0.0	62.86	90.91
group_3977	UPI00043694BE	<i>HR60_08380</i>	Hydrolase	5.2.0	37.14	9.09
group_3979	A0A3A7GK99	<i>adda</i>	ATP-dependent helicase/nuclease subunit A (EC 3.1.-.-) (EC 3.6.4.12) (ATP-dependent helicase/nuclease AddA)	3.3.0	37.14	9.09
group_3978	A0A2Z5BY92	<i>RK57_04995</i>	DUF523 domain-containing protein	5.2.0	37.14	9.09
group_2127	Q8Y482	<i>lmo2573</i>	Zinc-type alcohol dehydrogenase-like protein	2.1.1	62.86	90.91
pleD	A0A3A8BW24	<i>pleD</i>	Response regulator PleD	5.2.0	62.86	90.91
group_5614	A0A3A6XF35	<i>addb</i>	ATP-dependent helicase/deoxyribonuclease subunit B (EC 3.1.-.-) (EC 3.6.4.12) (ATP-dependent helicase/nuclease AddB)	3.3.0	37.14	9.09
group_3306	A0A0B8QYA4	<i>LmNIHS28_00502</i>	Uncharacterized protein		37.14	9.09
argC	Q8Y6U1	<i>argC</i>	N-acetyl-gamma-glutamyl-phosphate reductase (AGPR) (EC 1.2.1.38)	2.2.0	62.86	90.91
argD	Q8Y6U4	<i>argD</i>	Acetylornithine aminotransferase (ACOAT) (EC 2.6.1.11)	2.2.0	62.86	90.91
glyS	Q8Y754	<i>glyS</i>	Glycine--tRNA ligase beta subunit (EC 6.1.1.14) (Glycyl-tRNA synthetase beta subunit) (GlyRS)	3.7.2	62.86	90.91
group_1908	A0A1D2IZW1	<i>nagA</i>	N-acetylglucosamine-6-phosphate deacetylase	2.1.1	62.86	90.91
glmS_3	A0A3A8C081	<i>glmS_2</i>	Glutamine--fructose-6-phosphate aminotransferase isomerizing (EC 2.6.1.16)	2.1.1	37.14	9.09
group_4569	Q8Y6H7	<i>lmo1707</i>	UPF0435 protein lmo1707	5.2.0	62.86	90.91
group_3624	Q8Y481	<i>lmo2574</i>	Lmo2574 protein	6.0.0	62.86	90.91
bglH_3	A0A3A8C1L2	<i>bglH_2</i>	Aryl-phospho-beta-D-glucosidase BglH (EC 3.2.1.86)	2.1.1	62.86	90.91
group_4703	A0A394ZKB6	<i>inlj_1</i>	Internalin-J (LPXTG cell wall anchor domain-containing protein) (Peptidoglycan-binding protein)	1.8.0	37.14	9.09
group_4318	Q8Y3P8	<i>bvrC</i>	BvrC protein	5.2.0	62.86	90.91
group_4494	Q8Y7H5	<i>lmo1304</i>	UPF0291 protein lmo1304	5.2.0	62.86	90.91
group_4497	UPI000BDF6015		DUF1033 family protein	5.2.0	62.86	90.91
group_4496	Q8Y7A8	<i>lmo1380</i>	Lmo1380 protein	6.0.0	62.86	90.91
group_4491	Q8Y7I1	<i>lmo1297</i>	Lmo1297 protein	4.2.0	62.86	90.91
group_4492	Q8Y7H8	<i>lmo1301</i>	Lmo1301 protein	5.2.0	62.86	90.91
group_4499	A0A1D2IVP2	<i>fabG</i>	3-oxoacyl-ACP reductase (EC 1.1.1.100)	2.4.0	62.86	90.91
xylF	Q8Y5F5	<i>lmo2109</i>	Lmo2109 protein	2.1.1	62.86	90.91
group_4191	A0A394Y4B3	<i>AF264_01750</i>	Transcriptional regulator	6.0.0	37.14	9.09
group_2269	A0A393RX26	<i>AF264_07710</i>	Uncharacterized protein	5.2.0	37.14	9.09
group_4402	A0A0E0UTV9	<i>LMM7_0781</i>	Uncharacterized protein	6.0.0	62.86	90.91

group_4369	Q8Y9K2	<i>lmo0525</i>	Lmo0525 protein	5.2.0	62.86	90.91
miaA	Q8Y7I3	<i>miaA</i>	tRNA dimethylallyltransferase (EC 2.5.1.75) (Dimethylallyl diphosphate:tRNA dimethylallyltransferase)	3.6.0	62.86	90.91
addA	Q8Y511	<i>addA</i>	ATP-dependent helicase/nuclease subunit A (EC 3.1.-.-) (EC 3.6.4.12) (ATP-dependent helicase/nuclease AddA)	3.3.0	62.86	90.91
group_4149	A0A393JKC4	<i>AF239_03205</i>	Uncharacterized protein	6.0.0	37.14	9.09
group_4148	A0A3A7F1F5	<i>pgca_1</i>	Phospho-sugar mutase (Phosphoglucomutase) (EC 5.4.2.2)	2.1.1	37.14	9.09
group_4147	A0A2Z5C668	<i>RK57_12295</i>	TetR/AcrR family transcriptional regulator	6.0.0	37.14	9.09
group_4146	A0A393PPX4	<i>AB922_01757</i>	Uncharacterized protein	6.0.0	37.14	9.09
group_4144	A0A3A7GNS4	<i>AF264_03680</i>	Putative 3-methyladenine DNA glycosylase (EC 3.2.2.-)	3.2.0	37.14	9.09
group_1286	Q8Y945	<i>lmo0695</i>	Lmo0695 protein	6.0.0	62.86	90.91
group_4225	A0A1T1Y143	<i>DC57_13835</i>	Uncharacterized protein		37.14	9.09
group_1283	Q8Y9E3	<i>lmo0587</i>	Putative secreted protein	6.0.0	62.86	90.91
group_4223	A0A241SLD8	<i>ltrA</i>	Low temperature requirement protein A	4.1.0	37.14	9.09
group_4221	A0A0E1R4Z6	<i>BN389_04160</i>	Uncharacterized protein		37.14	9.09
group_4382	Q8Y981	<i>lmo0652</i>	Lmo0652 protein	5.2.0	62.86	90.91
group_4384	A0A1C7PWW5	<i>CDR86_13880</i>	Endonuclease III domain-containing protein	5.2.0	62.86	90.91
group_4228	A0A394ZC38	<i>AB922_00937</i>	N-acetyltransferase		37.14	9.09
dasR	Q8Y5T1	<i>lmo1974</i>	Lmo1974 protein	3.5.2	62.86	90.91
group_3083	A0A3A8BST8	<i>gloC</i>	Hydroxyacylglutathione hydrolase GloC (EC 3.1.2.6)	5.2.0	37.14	9.09
group_3461	A0A0E1R2S8	<i>BN389_04180</i>	Uncharacterized protein		37.14	9.09
group_3469	A0A394Y9C8	<i>inlJ_15</i>	Cell surface protein (Internalin-J) (LPXTG cell wall anchor domain-containing protein)	1.8.0	37.14	9.09
group_4032	UPI0009A4F8FD		alpha/beta hydrolase	2.1.1	37.14	9.09
group_4031	A0A3A8BNZ3	<i>yvbK</i>	Putative N-acetyltransferase YvbK (EC 2.3.1.-)	5.2.0	37.14	9.09
group_4037	A0A3A7D8F9	<i>AF264_09645</i>	CPBP family intramembrane metalloprotease	5.2.0	37.14	9.09
group_4036	A0A3A7GG31	<i>sdrd</i>	Cell surface protein (LPXTG cell wall anchor domain-containing protein) (Serine-aspartate repeat-containing protein D)	1.8.0	37.14	9.09
group_4035	A0A2Z5C1Q5	<i>RK57_04100</i>	FeoB-associated Cys-rich membrane protein		37.14	9.09
group_4034	A0A2Z5BZ37	<i>RK57_04110</i>	DeoR/GlpR transcriptional regulator	3.5.2	37.14	9.09
group_3936	A0A392WP35	<i>AF251_13240</i>	Bacteriocin-associated integral membrane family protein (DUF1430 domain-containing protein)	1.2.0	37.14	9.09
group_3935	A0A3A7PI73	<i>AF251_13245</i>	Lactococcin 972 family bacteriocin	6.0.0	37.14	9.09
group_4038	A0A0B8R0U3	<i>LmNIHS28_01736</i>	TetR family transcriptional regulator		37.14	9.09
group_4136	A0A3A8C5J2	<i>ypdB</i>	Transcriptional regulatory protein YpdB	3.5.2	37.14	9.09
group_3932	A0A2Z5C1E0	<i>RK57_07485</i>	Uncharacterized protein		37.14	9.09
yhaO	Q8Y554	<i>lmo2222</i>	Lmo2222 protein	5.2.0	62.86	90.91
group_1862	Q8Y9U9	<i>lmo0421</i>	Lmo0421 protein	1.7.0	62.86	90.91
group_1861	Q8YA24	<i>lmo0341</i>	Lmo0341 protein	5.2.0	62.86	90.91
group_3510	Q8YAM4	<i>lmo0094</i>	Lmo0094 protein	6.0.0	62.86	90.91
group_3513	P33383	<i>lmo0206</i>	Uncharacterized protein Lmo0206	6.0.0	62.86	90.91

fmnP	A0A3A8BXM0	<i>fmnP</i>	Riboflavin transporter	5.2.0	62.86	90.91
dnaK_1	Q8Y7V8	<i>lmo1161</i>	Lmo1161 protein	2.1.1	62.86	90.91
group_3948	A0A1T1YKC2	<i>DC57_02040</i>	Uncharacterized protein	5.2.0	37.14	9.09
group_3949	A0A393RP85	<i>AF239_12775</i>	Acetamidase	5.2.0	37.14	9.09
group_3940	A0A3A7GBK9	<i>trpg</i>	Aminodeoxychorismate/anthranilate synthase component II (Anthranilate synthase component 2) (EC 4.1.3.27)	2.2.0	37.14	9.09
group_3947	A0A0B8R180	<i>LmNIHS28_00331</i>	Uncharacterized protein	6.0.0	37.14	9.09
group_1307	Q8Y7E2	<i>lmo1341</i>	Lmo1341 protein	1.10.0	62.86	90.91
group_5648	A0A0B8RAI5	<i>LmNIHS28_01933</i>	Cell surface protein		37.14	9.09
group_3587	A0A1D2IQ28	<i>rsgA</i>	Small ribosomal subunit biogenesis GTPase RsgA (EC 3.6.1.-)	5.2.0	62.86	90.91
group_1301	Q8Y7Z4	<i>lmo1125</i>	Lmo1125 protein	5.2.0	62.86	90.91
group_3588	Q8Y7E0	<i>lmo1343</i>	Lmo1343 protein	1.10.0	62.86	90.91
group_4599	A0A3A8BP41	<i>php_2</i>	Phosphotriesterase homology protein	2.4.0	62.86	90.91
ydfG	Q8Y5S9	<i>lmo1976</i>	Lmo1976 protein	2.1.1	62.86	90.91
rpe_3	A0A1D2INB4	<i>rpe</i>	Ribulose-phosphate 3-epimerase	2.1.1	62.86	90.91
lntA	Q8Y9T5	<i>lntA</i>	Listeria nuclear targeted protein A	6.0.0	62.86	90.91
group_4047	C1KWK5	<i>cca</i>	CCA tRNA nucleotidyltransferase (EC 2.7.7.72)	3.6.0	37.14	9.09
bag	A0A394ZRE6	<i>AF264_02310</i>	DUF975 domain-containing protein (DUF975 family protein)	5.2.0	37.14	9.09
crnA_2	A0A3A8BU09	<i>crnA_2</i>	Creatinine amidohydrolase (EC 3.5.2.10)	2.2.0	62.86	90.91
group_1942	UPI000CE9721B	<i>LMJF5203_01179</i>	Cell wall surface anchor protein	1.8.0	37.14	9.09
group_3887	A0A2Z5C1D2	<i>RK57_08200</i>	Crp/Fnr family transcriptional regulator	5.1.0	37.14	9.09
group_3886	A0A0B8QU91	<i>LmNIHS28_00102</i>	Uncharacterized protein	6.0.0	37.14	9.09
group_3883	A0A393UMT7	<i>AB922_03025</i>	Uncharacterized protein	6.0.0	37.14	9.09
group_4670	UPI00098E7F8A		hypothetical protein		62.86	90.91
group_3881	A0A3A8BR90	<i>folK</i>	2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase (EC 2.7.6.3)	2.5.0	37.14	9.09
hisK	Q8Y9F8	<i>hisJ</i>	HisJ protein	2.2.0	62.86	90.91
group_4227	A0A2Z5C2F1	<i>RK57_09645</i>	LPXTG cell wall anchor domain-containing protein		37.14	9.09
group_1305	Q8Y7Y4	<i>lmo1135</i>	Lmo1135 protein	6.0.0	62.86	90.91
comEA	A0A3A8BUN0	<i>comEA</i>	ComE operon protein 1	1.10.0	62.86	90.91
group_4048	A0A393S206	<i>AB922_00453</i>	Thioredoxin	1.4.0	37.14	9.09
group_4356	UPI00074D66E8	<i>LM7424_90077</i>	Uncharacterized protein	6.0.0	62.86	90.91
group_4355	Q8Y9X1	<i>lmo0397</i>	Lmo0397 protein	5.2.0	62.86	90.91
group_4079	UPI00003CABCA	<i>BN389_14870</i>	Uncharacterized protein	6.0.0	37.14	9.09
group_4078	A0A3A2NXS6	<i>comea</i>	ComE operon protein 1 (ComEA family DNA-binding protein) (Competence protein ComEA)	1.10.0	37.14	9.09
group_4077	A0A3A8BV07	<i>tylM1</i>	dTDP-3-amino-3,6-dideoxy-alpha-D-glucopyranose N,N-dimethyltransferase (EC 2.1.1.235)	5.2.0	37.14	9.09
group_4076	A0A3A8BU71	<i>iscS_2</i>	Cysteine desulfurase IscS (EC 2.8.1.7)	2.5.0	37.14	9.09
group_4074	A0A3A8BU44	<i>rne</i>	Ribonuclease E (EC 3.1.26.12)	2.3.0	37.14	9.09
group_4073	A0A241SQE4	<i>folC</i>	Folylpolyglutamate synthase	2.5.0	37.14	9.09

group_4072	A0A3A8BUT3	<i>CFSAN002345_000149</i>	Uncharacterized protein	2.5.0	37.14	9.09
group_4071	Q71Z79	<i>argD</i>	Acetylornithine aminotransferase (ACOAT) (EC 2.6.1.11)	2.2.0	37.14	9.09
group_4070	Q71Z78	<i>argB</i>	Acetylglutamate kinase (EC 2.7.2.8) (N-acetyl-L-glutamate 5-phosphotransferase) (NAG kinase) (NAGK)	2.2.0	37.14	9.09
group_703	A0A3A8C0B4	<i>atpG_1</i>	ATP synthase gamma chain, sodium ion specific	1.4.0	62.86	90.91
group_706	Q8YAN0	<i>lmo0087</i>	Lmo0087 protein	5.1.0	62.86	90.91
group_4170	A0A2Z5C307	<i>RK57_11240</i>	Crp/Fnr family transcriptional regulator		37.14	9.09
fgs	Q8Y6Y0	<i>folC</i>	FolC protein	2.5.0	62.86	90.91
group_4179	A0A3A7PLI4	<i>pknB</i>	Serine/threonine protein kinase (Serine/threonine-protein kinase PknB) (EC 2.7.11.1)	3.8.0	37.14	9.09
group_1137	Q8Y7E3	<i>lmo1340</i>	Lmo1340 protein	5.2.0	62.86	90.91
group_4174	A0A392Y8U3	<i>AF264_02300</i>	GntR family transcriptional regulator	3.5.2	37.14	9.09
glcR	Q8Y5F7	<i>lmo2107</i>	Lmo2107 protein	3.5.2	62.86	90.91
group_4189	C1L0J0	<i>hisE</i>	Phosphoribosyl-ATP pyrophosphatase (PRA-PH) (EC 3.6.1.31)	2.2.0	37.14	9.09
group_4188	C1L0J4	<i>hisH</i>	Imidazole glycerol phosphate synthase subunit HisH (EC 4.3.2.10) (IGP synthase glutaminase subunit) (EC 3.5.1.2)	2.2.0	37.14	9.09
group_4400	Q8Y8Z3	<i>lmo0749</i>	Lmo0749 protein		62.86	90.91
group_4183	A0A3A8CAW5	<i>glpE_2</i>	Thiosulfate sulfurtransferase GlpE (EC 2.8.1.1)	4.1.0	37.14	9.09
group_4172	UPI000BE051DD		transposase		37.14	9.09
group_4181	A0A3A7TYK7	<i>speG_1</i>	N-acetyltransferase (Spermidine N(1)-acetyltransferase) (EC 2.3.1.57)	5.2.0	37.14	9.09
group_4180	A0A0B8RG88	<i>LmNIHS28_00920</i>	Uncharacterized protein	5.1.0	37.14	9.09
yxIG	Q8Y550	<i>lmo2226</i>	Lmo2226 protein	5.2.0	62.86	90.91
rpiB_3	G9G5K4	<i>rpiB</i>	Ribose-5-phosphate isomerase B	2.1.1	62.86	90.91
group_4171	A0A393D3V6	<i>AF264_02350</i>	Cell surface protein (LPXTG cell wall anchor domain-containing protein)		37.14	9.09
group_3412	A0A393RT87	<i>AF264_02105</i>	Uncharacterized protein	6.0.0	37.14	9.09
polC_2	Q8Y7E7	<i>lmo1336</i>	5-formyltetrahydrofolate cyclo-ligase (EC 6.3.3.2)	2.5.0	62.86	90.91
pgcA_1	Q8Y8N1	<i>lmo0865</i>	Lmo0865 protein	2.1.1	62.86	90.91
mngB_1	A0A255C9M1	<i>CDR86_08635</i>	Alpha-mannosidase	2.1.1	62.86	90.91
group_1736	Q8Y8Q6	<i>lmo0840</i>	Lmo0840 protein	5.2.0	62.86	90.91
group_3319	A0A3A2NVJ1	<i>AB922_01742</i>	Uncharacterized protein		37.14	9.09
hprA	Q8Y6K0	<i>lmo1684</i>	Lmo1684 protein	2.1.1	62.86	90.91
ecfA2	A0A0H3GF97	<i>ecfA</i>	Energy-coupling factor transporter ATP-binding protein EcfA (ECF transporter A component EcfA) (EC 3.6.3.-)	1.2.0	62.86	90.91
group_2353	Q8VMX1		Putative Gp2		37.14	9.09
group_4388	Q8Y917	<i>lmo0725</i>	Putative peptidoglycan bound protein (LPXTG motif)	1.8.0	62.86	90.91
group_2380	A0A0E1R602	<i>yjaB</i>	Uncharacterized N-acetyltransferase YjaB (EC 2.3.1.-)	5.2.0	37.14	9.09
group_5075	A0A3A8B0G1	<i>levS</i>	Cell invasion LPXTG protein Vip (Levansucrase) (EC 2.4.1.10)	1.8.0	37.14	9.09
group_2577	Q8Y905	<i>lmo0737</i>	Lmo0737 protein	5.2.0	62.86	90.91

group_4301	Q8Y452	<i>lmo2603</i>	Lmo2603 protein	5.2.0	62.86	90.91
group_2208	A0A0B8RAD6	<i>LmNIHS28_01888</i>	Serine/threonine protein phosphatase	5.2.0	37.14	9.09
hisE	Q8Y9G7	<i>hisE</i>	Phosphoribosyl-ATP pyrophosphatase (PRA-PH) (EC 3.6.1.31)	2.2.0	62.86	90.91
group_864	Q8Y9X3	<i>lmo0395</i>	Lmo0395 protein	4.2.0	62.86	90.91
inIJ_11	A0A393CQT2	<i>inlj_6</i>	Cell surface protein (Internalin-J)	1.8.0	37.14	9.09
group_4192	A0A394ZNT3	<i>mta</i>	HTH-type transcriptional activator mta (MerR family transcriptional regulator)	3.5.2	37.14	9.09
group_4039	A0A3A8BN86	<i>ubiG</i>	Ubiquinone biosynthesis O-methyltransferase (EC 2.1.1.222)		37.14	9.09
group_4419	Q8Y8M8	<i>lmo0868</i>	Lmo0868 protein	6.0.0	62.86	90.91
group_949	A0A0E1R447	<i>manZ_2</i>	Mannose permease IID component	1.2.0	62.86	90.91
group_4415	Q8Y8Q3	<i>lmo0843</i>	Lmo0843 protein	5.2.0	62.86	90.91
group_4417	Q8Y8P6	<i>lmo0850</i>	Lmo0850 protein	6.0.0	62.86	90.91
group_4229	A0A2Z5C0J8	<i>RK57_09605</i>	Triosephosphate isomerase (EC 5.3.1.1)	2.1.2	37.14	9.09
group_4411	Q8Y8R3	<i>lmo0832</i>	Lmo0832 protein	4.4.0	62.86	90.91
group_4214	A0A2Z5C2C0	<i>RK57_09950</i>	Uncharacterized protein	6.0.0	37.14	9.09
group_4213	A0A3A2LR66	<i>inla_6</i>	Internalin (Internalin-A) (LPXTG cell wall anchor domain-containing protein)	1.8.0	37.14	9.09
inIJ_6	Q8Y8R0	<i>lmo0835</i>	Putative peptidoglycan bound protein (LPXTG motif)	1.8.0	62.86	90.91
group_4182	A0A3A8BWT2	<i>inlB_1</i>	Internalin B	1.8.0	37.14	9.09
kdgA	A0A2A6A934	<i>CDR86_00865</i>	Aldolase	2.1.1	62.86	90.91
group_4187	A0A1S7FNB3	<i>DC57_12750</i>	Histidinol-phosphatase	2.2.0	37.14	9.09
group_3171	A0A0E1RCR1	<i>yozG</i>	Uncharacterized HTH-type transcriptional regulator YozG	5.2.0	37.14	9.09
yflN	Q8Y6A5	<i>lmo1790</i>	Lmo1790 protein	5.2.0	62.86	90.91
yneA	Q8Y7H6	<i>yneA</i>	Cell division suppressor protein YneA	5.2.0	62.86	90.91
cca	Q8Y5Z8	<i>cca</i>	CCA tRNA nucleotidyltransferase (EC 2.7.7.72)	3.6.0	62.86	90.91
group_3921	A0A1S7FGU9	<i>DC57_00570</i>	LD-carboxypeptidase	4.5.0	37.14	9.09
nth_2	A0A3A7HTM1	<i>nth_1</i>	Endonuclease III (EC 4.2.99.18) (Endonuclease III domain-containing protein)	5.2.0	37.14	9.09
group_4044	A0A393CLM7	<i>AF264_09030</i>	DUF5011 domain-containing protein		37.14	9.09
group_4045	A0A0E0UXG9	<i>aroH</i>	Chorismate mutase AroH (EC 5.4.99.5)	2.2.0	37.14	9.09
group_4042	A0A2Z5BZ76	<i>RK57_03415</i>	Uncharacterized protein	5.2.0	37.14	9.09
group_4043	A0A3A8BVH1	<i>act</i>	Methanol dehydrogenase activator (EC 3.-.-.-)	5.2.0	37.14	9.09
gdh	A0A3A8BLH6	<i>gdh_2</i>	Glucose 1-dehydrogenase (EC 1.1.1.47)	2.1.1	62.86	90.91
group_3922	A0A1S7FH11	<i>cutC</i>	Copper homeostasis protein CutC	4.2.0	37.14	9.09
cssS	Q8Y857	<i>lmo1061</i>	Histidine kinase (EC 2.7.13.3)	1.3.0	62.86	90.91
group_2610	Q8Y6G4	<i>lmo1723</i>	Lmo1723 protein	6.0.0	62.86	90.91
group_3210	A0A393VWD9	<i>AB922_02198</i>	NUDIX domain-containing protein		37.14	9.09
group_3219	A0A3A2WX84	<i>cbie</i>	Cobalt-precorrin-7 (C(5))-methyltransferase (Cobalt-precorrin-7 C(5)-methyltransferase) (EC 2.1.1.289)	2.5.0	37.14	9.09
nudF	Q8Y5U0	<i>lmo1965</i>	Lmo1965 protein	5.2.0	62.86	90.91
rne	Q8Y6Y8	<i>lmo1543</i>	Lmo1543 protein	2.3.0	62.86	90.91

group_3593	Q8Y6N1	<i>lmo1653</i>	Putative cell surface protein	6.0.0	62.86	90.91
group_3959	A0A394ZKW3	<i>gbpa</i>	Chitin-binding protein (GlcNAc-binding protein A)	2.1.1	37.14	9.09
group_3958	A0A2Z5BYZ7	<i>RK57_05850</i>	Uncharacterized protein	6.0.0	37.14	9.09
group_3951	A0A1T1YDG1	<i>DC57_02225</i>	Uncharacterized protein	6.0.0	37.14	9.09
group_3952	A0A3A2JZK0	<i>AF239_12415</i>	Zinc-type alcohol dehydrogenase-like protein	2.1.1	37.14	9.09
group_3957	A0A3A6WIB6	<i>AF239_12100</i>	Amidophosphoribosyltransferase (ComF family protein)	1.10.0	37.14	9.09
group_3956	A0A3A8BKJ7	<i>comFA</i>	ComF operon protein 1 (EC 3.6.4.12)	1.10.0	37.14	9.09
group_3328	A0A394Y0E1	<i>AF264_03215</i>	Cell surface protein (LPXTG cell wall anchor domain-containing protein)	1.8.0	37.14	9.09
group_897	Q8Y7R0	<i>lmo1212</i>	Lmo1212 protein	5.2.0	62.86	90.91
group_4466	A0A3A7HYF6	<i>DYZ90_00006</i>	Uncharacterized protein	6.0.0	62.86	90.91
group_4335	A0A1D2J1W2	<i>CDR86_05500</i>	Internalin	1.8.0	62.86	90.91
group_4584	Q8Y600	<i>lmo1903</i>	Lmo1903 protein	1.4.0	62.86	90.91
phnA	Q8Y778	<i>lmo1418</i>	Lmo1418 protein	2.6.0	62.86	90.91
group_4516	Q8Y6P9	<i>lmo1635</i>	Lmo1635 protein	5.2.0	62.86	90.91
group_4517	Q8Y6P4	<i>lmo1640</i>	Lmo1640 protein	6.0.0	62.86	90.91
murQ	C1KVV7	<i>murQ</i>	N-acetylmuramic acid 6-phosphate etherase (MurNAc-6-P etherase) (EC 4.2.1.126)		37.14	9.09
group_4386	A0A3A7EMK5	<i>AE233_02029</i>	Uncharacterized protein	1.8.0	62.86	90.91
rsgA_2	A0A0B8R6Z0	<i>rsgA</i>	Small ribosomal subunit biogenesis GTPase RsgA (EC 3.6.1.-)	5.2.0	37.14	9.09
azoR1_1	A0A3A8BPK0	<i>azoR1</i>	FMN-dependent NADH-azoreductase 1 (EC 1.7.-.-)	1.4.0	37.14	9.09
group_3135	A0A0E1R796	<i>yteJ</i>	Uncharacterized membrane protein yteJ	5.2.0	37.14	9.09
group_4138	A0A1S7FMA8	<i>DC57_10750</i>	Uncharacterized protein	5.2.0	37.14	9.09
group_4347	Q8YA09	<i>lmo0357</i>	Lmo0357 protein	1.2.0	62.86	90.91
group_4346	Q8YA13	<i>lmo0353</i>	Lmo0353 protein	5.2.0	62.86	90.91
inlA_8	UPI00073B62EC	<i>AOB47_624c</i>	Internalin-like protein	1.8.0	62.86	90.91
group_4082	A0A2Z5C055	<i>RK57_00410</i>	DUF2975 domain-containing protein		37.14	9.09
group_4080	A0A3A2XB09	<i>glys</i>	Glycine--tRNA ligase beta subunit (EC 6.1.1.14) (Glycyl-tRNA synthetase beta subunit) (GlyRS)	3.7.2	37.14	9.09
group_4081	A0A0E0UW34	<i>LMM7_1529</i>	Putative branched-chain amino acid export protein (BAAC homeostasis)	5.2.0	37.14	9.09
group_4086	A0A0B8R1M7	<i>LmNIHS28_01991</i>	Uncharacterized protein	6.0.0	37.14	9.09
group_4087	A0A2Z5BXN3	<i>RK57_00065</i>	Type II secretion system protein	1.10.0	37.14	9.09
group_4084	A0A3A7KDD8	<i>proC_1</i>	Pyrroline-5-carboxylate reductase (EC 1.5.1.2)	2.2.0	37.14	9.09
group_4069	C1KVN8	<i>argC</i>	N-acetyl-gamma-glutamyl-phosphate reductase (AGPR) (EC 1.2.1.38)	2.2.0	37.14	9.09
group_3987	A0A3A8BPP2	<i>yxIG</i>	Putative transmembrane protein YxlG	5.2.0	37.14	9.09
group_3984	A0A3A8BNU1	<i>adaB</i>	Methylated-DNA--protein-cysteine methyltransferase, inducible (EC 2.1.1.63)	3.2.0	37.14	9.09
group_3985	UPI00086E8416		GntR family transcriptional regulator	3.5.2	37.14	9.09
group_3983	A0A0E1RA49	<i>yqjT</i>	Uncharacterized protein yqjT	5.2.0	37.14	9.09

group_3980	A0A0E1RA70	<i>yisK</i>	Uncharacterized protein yisK	5.2.0	37.14	9.09
group_3981	UPI0000F53EDE	<i>ARJ20_15280</i>	GNAT family N-acetyltransferase	5.2.0	37.14	9.09
group_4165	G9G5K0		Internalin protein	1.8.0	37.14	9.09
group_4167	A0A241SMW0	<i>A410_0767</i>	Uncharacterized protein	1.8.0	37.14	9.09
group_4166	UPI00003CA86A	<i>ARJ20_09330</i>	LPXTG cell wall anchor domain-containing protein	1.8.0	37.14	9.09
group_4161	A0A3A6WTN7	<i>ydde</i>	PhzF family phenazine biosynthesis protein (Putative isomerase YddE) (EC 5.1.-.-)	5.2.0	37.14	9.09
group_4133	A0A0E1R4P0	<i>BN389_10880</i>	Uncharacterized protein		37.14	9.09
czcR	A0A3A8CCY3	<i>czcR</i>	Transcriptional activator protein CzcR	3.5.2	62.86	90.91
group_4169	A0A1T1YRJ7	<i>DC57_12265</i>	Carboxymuconolactone decarboxylase	5.2.0	37.14	9.09
group_3396	A0A392Y5A5	<i>inlj_7</i>	Cell surface protein (Internalin-J) (LPXTG cell wall anchor domain-containing protein)		37.14	9.09
group_2864	A0A394XIB0	<i>inlj_9</i>	Cell wall anchor protein (Internalin-J) (LPXTG cell wall anchor domain-containing protein)		37.14	9.09
group_4137	A0A2Z5C2J4	<i>RK57_12860</i>	Teichoic acid D-Ala incorporation-associated protein DltX		37.14	9.09
group_4185	A0A393RUI1	<i>AF264_01965</i>	Uncharacterized protein	6.0.0	37.14	9.09
group_4134	A0A3A7GGN8	<i>thif</i>	Molybdopterin biosynthesis protein MoeB (Sulfur carrier protein ThiS adenylyltransferase) (EC 2.7.7.73)	2.5.0	37.14	9.09
group_3769	UPI000984CE83		hypothetical protein		37.14	9.09
group_3408	A0A3A7C5V3	<i>stth</i>	Cysteine hydrolase (Streptothricin hydrolase) (EC 3.5.2.19)	5.2.0	37.14	9.09
group_1192	A0A3A8C9D9	<i>artQ_1</i>	Arginine transport system permease protein ArtQ	1.2.0	37.14	9.09
group_4100	A0A1S7FLP7	<i>DC57_09570</i>	ABC transporter permease	5.2.0	37.14	9.09
yknZ_2	A0A393R639	<i>yknZ_1</i>	ABC transporter permease (FtsX-like permease family protein) (Putative ABC transporter permease YknZ)		37.14	9.09
mta	A0A3A8CEM4	<i>mta</i>	HTH-type transcriptional activator mta	3.5.2	62.86	90.91
yusV_2	Q8Y587	<i>lmo2182</i>	Lmo2182 protein	1.2.0	62.86	90.91
cobC	A0A1D2IT42	<i>cobC</i>	Alpha-ribazole phosphatase	2.5.0	62.86	90.91
group_4628	Q8Y518	<i>lmo2260</i>	Lmo2260 protein	5.2.0	62.86	90.91
yvbK	Q8Y5E7	<i>lmo2117</i>	Lmo2117 protein	5.2.0	62.86	90.91
inIJ_4	A0A1D2IXY9	<i>CDR86_09540</i>	Cell surface protein	1.8.0	62.86	90.91
mglA	A0A3A8C417	<i>mglA</i>	Galactose/methyl galactoside import ATP-binding protein MglA (EC 3.6.3.17)	1.2.0	62.86	90.91
fabG_3	A0A3A8BVY0	<i>fabG_1</i>	3-oxoacyl-[acyl-carrier-protein] reductase FabG (EC 1.1.1.100)	2.4.0	37.14	9.09
inIJ_7	UPI000BDF441A		LPXTG cell wall anchor domain-containing protein	1.8.0	62.86	90.91
inIJ_1	Q8YAF4	<i>lmo0175</i>	Putative peptidoglycan bound protein (LPXTG motif)	1.8.0	62.86	90.91
group_4088	A0A393RS12	<i>AF264_05675</i>	Competence protein ComG	1.10.0	37.14	9.09
inIJ_8	UPI00043541E8	<i>HR60_04430</i>	Cell surface protein		37.14	9.09
group_2561	UPI000D72CB8D		IS3 family transposase	4.4.0	62.86	90.91
isdC	Q8Y585	<i>hbp1</i>	Hemin/hemoglobin-binding protein 1 (Hn/Hb-binding protein 1) (Cell wall protein Lmo2186)	1.8.0	62.86	90.91
group_4151	A0A3A8BXI7	<i>yabJ</i>	2-iminobutanoate/2-iminopropanoate deaminase (EC 3.5.99.10)	5.2.0	37.14	9.09

group_2568	Q8Y9X8	<i>ltrA</i>	Low temperature requirement protein A	4.1.0	62.86	90.91
group_4152	A0A0E1R689	<i>ysdA</i>	Uncharacterized protein ysdA	5.2.0	37.14	9.09
group_3567	Q8Y7Y2	<i>lmo1137</i>	Lmo1137 protein	6.0.0	62.86	90.91
argJ_1	Q8Y6U7	<i>lmo1584</i>	Lmo1584 protein	5.2.0	62.86	90.91
group_4025	A0A2Z5BZU3	<i>RK57_04520</i>	ABC transporter ATP-binding protein	1.2.0	37.14	9.09
group_4153	A0A3A7KR34	<i>inlJ_12</i>	Internalin-J (Peptidoglycan-binding protein)	1.8.0	37.14	9.09
group_4330	Q8YAN2	<i>lmo0085</i>	Lmo0085 protein	5.1.0	62.86	90.91
group_4331	Q8YAL4	<i>lmo0104</i>	Lmo0104 protein	6.0.0	62.86	90.91
uvrA_2	Q8Y4F6	<i>uvrA</i>	UvrABC system protein A (UvrA protein) (Excinuclease ABC subunit A)	3.2.0	62.86	90.91
adaB	Q8Y534	<i>lmo2242</i>	Lmo2242 protein	3.2.0	62.86	90.91
pduX	Q8Y7U9	<i>lmo1170</i>	Lmo1170 protein	5.2.0	62.86	90.91
glpE	A0A3A8C167	<i>glpE_1</i>	Thiosulfate sulfurtransferase GlpE (EC 2.8.1.1)	4.1.0	62.86	90.91
group_4424	A0A1D2IWW8	<i>CDR86_10445</i>	Putative 3-methyladenine DNA glycosylase (EC 3.2.2.-)	3.2.0	62.86	90.91
tylM1	A0A3A8BVR5	<i>tylM1</i>	dTDP-3-amino-3,6-dideoxy-alpha-D-glucopyranose N,N-dimethyltransferase (EC 2.1.1.235)	5.2.0	62.86	90.91
group_1979	A0A0H3GEH2	<i>LMRG_00323</i>	Uncharacterized protein	6.0.0	42.86	72.73
group_1012	A0A0E1RAY4	<i>lytG_4</i>	Exo-glucosaminidase lytG (EC 3.2.1.-)	1.8.0	57.14	27.27
group_1902	Q8Y6T5	<i>lmo1597</i>	Lmo1597 protein	6.0.0	42.86	72.73
group_4145	A0A3A7PI72	<i>AF239_03595</i>	Permease (Putative two-component membrane permease complex subunit)	5.2.0	57.14	27.27
group_380	Q8YA34	<i>lmo0331</i>	Lmo0331 protein	1.8.0	42.86	72.73
group_4513	A0A0H3GHA0	<i>LMRG_02946</i>	Uncharacterized protein		42.86	72.73
group_3986	A0A3A8BQ69	<i>yxIE</i>	Negative regulatory protein YxIE		57.14	27.27
group_4422	Q8Y8I2	<i>lmo0920</i>	Lmo0920 protein	5.2.0	42.86	72.73
group_3797	A0A3A2L4U9	<i>AF238_14470</i>	Uncharacterized protein		17.14	45.45
group_5509	A0A3A2KDS0	<i>AF273_15200</i>	Uncharacterized protein		17.14	45.45
group_1918	A0A3A7H7K5	<i>AF818_02937</i>	Uncharacterized protein		8.57	31.82
group_951	A0A1S7FGJ9	<i>DC57_00020</i>	Terminase	4.3.0	20.00	0.00
fusA_2	A0A3A8BXI3	<i>php</i>	Phosphotriesterase homology protein	2.4.0	80.00	100.00
wapA	A0A0E1R9W5	<i>wapA_2</i>	Wall-associated protein		20.00	0.00
metN2	UPI000D5F7FE8		ATP-binding cassette domain-containing protein		20.00	0.00
group_4763	A0A3A7V582	<i>AF247_13185</i>	DUF2712 domain-containing protein		20.00	0.00
group_4766	A0A0B8R0W5	<i>LmNIHS28_00352</i>	Membrane protein		20.00	0.00
group_4765	A0A3A2JQ03	<i>AF247_13175</i>	Uncharacterized protein		20.00	0.00
group_4764	A0A0B8R164	<i>LmNIHS28_00351</i>	Membrane protein		20.00	0.00
group_4768	A0A393LYV4	<i>AF247_13160</i>	Uncharacterized protein		20.00	0.00
csbB	Q93RN0	<i>mtrA</i>	Dolichol-phosphate mannosyltransferase MtrA (Hypothetical glycosyl transferase)	1.1.0	71.43	95.45
group_4110	A0A1S7FLY5	<i>DC57_10005</i>	Uncharacterized protein	6.0.0	28.57	4.55
group_4113	UPI0004311060	<i>HR60_02825</i>	Membrane protein		28.57	4.55

group_2486	A0A3A7PTC4	<i>AF251_01345</i>	DNA double-strand break repair Rad50 ATPase		28.57	4.55
tagH	UPI000BDFED64		teichoic acids export ABC transporter ATP-binding subunit TagH	1.1.0	71.43	95.45
malP	Q8Y5E3	<i>lmo2121</i>	Lmo2121 protein	2.1.1	71.43	95.45
group_4194	A0A3A8BYI6	<i>CFSAN002345_001197</i>	Uncharacterized protein		28.57	4.55
group_1153	A0A0E0UUS7	<i>pncB</i>	Nicotinate phosphoribosyltransferase (EC 6.3.4.21)	5.2.0	28.57	4.55
group_230	A0A394ZCQ5	<i>AF274_10260</i>	Helix-turn-helix domain-containing protein (Transposase)	4.4.0	28.57	4.55
tatAy	Q8YA04	<i>tatA</i>	Sec-independent protein translocase protein TatA	5.2.0	71.43	95.45
group_4224	A0A3A7A655	<i>AF241_00720</i>	Peptidase (Putative peptidase) (EC 3.4.21.-)	2.2.0	28.57	4.55
group_2501	A0A394ZN44	<i>AF264_00790</i>	YafY family transcriptional regulator	3.5.2	28.57	4.55
group_4176	A0A0B8RDT5	<i>LmNIHS28_00904</i>	Uncharacterized protein		28.57	4.55
group_4175	A0A3A6WQ80	<i>AB922_01521</i>	Uncharacterized protein		28.57	4.55
group_2381	A0A394ZTP0	<i>AF264_04540</i>	Uncharacterized protein	5.1.0	28.57	4.55
group_4112	A0A0B8RBG4	<i>LmNIHS28_00797</i>	Uncharacterized protein	6.0.0	28.57	4.55
group_4195	A0A0B8RHP3	<i>LmNIHS28_01665</i>	Uncharacterized protein		28.57	4.55
efeU	Q8YA02	<i>lmo0365</i>	Lmo0365 protein	5.2.0	71.43	95.45
efeM	Q8YA01	<i>lmo0366</i>	Lmo0366 protein	1.2.0	71.43	95.45
rmlC	A0A1C7Q2S5	<i>rfbC</i>	dTDP-4-dehydrorhamnose 3,5-epimerase (EC 5.1.3.13) (Thymidine diphospho-4-keto-rhamnose 3,5-epimerase)	1.1.0	71.43	95.45
group_3251	A0A393RS34	<i>AF264_04600</i>	Uncharacterized protein	6.0.0	28.57	4.55
tatC2	Q8YA05	<i>tatC</i>	Sec-independent protein translocase protein TatC	5.2.0	71.43	95.45
group_770	A0A3A2WV59	<i>feoB</i>	Ferrous iron transport protein B	1.2.0	42.86	13.64
inlA_7	L7X106	<i>inlA</i>	Internalin A	1.8.0	57.14	86.36
group_940	A0A0B8REA6	<i>LmNIHS28_00065</i>	Uncharacterized protein		42.86	13.64
group_746	A0A0B8R487	<i>LmNIHS28_01552</i>	ABC transporter permease	1.2.0	42.86	13.64
feoB	A0A1D2IZV3	<i>feoB</i>	Ferrous iron transport protein B	1.2.0	60.00	86.36
group_4321	A0A090IU55	<i>Bacillus thermoamylovorans</i>	Uncharacterized protein		60.00	86.36
group_2732	A0A393U4Y6	<i>AF255_14330</i>	DUF2974 domain-containing protein	6.0.0	40.00	13.64
group_5515	UPI000BE047C1		DUF1310 family protein	5.1.0	40.00	13.64
group_1980	A0A392WP24	<i>AF255_14340</i>	DUF1310 domain-containing protein (DUF1310 family protein)	5.1.0	40.00	13.64
group_745	Q8Y4R3	<i>lmo2371</i>	Lmo2371 protein	1.2.0	60.00	86.36
group_918	UPI0007666023	<i>ERS409620_01314</i>	Uncharacterized conserved protein		11.43	36.36
group_2730	A0A392X2X8	<i>AF238_14485</i>	Uncharacterized protein		11.43	36.36
group_2069	A0A0H3GGP2	<i>LMRG_02453</i>	Mannose-specific PTS system IID component	1.2.0	11.43	36.36
group_475	Q8Y9K3	<i>lmo0524</i>	Lmo0524 protein	1.2.0	11.43	36.36
group_5654	A0A394RQC8	<i>AB922_02753</i>	Ribonuclease BN		5.71	27.27
group_3511	Q8YAH5	<i>lmo0151</i>	Lmo0151 protein	6.0.0	5.71	27.27
group_1986	UPI00047C87C6		hypothetical protein	4.3.0	5.71	27.27
group_481	A0A3A7DXN2	<i>AB922_02752</i>	Uncharacterized protein		5.71	27.27

group_3525	Q8Y9Y8	<i>lmo0379</i>	Lmo0379 protein	6.0.0	54.29	81.82
bioC	Q8Y7H2	<i>lmo1308</i>	Lmo1308 protein	3.8.0	54.29	81.82

¥ Non *L. monocytogenes* species

† Description for each functional category code is presented below

- [1.1.0] Cell envelope and cellular processes > Cell wall
- [1.2.0] Cell envelope and cellular processes > Transport/binding proteins and lipoproteins
- [1.3.0] Cell envelope and cellular processes > Sensors (signal transduction)
- [1.4.0] Cell envelope and cellular processes > Membrane bioenergetics
- [1.5.0] Cell envelope and cellular processes > Mobility and chemotaxis
- [1.6.0] Cell envelope and cellular processes > Protein secretion
- [1.7.0] Cell envelope and cellular processes > Cell division
- [1.8.0] Cell envelope and cellular processes > Cell surface proteins
- [1.9.0] Cell envelope and cellular processes > Soluble internalin
- [1.10.0] Cell envelope and cellular processes > Transformation/competence
- [2.1.0] Intermediary metabolism > Metabolism of carbohydrates and related molecule
- [2.1.1] Intermediary metabolism > Metabolism of carbohydrates and related molecule > Specific pathways
- [2.1.2] Intermediary metabolism > Metabolism of carbohydrates and related molecule > Main glycolytic pathways
- [2.1.3] Intermediary metabolism > Metabolism of carbohydrates and related molecule > TCA cycle
- [2.2.0] Intermediary metabolism > Metabolism of amino acids and related molecules
- [2.3.0] Intermediary metabolism > Metabolism of nucleotides and nucleic acids
- [2.4.0] Intermediary metabolism > Metabolism of lipids
- [2.5.0] Intermediary metabolism > Metabolism of coenzymes and prosthetic groups
- [2.6.0] Intermediary metabolism > Metabolism of phosphate
- [3.1.0] Information pathways > DNA replication
- [3.2.0] Information pathways > DNA restriction/modification and repair
- [3.3.0] Information pathways > DNA recombination
- [3.4.0] Information pathways > DNA packaging and segregation
- [3.5.1] Information pathways > RNA synthesis > Initiation
- [3.5.2] Information pathways > RNA synthesis > Regulation
- [3.5.3] Information pathways > RNA synthesis > Elongation
- [3.5.4] Information pathways > RNA synthesis > Termination
- [3.6.0] Information pathways > RNA modification
- [3.7.1] Information pathways > Protein synthesis > Ribosomal proteins
- [3.7.2] Information pathways > Protein synthesis > Aminoacyl-tRNA synthetases
- [3.7.3] Information pathways > Protein synthesis > Initiation
- [3.7.4] Information pathways > Protein synthesis > Elongation
- [3.7.5] Information pathways > Protein synthesis > Termination
- [3.8.0] Information pathways > Protein modification
- [3.9.0] Information pathways > Protein folding
- [4.1.0] Other functions > Adaptation to atypical conditions
- [4.2.0] Other functions > Detoxification

[4.3.0] Other functions > Phage-related functions

[4.4.0] Other functions > Transposon and IS

[4.5.0] Other functions > Miscellaneous

[5.1.0] Similar to unknown proteins > From Listeria

[5.2.0] Similar to unknown proteins > From other organisms

[6.0.0] No similarity

Supplementary Table 5. List of genes associated with biofilm production in BHI media at 10°C after pan-GWAS ($p < 0.05$).

GWAS name	Uniprot Entry	Organism ¥	Gene name	Protein names	Function al category †	% in weak biofilm formers	% in strong biofilm formers
group_4197	UPI00098E3EF0			hypothetical protein		66.67	13.33
group_7000	A0A2Z5Z219	<i>Lactococcus lactis</i>	<i>E05_32090</i>	Uncharacterized protein		3.70	50.00
group_3869	A0A394RPA7		<i>AF242_15480</i>	Uncharacterized protein		37.04	0.00
group_3762	A0A142EC64		<i>pA144_0007</i>	Uncharacterized protein		37.04	0.00
group_940	A0A0B8REA6		<i>LmNIHS28_00065</i>	Uncharacterized protein		55.56	10.00
group_377	UPI00074D6BC6		<i>LM83088_80034</i>	Uncharacterized protein	5.2.0	62.96	16.67
group_4590	Q8Y5Z0		<i>lmo1913</i>	Lmo1913 protein	5.2.0	7.41	50.00
group_3040	A0A3A7GE33		<i>AF264_08870</i>	Glycoside transferase	5.2.0	92.59	50.00
group_3986	A0A3A8BQ69		<i>yxIE</i>	Negative regulatory protein YxIE		70.37	23.33
group_6240	A0A2H1SK93	<i>Xanthomonas citri</i>	<i>C</i>	C protein		33.33	0.00
group_397	A0A0B8R5D0		<i>LmNIHS28_00068</i>	Uncharacterized protein	5.1.0	66.67	100.00
group_1807	UPI000BE00DE2			hypothetical protein		59.26	13.33
group_3733	A0A393N9I6		<i>D3C41_12950</i>	Uncharacterized protein		40.74	3.33
group_5799	UPI00092FB1F5			arsenic metallochaperone ArsD family protein		40.74	3.33
group_2657	A0A2Z5C560		<i>RK57_09450</i>	Endonuclease	5.2.0	0.00	33.33
group_2742	A0A3A7TM14		<i>AF856_01591</i>	AP2 domain-containing protein	4.3.0	51.85	10.00
group_6265	UPI00076722D3		<i>AXF25_01535</i>	Uncharacterized protein		29.63	0.00
group_3877	A0A3A7UV92		<i>ID87_02058</i>	Uncharacterized protein		29.63	0.00
group_6263	UPI000507E686		<i>AF821_01501</i>	Uncharacterized protein		29.63	0.00
group_6279	A0A3A7NV98		<i>AFX80_00020</i>	Uncharacterized protein	4.3.0	29.63	0.00
group_2757	A0A060UT12	<i>Acidithiobacill us ferrivorans</i>	<i>F</i>	Capsid protein F		29.63	0.00
bcgIB	UPI0009850DB7		<i>CJV36_12055</i>	Uncharacterized protein		29.63	0.00
bcgIA	UPI00074D58A5		<i>CJV36_12060</i>	Adenine methyltransferase		29.63	0.00
group_6271	UPI00053BE8EB		<i>DSD43_08455</i>	Uncharacterized protein		29.63	0.00
group_6276	A0A3A7EN18		<i>AFX46_00136</i>	XRE family transcriptional regulator		29.63	0.00
group_6243	A0A060US63	<i>Acidithiobacill us ferrivorans</i>	<i>G</i>	Major spike protein G		29.63	0.00
group_938	Q8YAG9		<i>lmo0157</i>	Lmo0157 protein	3.2.0	29.63	0.00
hsdM	A0A3A7RFF8		<i>hsdM</i>	SAM-dependent DNA methyltransferase (Type I restriction enzyme EcoKI M protein) (EC 2.1.1.72)		29.63	0.00
group_6273	A0A3A7UXE8		<i>AF273_02455</i>	Uncharacterized protein		29.63	0.00

group_6253	UPI000BE1046E	<i>Enterococcus faecalis TX0630</i>		relaxase	29.63	0.00	
group_6255	E6EXY6		<i>HMPREF9511_0168</i> 3	Uncharacterized protein	29.63	0.00	
group_6254	UPI00098E5223			plasmid mobilization relaxosome protein MobC	29.63	0.00	
group_6256	UPI0004D69275		<i>ARJ20_16365</i>	LPXTG cell wall anchor domain-containing protein	29.63	0.00	
group_6258	UPI000BE07A8C			CHAP domain-containing protein	29.63	0.00	
group_3878	A0A393A2Z5		<i>DOZ93_04615</i>	XRE family transcriptional regulator	29.63	0.00	
group_3876	UPI00074D51A1		<i>LM800396_140057</i>	Uncharacterized protein	29.63	0.00	
group_3874	A0A0V7YCU8	<i>Enterococcus faecium (Streptococcus faecium)</i>		<i>AOY33_09325</i>	Uncharacterized protein	29.63	0.00
group_3875	A0A3A7Q520			<i>AEZ78_00963</i>	Uncharacterized protein	29.63	0.00
group_6264	A0A0H3GD71			<i>LMRG_02934</i>	Uncharacterized protein	29.63	0.00
group_6266	A0A3A7MCD0			<i>AF821_01506</i>	Uncharacterized protein	29.63	0.00
group_6267	A0A0H3G912			<i>LMRG_02574</i>	GNAT family acetyltransferase	29.63	0.00
group_6261	UPI00074D5B8B			<i>LM800396_140058</i>	Uncharacterized protein	29.63	0.00
group_6262	A0A3A7YC45		<i>AF821_01500</i>	Uncharacterized protein	29.63	0.00	
group_6268	A0A3A7URE0		<i>ID87_02064</i>	Uncharacterized protein	29.63	0.00	
hsdR	A0A3A7Y0A7		<i>hsdR</i>	Type I restriction endonuclease subunit R (Type-I restriction enzyme R protein) (EC 3.1.21.3)	29.63	0.00	
group_6260	Q2V4W9		<i>pCT0002</i>	Uncharacterized protein	29.63	0.00	
group_6272	A0A3A7V8A6		<i>AF252_02435</i>	Sugar-phosphate nucleotidyltransferase	29.63	0.00	
group_294	UPI000BE003A6			helicase SNF2	29.63	0.00	
yofA	A0A393QJ60		<i>yofA</i>	HTH-type transcriptional regulator YofA (LysR family transcriptional regulator)	29.63	0.00	
group_3873	UPI0004D8BD21		<i>ARJ20_16270</i>	Uncharacterized protein	29.63	0.00	
group_6281	A0A3A7NH96		<i>AFX80_00025</i>	Uncharacterized protein	29.63	0.00	
group_6284	A0A0H3GFH8		<i>LMRG_02220</i>	Uncharacterized protein	6.0.0	29.63	0.00
group_6270	UPI000678F014		<i>KO07_03320</i>	Uncharacterized protein	29.63	0.00	
group_6277	A0A393A7N5		<i>DOZ93_04605</i>	Phage antirepressor	29.63	0.00	
group_6280	A0A3A7NSF4		<i>AFX80_00023</i>	Uncharacterized protein	29.63	0.00	
group_2760	UPI00086F2DD0			DUF1738 domain-containing protein	29.63	0.00	
yxIE	UPI000E759913		<i>yxIE</i>	Negative regulatory protein YxIE	5.2.0	29.63	73.33
group_5404	A0A142EC67		<i>pA144_0010</i>	Uncharacterized protein	37.04	3.33	
group_3681	A0A3A7KXY9		<i>AF818_02931</i>	Uncharacterized protein	37.04	3.33	
group_3864	A0A3A7IJW5		<i>AB922_01480</i>	Uncharacterized protein	37.04	3.33	
group_3761	A0A142EC65		<i>pA144_0008</i>	Uncharacterized protein	37.04	3.33	

group_5405	A0A142EC66	<i>pA144_0009</i>	Uncharacterized protein		37.04	3.33
group_4329	Q8YAN5	<i>lmo0082</i>	Lmo0082 protein	6.0.0	0.00	30.00
group_4328	Q8YAN7	<i>lmo0080</i>	Lmo0080 protein	6.0.0	0.00	30.00
group_2557	UPI0009B0B9A0		hypothetical protein	6.0.0	0.00	30.00
group_2729	A0A392X2X8	<i>AF238_14485</i>	Uncharacterized protein		7.41	43.33
group_6242	A0A2I2M4I9	<i>Tenacibaculum dicentrarchi</i> J	DNA-binding protein J		25.93	0.00
group_3871	A0A060UXK7	<i>Acidithiobacillus ferrivorans</i> H	Minor spike protein H		25.93	0.00
group_6269	A0A3A7V3E1	<i>immR_3</i>	HTH-type transcriptional regulator ImmR		25.93	0.00
group_295	UPI00042E7F14	<i>ARK89_15370</i>	Uncharacterized protein		25.93	0.00
group_6278	A0A393AES1	<i>DOZ93_04600</i>	Uncharacterized protein		25.93	0.00
group_1987	A0A394RZ82	<i>AF240_05480</i>	Uncharacterized protein		40.74	6.67
group_2752	A0A0H3GD86	<i>LMRG_02933</i>	Uncharacterized protein		33.33	3.33
group_5994	A0A0H3GDM5	<i>LMRG_00003</i>	Uncharacterized protein	6.0.0	33.33	3.33
nfrA1_1	A0A3A7H264	<i>nfra1_2</i>	FMN reductase (NADPH) (EC 1.5.1.38) (NADPH-dependent oxidoreductase)	1.4.0	66.67	96.67
gltR_1	A0A0B8QZ17	<i>LmNIHS28_01096</i>	LysR family transcriptional regulator	3.5.2	66.67	96.67
group_6291	UPI000BDFECA9		DUF262 domain-containing protein	5.2.0	33.33	3.33
group_2556	Q8YAP6	<i>lmo0071</i>	Lmo0071 protein	6.0.0	7.41	40.00
group_4470	A0A1D2IW15	<i>pduM</i>	Microcompartment protein PduM	6.0.0	18.52	56.67
group_2195	A0A393SL84	<i>coiA</i>	Competence protein CoiA	1.10.0	59.26	23.33
group_2547	Q8Y403	<i>lmo2675</i>	Lmo2675 protein	6.0.0	40.74	76.67
group_3636	A0A3A2YAK1	<i>cas5b</i>	Type I-B CRISPR-associated protein Cas5		29.63	66.67
cas1	UPI00092E4084	<i>B0X19_02870</i>	CRISPR-associated endonuclease Cas1		29.63	66.67
cas2	A0A0E0UTU7	<i>cas2</i>	CRISPR-associated endoribonuclease Cas2 (EC 3.1.-.-)		29.63	66.67
group_2659	A0A3A7SZG9	<i>cas6</i>	CRISPR-associated endoribonuclease Cas6		29.63	66.67
cas3	UPI00083D7946		CRISPR-associated helicase/endoribonuclease Cas3		29.63	66.67
group_1062	A0A393CV23	<i>AF264_09920</i>	Glycoside hydrolase family 65 protein	2.1.1	37.04	6.67
group_401	A0A394XJ12	<i>AF264_14015</i>	Uncharacterized protein		37.04	6.67
group_6040	A0A3A7RS18	<i>AF818_02929</i>	Uncharacterized protein		37.04	6.67
parC	A0A3A7I7R9	<i>parc</i>	DNA topoisomerase 4 subunit A (EC 5.99.1.3) (Topoisomerase IV subunit A)	3.4.0	77.78	100.00
group_1672	A0A0H3GJX6	<i>parC</i>	DNA topoisomerase 4 subunit A (EC 5.99.1.3) (Topoisomerase IV subunit A)	3.4.0	22.22	0.00
ycjO_2	A0A3A7GFW1	<i>AF264_13565</i>	Transglutaminase family protein	6.0.0	22.22	0.00
group_846	A0A0B8R577	<i>hflX</i>	GTPase HflX (GTP-binding protein HflX)	4.5.0	22.22	0.00
tkf_3	A0A0D8X574	<i>CDR86_05070</i>	Uncharacterized protein	5.2.0	22.22	0.00
group_1855	UPI000BDFDF92		DUF1310 family protein	5.1.0	11.11	43.33

group_6011	A0A3A7NYZ5	<i>AFX80_00022</i>	Uncharacterized protein		29.63	3.33
group_5722	UPI0009853537		hypothetical protein		29.63	3.33
group_2750	A0A0H3GCJ6	<i>LMRG_02892</i>	Uncharacterized protein		29.63	3.33
group_1810	UPI000E6BA985	<i>D3C26_06200</i>	Uncharacterized protein		29.63	3.33
group_488	A0A3A7U2K0	<i>AF856_02018</i>	Carbohydrate deacetylase (EC 3.5.1.-) (ChbG/HpnK family deacetylase)	5.2.0	29.63	3.33
group_3812	A0A2A6AA43	<i>CDR86_02440</i>	N-acetyltransferase		29.63	3.33
group_5916	A0A0H3GCY0	<i>LMRG_02891</i>	Uncharacterized protein		29.63	3.33
group_5915	A0A0H3G8Y5	<i>LMRG_02330</i>	Uncharacterized protein	6.0.0	29.63	3.33
group_6074	A0A3A7NHD5	<i>AFX80_00024</i>	Uncharacterized protein		29.63	3.33
group_6283	A0A393KIZ1	<i>AFX44_02360</i>	Uncharacterized protein		29.63	3.33
group_3841	UPI000E6B9871		hypothetical protein		29.63	3.33
group_1884	UPI000E718624		hypothetical protein	5.2.0	29.63	3.33
group_474	A0A393CRL8	<i>AF264_01650</i>	Putative sulfate transporter (SulP family inorganic anion transporter)	1.2.0	51.85	16.67
group_3527	UPI000E751432		hypothetical protein		0.00	23.33
draG	Q8YAAQ0	<i>lmo0067</i>	Lmo0067 protein	3.8.0	0.00	23.33
group_4268	A0A3A7G7B2	<i>AB922_00990</i>	Uncharacterized protein		7.41	36.67
group_4269	A0A2A5ZK54	<i>CDR86_14750</i>	Uncharacterized protein		7.41	36.67
group_3934	A0A0B8RC01	<i>LmNIHS28_00239</i>	Uncharacterized protein	6.0.0	92.59	63.33
group_4271	A0A2A5ZJX3	<i>CDR86_14735</i>	Uncharacterized protein		7.41	36.67
group_4270	A0A3A7G421	<i>AB922_00993</i>	Uncharacterized protein		7.41	36.67
group_3495	UPI000E72C99E		hypothetical protein		7.41	36.67
group_5655	UPI000BE0F385		hypothetical protein		40.74	10.00
group_3519	Q8YA40	<i>lmo0324</i>	Lmo0324 protein	6.0.0	3.70	30.00
group_4478	A0A1D2ISE5	<i>CDR86_11995</i>	Uncharacterized protein		3.70	30.00
immR_1	A0A394V9S3	<i>AF261_05410</i>	XRE family transcriptional regulator		3.70	30.00
nifS	Q8Y5N5	<i>lmo2022</i>	Lmo2022 protein	2.5.0	22.22	56.67
group_3827	A0A392XHQ2	<i>pduM</i>	Microcompartment protein PduM	6.0.0	51.85	20.00
group_1969	A0A0E0V124	<i>gidA</i>	tRNA uridine 5-carboxymethylaminomethyl modification enzyme MnmG (Glucose-inhibited division protein A)	1.7.0	51.85	20.00
group_2660	A0A3A7IMJ8	<i>cas8a1</i>	Type I-B CRISPR-associated protein Cas8b1/Cst1		29.63	63.33
group_4686	A0A393MBE2	<i>cas7i</i>	Type I-B CRISPR-associated protein Cas7/Cst2/DevR		29.63	63.33
group_1346	A0A3A7FZC8	<i>AF951_02536</i>	Uncharacterized protein		44.44	13.33
tagB_1	A0A3A8BZ54	<i>tarL_2</i>	Teichoic acid ribitol-phosphate polymerase TarL (EC 2.7.8.14)	1.1.0	55.56	86.67
tagG	UPI000BE10CE8		ABC transporter permease	1.1.0	55.56	86.67
group_2684	A0A393U116	<i>AF273_04990</i>	XRE family transcriptional regulator		11.11	40.00
group_1396	A0A0H3GGU0	<i>LMRG_02850</i>	Uncharacterized protein		88.89	60.00
group_3915	A0A0H3G8X6	<i>LMRG_02849</i>	Uncharacterized protein		88.89	60.00
group_2751	UPI0000F3E668	<i>LMRG_00004</i>	Uncharacterized protein	6.0.0	33.33	6.67

csbB	Q93RN0	<i>mtrA</i>	Dolichol-phosphate mannosyltransferase MtrA (Hypothetical glycosyl transferase)	1.1.0	66.67	93.33
group_1153	A0A0E0UUS7	<i>pncB</i>	Nicotinate phosphoribosyltransferase (EC 6.3.4.21)	5.2.0	33.33	6.67
group_3850	A0A0H3GHG8	<i>LMRG_00005</i>	Uncharacterized protein		33.33	6.67
group_307	UPI00027E8422	<i>D3B99_03045</i>	Uncharacterized protein		33.33	6.67
group_6068	A0A3A7VX21	<i>AF951_02474</i>	Uncharacterized protein		33.33	6.67
tagH	UPI000BDFED64		teichoic acids export ABC transporter ATP-binding subunit TagH	1.1.0	66.67	93.33
malP	Q8Y5E3	<i>lmo2121</i>	Lmo2121 protein	2.1.1	66.67	93.33
rmlC	A0A1C7Q2S5	<i>rfbC</i>	dTDP-4-dehydrothymine 3,5-epimerase (EC 5.1.3.13) (Thymidine diphospho-4-keto-thymine 3,5-epimerase)	1.1.0	66.67	93.33
znuC_4	A0A3A7NPD6	<i>znuC_2</i>	ABC transporter ATP-binding protein (Zinc import ATP-binding protein ZnuC) (EC 3.6.3.-)		33.33	6.67
group_1990	A0A3A7UE98	<i>AF951_02473</i>	Uncharacterized protein		33.33	6.67
group_2474	UPI000D72D1E5		DHA2 family efflux MFS transporter permease subunit	1.2.0	66.67	33.33
group_1144	A0A0E1RCC6	<i>yneQ</i>	Uncharacterized protein yneQ	5.2.0	81.48	100.00
group_220	Q8Y3J2	<i>lmo2843</i>	Lmo2843 protein	6.0.0	81.48	100.00
group_1241	Q723T1	<i>iolA</i>	Malonate-semialdehyde dehydrogenase (MSA dehydrogenase) (EC 1.2.1.27)	2.1.1	18.52	0.00
hflX_1	Q8Y8Y0	<i>hflX</i>	GTPase HflX (GTP-binding protein HflX)	4.5.0	81.48	100.00
group_1798	UPI000EFDE50F		6-phospho-beta-glucosidase	2.1.1	25.93	3.33
group_487	A0A3A7GDL7	<i>AF264_00475</i>	Carbohydrate deacetylase (EC 3.5.1.-) (ChbG/HpnK family deacetylase)	5.2.0	74.07	96.67
group_151	C1KYJ3	<i>rpoB</i>	DNA-directed RNA polymerase subunit beta (RNAP subunit beta) (EC 2.7.7.6) (RNA polymerase subunit beta) (Transcriptase subunit beta)	3.5.3	25.93	3.33
mco	UPI000A1FFD33		copper oxidase		25.93	3.33
group_2708	A0A2Z5C305	<i>RK57_11985</i>	RNA-directed DNA polymerase		25.93	3.33
licH_1	UPI000EFDE50F		6-phospho-beta-glucosidase	2.1.1	74.07	96.67
group_3917	A0A0H3G8X1	<i>LMRG_02492</i>	Uncharacterized protein		48.15	16.67
group_2056	A0A3A6WUY8	<i>AF251_14005</i>	Uncharacterized protein		48.15	16.67
group_4800	A0A394Y6H5	<i>AF255_14190</i>	Uncharacterized protein	6.0.0	7.41	33.33
group_3505	Q8Y3M7	<i>lmo2808</i>	Lmo2808 protein	5.1.0	7.41	33.33
group_1262	UPI000873C4F1		DUF1310 family protein	5.1.0	14.81	43.33
group_2559	UPI000B54942D		DUF3130 family protein	5.1.0	14.81	43.33
group_697	A0A1T1YBY4	<i>DC57_15090</i>	Type VII secretion effector	5.1.0	85.19	56.67
group_1151	UPI0008739F0D		antibiotic biosynthesis monooxygenase	5.2.0	100.00	80.00
group_150	C1KYJ3	<i>rpoB</i>	DNA-directed RNA polymerase subunit beta (RNAP subunit beta) (EC 2.7.7.6)	3.5.3	0.00	20.00
group_4297	D7PCG3		Uncharacterized protein		0.00	20.00
group_4299	D7PCG1		CRISPR-associated Cas5 family protein		0.00	20.00
group_4298	D7PCG2		Uncharacterized protein		0.00	20.00

group_700	A0A3A7G652	<i>AF264_14680</i>	Uncharacterized protein	4.3.0	100.00	80.00
hhaIM	A0A3A2V7Q5	<i>dcm</i>	Cytosine-specific methyltransferase (EC 2.1.1.37)		0.00	20.00
group_4462	Q8Y824	<i>lmo1094</i>	Lmo1094 protein	5.2.0	0.00	20.00
group_4257	UPI000C869397		hypothetical protein		0.00	20.00
group_4256	UPI000E254038	<i>AFT78_15980</i>	IS3 family transposase		0.00	20.00
group_4258	D7PCF5		Uncharacterized protein		0.00	20.00
sau3AIR	A0A3A7FE85	<i>sau3air</i>	Restriction endonuclease (Type-2 restriction enzyme Sau3AI) (EC 3.1.21.4)		0.00	20.00
group_4300	D7PCG0		Uncharacterized protein		0.00	20.00
group_4253	D7PCF8		Uncharacterized protein		0.00	20.00
group_876	A0A1D2IYH2	<i>CDR86_08530</i>	Uncharacterized protein	6.0.0	18.52	50.00
group_80	Q8YAQ1	<i>lmo0066</i>	Lmo0066 protein	4.5.0	18.52	50.00
group_1298	Q8Y842	<i>lmo1076</i>	Lmo1076 protein	1.1.0	62.96	90.00
group_2563	Q8YAA1	<i>lmo0253</i>	Lmo0253 protein	4.2.0	3.70	26.67
group_161	A0A1D2IS76	<i>essC</i>	Type VII secretion protein EssC	5.2.0	18.52	46.67
blaI	A0A3A8BYR2	<i>blaI</i>	Penicillinase repressor	3.5.2	18.52	46.67
group_2564	Q8YAA0	<i>lmo0254</i>	Lmo0254 protein	6.0.0	18.52	46.67
group_3506	Q8YAQ2	<i>lmo0065</i>	Lmo0065 protein	6.0.0	18.52	46.67
group_717	A0A0B8R8Y8	<i>LmNIHS28_00262</i>	Multidrug ABC transporter permease	1.2.0	81.48	53.33
group_3520	Q8YA27	<i>lmo0338</i>	Lmo0338 protein	6.0.0	29.63	60.00
group_2567	Q7AP83	<i>lmo0320</i>	Lmo0320 protein	1.8.0	29.63	60.00
group_94	UPI00083E5C54	<i>AF252_11575</i>	Class I SAM-dependent methyltransferase (Fragment)		40.74	13.33
copB	UPI000E76FAAA		copper-translocating P-type ATPase		40.74	13.33
group_3806	A0A3A2LE02	<i>AEZ78_01356</i>	Uncharacterized protein		40.74	13.33
group_70	UPI0001D010FD	<i>AF264_00610</i>	Uncharacterized protein	5.1.0	59.26	30.00
group_2550	A0A3A2SL16	<i>licT_2</i>	PRD domain-containing protein (Transcription antiterminator LicT)	3.5.2	59.26	30.00
emrY	A0A3A8BX24	<i>emrY</i>	Putative multidrug resistance protein EmrY	1.2.0	37.04	66.67
group_1233	A0A0B8R4N6	<i>LmNIHS28_01797</i>	Uncharacterized protein	6.0.0	62.96	33.33
group_1860	Q8YA42	<i>lmo0322</i>	Lmo0322 protein	5.2.0	70.37	93.33
group_4446	Q8Y839	<i>lmo1079</i>	Lmo1079 protein	5.2.0	70.37	93.33
group_4123	A0A0E1R4Q8	<i>ispD2</i>	Ribitol-5-phosphate cytidyltransferase (EC 2.7.7.40)		29.63	6.67
group_477	Q8Y9M5	<i>lmo0501</i>	Lmo0501 protein	3.5.2	70.37	93.33
group_4125	UPI000D66CEA1	<i>DF274_15095</i>	Uncharacterized protein (Fragment)		29.63	6.67
group_4124	A0A3A8BY01	<i>gtab</i>	UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) (UDP-glucose pyrophosphorylase)		29.63	6.67
group_4127	A0A3A7GRB2	<i>AF264_04425</i>	Uncharacterized protein		29.63	6.67
group_4049	A0A3A8BMB0	<i>blaSE</i>	Serine protease (EC 3.4.21.-)		29.63	6.67
group_4454	Q8Y831	<i>tarJ</i>	Ribulose-5-phosphate reductase (Ribulose-5-P reductase) (EC 1.1.1.405) (Ribitol-5-phosphate dehydrogenase)	2.1.0	70.37	93.33
group_4119	UPI000035D008	<i>APS76_03080</i>	CDP-glycerol glycerophosphotransferase family protein		29.63	6.67
group_3810	UPI000679072E		DUF4352 domain-containing protein		29.63	6.67

tagB_2	A0A1D2ISQ5	<i>CDR86_11250</i>	Glycosyl transferase family 2	1.1.0	70.37	93.33
group_6039	A0A393Q6N1	<i>AF951_01447</i>	Uncharacterized protein		29.63	6.67
pncB2	A0A0D8X9Q4	<i>CDR86_11285</i>	Nicotinate phosphoribosyltransferase (EC 6.3.4.21)	5.2.0	70.37	93.33
group_3954	UPI000E3C8303		cell wall teichoic acid glycosylation protein GtcA		29.63	6.67
group_3454	A0A0B8RAV3	<i>LmNIHS28_01817</i>	Uncharacterized protein		29.63	6.67
group_3882	A0A3A6WVM4	<i>AF241_14355</i>	Uncharacterized protein	4.3.0	29.63	6.67
group_4672	UPI0009305ABB		GtrA family protein	1.1.0	70.37	93.33
gutB	A0A3A7GLG3	<i>tarj</i>	Ribulose-5-phosphate reductase (Ribulose-5-P reductase) (EC 1.1.1.405) (Ribitol-5-phosphate dehydrogenase)		29.63	6.67
gtaB	UPI000931810D		UTP--glucose-1-phosphate uridylyltransferase GalU	1.1.0	70.37	93.33
group_4677	A0A393QPI9	<i>AF238_05485</i>	VRR-NUC domain-containing protein		29.63	6.67
group_1891	Q8Y7T3	<i>lmo1188</i>	Lmo1188 protein	6.0.0	70.37	93.33
group_4126	A0A3A7GN59	<i>tarl</i>	CDP-glycerol:glycerophosphate glycerophosphotransferase (Teichoic acid poly(Ribitol-phosphate) polymerase) (EC 2.7.8.-)		29.63	6.67
ispD2_1	UPI0004D75A86	<i>HT50_11035</i>	2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase (Fragment)	2.1.0	70.37	93.33
group_2892	UPI0009B09F82		GW domain-containing glycosaminoglycan-binding protein	1.8.0	29.63	6.67
tagD	A0A1C7PZ73	<i>tagD</i>	Glycerol-3-phosphate cytidylyltransferase	1.1.0	70.37	93.33
epsJ	A0A3A7GEL8	<i>epsj</i>	Glycosyltransferase family 2 protein (Putative glycosyltransferase EpsJ) (EC 2.4.-.-)		29.63	6.67
lytG_5	A0A3A8BW61	<i>lytG_3</i>	Exo-glucosaminidase LytG (EC 3.2.1.-)		29.63	6.67
group_4131	A0A3A8BVC9	<i>tagG</i>	Transport permease protein		29.63	6.67
group_3705	A0A3A7DYA1	<i>AF249_03765</i>	DUF1541 domain-containing protein		29.63	6.67
arnT	A0A3A7F315	<i>arnt</i>	Phospholipid carrier-dependent glycosyltransferase (Undecaprenyl phosphate-alpha-4-amino-4-deoxy-L-arabinose arabinosyl transferase) (EC 2.4.2.43)		29.63	6.67
rmlD	A0A1D2ISS6	<i>rfbD</i>	dTDP-4-dehydrorhamnose reductase (EC 1.1.1.133)	1.1.0	70.37	93.33
tagB_3	Q8Y830	<i>tagB</i>	TagB protein	1.1.0	70.37	93.33
epsJ_1	Q8Y9M9	<i>lmo0497</i>	Lmo0497 protein	1.1.0	70.37	93.33
ykoT	UPI000035CFFF	<i>NT04LM_1735</i>	Glycosyl transferase, group 2 family protein		29.63	6.67
tagF	A0A3A8BW41	<i>tagF</i>	Teichoic acid poly(Glycerol phosphate) polymerase (EC 2.7.8.12)		29.63	6.67
group_3925	A0A3A8BY26	<i>CFSAN002345_001436</i>	Uncharacterized protein		29.63	6.67
rmlA1	A0A0D8X3Y7	<i>rfbA</i>	Glucose-1-phosphate thymidylyltransferase (EC 2.7.7.24)	1.1.0	70.37	93.33
group_3562	Q8Y850	<i>lmo1068</i>	Lmo1068 protein	6.0.0	70.37	93.33
rffG	A0A1D2IST6	<i>rfbB</i>	dTDP-glucose 4,6-dehydratase (EC 4.2.1.46)	1.1.0	70.37	93.33
group_2384	UPI000766C630	<i>ERS409610_00158</i>	Uncharacterized protein		29.63	6.67
group_4237	A0A394YEX0	<i>AF264_00540</i>	Endonuclease (Endonuclease/exonuclease/phosphatase family protein)	5.2.0	29.63	6.67
group_4030	A0A0B8R4F9	<i>LmNIHS28_01899</i>	Teichoic acid biosynthesis protein		29.63	6.67
group_3939	A0A0B8QQZ7	<i>LmNIHS28_00261</i>	Membrane protein		29.63	6.67

group_3938	Q9ZIC5	<i>LmNIHS28_00260</i>	Uncharacterized protein		29.63	6.67
group_4132	A0A3A2P6F9	<i>AF241_04305</i>	DUF5068 domain-containing protein		29.63	6.67
group_4130	UPI000D66B0A6	<i>tagH</i>	Teichoic acids export ABC transporter ATP-binding subunit TagH (Fragment)		29.63	6.67
group_4238	A0A394Y3M2	<i>AF264_00535</i>	PH domain-containing protein		29.63	6.67
epsJ_3	A0A3A8CCS3	<i>epsJ_2</i>	Putative glycosyltransferase EpsJ (EC 2.4.-.-)	1.1.0	70.37	93.33
epsJ_2	A0A3A7NTY9	<i>epsJ_2</i>	Glycosyltransferase (Putative glycosyltransferase EpsJ) (EC 2.4.-.-)	1.1.0	70.37	93.33
group_965	UPI000D6455E8	<i>DF273_02615</i>	Uncharacterized protein (Fragment)		29.63	6.67
epsJ_4	A0A3A8BXQ8	<i>epsJ_1</i>	Putative glycosyltransferase EpsJ (EC 2.4.-.-)	1.1.0	70.37	93.33
sdpR	A0A3A8BPZ1	<i>sdpR</i>	Transcriptional repressor SdpR	3.5.2	29.63	6.67
group_4426	Q8Y8H1	<i>lmo0933</i>	Lmo0933 protein	1.1.0	70.37	93.33
group_4118	UPI000E6B7FBF		glycerol-3-phosphate cytidyltransferase		29.63	6.67
group_3885	A0A393D4V0	<i>AF264_14565</i>	Pyruvyl-transferase		29.63	6.67
group_5438	A0A2A6A383	<i>CDR86_14065</i>	Phage major capsid protein		44.44	16.67
group_5436	A0A2A6A494	<i>CDR86_14040</i>	Phage tail protein		44.44	16.67
group_5437	A0A2A6A2S9	<i>CDR86_14060</i>	Uncharacterized protein		44.44	16.67
group_5450	A0A3A2JSK3	<i>AF847_01777</i>	Uncharacterized protein		44.44	16.67
group_5455	A0A2A6A624	<i>CDR86_09860</i>	Uncharacterized protein		44.44	16.67
group_5440	A0A3A2Q1E8	<i>AF847_01796</i>	Phage portal protein		44.44	16.67
group_2724	A0A2A6A2X1	<i>CDR86_14035</i>	Uncharacterized protein		44.44	16.67
group_3870	A0A2A6A392	<i>CDR86_14115</i>	RNA polymerase subunit sigma		44.44	16.67
group_2723	A0A2A6A314	<i>CDR86_14025</i>	Phage tail protein		44.44	16.67
group_3781	A0A3A7A859	<i>AF847_01778</i>	Uncharacterized protein		44.44	16.67
group_5441	A0A2A6A2T7	<i>CDR86_14110</i>	Site-specific integrase		44.44	16.67
group_3775	A0A2A5ZJU3	<i>CDR86_14055</i>	Head-tail adaptor protein		44.44	16.67
smc_5	A0A3A2L5G2	<i>AF249_02565</i>	Phage tail tape measure protein		44.44	16.67
group_3773	A0A2A6A3R8	<i>CDR86_14045</i>	Uncharacterized protein		44.44	16.67
group_3774	A0A2A5ZKW1	<i>CDR86_14050</i>	Uncharacterized protein		44.44	16.67
group_3776	A0A2A5ZK62	<i>CDR86_14085</i>	Terminase large subunit		44.44	16.67
group_5452	A0A2A5ZM51	<i>CDR86_09880</i>	DUF771 domain-containing protein		44.44	16.67
group_2698	A0A3A2JNT0	<i>D3C46_16425</i>	Uncharacterized protein		44.44	16.67
group_3771	A0A2A6A353	<i>CDR86_14020</i>	Uncharacterized protein		44.44	16.67
group_2597	A0A393F8Q4	<i>D3B62_10335</i>	Uncharacterized protein		14.81	40.00
group_132	UPI00086E3AD4		hypothetical protein		7.41	30.00
group_4242	A0A0B8QZ13	<i>LmNIHS28_01086</i>	Uncharacterized protein	6.0.0	92.59	70.00
group_3647	A0A393KD14	<i>AF247_14610</i>	Uncharacterized protein		7.41	30.00
group_2691	A0A2A6A8L3	<i>CDR86_05350</i>	Uncharacterized protein		7.41	30.00
group_3504	Q8Y3N1	<i>lmo2804</i>	Lmo2804 protein	6.0.0	7.41	30.00
group_4200	A0A3A2WRU5	<i>AF241_01120</i>	Uncharacterized protein		14.81	0.00
group_4201	UPI00098E5B68	<i>DOV17_10730</i>	Uncharacterized protein		14.81	0.00
group_4202	A0A0B8RHX0	<i>LmNIHS28_01805</i>	Uncharacterized protein		14.81	0.00

group_4203	A0A0B8R119	<i>LmNIHS28_01806</i>	Uncharacterized protein		14.81	0.00
group_4205	A0A0B8RA54	<i>LmNIHS28_01808</i>	Uncharacterized protein		14.81	0.00
group_4206	UPI000873BE8A		hypothetical protein		14.81	0.00
group_4204	A0A0B8RAJ2	<i>LmNIHS28_01807</i>	Uncharacterized protein		14.81	0.00
group_4199	A0A0B8RG01	<i>LmNIHS28_01804</i>	Uncharacterized protein		14.81	0.00
group_4211	A0A0B8QZH0	<i>LmNIHS28_01814</i>	Uncharacterized protein		14.81	0.00
araR	A0A3A8C7S0	<i>araR</i>	Arabinose metabolism transcriptional repressor	3.5.2	85.19	100.00
group_2942	A0A3A7F258	<i>AF258_10415</i>	DUF87 domain-containing protein		14.81	0.00
group_6241	A0A060USR2	<i>Acidithiobacillus ferrivorans</i> D	Scaffolding protein D		14.81	0.00
group_1809	UPI00073B1B95	<i>AN945_2724c</i>	Uncharacterized protein		14.81	0.00
group_2489	UPI000254880C	<i>AJZ74_11435</i>	PBS lyase		14.81	0.00
group_3545	A0A3A7QRH6	<i>AF249_03255</i>	Glycoside hydrolase family 125 protein	5.2.0	85.19	100.00
group_6259	UPI000B8EE202		hypothetical protein		14.81	0.00
group_147	UPI00098E3A42		BspA family leucine-rich repeat surface protein	1.8.0	14.81	0.00
group_3549	Q8Y8X1	<i>lmo0771</i>	Lmo0771 protein	6.0.0	85.19	100.00
group_3872	UPI000B8EE202		hypothetical protein		14.81	0.00
group_4163	A0A0E0UTX3	<i>LMM7_0796</i>	Uncharacterized protein	6.0.0	14.81	0.00
group_4210	A0A0B8RA58	<i>LmNIHS28_01813</i>	Uncharacterized protein		14.81	0.00
ugpA	A0A3A8CAJ6	<i>ugpA</i>	sn-glycerol-3-phosphate transport system permease protein UgpA	1.2.0	85.19	100.00
iolA	A0A1D2IYM0	<i>mmsA</i>	Malonate-semialdehyde dehydrogenase (MSA dehydrogenase) (EC 1.2.1.27)	2.1.1	85.19	100.00
ugpB	Q8Y8X4	<i>lmo0768</i>	Lmo0768 protein	1.2.0	85.19	100.00
group_606	A0A2Z5C4G3	<i>RK57_13575</i>	MerR family transcriptional regulator	3.5.2	14.81	0.00
group_2702	A0A0S4KTT7	<i>Candidatus Nitrospira inopinata</i> NITINOP_1625	Uncharacterized protein		14.81	0.00
group_2794	UPI00098D5DEC		XkdX family protein		14.81	0.00
group_1214	UPI000E72BE72	<i>AFX66_02803</i>	Uncharacterized protein	6.0.0	14.81	0.00
group_2796	A0A394ZCH8	<i>AF274_11785</i>	Phage tail family protein		14.81	0.00
group_5108	A0A2Z5C608	<i>RK57_11975</i>	Uncharacterized protein		14.81	0.00
group_4207	A0A0B8RHX3	<i>LmNIHS28_01810</i>	Membrane protein		14.81	0.00
group_4208	A0A394XPH6	<i>AF241_01080</i>	Uncharacterized protein		14.81	0.00
araQ_4	Q8Y8X5	<i>lmo0767</i>	Lmo0767 protein	1.2.0	85.19	100.00
group_2795	UPI0004D43DC4	<i>CJ756_11065</i>	Uncharacterized protein		14.81	0.00
group_5107	UPI000D654808	<i>DF278_15490</i>	Transcriptional regulator (Fragment)		14.81	0.00
group_4209	A0A0B8R4P7	<i>LmNIHS28_01812</i>	Uncharacterized protein		14.81	0.00
lptB	A0A3A7JHL1	<i>nata_1</i>	ABC transporter ATP-binding protein NatA (ATP-binding cassette domain-containing protein) (DUF4162 domain-containing protein)	1.2.0	85.19	100.00
group_1873	Q8Y8X3	<i>lmo0769</i>	Lmo0769 protein	2.1.1	85.19	100.00

group_195	A0A0E1R2K1	<i>BN389_01650</i>	Uncharacterized protein		22.22	3.33
group_3895	A0A394QVX1	<i>AF241_14025</i>	Uncharacterized protein	4.3.0	22.22	3.33
group_14	A0A0F5Z6U3	<i>UQ68_03245</i>	Holin	4.3.0	22.22	3.33
mnmg	A0A0E0V124	<i>gida</i>	tRNA uridine 5-carboxymethylaminomethyl modification enzyme MnmG (Glucose-inhibited division protein A)	1.7.0	51.85	80.00
group_2040	A0A3A7F101	<i>AF264_14455</i>	Ribonuclease (EC 3.1.-.-)	5.2.0	51.85	80.00
group_3916	A0A3A7D3S5	<i>AF251_14010</i>	Uncharacterized protein		48.15	20.00
group_3700	UPI000984B87F		hypothetical protein		33.33	10.00
group_3858	A0A0H3GDJ9	<i>LMRG_02591</i>	Uncharacterized protein		33.33	10.00

‡ Non *L. monocytogenes* species

† Description for each functional category code is presented below

[1.1.0] Cell envelope and cellular processes > Cell wall

[1.2.0] Cell envelope and cellular processes > Transport/binding proteins and lipoproteins

[1.3.0] Cell envelope and cellular processes > Sensors (signal transduction)

[1.4.0] Cell envelope and cellular processes > Membrane bioenergetics

[1.5.0] Cell envelope and cellular processes > Mobility and chemotaxis

[1.6.0] Cell envelope and cellular processes > Protein secretion

[1.7.0] Cell envelope and cellular processes > Cell division

[1.8.0] Cell envelope and cellular processes > Cell surface proteins

[1.9.0] Cell envelope and cellular processes > Soluble internalin

[1.10.0] Cell envelope and cellular processes > Transformation/competence

[2.1.0] Intermediary metabolism > Metabolism of carbohydrates and related molecule

[2.1.1] Intermediary metabolism > Metabolism of carbohydrates and related molecule > Specific pathways

[2.1.2] Intermediary metabolism > Metabolism of carbohydrates and related molecule > Main glycolytic pathways

[2.1.3] Intermediary metabolism > Metabolism of carbohydrates and related molecule > TCA cycle

[2.2.0] Intermediary metabolism > Metabolism of amino acids and related molecules

[2.3.0] Intermediary metabolism > Metabolism of nucleotides and nucleic acids

[2.4.0] Intermediary metabolism > Metabolism of lipids

[2.5.0] Intermediary metabolism > Metabolism of coenzymes and prosthetic groups

[2.6.0] Intermediary metabolism > Metabolism of phosphate

[3.1.0] Information pathways > DNA replication

[3.2.0] Information pathways > DNA restriction/modification and repair

[3.3.0] Information pathways > DNA recombination

[3.4.0] Information pathways > DNA packaging and segregation

[3.5.1] Information pathways > RNA synthesis > Initiation

[3.5.2] Information pathways > RNA synthesis > Regulation

[3.5.3] Information pathways > RNA synthesis > Elongation

[3.5.4] Information pathways > RNA synthesis > Termination

[3.6.0] Information pathways > RNA modification

[3.7.1] Information pathways > Protein synthesis > Ribosomal proteins

[3.7.2] Information pathways > Protein synthesis > Aminoacyl-tRNA synthetases

- [3.7.3] Information pathways > Protein synthesis > Initiation
- [3.7.4] Information pathways > Protein synthesis > Elongation
- [3.7.5] Information pathways > Protein synthesis > Termination
- [3.8.0] Information pathways > Protein modification
- [3.9.0] Information pathways > Protein folding
- [4.1.0] Other functions > Adaptation to atypical conditions
- [4.2.0] Other functions > Detoxification
- [4.3.0] Other functions > Phage-related functions
- [4.4.0] Other functions > Transposon and IS
- [4.5.0] Other functions > Miscellaneous
- [5.1.0] Similar to unknown proteins > From Listeria
- [5.2.0] Similar to unknown proteins > From other organisms
- [6.0.0] No similarity

Supplementary Table 6. List of genes associated with biofilm production in dBHI media at 10°C after pan-GWAS ($p < 0.05$).

GWAS name	Uniprot Entry	Organism ¥	Gene name	Protein names	Function al category †	% in weak biofilm formers	% in strong biofilm formers
group_3627	A0A2A6A9Q5		<i>CDR86_05420</i>	Uncharacterized protein		67.44	7.14
group_1972	A0A1D2IW59		<i>CDR86_05425</i>	Uncharacterized protein		65.12	7.14
group_194	A0A394YAU8		<i>AF255_15365</i>	Uncharacterized protein		79.07	21.43
group_4801	A0A3A2R9E5		<i>D3B46_07385</i>	Uncharacterized protein		0.00	35.71
clpP1	A0A3A7GTR6		<i>clpP1</i>	ATP-dependent Clp protease proteolytic subunit		48.84	0.00
group_1969	A0A0E0V124		<i>gidA</i>	tRNA uridine 5-carboxymethylaminomethyl modification enzyme MnmG (Glucose-inhibited division protein A)	1.7.0	46.51	0.00
group_1323	A0A393NY83		<i>AF252_05645</i>	Terminase large subunit		69.77	21.43
group_1930	UPI000987417B		<i>C7K67_12540</i>	Uncharacterized protein		69.77	21.43
group_1936	UPI0001E38E7D		<i>lmo4a_1264</i>	hypothetical protein		69.77	21.43
group_911	A0A394UBA6		<i>AF237_14510</i>	Phage portal protein		69.77	21.43
group_396	UPI00086EB4E1			hypothetical protein		69.77	21.43
mnmG	A0A0E0V124		<i>gidA</i>	tRNA uridine 5-carboxymethylaminomethyl modification enzyme MnmG (Glucose-inhibited division protein A)	1.7.0	55.81	100.00
group_877	UPI000D65622D		<i>DF271_11275</i>	Uncharacterized protein (Fragment)	6.0.0	9.30	50.00
group_143	A0A3A2J7V9		<i>AF247_01180</i>	BspA family leucine-rich repeat surface protein	1.8.0	9.30	50.00
group_3728	UPI00087574F4		<i>CKA04_00075</i>	DUF4274 domain-containing protein		0.00	28.57
group_3729	A0A3A7CPM3		<i>AFX42_02321</i>	Uncharacterized protein		0.00	28.57
group_5173	A0A2Z5C0M4		<i>RK57_09705</i>	Peptidase	2.2.0	0.00	28.57
group_5174	A0A3A2SNR2		<i>D3B74_12110</i>	YafY family transcriptional regulator	3.5.2	0.00	28.57
group_3730	A0A393IN51		<i>AFX42_02319</i>	Uncharacterized protein	6.0.0	0.00	28.57
group_5189	A0A3A7P9Y2		<i>AFX42_02323</i>	Uncharacterized protein		0.00	28.57
group_876	A0A1D2IYH2		<i>CDR86_08530</i>	Uncharacterized protein	6.0.0	23.26	71.43
group_1275	Q8YA41		<i>lmo0323</i>	Lmo0323 protein	5.2.0	74.42	28.57
group_620	A0A0E0UTZ8		<i>rarD</i>	Putative chloramphenicol resistance permease	5.2.0	46.51	92.86
group_4408	Q8Y8U3		<i>lmo0800</i>	Lmo0800 protein	5.2.0	53.49	7.14
group_2584	Q8Y8U2		<i>lmo0801</i>	Lmo0801 protein	1.8.0	53.49	7.14
group_4160	A0A0E1RAZ5		<i>yqkB</i>	Uncharacterized protein yqkB	5.2.0	46.51	92.86
ibpA	A0A1B2LR36		<i>pLM-C-273_00100</i>	Protein involved in cell division		51.16	7.14
group_1422	A0A3A2RW22		<i>AF251_13400</i>	DUF1310 domain-containing protein (DUF1310 family protein)	5.1.0	32.56	78.57
group_1939	A0A2A6A897		<i>CDR86_05340</i>	Phage tail protein		67.44	21.43
group_1374	UPI000990612F			hypothetical protein	6.0.0	67.44	21.43
group_4931	A0A393UJY3		<i>AB922_03066</i>	Dihydroorotate dehydrogenase (Quinone)	5.1.0	6.98	42.86
group_1423	A0A393L0Q4		<i>AF264_13385</i>	DUF1310 domain-containing protein (DUF1310 family protein)	5.1.0	39.53	85.71
group_4273	UPI0008759A67			XRE family transcriptional regulator		48.84	7.14
group_2656	UPI000766639A		<i>ERS409650_01636</i>	Uncharacterized protein		48.84	7.14

group_4683	A0A393SKA6	<i>AF239_00415</i>	Uncharacterized protein	6.0.0	11.63	50.00
group_475	Q8Y9K3	<i>lmo0524</i>	Lmo0524 protein	1.2.0	11.63	50.00
group_609	A0A1S7FLU5	<i>DC57_10100</i>	Uncharacterized protein	6.0.0	88.37	50.00
group_2732	A0A393U4Y6	<i>AF255_14330</i>	DUF2974 domain-containing protein	6.0.0	39.53	0.00
group_5515	UPI000BE047C1		DUF1310 family protein	5.1.0	39.53	0.00
group_1980	A0A392WP24	<i>AF255_14340</i>	DUF1310 domain-containing protein (DUF1310 family protein)	5.1.0	39.53	0.00
group_1927	A0A393EP38	<i>DPM34_15090</i>	HNH endonuclease		58.14	14.29
group_2538	D7PCF0		Putative transposase		37.21	0.00
group_913	A0A394RXF7	<i>AF236_05635</i>	Uncharacterized protein		65.12	21.43
actA	Q6E9G6	<i>actA</i>	ActA (Actin nucleator protein ActA)	1.8.0	95.35	64.29
group_925	A0A0E0USB0	<i>prs</i>	Ribose-phosphate pyrophosphokinase (RPPK) (EC 2.7.6.1) (5-phospho-D-ribose 5-phosphate)		95.35	64.29
group_4930	UPI000BE0165D		actin assembly-inducing protein ActA	1.8.0	4.65	35.71
mgtB	A0A1D2IRU1	<i>mgtA</i>	Magnesium-translocating P-type ATPase	1.2.0	72.09	28.57
group_2548	UPI000874D6A9		polysaccharide deacetylase		72.09	28.57
group_2657	A0A2Z5C560	<i>RK57_09450</i>	Endonuclease	5.2.0	9.30	42.86
group_1932	A0A393D0P3	<i>AF261_15130</i>	Phage major capsid protein		46.51	7.14
group_2542	UPI000BE0CF3F		hypothetical protein		46.51	7.14
group_4274	A0A142EC60	<i>pA144_0003</i>	Uncharacterized protein		46.51	7.14
group_2650	A0A3A7NB70	<i>AF818_02916</i>	Uncharacterized protein		46.51	7.14
group_2655	UPI00070C5611		hypothetical protein		46.51	7.14
group_1858	A0A3A7Q0D0	<i>folK</i>	2-amino-4-hydroxy-6-hydroxymethyldihydropteridine diphosphokinase (EC 2.7.6.3)	2.5.0	46.51	7.14
group_1923	A0A393FBY8	<i>AF252_05580</i>	Uncharacterized protein		46.51	7.14
group_1228	A0A2Z5C2Q2	<i>RK57_10170</i>	DUF917 domain-containing protein	5.2.0	97.67	71.43
group_3707	UPI00003CAC0A	<i>AF251_12155</i>	Uncharacterized protein		2.33	28.57
group_728	A0A393CRH4	<i>mgtA</i>	Magnesium-translocating P-type ATPase (Magnesium-transporting ATPase, P-type 1) (EC 3.6.3.2)	1.2.0	30.23	71.43
group_1269	UPI00083DD376		hypothetical protein	6.0.0	69.77	28.57
group_1894	A0A3A6ZFF6	<i>AE052_00014</i>	Uncharacterized protein		44.19	7.14
group_4475	A0A0E0UVZ2	<i>LMM7_1248</i>	Uncharacterized protein		44.19	7.14
group_2731	A0A0H3GJX1	<i>LMRG_01889</i>	Uncharacterized protein	5.1.0	44.19	7.14
group_919	UPI00093013A0		A-kinase anchor protein 11	6.0.0	55.81	14.29
group_622	A0A0B8R4R4	<i>rarD</i>	EamA family transporter (Permease)	5.2.0	55.81	14.29
group_4344	Q8YA33	<i>lmo0332</i>	Lmo0332 protein	6.0.0	55.81	14.29
group_5435	A0A3A2KJM7	<i>AF255_07855</i>	Uncharacterized protein		34.88	0.00
group_904	A0A3A7P9G8	<i>inlJ_10</i>	Class 1 internalin InlL (Internalin-J)	1.8.0	34.88	0.00
group_3769	UPI000984CE83		hypothetical protein		34.88	0.00
group_1843	A0A1S7FP06	<i>DC57_14095</i>	6-phospho-beta-glucosidase	2.1.1	62.79	21.43
group_5843	A0A3A2R8P7	<i>D3B69_09405</i>	DUF5081 family protein	6.0.0	0.00	21.43
group_5842	A0A3A2NZC0	<i>D3B69_09410</i>	WXG100 family type VII secretion target	6.0.0	0.00	21.43

purM	C1KW66	<i>purM</i>	Phosphoribosylformylglycinamide cyclo-ligase (EC 6.3.3.1) (AIR synthase) (AIRS) (Phosphoribosyl-aminoimidazole synthetase)	2.3.0	100.00	78.57
group_506	A0A393UJW4	<i>AB922_03046</i>	Alpha-amylase	6.0.0	0.00	21.43
group_360	UPI000CDB419D	<i>CXR83_06020</i>	Cell surface protein	1.8.0	0.00	21.43
group_5844	A0A392YQG8	<i>AF844_02972</i>	Uncharacterized protein	6.0.0	0.00	21.43
group_5841	A0A3A7BU98	<i>D3B69_09415</i>	Chorismate synthase	6.0.0	0.00	21.43
group_5840	A0A3A7BL13	<i>D3B69_08805</i>	ATP-binding protein		0.00	21.43
group_3763	A0A3A7Q2Y8	<i>D3C16_05975</i>	Restriction endonuclease subunit S		0.00	21.43
group_5838	A0A3A2NKZ5	<i>D3B79_09090</i>	Uncharacterized protein		0.00	21.43
group_5839	A0A3A2TU61	<i>D3B69_08800</i>	SIR2 family protein		0.00	21.43
group_5835	A0A3A7QPE8	<i>AF840_01803</i>	Uncharacterized protein		0.00	21.43
group_5836	A0A3A2RH67	<i>D3B69_08785</i>	Appr-1-p processing protein		0.00	21.43
group_5837	UPI00098E44F1		Appr-1-p processing protein		0.00	21.43
group_5833	C6ZXJ8	<i>purM</i>	Phosphoribosylformylglycinamide cyclo-ligase (EC 6.3.3.1) (AIR synthase) (AIRS) (Phosphoribosyl-aminoimidazole synthetase)	2.3.0	0.00	21.43
group_1943	A0A394VD49	<i>AF261_05405</i>	Imma/IrrE family metallo-endopeptidase		32.56	0.00
tnpR	D7PCF4		Putative resolvase		53.49	14.29
cadA	UPI0009305248		cadmium-translocating P-type ATPase	1.2.0	53.49	14.29
group_1343	A0A394ZJX3	<i>AF243_05235</i>	DNA-binding protein		53.49	14.29
hin_2	UPI000BE029CD		recombinase family protein		53.49	14.29
group_3497	D7PCH4	<i>CDR86_15050</i>	DDE transposase (Transposase)		53.49	14.29
group_1295	Q8Y8G5	<i>lmo0939</i>	Lmo0939 protein	6.0.0	81.40	42.86
group_4664	Q8Y4K6	<i>lmo2432</i>	Lmo2432 protein	6.0.0	81.40	42.86
nfrA1_2	A0A3A8BZV6	<i>nfrA1_1</i>	FMN reductase (NADPH) (EC 1.5.1.38)	1.4.0	81.40	42.86
accB	A0A1D2IQ93	<i>accB</i>	Biotin carboxyl carrier protein of acetyl-CoA carboxylase	2.4.0	81.40	42.86
sttH	Q8Y9A3	<i>lmo0629</i>	Lmo0629 protein	5.2.0	81.40	42.86
yfkJ	Q8Y8G6	<i>lmo0938</i>	Lmo0938 protein	3.8.0	81.40	42.86
group_3621	Q8Y4Q9	<i>lmo2375</i>	Lmo2375 protein	6.0.0	81.40	42.86
group_3297	A0A394XZE5	<i>AF264_03740</i>	SMI1/KNR4 family protein	6.0.0	18.60	57.14
group_2913	A0A2Z5BYV4	<i>RK57_05535</i>	Uncharacterized protein	6.0.0	18.60	57.14
group_4150	A0A394XVS5	<i>gata_1</i>	Amidase (EC 3.5.1.4) (Glutamyl-tRNA(Gln) amidotransferase subunit A) (EC 6.3.5.7)	1.1.0	18.60	57.14
group_4142	A0A3A8BVY8	<i>nfrA1_1</i>	FMN reductase (NADPH) (EC 1.5.1.38)	1.4.0	18.60	57.14
group_4141	A0A3A8C3E2	<i>yfkJ</i>	Low molecular weight protein-tyrosine-phosphatase YfkJ (EC 3.1.3.48)		18.60	57.14
group_3187	A0A393RR72	<i>accB</i>	Biotin carboxyl carrier protein of acetyl-CoA carboxylase	2.4.0	18.60	57.14
group_2560	UPI000BE05954		hypothetical protein	5.1.0	32.56	71.43
group_1845	Q9EXF8	<i>bglA</i>	Beta-glucosidase (EC 3.2.1.21) (Glycoside hydrolase family 1 protein)	2.1.1	39.53	78.57
group_665	A0A394VEJ2	<i>AF261_05390</i>	Site-specific integrase		60.47	21.43
group_1963	UPI00098E7CD3		superoxide dismutase	6.0.0	60.47	21.43

group_3668	A0A3A2JQP2	<i>D3B79_08735</i>	PBSX family phage terminase large subunit		6.98	35.71
group_1875	Q8Y8S0	<i>lmo0824</i>	Lmo0824 protein	6.0.0	79.07	42.86
mhqA_2	Q8Y8Y4	<i>lmo0758</i>	Lmo0758 protein	5.2.0	79.07	42.86
group_4155	A0A3A2X5P1	<i>AF264_03135</i>	Winged helix DNA-binding domain-containing protein	6.0.0	20.93	57.14
group_2658	A0A2Z5C293	<i>RK57_09780</i>	Uncharacterized protein	6.0.0	20.93	57.14
trxA_3	UPI000BDFC1FB		thioredoxin	1.4.0	79.07	42.86
group_745	Q8Y4R3	<i>lmo2371</i>	Lmo2371 protein	1.2.0	79.07	42.86
group_3355	A0A3A8BXQ6	<i>mhqA_2</i>	Putative ring-cleaving dioxygenase MhqA (EC 1.13.11.-)	5.2.0	20.93	57.14
group_4176	A0A0B8RDT5	<i>LmNIHS28_00904</i>	Uncharacterized protein		11.63	42.86
group_4175	A0A3A6WQ80	<i>AB922_01521</i>	Uncharacterized protein		11.63	42.86
group_1749	A0A2Z5C202	<i>RK57_12045</i>	Uncharacterized protein	6.0.0	11.63	42.86
group_3501	Q8Y3Z3	<i>lmo2686</i>	Lmo2686 protein	6.0.0	74.42	35.71
group_2648	A0A394T3U8	<i>AF252_05595</i>	DUF669 domain-containing protein		41.86	7.14
group_3626	A0A3A2TXX4	<i>AF238_05490</i>	Uncharacterized protein		41.86	7.14
group_3962	A0A393CS61	<i>inlB_2</i>	Internalin B (Lmo2445 family class 3 internalin)	1.8.0	23.26	57.14
kdpC	Q8Y3Z8	<i>kdpC</i>	Potassium-transporting ATPase KdpC subunit	1.2.0	76.74	42.86
group_2223	A0A0B8R893	<i>AJL15_12980</i>	Transcriptional regulator	5.2.0	23.26	57.14
group_4666	A0A0H3GN16	<i>LMRG_01803</i>	Internalin	1.8.0	76.74	42.86
group_2646	Q8Y4H5	<i>lmo2466</i>	Lmo2466 protein	6.0.0	76.74	42.86
group_3946	C1KZN4	<i>kdpC</i>	Potassium-transporting ATPase KdpC subunit	1.2.0	23.26	57.14
group_746	A0A0B8R487	<i>LmNIHS28_01552</i>	ABC transporter permease	1.2.0	23.26	57.14
group_2612	A0A0H3GHY8	<i>LMRG_02831</i>	Uncharacterized protein	5.2.0	76.74	42.86
group_1443	Q8Y3Y2	<i>lmo2697</i>	Lmo2697 protein	5.2.0	76.74	42.86
group_2647	A0A3A2YHL0	<i>AF252_05590</i>	ATP-dependent helicase (DEAD/DEAH box helicase)		30.23	0.00
group_5469	UPI00074D5C6E	<i>DB955_12755</i>	Uncharacterized protein		27.91	0.00
group_5799	UPI00092FB1F5		arsenic metallochaperone ArsD family protein		27.91	0.00
group_2594	Q8Y7Z5	<i>lmo1124</i>	Lmo1124 protein	5.1.0	51.16	14.29
group_4465	Q8Y7Z7	<i>lmo1122</i>	Lmo1122 protein	5.1.0	51.16	14.29
group_3888	A0A0B8RBN9	<i>LmNIHS28_00109</i>	Uncharacterized protein	6.0.0	16.28	50.00
group_1946	A0A0B8REH4	<i>LmNIHS28_00150</i>	Membrane protein		16.28	50.00
group_4099	UPI000D648E93	<i>DF275_07015</i>	Uncharacterized protein (Fragment)		16.28	50.00
inlJ_10	UPI000987BEBC		LPXTG cell wall anchor domain-containing protein		16.28	50.00
group_1250	A0A1S7FP90	<i>DC57_14415</i>	Uncharacterized protein		16.28	50.00
group_3727	A0A3A2TE22	<i>int-tn</i>	Site-specific integrase (Transposase)		4.65	28.57
group_5179	A0A393N0K8	<i>AB922_01353</i>	Putative type I restriction enzyme P M protein (EC 2.1.1.72) (Type I restriction-modification system subunit M)		4.65	28.57
group_5178	A0A3A2PDJ1	<i>D3B74_06000</i>	Type I restriction endonuclease subunit R		4.65	28.57
group_3648	UPI000EF5AE28		DUF1310 family protein		4.65	28.57
group_569	A0A1S7FIY4	<i>DC57_04745</i>	Phosphotransferase family protein	5.2.0	95.35	71.43
group_5020	A0A3A8BWY7	<i>CFSAN002345_002255</i>	Uncharacterized protein		4.65	28.57

group_50	A0A3A2LQV6	<i>AFX52_01641</i>	LPXTG cell wall anchor domain-containing protein	6.0.0	4.65	28.57
group_1933	A0A3A2P3J3	<i>D3B70_02255</i>	Phage tail protein		48.84	14.29
group_4259	A0A393F3Q7	<i>AB922_00274</i>	Uncharacterized protein		48.84	14.29
clpC_2	UPI000930EE1D		ATP-dependent Clp protease ATP-binding subunit		48.84	14.29
group_125	A0A3A7AAN2	<i>AF247_14620</i>	Uncharacterized protein	6.0.0	48.84	14.29
group_3490	UPI000931EA20		ParA family protein		48.84	14.29
pdxT	Q71XR2	<i>pdxT</i>	Pyridoxal 5'-phosphate synthase subunit PdxT (EC 4.3.3.6) (Pdx2) (Pyridoxal 5'-phosphate synthase glutaminase subunit) (EC 3.5.1.2)	5.2.0	41.86	78.57
group_399	A0A393LD96	<i>AF247_14630</i>	Uncharacterized protein		69.77	35.71
group_5074	A0A3A7JEW8	<i>AF844_02399</i>	Uncharacterized protein		9.30	35.71
group_2053	UPI000D65D056	<i>DF275_03155</i>	Uncharacterized protein (Fragment)		9.30	35.71
group_2054	A0A394XJ48	<i>AF264_14055</i>	Uncharacterized protein		9.30	35.71
group_3649	A0A3A7V9B4	<i>AF247_13985</i>	DUF2974 domain-containing protein	6.0.0	9.30	35.71
group_3912	A0A3A7LWM6	<i>AF251_14090</i>	Uncharacterized protein		9.30	35.71
group_926	A0A0E0USB0	<i>prs</i>	Ribose-phosphate pyrophosphokinase (RPPK) (EC 2.7.6.1) (5-phospho-D- ribosyl alpha-1-diphosphate)	na	9.30	35.71
group_2811	A0A394TF27	<i>AF251_14070</i>	Uncharacterized protein		9.30	35.71
group_3913	A0A392YE30	<i>AF251_14085</i>	Uncharacterized protein		9.30	35.71
group_197	A0A0H3G937	<i>LMRG_02391</i>	Uncharacterized protein	5.1.0	55.81	21.43
dinB_3	D7PCE7		Putative DNA-directed DNA polymerase		62.79	28.57
group_3569	Q8Y7Y0	<i>lmo1139</i>	Lmo1139 protein	6.0.0	62.79	28.57
group_4612	Q8Y5J1	<i>lmo2070</i>	Lmo2070 protein	5.2.0	81.40	50.00
group_3197	A0A3A7EY63	<i>AB922_02243</i>	N-acetyltransferase	5.2.0	18.60	50.00
group_3196	Q720B7	<i>LMOf2365_1322</i>	UPF0291 protein LMOF2365_1322	5.2.0	18.60	50.00
group_4614	A0A2A5ZFW1	<i>CDR86_01560</i>	FeoB-associated Cys-rich membrane protein		81.40	50.00
licT_3	Q8Y3P6	<i>bvrA</i>	Transcription antiterminator	3.5.2	81.40	50.00
inlB_2	Q8Y9H9	<i>lmo0549</i>	Lmo0549 protein	1.9.0	81.40	50.00
manX_4	Q8YAU2	<i>lmo0021</i>	Lmo0021 protein	1.2.0	81.40	50.00
tpiA_1	Q8YA20	<i>tpiA2</i>	Probable triosephosphate isomerase 2 (TIM 2) (TPI 2) (EC 5.3.1.1) (Triose-phosphate isomerase 2)	2.1.2	81.40	50.00
group_4054	A0A394RA98	<i>AF239_08275</i>	HD domain-containing protein	5.2.0	18.60	50.00
group_4057	A0A3A7ML43	<i>AF251_07735</i>	2-methyl-6-phytyl-1,4-hydroquinone methyltransferase (EC 2.1.1.295) (Class I SAM-dependent methyltransferase)	5.2.0	18.60	50.00
group_4050	A0A3A8BL21	<i>thiN</i>	Thiamine pyrophosphokinase (EC 2.7.6.2)	2.5.0	18.60	50.00
group_4053	A0A0B8R933	<i>LmNIHS28_02291</i>	Uncharacterized protein	6.0.0	18.60	50.00
group_4052	A0A2Z5BX03	<i>RK57_02435</i>	DUF1697 domain-containing protein	5.2.0	18.60	50.00
group_4059	A0A3A8BR73	<i>fosX</i>	Fosfomycin resistance protein FosX	4.1.0	18.60	50.00
group_4058	UPI0004366B26	<i>HR60_00125</i>	UPF0435 protein HR60_00125	5.2.0	18.60	50.00
group_820	A0A393CUI8	<i>AF264_04565</i>	Alpha/beta hydrolase	6.0.0	18.60	50.00
group_2626	Q8Y593	<i>lmo2176</i>	Lmo2176 protein	3.5.2	81.40	50.00
group_2627	Q8Y582	<i>lmo2189</i>	Lmo2189 protein	1.10.0	81.40	50.00

group_2629	Q8Y512	<i>lmo2266</i>	Lmo2266 protein	5.2.0	81.40	50.00
group_3612	Q8Y531	<i>lmo2245</i>	Lmo2245 protein	5.2.0	81.40	50.00
glmS_3	A0A3A8C081	<i>glmS_2</i>	Glutamine--fructose-6-phosphate aminotransferase isomerizing (EC 2.6.1.16)	2.1.1	18.60	50.00
glmS_1	A0A3A8C038	<i>glmS_2</i>	Glutamine--fructose-6-phosphate aminotransferase isomerizing (EC 2.6.1.16)	2.1.1	81.40	50.00
group_3537	Q8Y973	<i>lmo0660</i>	Lmo0660 protein	4.4.0	81.40	50.00
group_3535	UPI000EF5BE8A		DUF975 family protein	5.2.0	81.40	50.00
group_3534	A0A3A8CFC5	<i>speG_1</i>	Spermidine N(1)-acetyltransferase (EC 2.3.1.57)	5.2.0	81.40	50.00
group_3539	Q8Y8Z5	<i>lmo0747</i>	Lmo0747 protein	6.0.0	81.40	50.00
ulaB_2	A0A3A8BNH7	<i>ulaB_2</i>	Ascorbate-specific PTS system EIIB component (EC 2.7.1.194)	1.2.0	81.40	50.00
ytnP	Q8Y6R9	<i>lmo1614</i>	Lmo1614 protein	5.2.0	81.40	50.00
addB	Q8Y510	<i>addB</i>	ATP-dependent helicase/deoxyribonuclease subunit B (EC 3.1.-.-) (EC 3.6.4.12) (ATP-dependent helicase/nuclease AddB)	3.3.0	81.40	50.00
addA	Q8Y511	<i>addA</i>	ATP-dependent helicase/nuclease subunit A (EC 3.1.-.-) (EC 3.6.4.12) (ATP-dependent helicase/nuclease AddA)	3.3.0	81.40	50.00
group_225	UPI0001D010DE	<i>inlj_14</i>	Internalin-J	1.8.0	18.60	50.00
group_3965	A0A3A7GK80	<i>mggb</i>	Bifunctional metallophosphatase/5'-nucleotidase (Mannosylglucosyl-3-phosphoglycerate phosphatase) (EC 3.1.3.-)	5.2.0	18.60	50.00
group_3963	A0A3A7G3T8	<i>AF251_11130</i>	Uncharacterized protein	6.0.0	18.60	50.00
group_3339	A0A393CSM1	<i>AF264_03070</i>	DUF3130 family protein (TIGR04197 family type VII secretion effector)		18.60	50.00
proC_2	A0A3A8C3U2	<i>proC_1</i>	Pyrroline-5-carboxylate reductase (EC 1.5.1.2)	2.2.0	81.40	50.00
sigW	Q8Y9U7	<i>lmo0423</i>	Lmo0423 protein	3.5.1	81.40	50.00
group_1244	A0A393CR87	<i>AF264_00605</i>	Ribonuclease P	5.1.0	18.60	50.00
group_4573	Q8Y6D7	<i>lmo1750</i>	Lmo1750 protein	5.2.0	81.40	50.00
group_4577	Q8Y6B2	<i>lmo1779</i>	Lmo1779 protein	6.0.0	81.40	50.00
group_4575	Q8Y6B4	<i>lmo1777</i>	Lmo1777 protein	5.2.0	81.40	50.00
ybjG	Q8Y6R1	<i>lmo1623</i>	Lmo1623 protein	5.2.0	81.40	50.00
cbiE	A0A3A8C045	<i>cbiE</i>	Cobalt-precorrin-7 C(5)-methyltransferase (EC 2.1.1.289)	2.5.0	81.40	50.00
yjaB	A0A3A8BXM4	<i>yjaB</i>	Putative N-acetyltransferase YjaB (EC 2.3.1.-)	5.2.0	81.40	50.00
ulaC_3	A0A3A8BN71	<i>ulaC_3</i>	Ascorbate-specific PTS system EIIA component (EC 2.7.1.194)	1.2.0	81.40	50.00
group_4504	Q8Y751	<i>lmo1461</i>	Lmo1461 protein	6.0.0	81.40	50.00
group_4503	Q8Y760	<i>lmo1443</i>	Lmo1443 protein	5.2.0	81.40	50.00
group_4500	Q8Y785	<i>lmo1410</i>	Lmo1410 protein	6.0.0	81.40	50.00
group_4509	Q8Y6X6	<i>lmo1555</i>	Lmo1555 protein	2.5.0	81.40	50.00
group_4489	A0A1D2IPZ2	<i>dprA</i>	DNA-protecting protein DprA	3.8.0	81.40	50.00
group_3028	A0A2Z5BXF4	<i>RK57_03270</i>	Riboflavin transporter	5.2.0	18.60	50.00
group_2916	A0A393D408	<i>trxa_4</i>	Thioredoxin (Thioredoxin 1)	1.4.0	18.60	50.00
group_4371	Q8Y9I3	<i>lmo0545</i>	Lmo0545 protein	6.0.0	81.40	50.00
group_4374	Q8Y9B7	<i>lmo0615</i>	Lmo0615 protein	6.0.0	81.40	50.00

group_4375	Q8Y9B5	<i>lmo0617</i>	Lmo0617 protein	5.1.0	81.40	50.00
group_4472	Q8Y7Q8	<i>lmo1214</i>	Lmo1214 protein	6.0.0	81.40	50.00
group_1303	Q8Y7Z1	<i>lmo1128</i>	Lmo1128 protein	6.0.0	81.40	50.00
group_4090	A0A3A7N8T5	<i>bioC</i>	Class I SAM-dependent methyltransferase (Malonyl-[acyl-carrier protein] O-methyltransferase) (EC 2.1.1.197)	3.8.0	18.60	50.00
group_4093	C1L2K1	<i>miaA</i>	tRNA dimethylallyltransferase (EC 2.5.1.75) (Dimethylallyl diphosphate:tRNA dimethylallyltransferase)	3.6.0	18.60	50.00
group_4092	A0A0E1R7G6	<i>ynbB</i>	Uncharacterized protein ynbB	4.2.0	18.60	50.00
group_4095	C1L2I1	<i>rnhB</i>	Ribonuclease HII (RNase HII) (EC 3.1.26.4)	3.1.0	18.60	50.00
group_4094	A0A2Z5C362	<i>dprA</i>	DNA-protecting protein DprA		18.60	50.00
group_4096	A0A2Z5C3E4	<i>RK57_14300</i>	Uncharacterized protein	1.2.0	18.60	50.00
group_4623	Q8Y555	<i>lmo2221</i>	Lmo2221 protein	5.2.0	81.40	50.00
group_4152	A0A0E1R689	<i>ysdA</i>	Uncharacterized protein ysdA	5.2.0	18.60	50.00
group_4621	Q8Y592	<i>lmo2177</i>	Lmo2177 protein	5.2.0	81.40	50.00
group_4154	A0A1T1YQG4	<i>DC57_11460</i>	Transposase	4.4.0	18.60	50.00
group_4252	A0A2Z5C1U4	<i>RK57_09025</i>	Uncharacterized protein	6.0.0	18.60	50.00
thiO	A0A3A8BP94	<i>thiO</i>	Glycine oxidase (EC 1.4.3.19)	2.2.0	81.40	50.00
group_4392	A0A3A8CAQ5	<i>rbsR_1</i>	Ribose operon repressor	3.5.2	81.40	50.00
group_4396	A0A3A8C7X5	<i>bglF_2</i>	PTS system beta-glucoside-specific EIIBCA component	1.2.0	81.40	50.00
thiF	Q8Y868	<i>lmo1049</i>	Lmo1049 protein	2.5.0	81.40	50.00
group_3589	Q8Y784	<i>lmo1411</i>	Lmo1411 protein	5.2.0	81.40	50.00
group_2703	A0A393RS60	<i>inlK</i>	Class 1 internalin InlK (LPXTG cell wall anchor domain-containing protein)	1.8.0	18.60	50.00
group_3979	A0A3A7GK99	<i>adda</i>	ATP-dependent helicase/nuclease subunit A (EC 3.1.-.-) (EC 3.6.4.12) (ATP-dependent helicase/nuclease AddA)	3.3.0	18.60	50.00
group_3470	A0A392X3L4	<i>AF241_00505</i>	Superoxide dismutase	6.0.0	18.60	50.00
inlA_11	A0A394Y342	<i>inlA_4</i>	Internalin (Internalin-A) (LPXTG cell wall anchor domain-containing protein)	1.8.0	18.60	50.00
group_3478	A0A0E1R3M5	<i>inlA_2</i>	Internalin-A	1.8.0	18.60	50.00
inlA_3	UPI000BDFD377		lmo1136 family class 1 internalin	1.8.0	81.40	50.00
ulaA_2	Q8Y5T4	<i>lmo1971</i>	Lmo1971 protein	1.2.0	81.40	50.00
inlA_1	Q8Y7I7	<i>lmo1290</i>	Lmo1290 protein	1.8.0	81.40	50.00
group_4024	UPI000035D3A8	<i>isdE</i>	Heme ABC transporter substrate-binding protein IsdE	1.2.0	18.60	50.00
group_4025	A0A2Z5BZU3	<i>RK57_04520</i>	ABC transporter ATP-binding protein	1.2.0	18.60	50.00
group_4026	A0A0D4CB02	<i>AJL15_12175</i>	Uncharacterized protein	5.2.0	18.60	50.00
group_4027	A0A2Z5BZF4	<i>RK57_04485</i>	TetR/AcrR family transcriptional regulator		18.60	50.00
group_4020	A0A3A7JKS7	<i>yhaO</i>	Exonuclease SbcCD subunit D (Putative metallophosphoesterase YhaO)	5.2.0	18.60	50.00
group_4021	A0A0B8QRP4	<i>LmNIHS28_01575</i>	Uncharacterized protein	5.2.0	18.60	50.00
group_4022	A0A0B8RAU1	<i>LmNIHS28_02204</i>	Membrane protein	6.0.0	18.60	50.00
group_4023	UPI0001EBA5A3	<i>NT04LM_3257</i>	Heme uptake protein IsdC	1.8.0	18.60	50.00

group_3923	A0A2Z5BZQ8	<i>RK57_07860</i>	PTS fructose transporter subunit IIA	1.2.0	18.60	50.00
albF	Q8Y797	<i>lmo1393</i>	Lmo1393 protein	2.2.0	81.40	50.00
group_5614	A0A3A6XF35	<i>addb</i>	ATP-dependent helicase/deoxyribonuclease subunit B (EC 3.1.-.-) (EC 3.6.4.12) (ATP-dependent helicase/nuclease AddB)	3.3.0	18.60	50.00
group_3927	A0A0B8RBU5	<i>LmNIHS28_00179</i>	RNA-binding protein	5.2.0	18.60	50.00
lutR_1	A0A3A8CF58	<i>lutR_2</i>	HTH-type transcriptional regulator LutR	3.5.2	81.40	50.00
group_3500	Q8Y451	<i>lmo2604</i>	Lmo2604 protein	5.2.0	81.40	50.00
macB_4	A0A3A8BUW4	<i>yknY_2</i>	Putative ABC transporter ATP-binding protein YknY (EC 3.6.3.-)		18.60	50.00
aguA_2	A0A0H3G891	<i>aguA</i>	Putative agmatine deiminase (EC 3.5.3.12) (Agmatine iminohydrolase)	5.2.0	81.40	50.00
argB	A0A1D2IV64	<i>argB</i>	Acetylglutamate kinase (EC 2.7.2.8) (N-acetyl-L-glutamate 5-phosphotransferase) (NAG kinase) (NAGK)	2.2.0	81.40	50.00
group_4055	A0A2Z5BWW4	<i>RK57_02265</i>	Molybdate metabolism regulator	5.2.0	18.60	50.00
group_662	Q8Y7Z0	<i>lmo1129</i>	Lmo1129 protein	5.2.0	81.40	50.00
group_3571	Q8Y7X3	<i>lmo1146</i>	Lmo1146 protein	5.2.0	81.40	50.00
group_4440	Q8Y855	<i>lmo1063</i>	Lmo1063 protein	1.2.0	81.40	50.00
ypdB	Q8Y8C4	<i>lmo0984</i>	Lmo0984 protein	3.5.2	81.40	50.00
group_2953	UPI0001B4220F	<i>ARJ20_02020</i>	LPXTG cell wall anchor domain-containing protein		18.60	50.00
group_4085	A0A0E0UWI3	<i>LMM7_1468</i>	Uncharacterized protein	5.2.0	18.60	50.00
panC	Q8Y602	<i>panC</i>	Pantothenate synthetase (PS) (EC 6.3.2.1) (Pantoate--beta-alanine ligase) (Pantoate-activating enzyme)	2.5.0	81.40	50.00
group_4432	A0A0H3GJ44	<i>LMRG_02074</i>	Uncharacterized protein		81.40	50.00
group_4430	Q8Y8D8	<i>lmo0966</i>	Lmo0966 protein	5.2.0	81.40	50.00
group_2353	Q8VMX1		Putative Gp2		18.60	50.00
group_4438	Q8Y856	<i>lmo1062</i>	Lmo1062 protein	1.2.0	81.40	50.00
group_4667	Q8Y4F2	<i>lmo2492</i>	Lmo2492 protein	6.0.0	81.40	50.00
group_4190	A0A3A7GJ00	<i>inla_3</i>	Internalin-A (Leucine-rich repeat domain-containing protein)	1.9.0	18.60	50.00
group_4219	A0A2Z5C2B1	<i>RK57_09890</i>	GntR family transcriptional regulator		18.60	50.00
group_4218	A0A393CNN4	<i>AF240_00940</i>	Uncharacterized protein		18.60	50.00
group_4216	UPI000035CDC6	<i>BN389_04240</i>	Uncharacterized protein		18.60	50.00
group_4215	A0A0B8R4Y8	<i>LmNIHS28_01937</i>	ATPase	5.2.0	18.60	50.00
group_2775	A0A393S3L9	<i>AF264_15050</i>	Uncharacterized protein	6.0.0	18.60	50.00
group_4213	A0A3A2LR66	<i>inla_6</i>	Internalin (Internalin-A) (LPXTG cell wall anchor domain-containing protein)	1.8.0	18.60	50.00
group_4668	Q8Y4D7	<i>comFC</i>	ComFC protein	1.10.0	81.40	50.00
group_4669	Q8Y4D6	<i>comFA</i>	ComFA protein	1.10.0	81.40	50.00
pknB	A0A3A8C235	<i>pknB</i>	Serine/threonine-protein kinase PknB (EC 2.7.11.1)	3.8.0	81.40	50.00
hcnC	A0A3A7J837	<i>hcnC</i>	FAD-binding oxidoreductase (Hydrogen cyanide synthase subunit HcnC) (EC 1.4.99.5)	2.2.0	18.60	50.00
group_4168	A0A0B8R2G1	<i>LmNIHS28_00854</i>	Flagellar hook protein	6.0.0	18.60	50.00
group_897	Q8Y7R0	<i>lmo1212</i>	Lmo1212 protein	5.2.0	81.40	50.00

group_4167	A0A241SMW0	<i>A410_0767</i>	Uncharacterized protein	1.8.0	18.60	50.00
adrA	A0A0E1REZ1	<i>yhcK</i>	Uncharacterized protein yhcK	5.2.0	18.60	50.00
group_4322	Q8Y3I4	<i>lmo2852</i>	Lmo2852 protein	5.2.0	81.40	50.00
group_4324	Q8YAT7	<i>cutC</i>	Copper homeostasis protein CutC	4.2.0	81.40	50.00
group_4068	A0A3A7T7A5	<i>ytnP</i>	MBL fold metallo-hydrolase (Putative quorum-quenching lactonase YtnP) (EC 3.1.1.-)	5.2.0	18.60	50.00
cobU	A0A3A8BXJ5	<i>cobU</i>	Bifunctional adenosylcobalamin biosynthesis protein CobU (EC 2.7.1.156)	2.5.0	81.40	50.00
ytrA_4	A0A3A8BN52	<i>ytrA_3</i>	HTH-type transcriptional repressor YtrA	3.5.2	81.40	50.00
rnhB	Q8Y7K4	<i>rnhB</i>	Ribonuclease HII (RNase HII) (EC 3.1.26.4)	3.1.0	81.40	50.00
group_4060	A0A3A2X1R4	<i>AF264_07635</i>	Uncharacterized protein	6.0.0	18.60	50.00
group_4061	A0A393RQY0	<i>ybbh_2</i>	MurR/RpiR family transcriptional regulator (Putative HTH-type transcriptional regulator YbbH)		18.60	50.00
group_4063	A0A0B8R8T3	<i>LmNIHS28_01308</i>	Permease		18.60	50.00
group_4064	UPI000035D1DA	<i>SAMD00023519_01157</i>	Cell surface protein		18.60	50.00
group_4065	A0A2Z5BWP2	<i>RK57_01585</i>	Uncharacterized protein	6.0.0	18.60	50.00
group_4066	UPI0004352777	<i>X846_1709</i>	Uncharacterized protein	5.2.0	18.60	50.00
group_4067	A0A0E1R8B1	<i>yodM</i>	Putative lipid phosphate phosphatase yodM (EC 3.1.3.-)	5.2.0	18.60	50.00
group_4103	A0A3A7Z0I1	<i>pduX</i>	L-threonine kinase (EC 2.7.1.177) (Propanediol utilization protein)	5.2.0	18.60	50.00
group_4102	A0A0B8R3Z5	<i>LmNIHS28_00732</i>	DNA topology modulation protein	5.2.0	18.60	50.00
group_4101	A0A0B8QUW8	<i>LmNIHS28_00730</i>	Uncharacterized protein	6.0.0	18.60	50.00
group_4100	A0A1S7FLP7	<i>DC57_09570</i>	ABC transporter permease	5.2.0	18.60	50.00
group_4107	A0A3A8BV76	<i>cobU</i>	Bifunctional adenosylcobalamin biosynthesis protein CobU (EC 2.7.1.156)		18.60	50.00
group_4106	A0A2Z5C4I3	<i>cobC</i>	Alpha-ribazole phosphatase	2.5.0	18.60	50.00
group_4105	A0A0E1R5F1	<i>eutJ</i>	Ethanolamine utilization protein eutJ	2.1.1	18.60	50.00
cobC	A0A1D2IT42	<i>cobC</i>	Alpha-ribazole phosphatase	2.5.0	81.40	50.00
group_4108	A0A0B8R7E7	<i>LmNIHS28_00778</i>	Alpha-L-fucosidase	5.2.0	18.60	50.00
fruA_9	A0A3A8BML0	<i>fruA_3</i>	PTS system fructose-specific EIIABC component	1.2.0	18.60	50.00
nagA_1	A0A3A7N225	<i>nagA_1</i>	N-acetylglucosamine-6-phosphate deacetylase (EC 3.5.1.25)	2.1.1	18.60	50.00
pduX	Q8Y7U9	<i>lmo1170</i>	Lmo1170 protein	5.2.0	81.40	50.00
cpnA	A0A3A8BW91	<i>cpnA</i>	Cyclopentanol dehydrogenase (EC 1.1.1.163)	2.1.1	18.60	50.00
group_3606	Q8Y5F8	<i>lmo2106</i>	Lmo2106 protein	5.2.0	81.40	50.00
group_3541	Q8Y8Z4	<i>lmo0748</i>	Lmo0748 protein	6.0.0	81.40	50.00
group_3977	UPI00043694BE	<i>HR60_08380</i>	Hydrolase	5.2.0	18.60	50.00
group_3978	A0A2Z5BY92	<i>RK57_04995</i>	DUF523 domain-containing protein	5.2.0	18.60	50.00
group_2127	Q8Y482	<i>lmo2573</i>	Zinc-type alcohol dehydrogenase-like protein	2.1.1	81.40	50.00
pleD	A0A3A8BW24	<i>pleD</i>	Response regulator PleD	5.2.0	81.40	50.00

argC	Q8Y6U1	<i>argC</i>	N-acetyl-gamma-glutamyl-phosphate reductase (AGPR) (EC 1.2.1.38) (N-acetyl-glutamate semialdehyde dehydrogenase) (NAGSA dehydrogenase)	2.2.0	81.40	50.00
argD	Q8Y6U4	<i>argD</i>	Acetylornithine aminotransferase (ACOAT) (EC 2.6.1.11)	2.2.0	81.40	50.00
glyS	Q8Y754	<i>glyS</i>	Glycine--tRNA ligase beta subunit (EC 6.1.1.14) (Glycyl-tRNA synthetase beta subunit) (GlyRS)	3.7.2	81.40	50.00
group_1908	A0A1D2IZW1	<i>nagA</i>	N-acetylglucosamine-6-phosphate deacetylase	2.1.1	81.40	50.00
group_3886	A0A0B8QU91	<i>LmNIHS28_00102</i>	Uncharacterized protein	6.0.0	18.60	50.00
group_4569	Q8Y6H7	<i>lmo1707</i>	UPF0435 protein lmo1707	5.2.0	81.40	50.00
group_3624	Q8Y481	<i>lmo2574</i>	Lmo2574 protein	6.0.0	81.40	50.00
bglH_3	A0A3A8C1L2	<i>bglH_2</i>	Aryl-phospho-beta-D-glucosidase BglH (EC 3.2.1.86)	2.1.1	81.40	50.00
group_4703	A0A394ZKB6	<i>inlj_1</i>	Internalin-J (LPXTG cell wall anchor domain-containing protein) (Peptidoglycan-binding protein)	1.8.0	18.60	50.00
group_4318	Q8Y3P8	<i>bvrC</i>	BvrC protein	5.2.0	81.40	50.00
group_4494	Q8Y7H5	<i>lmo1304</i>	UPF0291 protein lmo1304	5.2.0	81.40	50.00
group_4497	UPI000BDF6015		DUF1033 family protein	5.2.0	81.40	50.00
group_4496	Q8Y7A8	<i>lmo1380</i>	Lmo1380 protein	6.0.0	81.40	50.00
group_4491	Q8Y7I1	<i>lmo1297</i>	Lmo1297 protein	4.2.0	81.40	50.00
group_4492	Q8Y7H8	<i>lmo1301</i>	Lmo1301 protein	5.2.0	81.40	50.00
group_4499	A0A1D2IVP2	<i>fabG</i>	3-oxoacyl-ACP reductase (EC 1.1.1.100)	2.4.0	81.40	50.00
xylF	Q8Y5F5	<i>lmo2109</i>	Lmo2109 protein	2.1.1	81.40	50.00
ydfG	Q8Y5S9	<i>lmo1976</i>	Lmo1976 protein	2.1.1	81.40	50.00
group_2269	A0A393RX26	<i>AF264_07710</i>	Uncharacterized protein	5.2.0	18.60	50.00
group_4402	A0A0E0UTV9	<i>LMM7_0781</i>	Uncharacterized protein	6.0.0	81.40	50.00
group_4369	Q8Y9K2	<i>lmo0525</i>	Lmo0525 protein	5.2.0	81.40	50.00
miaA	Q8Y7I3	<i>miaA</i>	tRNA dimethylallyltransferase (EC 2.5.1.75) (Dimethylallyl diphosphate:tRNA dimethylallyltransferase)	3.6.0	81.40	50.00
pgcA_1	Q8Y8N1	<i>lmo0865</i>	Lmo0865 protein	2.1.1	81.40	50.00
group_4148	A0A3A7F1F5	<i>pgca_1</i>	Phospho-sugar mutase (Phosphoglucomutase) (EC 5.4.2.2)	2.1.1	18.60	50.00
group_4147	A0A2Z5C668	<i>RK57_12295</i>	TetR/AcrR family transcriptional regulator	6.0.0	18.60	50.00
group_4146	A0A393PPX4	<i>AB922_01757</i>	Uncharacterized protein	6.0.0	18.60	50.00
group_4144	A0A3A7GNS4	<i>AF264_03680</i>	Putative 3-methyladenine DNA glycosylase (EC 3.2.2.-)	3.2.0	18.60	50.00
group_1286	Q8Y945	<i>lmo0695</i>	Lmo0695 protein	6.0.0	81.40	50.00
group_4225	A0A1T1YI43	<i>DC57_13835</i>	Uncharacterized protein		18.60	50.00
group_1283	Q8Y9E3	<i>lmo0587</i>	Putative secreted protein	6.0.0	81.40	50.00
group_4223	A0A241SLD8	<i>ltrA</i>	Low temperature requirement protein A	4.1.0	18.60	50.00
group_4221	A0A0E1R4Z6	<i>BN389_04160</i>	Uncharacterized protein		18.60	50.00
group_4382	Q8Y981	<i>lmo0652</i>	Lmo0652 protein	5.2.0	81.40	50.00
group_4384	A0A1C7PWW5	<i>CDR86_13880</i>	Endonuclease III domain-containing protein	5.2.0	81.40	50.00
group_4228	A0A394ZC38	<i>AB922_00937</i>	N-acetyltransferase		18.60	50.00
dasR	Q8Y5T1	<i>lmo1974</i>	Lmo1974 protein	3.5.2	81.40	50.00

group_3083	A0A3A8BST8	<i>gloC</i>	Hydroxyacylglutathione hydrolase GloC (EC 3.1.2.6)	5.2.0	18.60	50.00
group_3461	A0A0E1R2S8	<i>BN389_04180</i>	Uncharacterized protein		18.60	50.00
group_3469	A0A394Y9C8	<i>inlJ_15</i>	Cell surface protein (Internalin-J) (LPXTG cell wall anchor domain-containing protein)	1.8.0	18.60	50.00
group_4032	UPI0009A4F8FD		alpha/beta hydrolase	2.1.1	18.60	50.00
group_4031	A0A3A8BNZ3	<i>yvbK</i>	Putative N-acetyltransferase YvbK (EC 2.3.1.-)	5.2.0	18.60	50.00
group_4037	A0A3A7D8F9	<i>AF264_09645</i>	CPBP family intramembrane metalloprotease	5.2.0	18.60	50.00
group_4036	A0A3A7GG31	<i>sdrd</i>	Cell surface protein (LPXTG cell wall anchor domain-containing protein) (Serine-aspartate repeat-containing protein D)	1.8.0	18.60	50.00
group_4035	A0A2Z5C1Q5	<i>RK57_04100</i>	FeoB-associated Cys-rich membrane protein		18.60	50.00
group_4034	A0A2Z5BZ37	<i>RK57_04110</i>	DeoR/GlpR transcriptional regulator	3.5.2	18.60	50.00
group_3936	A0A392WP35	<i>AF251_13240</i>	Bacteriocin-associated integral membrane family protein (DUF1430 domain-containing protein)	1.2.0	18.60	50.00
group_4038	A0A0B8R0U3	<i>LmNIHS28_01736</i>	TetR family transcriptional regulator		18.60	50.00
group_4136	A0A3A8C5J2	<i>ypdB</i>	Transcriptional regulatory protein YpdB	3.5.2	18.60	50.00
group_3932	A0A2Z5C1E0	<i>RK57_07485</i>	Uncharacterized protein		18.60	50.00
group_4134	A0A3A7GGN8	<i>thif</i>	Molybdopterin biosynthesis protein MoeB (Sulfur carrier protein ThiS adenylyltransferase) (EC 2.7.7.73)	2.5.0	18.60	50.00
yhaO	Q8Y554	<i>lmo2222</i>	Lmo2222 protein	5.2.0	81.40	50.00
group_3966	A0A2Z5BYS6	<i>RK57_05330</i>	Crp/Fnr family transcriptional regulator		18.60	50.00
group_1862	Q8Y9U9	<i>lmo0421</i>	Lmo0421 protein	1.7.0	81.40	50.00
group_1861	Q8YA24	<i>lmo0341</i>	Lmo0341 protein	5.2.0	81.40	50.00
group_3510	Q8YAM4	<i>lmo0094</i>	Lmo0094 protein	6.0.0	81.40	50.00
group_3513	P33383	<i>lmo0206</i>	Uncharacterized protein Lmo0206	6.0.0	81.40	50.00
fmnP	A0A3A8BXM0	<i>fmnP</i>	Riboflavin transporter	5.2.0	81.40	50.00
group_4091	B8DG24	<i>yneA</i>	Cell division suppressor protein YneA	5.2.0	18.60	50.00
dnaK_1	Q8Y7V8	<i>lmo1161</i>	Lmo1161 protein	2.1.1	81.40	50.00
group_3948	A0A1T1YKC2	<i>DC57_02040</i>	Uncharacterized protein	5.2.0	18.60	50.00
group_3949	A0A393RP85	<i>AF239_12775</i>	Acetamidase	5.2.0	18.60	50.00
group_3940	A0A3A7GBK9	<i>trpg</i>	Aminodeoxychorismate/anthranilate synthase component II (Anthranilate synthase component 2) (EC 4.1.3.27)	2.2.0	18.60	50.00
group_3947	A0A0B8R180	<i>LmNIHS28_00331</i>	Uncharacterized protein	6.0.0	18.60	50.00
group_1307	Q8Y7E2	<i>lmo1341</i>	Lmo1341 protein	1.10.0	81.40	50.00
group_5648	A0A0B8RAI5	<i>LmNIHS28_01933</i>	Cell surface protein		18.60	50.00
group_3587	A0A1D2IQ28	<i>rsgA</i>	Small ribosomal subunit biogenesis GTPase RsgA (EC 3.6.1.-)	5.2.0	81.40	50.00
group_1301	Q8Y7Z4	<i>lmo1125</i>	Lmo1125 protein	5.2.0	81.40	50.00
group_3588	Q8Y7E0	<i>lmo1343</i>	Lmo1343 protein	1.10.0	81.40	50.00
group_4599	A0A3A8BP41	<i>php_2</i>	Phosphotriesterase homology protein	2.4.0	81.40	50.00
group_4356	UPI00074D66E8	<i>LM7424_90077</i>	Uncharacterized protein	6.0.0	81.40	50.00
inlJ_11	A0A393CQT2	<i>inlj_6</i>	Cell surface protein (Internalin-J)	1.8.0	18.60	50.00
IntA	Q8Y9T5	<i>IntA</i>	Listeria nuclear targeted protein A	6.0.0	81.40	50.00

bag	A0A394ZRE6	<i>AF264_02310</i>	DUF975 domain-containing protein (DUF975 family protein)	5.2.0	18.60	50.00
crnA_2	A0A3A8BU09	<i>crnA_2</i>	Creatinine amidohydrolase (EC 3.5.2.10)	2.2.0	81.40	50.00
group_1942	UPI000CE9721B	<i>LMJF5203_01179</i>	Cell wall surface anchor protein	1.8.0	18.60	50.00
group_3887	A0A2Z5C1D2	<i>RK57_08200</i>	Crp/Fnr family transcriptional regulator	5.1.0	18.60	50.00
hisE	Q8Y9G7	<i>hisE</i>	Phosphoribosyl-ATP pyrophosphatase (PRA-PH) (EC 3.6.1.31)	2.2.0	81.40	50.00
group_3883	A0A393UMT7	<i>AB922_03025</i>	Uncharacterized protein	6.0.0	18.60	50.00
group_4670	UPI00098E7F8A		hypothetical protein		81.40	50.00
group_3881	A0A3A8BR90	<i>folK</i>	2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase (EC 2.7.6.3)	2.5.0	18.60	50.00
hisK	Q8Y9F8	<i>hisJ</i>	HisJ protein	2.2.0	81.40	50.00
group_4227	A0A2Z5C2F1	<i>RK57_09645</i>	LPXTG cell wall anchor domain-containing protein		18.60	50.00
group_1305	Q8Y7Y4	<i>lmo1135</i>	Lmo1135 protein	6.0.0	81.40	50.00
group_4079	UPI00003CABCA	<i>BN389_14870</i>	Uncharacterized protein	6.0.0	18.60	50.00
comEA	A0A3A8BUN0	<i>comEA</i>	ComE operon protein 1	1.10.0	81.40	50.00
group_4159	A0A3A7G936	<i>AF264_03075</i>	Ribonuclease P		18.60	50.00
group_4048	A0A393S206	<i>AB922_00453</i>	Thioredoxin	1.4.0	18.60	50.00
rpe_3	A0A1D2INB4	<i>rpe</i>	Ribulose-phosphate 3-epimerase	2.1.1	81.40	50.00
group_4355	Q8Y9X1	<i>lmo0397</i>	Lmo0397 protein	5.2.0	81.40	50.00
group_4578	A0A3A8BJ82	<i>azoR_2</i>	FMN-dependent NADH-azoreductase (EC 1.7.-.-)	1.4.0	81.40	50.00
group_842	Q8Y8S6	<i>lmo0818</i>	Lmo0818 protein	1.2.0	81.40	50.00
group_4078	A0A3A2NXS6	<i>comea</i>	ComE operon protein 1 (ComEA family DNA-binding protein) (Competence protein ComEA)	1.10.0	18.60	50.00
group_4077	A0A3A8BV07	<i>tylM1</i>	dTDP-3-amino-3,6-dideoxy-alpha-D-glucopyranose N,N-dimethyltransferase (EC 2.1.1.235)	5.2.0	18.60	50.00
group_4076	A0A3A8BU71	<i>iscS_2</i>	Cysteine desulfurase IscS (EC 2.8.1.7)	2.5.0	18.60	50.00
group_4074	A0A3A8BU44	<i>rne</i>	Ribonuclease E (EC 3.1.26.12)	2.3.0	18.60	50.00
group_4073	A0A241SQE4	<i>folC</i>	Folypolyglutamate synthase	2.5.0	18.60	50.00
group_4072	A0A3A8BUT3	<i>CFSAN002345_000149</i>	Uncharacterized protein	2.5.0	18.60	50.00
group_4071	Q71Z79	<i>argD</i>	Acetylornithine aminotransferase (ACOAT) (EC 2.6.1.11)	2.2.0	18.60	50.00
group_4070	Q71Z78	<i>argB</i>	Acetylglutamate kinase (EC 2.7.2.8) (N-acetyl-L-glutamate 5-phosphotransferase) (NAG kinase) (NAGK)	2.2.0	18.60	50.00
group_703	A0A3A8C0B4	<i>atpG_1</i>	ATP synthase gamma chain, sodium ion specific	1.4.0	81.40	50.00
group_4174	A0A392Y8U3	<i>AF264_02300</i>	GntR family transcriptional regulator	3.5.2	18.60	50.00
group_706	Q8YAN0	<i>lmo0087</i>	Lmo0087 protein	5.1.0	81.40	50.00
group_4170	A0A2Z5C307	<i>RK57_11240</i>	Crp/Fnr family transcriptional regulator		18.60	50.00
group_4171	A0A393D3V6	<i>AF264_02350</i>	Cell surface protein (LPXTG cell wall anchor domain-containing protein)		18.60	50.00
fgs	Q8Y6Y0	<i>folC</i>	FolC protein	2.5.0	81.40	50.00
group_4179	A0A3A7PLI4	<i>pknB</i>	Serine/threonine protein kinase (Serine/threonine-protein kinase PknB) (EC 2.7.11.1)	3.8.0	18.60	50.00

group_1137	Q8Y7E3	<i>lmo1340</i>	Lmo1340 protein	5.2.0	81.40	50.00
glcR	Q8Y5F7	<i>lmo2107</i>	Lmo2107 protein	3.5.2	81.40	50.00
group_4189	C1L0J0	<i>hisE</i>	Phosphoribosyl-ATP pyrophosphatase (PRA-PH) (EC 3.6.1.31)	2.2.0	18.60	50.00
group_4188	C1L0J4	<i>hisH</i>	Imidazole glycerol phosphate synthase subunit HisH (EC 4.3.2.10) (IGP synthase glutaminase subunit) (EC 3.5.1.2)	2.2.0	18.60	50.00
group_4400	Q8Y8Z3	<i>lmo0749</i>	Lmo0749 protein	na	81.40	50.00
group_4183	A0A3A8CAW5	<i>glpE_2</i>	Thiosulfate sulfurtransferase GlpE (EC 2.8.1.1)	4.1.0	18.60	50.00
group_4172	UPI000BE051DD		transposase		18.60	50.00
group_4181	A0A3A7TYK7	<i>speG_1</i>	N-acetyltransferase (Spermidine N(1)-acetyltransferase) (EC 2.3.1.57)	5.2.0	18.60	50.00
group_4180	A0A0B8RG88	<i>LmNIHS28_00920</i>	Uncharacterized protein	5.1.0	18.60	50.00
yxIG	Q8Y550	<i>lmo2226</i>	Lmo2226 protein	5.2.0	81.40	50.00
group_4185	A0A393RUI1	<i>AF264_01965</i>	Uncharacterized protein	6.0.0	18.60	50.00
rpiB_3	G9G5K4	<i>rpiB</i>	Ribose-5-phosphate isomerase B	2.1.1	81.40	50.00
group_3412	A0A393RT87	<i>AF264_02105</i>	Uncharacterized protein	6.0.0	18.60	50.00
polC_2	Q8Y7E7	<i>lmo1336</i>	5-formyltetrahydrofolate cyclo-ligase (EC 6.3.3.2)	2.5.0	81.40	50.00
mngB_1	A0A255C9M1	<i>CDR86_08635</i>	Alpha-mannosidase	2.1.1	81.40	50.00
group_4149	A0A393JKC4	<i>AF239_03205</i>	Uncharacterized protein	6.0.0	18.60	50.00
group_1736	Q8Y8Q6	<i>lmo0840</i>	Lmo0840 protein	5.2.0	81.40	50.00
group_3319	A0A3A2NVJ1	<i>AB922_01742</i>	Uncharacterized protein		18.60	50.00
hrtA_3	UPI00067846F2		ATP-binding cassette domain-containing protein		18.60	50.00
ecfA2	A0A0H3GF97	<i>ecfA</i>	Energy-coupling factor transporter ATP-binding protein EcfA (ECF transporter A component EcfA) (EC 3.6.3.-)	1.2.0	81.40	50.00
group_4388	Q8Y917	<i>lmo0725</i>	Putative peptidoglycan bound protein (LPXTG motif)	1.8.0	81.40	50.00
group_2380	A0A0E1R602	<i>yjaB</i>	Uncharacterized N-acetyltransferase YjaB (EC 2.3.1.-)	5.2.0	18.60	50.00
group_5075	A0A3A8B0G1	<i>levS</i>	Cell invasion LPXTG protein Vip (Levansucrase) (EC 2.4.1.10)	1.8.0	18.60	50.00
group_2577	Q8Y905	<i>lmo0737</i>	Lmo0737 protein	5.2.0	81.40	50.00
group_4301	Q8Y452	<i>lmo2603</i>	Lmo2603 protein	5.2.0	81.40	50.00
group_2208	A0A0B8RAD6	<i>LmNIHS28_01888</i>	Serine/threonine protein phosphatase	5.2.0	18.60	50.00
group_4191	A0A394Y4B3	<i>AF264_01750</i>	Transcriptional regulator	6.0.0	18.60	50.00
group_3396	A0A392Y5A5	<i>inlj_7</i>	Cell surface protein (Internalin-J) (LPXTG cell wall anchor domain-containing protein)		18.60	50.00
group_4192	A0A394ZNT3	<i>mta</i>	HTH-type transcriptional activator mta (MerR family transcriptional regulator)	3.5.2	18.60	50.00
group_4039	A0A3A8BN86	<i>ubiG</i>	Ubiquinone biosynthesis O-methyltransferase (EC 2.1.1.222)		18.60	50.00
group_4419	Q8Y8M8	<i>lmo0868</i>	Lmo0868 protein	6.0.0	81.40	50.00
group_949	A0A0E1R447	<i>manZ_2</i>	Mannose permease IID component	1.2.0	81.40	50.00
group_4415	Q8Y8Q3	<i>lmo0843</i>	Lmo0843 protein	5.2.0	81.40	50.00
group_4417	Q8Y8P6	<i>lmo0850</i>	Lmo0850 protein	6.0.0	81.40	50.00
group_4229	A0A2Z5C0J8	<i>RK57_09605</i>	Triosephosphate isomerase (EC 5.3.1.1)	2.1.2	18.60	50.00
group_4411	Q8Y8R3	<i>lmo0832</i>	Lmo0832 protein	4.4.0	81.40	50.00

group_4214	A0A2Z5C2C0	<i>RK57_09950</i>	Uncharacterized protein	6.0.0	18.60	50.00
mgIA	A0A3A8C417	<i>mgIA</i>	Galactose/methyl galactoside import ATP-binding protein MglA (EC 3.6.3.17)	1.2.0	81.40	50.00
inIJ_6	Q8Y8R0	<i>lmo0835</i>	Putative peptidoglycan bound protein (LPXTG motif)	1.8.0	81.40	50.00
group_4182	A0A3A8BWT2	<i>inIB_1</i>	Internalin B	1.8.0	18.60	50.00
kdgA	A0A2A6A934	<i>CDR86_00865</i>	Aldolase	2.1.1	81.40	50.00
group_4187	A0A1S7FNB3	<i>DC57_12750</i>	Histidinol-phosphatase	2.2.0	18.60	50.00
group_3171	A0A0E1RCR1	<i>yoZG</i>	Uncharacterized HTH-type transcriptional regulator YozG	5.2.0	18.60	50.00
yflN	Q8Y6A5	<i>lmo1790</i>	Lmo1790 protein	5.2.0	81.40	50.00
yneA	Q8Y7H6	<i>yneA</i>	Cell division suppressor protein YneA	5.2.0	81.40	50.00
cca	Q8Y5Z8	<i>cca</i>	CCA tRNA nucleotidyltransferase (EC 2.7.7.72)	3.6.0	81.40	50.00
group_3921	A0A1S7FGU9	<i>DC57_00570</i>	LD-carboxypeptidase	4.5.0	18.60	50.00
nth_2	A0A3A7HTM1	<i>nth_1</i>	Endonuclease III (EC 4.2.99.18) (Endonuclease III domain-containing protein)	5.2.0	18.60	50.00
group_4047	C1KWK5	<i>cca</i>	CCA tRNA nucleotidyltransferase (EC 2.7.7.72)	3.6.0	18.60	50.00
group_4044	A0A393CLM7	<i>AF264_09030</i>	DUF5011 domain-containing protein		18.60	50.00
group_4045	A0A0E0UXG9	<i>aroH</i>	Chorismate mutase AroH (EC 5.4.99.5)	2.2.0	18.60	50.00
group_4042	A0A2Z5BZ76	<i>RK57_03415</i>	Uncharacterized protein	5.2.0	18.60	50.00
group_4043	A0A3A8BVH1	<i>act</i>	Methanol dehydrogenase activator (EC 3.-.-.-)	5.2.0	18.60	50.00
gdh	A0A3A8BLH6	<i>gdh_2</i>	Glucose 1-dehydrogenase (EC 1.1.1.47)	2.1.1	81.40	50.00
group_3922	A0A1S7FH11	<i>cutC</i>	Copper homeostasis protein CutC	4.2.0	18.60	50.00
cssS	Q8Y857	<i>lmo1061</i>	Histidine kinase (EC 2.7.13.3)	1.3.0	81.40	50.00
group_2610	Q8Y6G4	<i>lmo1723</i>	Lmo1723 protein	6.0.0	81.40	50.00
group_3210	A0A393VWD9	<i>AB922_02198</i>	NUDIX domain-containing protein		18.60	50.00
group_3219	A0A3A2WX84	<i>cbie</i>	Cobalt-precorrin-7 (C(5))-methyltransferase (Cobalt-precorrin-7 C(5)-methyltransferase) (EC 2.1.1.289)	2.5.0	18.60	50.00
group_3981	UPI0000F53EDE	<i>ARJ20_15280</i>	GNAT family N-acetyltransferase	5.2.0	18.60	50.00
group_1492	A0A393D637	<i>AF264_11325</i>	Uncharacterized protein	6.0.0	18.60	50.00
thiN	A0A3A8BXM3	<i>thiN</i>	Thiamine pyrophosphokinase (EC 2.7.6.2)	2.5.0	81.40	50.00
nudF	Q8Y5U0	<i>lmo1965</i>	Lmo1965 protein	5.2.0	81.40	50.00
rne	Q8Y6Y8	<i>lmo1543</i>	Lmo1543 protein	2.3.0	81.40	50.00
group_4157	UPI000939B687		hypothetical protein		18.60	50.00
group_3959	A0A394ZKW3	<i>gbpa</i>	Chitin-binding protein (GlcNAc-binding protein A)	2.1.1	18.60	50.00
group_3958	A0A2Z5BYZ7	<i>RK57_05850</i>	Uncharacterized protein	6.0.0	18.60	50.00
group_2568	Q8Y9X8	<i>ltrA</i>	Low temperature requirement protein A	4.1.0	81.40	50.00
group_4487	Q8Y7L2	<i>lmo1265</i>	Lmo1265 protein	1.2.0	81.40	50.00
group_3951	A0A1T1YDG1	<i>DC57_02225</i>	Uncharacterized protein	6.0.0	18.60	50.00
group_3952	A0A3A2JZK0	<i>AF239_12415</i>	Zinc-type alcohol dehydrogenase-like protein	2.1.1	18.60	50.00
group_3957	A0A3A6WIB6	<i>AF239_12100</i>	Amidophosphoribosyltransferase (ComF family protein)	1.10.0	18.60	50.00
group_3593	Q8Y6N1	<i>lmo1653</i>	Putative cell surface protein	6.0.0	81.40	50.00
group_4466	A0A3A7HYF6	<i>DYZ90_00006</i>	Uncharacterized protein	6.0.0	81.40	50.00

group_4584	Q8Y600	<i>lmo1903</i>	Lmo1903 protein	1.4.0	81.40	50.00
phnA	Q8Y778	<i>lmo1418</i>	Lmo1418 protein	2.6.0	81.40	50.00
group_3956	A0A3A8BKJ7	<i>comFA</i>	ComF operon protein 1 (EC 3.6.4.12)	1.10.0	18.60	50.00
murQ	C1KVV7	<i>murQ</i>	N-acetylmuramic acid 6-phosphate etherase (MurNAc-6-P etherase) (EC 4.2.1.126)		18.60	50.00
group_3328	A0A394Y0E1	<i>AF264_03215</i>	Cell surface protein (LPXTG cell wall anchor domain-containing protein)	1.8.0	18.60	50.00
group_4516	Q8Y6P9	<i>lmo1635</i>	Lmo1635 protein	5.2.0	81.40	50.00
group_4517	Q8Y6P4	<i>lmo1640</i>	Lmo1640 protein	6.0.0	81.40	50.00
group_4386	A0A3A7EMK5	<i>AE233_02029</i>	Uncharacterized protein	1.8.0	81.40	50.00
rsgA_2	A0A0B8R6Z0	<i>rsgA</i>	Small ribosomal subunit biogenesis GTPase RsgA (EC 3.6.1.-)	5.2.0	18.60	50.00
azoR1_1	A0A3A8BPK0	<i>azoR1</i>	FMN-dependent NADH-azoreductase 1 (EC 1.7.-.-)	1.4.0	18.60	50.00
group_3135	A0A0E1R796	<i>yteJ</i>	Uncharacterized membrane protein yteJ	5.2.0	18.60	50.00
group_3306	A0A0B8QYA4	<i>LmNIHS28_00502</i>	Uncharacterized protein		18.60	50.00
group_4138	A0A1S7FMA8	<i>DC57_10750</i>	Uncharacterized protein	5.2.0	18.60	50.00
group_4347	Q8YA09	<i>lmo0357</i>	Lmo0357 protein	1.2.0	81.40	50.00
group_4346	Q8YA13	<i>lmo0353</i>	Lmo0353 protein	5.2.0	81.40	50.00
inlA_8	UPI00073B62EC	<i>AOB47_624c</i>	Internalin-like protein	1.8.0	81.40	50.00
group_4082	A0A2Z5C055	<i>RK57_00410</i>	DUF2975 domain-containing protein		18.60	50.00
group_4080	A0A3A2XB09	<i>glys</i>	Glycine--tRNA ligase beta subunit (EC 6.1.1.14) (Glycyl-tRNA synthetase beta subunit) (GlyRS)	3.7.2	18.60	50.00
group_4081	A0A0E0UW34	<i>LMM7_1529</i>	Putative branched-chain amino acid export protein (BAAC homeostasis)	5.2.0	18.60	50.00
group_4086	A0A0B8R1M7	<i>LmNIHS28_01991</i>	Uncharacterized protein	6.0.0	18.60	50.00
group_4087	A0A2Z5BXN3	<i>RK57_00065</i>	Type II secretion system protein	1.10.0	18.60	50.00
group_4084	A0A3A7KDD8	<i>proC_1</i>	Pyrroline-5-carboxylate reductase (EC 1.5.1.2)	2.2.0	18.60	50.00
group_4069	C1KVN8	<i>argC</i>	N-acetyl-gamma-glutamyl-phosphate reductase (AGPR) (EC 1.2.1.38)	2.2.0	18.60	50.00
group_3987	A0A3A8BPP2	<i>yxIG</i>	Putative transmembrane protein YxIG	5.2.0	18.60	50.00
group_3984	A0A3A8BNU1	<i>adaB</i>	Methylated-DNA--protein-cysteine methyltransferase, inducible (EC 2.1.1.63)	3.2.0	18.60	50.00
group_3985	UPI00086E8416		GntR family transcriptional regulator	3.5.2	18.60	50.00
group_3983	A0A0E1RA49	<i>yqjT</i>	Uncharacterized protein yqjT	5.2.0	18.60	50.00
group_3980	A0A0E1RA70	<i>yisK</i>	Uncharacterized protein yisK	5.2.0	18.60	50.00
group_4165	G9G5K0		Internalin protein	1.8.0	18.60	50.00
group_3399	A0A0E1R5P0	<i>yesJ</i>	Uncharacterized N-acetyltransferase YesJ (EC 2.3.1.-)	5.2.0	18.60	50.00
group_4166	UPI00003CA86A	<i>ARJ20_09330</i>	LPXTG cell wall anchor domain-containing protein	1.8.0	18.60	50.00
group_4161	A0A3A6WTN7	<i>ydde</i>	PhzF family phenazine biosynthesis protein (Putative isomerase Ydde) (EC 5.1.-.-)	5.2.0	18.60	50.00
group_4133	A0A0E1R4P0	<i>BN389_10880</i>	Uncharacterized protein		18.60	50.00
czcR	A0A3A8CCY3	<i>czcR</i>	Transcriptional activator protein CzcR	3.5.2	81.40	50.00

group_4169	A0A1T1YRJ7	<i>DC57_12265</i>	Carboxymuconolactone decarboxylase	5.2.0	18.60	50.00
group_3935	A0A3A7PI73	<i>AF251_13245</i>	Lactococcin 972 family bacteriocin	6.0.0	18.60	50.00
group_2864	A0A394XIB0	<i>inlj_9</i>	Cell wall anchor protein (Internalin-J) (LPXTG cell wall anchor domain-containing protein)		18.60	50.00
group_4137	A0A2Z5C2J4	<i>RK57_12860</i>	Teichoic acid D-Ala incorporation-associated protein DltX		18.60	50.00
group_3408	A0A3A7C5V3	<i>stth</i>	Cysteine hydrolase (Streptothricin hydrolase) (EC 3.5.2.19)	5.2.0	18.60	50.00
hprA	Q8Y6K0	<i>lmo1684</i>	Lmo1684 protein	2.1.1	81.40	50.00
group_1192	A0A3A8C9D9	<i>artQ_1</i>	Arginine transport system permease protein ArtQ	1.2.0	18.60	50.00
yknZ_2	A0A393R639	<i>yknZ_1</i>	ABC transporter permease (FtsX-like permease family protein) (Putative ABC transporter permease YknZ)		18.60	50.00
mta	A0A3A8CEM4	<i>mta</i>	HTH-type transcriptional activator mta	3.5.2	81.40	50.00
yusV_2	Q8Y587	<i>lmo2182</i>	Lmo2182 protein	1.2.0	81.40	50.00
group_4158	A0A3A7GM56	<i>AF264_03080</i>	Ribonuclease (EC 3.1.-.-)	5.1.0	18.60	50.00
group_4104	A0A2Z5C4F6	<i>pduM</i>	Microcompartment protein PduM	6.0.0	18.60	50.00
group_4628	Q8Y518	<i>lmo2260</i>	Lmo2260 protein	5.2.0	81.40	50.00
yvbK	Q8Y5E7	<i>lmo2117</i>	Lmo2117 protein	5.2.0	81.40	50.00
inlJ_4	A0A1D2IXY9	<i>CDR86_09540</i>	Cell surface protein	1.8.0	81.40	50.00
fabG_3	A0A3A8BVY0	<i>fabG_1</i>	3-oxoacyl-[acyl-carrier-protein] reductase FabG (EC 1.1.1.100)	2.4.0	18.60	50.00
inlJ_7	UPI000BDF441A		LPXTG cell wall anchor domain-containing protein	1.8.0	81.40	50.00
inlJ_1	Q8YAF4	<i>lmo0175</i>	Putative peptidoglycan bound protein (LPXTG motif)	1.8.0	81.40	50.00
group_4088	A0A393RS12	<i>AF264_05675</i>	Competence protein ComG	1.10.0	18.60	50.00
inlJ_8	UPI00043541E8	<i>HR60_04430</i>	Cell surface protein		18.60	50.00
group_4622	Q8Y578	<i>lmo2197</i>	Lmo2197 protein	6.0.0	81.40	50.00
group_2561	UPI000D72CB8D		IS3 family transposase	4.4.0	81.40	50.00
isdC	Q8Y585	<i>hbp1</i>	Hemin/hemoglobin-binding protein 1 (Hn/Hb-binding protein 1) (Cell wall protein Lmo2186)	1.8.0	81.40	50.00
group_4151	A0A3A8BXI7	<i>yabJ</i>	2-iminobutanoate/2-iminopropanoate deaminase (EC 3.5.99.10)	5.2.0	18.60	50.00
group_4424	A0A1D2IWW8	<i>CDR86_10445</i>	Putative 3-methyladenine DNA glycosylase (EC 3.2.2.-)	3.2.0	81.40	50.00
group_3567	Q8Y7Y2	<i>lmo1137</i>	Lmo1137 protein	6.0.0	81.40	50.00
argJ_1	Q8Y6U7	<i>lmo1584</i>	Lmo1584 protein	5.2.0	81.40	50.00
group_4335	A0A1D2J1W2	<i>CDR86_05500</i>	Internalin	1.8.0	81.40	50.00
group_4153	A0A3A7KR34	<i>inlJ_12</i>	Internalin-J (Peptidoglycan-binding protein)	1.8.0	18.60	50.00
group_4330	Q8YAN2	<i>lmo0085</i>	Lmo0085 protein	5.1.0	81.40	50.00
group_4331	Q8YAL4	<i>lmo0104</i>	Lmo0104 protein	6.0.0	81.40	50.00
uvrA_2	Q8Y4F6	<i>uvrA</i>	UvrABC system protein A (UvrA protein) (Excinuclease ABC subunit A)	3.2.0	81.40	50.00
sdrF	Q8Y5H7	<i>lmo2085</i>	Putative peptidoglycan bound protein (LPXTG motif)	1.8.0	81.40	50.00
adaB	Q8Y534	<i>lmo2242</i>	Lmo2242 protein	3.2.0	81.40	50.00
sdrD	Q8Y479	<i>lmo2576</i>	Peptidoglycan anchored protein (LPXTG motif)	1.8.0	81.40	50.00
glpE	A0A3A8C167	<i>glpE_1</i>	Thiosulfate sulfurtransferase GlpE (EC 2.8.1.1)	4.1.0	81.40	50.00

tylM1	A0A3A8BVR5	<i>tylM1</i>	dTDP-3-amino-3,6-dideoxy-alpha-D-glucopyranose N,N-dimethyltransferase (EC 2.1.1.235)	5.2.0	81.40	50.00
group_3663	UPI000CDA2F7B		hypothetical protein		2.33	21.43
group_4685	A0A393UMR2	<i>AB922_01315</i>	RNA-directed DNA polymerase (Reverse transcriptase)		2.33	21.43
group_5156	A0A393UMR0	<i>AB922_02994</i>	Uncharacterized protein		2.33	21.43
group_5829	A0A3A2NRD8	<i>D3B69_11250</i>	SLATT domain-containing protein		2.33	21.43
clpP_1	A0A0B8R8I5	<i>clpP</i>	ATP-dependent Clp protease proteolytic subunit (EC 3.4.21.92) (Endopeptidase Clp)	4.1.0	97.67	78.57
gatZ	UPI000436C1E8	<i>HR60_13125</i>	Sugar-phosphate kinase	2.1.1	97.67	78.57
group_5158	A0A393T090	<i>AF251_00420</i>	DUF1433 domain-containing protein	6.0.0	2.33	21.43
group_1772	A0A3A7DAW7	<i>yjjg_1</i>	HAD family hydrolase (Pyrimidine 5'-nucleotidase YjjG) (EC 3.1.3.5)	5.2.0	97.67	78.57
group_5119	A0A3A8BVS8	<i>CFSAN002345_001735</i>	Uncharacterized protein		2.33	21.43
group_5013	UPI00074D6A4B	<i>DLE78_04650</i>	N-acetyltransferase		2.33	21.43
group_5012	A0A3A2KHQ4	<i>AFX42_02307</i>	Uncharacterized protein		2.33	21.43
group_5010	UPI00074D6014	<i>DLE78_04630</i>	ATP-dependent Clp protease proteolytic subunit	4.1.0	2.33	21.43
group_5011	A0A393L9E6	<i>AFX42_02305</i>	Uncharacterized protein	6.0.0	2.33	21.43
group_5016	UPI000BE01261		hypothetical protein	6.0.0	2.33	21.43
group_5014	A0A3A7P6T3	<i>AFX42_02309</i>	Uncharacterized protein		2.33	21.43
group_5015	A0A3A2TJS8	<i>AFX42_02310</i>	Uncharacterized protein		2.33	21.43
group_5662	A0A3A7FE57	<i>AF947_01444</i>	Uncharacterized protein		2.33	21.43
manP_4	UPI000434E433	<i>HR60_13110</i>	PTS fructose transporter subunit IIA	1.2.0	97.67	78.57
manP_3	A0A0E1R4Q4	<i>frwC</i>	Fructose-like permease IIC component 2 (EC 2.7.1.69)	1.2.0	97.67	78.57
manP_2	A0A0E1R3Y0	<i>frwB_2</i>	Fructose-like phosphotransferase enzyme IIB component 2 (EC 2.7.1.69)	1.2.0	97.67	78.57
licR_4	A0A393DPZ5	<i>manR_2</i>	PRD domain-containing protein (Transcriptional regulator ManR)	3.5.2	97.67	78.57
group_5830	A0A3A2TSA1	<i>D3B69_11245</i>	Nucleotidyltransferase		2.33	21.43
group_2721	A0A142ECB6	<i>pA144_0059</i>	Uncharacterized protein		39.53	7.14
group_940	A0A0B8REA6	<i>LmNIHS28_00065</i>	Uncharacterized protein		39.53	7.14
group_3748	A0A142ECB7	<i>pA144_0060</i>	Uncharacterized protein		39.53	7.14
group_3773	A0A2A6A3R8	<i>CDR86_14045</i>	Uncharacterized protein		37.21	7.14
group_3771	A0A2A6A353	<i>CDR86_14020</i>	Uncharacterized protein		37.21	7.14
group_3775	A0A2A5ZJU3	<i>CDR86_14055</i>	Head-tail adaptor protein		37.21	7.14
group_3774	A0A2A5ZKW1	<i>CDR86_14050</i>	Uncharacterized protein		37.21	7.14
group_3776	A0A2A5ZK62	<i>CDR86_14085</i>	Terminase large subunit		37.21	7.14
group_5436	A0A2A6A494	<i>CDR86_14040</i>	Phage tail protein		37.21	7.14
group_2742	A0A3A7TM14	<i>AF856_01591</i>	AP2 domain-containing protein	4.3.0	37.21	7.14
group_2637	UPI00042EC15D	<i>AF237_14680</i>	PBSX family phage terminase large subunit		37.21	7.14
group_3870	A0A2A6A392	<i>CDR86_14115</i>	RNA polymerase subunit sigma		37.21	7.14
group_5452	A0A2A5ZM51	<i>CDR86_09880</i>	DUF771 domain-containing protein		37.21	7.14

group_5450	A0A3A2JSK3	<i>AF847_01777</i>	Uncharacterized protein		37.21	7.14
group_5455	A0A2A6A624	<i>CDR86_09860</i>	Uncharacterized protein		37.21	7.14
group_2724	A0A2A6A2X1	<i>CDR86_14035</i>	Uncharacterized protein		37.21	7.14
group_5438	A0A2A6A383	<i>CDR86_14065</i>	Phage major capsid protein		37.21	7.14
smc_5	A0A3A2L5G2	<i>AF249_02565</i>	Phage tail tape measure protein		37.21	7.14
group_2723	A0A2A6A314	<i>CDR86_14025</i>	Phage tail protein		37.21	7.14
group_5441	A0A2A6A2T7	<i>CDR86_14110</i>	Site-specific integrase		37.21	7.14
group_3781	A0A3A7A859	<i>AF847_01778</i>	Uncharacterized protein		37.21	7.14
group_3787	UPI000737C4C4		hypothetical protein		37.21	7.14
group_5440	A0A3A2Q1E8	<i>AF847_01796</i>	Phage portal protein		37.21	7.14
group_5437	A0A2A6A2S9	<i>CDR86_14060</i>	Uncharacterized protein		37.21	7.14
group_176	A0A3A6WMA8	<i>dape</i>	ArgE/DapE family deacylase (EC 3.5.1.18) (Succinyl-diaminopimelate desuccinylase)	2.2.0	20.93	50.00
group_4390	Q8Y916	<i>lmo0726</i>	Hypothetical CDS	6.0.0	79.07	50.00
group_1660	A0A3A8C6B9	<i>mgIA</i>	Galactose/methyl galactoside import ATP-binding protein MglA (EC 3.6.3.17)	1.2.0	20.93	50.00
group_860	Q8Y9U8	<i>lmo0422</i>	Lmo0422 protein	5.2.0	79.07	50.00
group_4658	Q8Y4U3	<i>lmo2339</i>	Lmo2339 protein	5.2.0	79.07	50.00
group_261	A0A393F884	<i>AF249_03970</i>	Cell surface protein (LPXTG cell wall anchor domain-containing protein)	1.8.0	79.07	50.00
inlA_4	A0A1D2IYS1	<i>CDR86_07930</i>	Internalin	1.8.0	79.07	50.00
group_1613	UPI000986F629	<i>D3C41_14375</i>	DEAD/DEAH box helicase	3.6.0	79.07	50.00
atpG_1	A0A3A7I128	<i>atpg_1</i>	ATP synthase gamma chain, sodium ion specific (F0F1 ATP synthase subunit gamma)	1.4.0	20.93	50.00
group_1398	A0A393D0P2	<i>aguA</i>	Putative agmatine deiminase (EC 3.5.3.12) (Agmatine iminohydrolase)	5.2.0	20.93	50.00
isdE_1	Q9EXG4	<i>fufA</i>	Heme ABC transporter substrate-binding protein IsdE (Lipoprotein)	1.2.0	79.07	50.00
group_4665	Q8Y4J5	<i>lmo2443</i>	Lmo2443 protein	6.0.0	79.07	50.00
group_761	Q8Y599	<i>lmo2170</i>	Lmo2170 protein	5.2.0	79.07	50.00
group_3112	A0A393SNY1	<i>AF264_07545</i>	Dehydrogenase	2.1.1	20.93	50.00
ogt_2	Q8Y8B2	<i>lmo0996</i>	Methylated-DNA--protein-cysteine methyltransferase (EC 2.1.1.63) (O-6-methylguanine-DNA-alkyltransferase)	3.2.0	79.07	50.00
dapE	A0A1D2IZ09	<i>CDR86_07935</i>	Succinyl-diaminopimelate desuccinylase	2.2.0	79.07	50.00
group_1653	A0A1S7FKW2	<i>DC57_08295</i>	Alkaline phosphatase family protein	2.6.0	20.93	50.00
group_239	A0A392XPZ3	<i>AF264_04535</i>	Uncharacterized protein	5.1.0	79.07	50.00
group_2013	A0A3A7BSY5	<i>inlj_16</i>	Internalin-J (LPXTG cell wall anchor domain-containing protein) (Peptidoglycan-binding protein)	1.8.0	20.93	50.00
artQ_1	A0A3A8BYD6	<i>artQ_1</i>	Arginine transport system permease protein ArtQ	1.2.0	79.07	50.00
group_3165	A0A3A7MIL3	<i>garB</i>	Glutathione amide reductase (EC 1.8.1.16) (NAD(P)/FAD-dependent oxidoreductase)	4.1.0	20.93	50.00

group_4135	A0A3A2VNJ8	<i>ogt</i>	Methylated-DNA--protein-cysteine methyltransferase (EC 2.1.1.63) (O-6-methylguanine-DNA-alkyltransferase)	3.2.0	20.93	50.00
group_1560	A0A3A8BMS5	<i>ydfG</i>	NADP-dependent 3-hydroxy acid dehydrogenase YdfG (EC 1.1.1.381)	2.1.1	20.93	50.00
group_2769	A0A1D2IW42	<i>CDR86_11860</i>	ABC transporter permease	5.2.0	79.07	50.00
group_2119	A0A241STG7	<i>cbiO</i>	Energy-coupling factor transporter ATP-binding protein EcfA (ECF transporter A component EcfA) (EC 3.6.3.-)	1.2.0	20.93	50.00
group_4593	Q8Y5W2	<i>lmo1943</i>	Lmo1943 protein	5.2.0	79.07	50.00
ywtF	A0A3A8BV30	<i>ywtF</i>	Putative transcriptional regulator YwtF	3.5.2	79.07	50.00
group_1000	A0A3A7RII6	<i>AE233_00940</i>	SMI1/KNR4 family protein	5.2.0	79.07	50.00
group_3048	Q71YB4	<i>panC</i>	Pantothenate synthetase (PS) (EC 6.3.2.1) (Pantoate--beta-alanine ligase) (Pantoate-activating enzyme)	2.5.0	20.93	50.00
fosX	Q8Y6I2	<i>fosX</i>	Fosfomycin resistance protein FosX	4.1.0	79.07	50.00
group_705	A0A2Z5C4I1	<i>RK57_08210</i>	Uncharacterized protein	5.1.0	20.93	50.00
group_1735	A0A0E0UV76	<i>LMM7_0870</i>	Putative transcriptional regulator, MarR family	5.2.0	20.93	50.00
artQ_2	Q8Y527	<i>arpJ</i>	ArpJ protein	1.2.0	79.07	50.00
ddrA	A0A0E0UUN7	<i>pduG</i>	Putative diol dehydratase-reactivating factor large subunit	2.1.1	79.07	50.00
group_1138	A0A394ZK64	<i>AF264_05670</i>	Uncharacterized protein	5.2.0	20.93	50.00
group_2575	Q8Y972	<i>lmo0661</i>	Lmo0661 protein	5.2.0	79.07	50.00
dnaX_1	A0A1D2IRD3	<i>dnaX</i>	DNA polymerase III subunit gamma/tau (EC 2.7.7.7)	3.1.0	79.07	50.00
group_4609	Q8Y5S4	<i>lmo1981</i>	Lmo1981 protein	5.2.0	79.07	50.00
topA	A0A1D2IVT6	<i>topA</i>	DNA topoisomerase 1 (EC 5.99.1.2) (DNA topoisomerase I)	3.4.0	79.07	50.00
group_2445	Q8Y9C4	<i>lmo0608</i>	Lmo0608 protein	1.2.0	79.07	50.00
group_649	A0A393CN22	<i>AF264_00975</i>	Mannosylglycerate hydrolase (EC 3.2.1.170)	2.1.1	20.93	50.00
skfE	A0A3A8BUB3	<i>skfE</i>	SkfA peptide export ATP-binding protein SkfE (EC 3.6.3.25)	1.2.0	79.07	50.00
group_4348	A0A0H3GDS2	<i>LMRG_00052</i>	Uncharacterized protein		79.07	50.00
garB	A0A3A7P5T5	<i>garB</i>	Glutathione amide reductase (EC 1.8.1.16) (NAD(P)/FAD-dependent oxidoreductase)	4.1.0	79.07	50.00
iscS_2	A0A3A8BUZ1	<i>iscS_2</i>	Cysteine desulfurase IscS (EC 2.8.1.7)	2.5.0	79.07	50.00
xseA_2	A0A0E1R607	<i>yqgN</i>	5-formyltetrahydrofolate cyclo-ligase (EC 6.3.3.2)	2.5.0	20.93	50.00
inlJ_5	A0A3A8C0G4	<i>inlJ_2</i>	Internalin-J	1.8.0	79.07	50.00
inlJ_9	Q8Y591	<i>lmo2178</i>	Putative peptidoglycan bound protein (LPXTG motif)	1.8.0	79.07	50.00
group_4336	Q8YAA5	<i>lmo0247</i>	Lmo0247 protein	6.0.0	79.07	50.00
group_1657	A0A3A8BUI8	<i>albF</i>	Putative zinc protease AlbF (EC 3.4.24.-)	2.2.0	20.93	50.00
group_251	Q8Y9P7	<i>lmo0477</i>	Putative secreted protein	5.2.0	74.42	42.86
sirC	Q8Y7X8	<i>lmo1141</i>	Lmo1141 protein	2.5.0	74.42	42.86
dhaM_1	A0A0E1R9L3	<i>dhaM</i>	PTS-dependent dihydroxyacetone kinase,phosphotransferase subunit dhaM (EC 2.7.1.-)	5.2.0	25.58	57.14
group_3681	A0A3A7KXY9	<i>AF818_02931</i>	Uncharacterized protein		25.58	0.00
group_3864	A0A3A7IJW5	<i>AB922_01480</i>	Uncharacterized protein		25.58	0.00
group_4242	A0A0B8QZ13	<i>LmNIHS28_01086</i>	Uncharacterized protein	6.0.0	74.42	100.00

¥ Non *L. monocytogenes* species

† Description for each functional category code is presented below

- [1.1.0] Cell envelope and cellular processes > Cell wall
- [1.2.0] Cell envelope and cellular processes > Transport/binding proteins and lipoproteins
- [1.3.0] Cell envelope and cellular processes > Sensors (signal transduction)
- [1.4.0] Cell envelope and cellular processes > Membrane bioenergetics
- [1.5.0] Cell envelope and cellular processes > Mobility and chemotaxis
- [1.6.0] Cell envelope and cellular processes > Protein secretion
- [1.7.0] Cell envelope and cellular processes > Cell division
- [1.8.0] Cell envelope and cellular processes > Cell surface proteins
- [1.9.0] Cell envelope and cellular processes > Soluble internalin
- [1.10.0] Cell envelope and cellular processes > Transformation/competence
- [2.1.0] Intermediary metabolism > Metabolism of carbohydrates and related molecule
- [2.1.1] Intermediary metabolism > Metabolism of carbohydrates and related molecule > Specific pathways
- [2.1.2] Intermediary metabolism > Metabolism of carbohydrates and related molecule > Main glycolytic pathways
- [2.1.3] Intermediary metabolism > Metabolism of carbohydrates and related molecule > TCA cycle
- [2.2.0] Intermediary metabolism > Metabolism of amino acids and related molecules
- [2.3.0] Intermediary metabolism > Metabolism of nucleotides and nucleic acids
- [2.4.0] Intermediary metabolism > Metabolism of lipids
- [2.5.0] Intermediary metabolism > Metabolism of coenzymes and prosthetic groups
- [2.6.0] Intermediary metabolism > Metabolism of phosphate
- [3.1.0] Information pathways > DNA replication
- [3.2.0] Information pathways > DNA restriction/modification and repair
- [3.3.0] Information pathways > DNA recombination
- [3.4.0] Information pathways > DNA packaging and segregation
- [3.5.1] Information pathways > RNA synthesis > Initiation
- [3.5.2] Information pathways > RNA synthesis > Regulation
- [3.5.3] Information pathways > RNA synthesis > Elongation
- [3.5.4] Information pathways > RNA synthesis > Termination
- [3.6.0] Information pathways > RNA modification
- [3.7.1] Information pathways > Protein synthesis > Ribosomal proteins
- [3.7.2] Information pathways > Protein synthesis > Aminoacyl-tRNA synthetases
- [3.7.3] Information pathways > Protein synthesis > Initiation
- [3.7.4] Information pathways > Protein synthesis > Elongation
- [3.7.5] Information pathways > Protein synthesis > Termination
- [3.8.0] Information pathways > Protein modification
- [3.9.0] Information pathways > Protein folding
- [4.1.0] Other functions > Adaptation to atypical conditions
- [4.2.0] Other functions > Detoxification
- [4.3.0] Other functions > Phage-related functions
- [4.4.0] Other functions > Transposon and IS

[4.5.0] Other functions > Miscellaneous

[5.1.0] Similar to unknown proteins > From Listeria

[5.2.0] Similar to unknown proteins > From other organisms

[6.0.0] No similarity

Supplementary Table 7. List of genes associated with biofilm production in BHI media supplemented with 0.85% NaCl at 10°C after pan-GWAS ($p < 0.05$).

GWAS name	Uniprot Entry	Organism ¥	Gene name	Protein names	Function al category †	% in weak biofilm formers	% in strong biofilm formers
group_5799	UPI00092FB1F5	<i>Enterococcus faecalis TX0630</i>		arsenic metallochaperone ArsD family protein		54.55	0.00
group_4197	UPI00098E3EF0			hypothetical protein		77.27	14.29
group_3762	A0A142EC64		<i>pA144_0007</i>	Uncharacterized protein		45.45	0.00
group_1807	UPI000BE00DE2			hypothetical protein		68.18	14.29
group_1810	UPI000E6BA985		<i>D3C26_06200</i>	Uncharacterized protein		40.91	0.00
group_940	A0A0B8REA6		<i>LmNIHS28_00065</i>	Uncharacterized protein		63.64	11.43
group_876	A0A1D2IYH2		<i>CDR86_08530</i>	Uncharacterized protein	6.0.0	4.55	54.29
group_5404	A0A142EC67		<i>pA144_0010</i>	Uncharacterized protein		45.45	2.86
group_3761	A0A142EC65		<i>pA144_0008</i>	Uncharacterized protein		45.45	2.86
group_5405	A0A142EC66		<i>pA144_0009</i>	Uncharacterized protein		45.45	2.86
group_6265	UPI00076722D3		<i>AXF25_01535</i>	Uncharacterized protein		36.36	0.00
bcgIA	UPI00074D58A5		<i>CJV36_12060</i>	Adenine methyltransferase		36.36	0.00
group_6263	UPI000507E686		<i>AF821_01501</i>	Uncharacterized protein		36.36	0.00
group_6279	A0A3A7NV98		<i>AFX80_00020</i>	Uncharacterized protein	4.3.0	36.36	0.00
group_6273	A0A3A7UXE8		<i>AF273_02455</i>	Uncharacterized protein		36.36	0.00
bcgIB	UPI0009850DB7		<i>CJV36_12055</i>	Uncharacterized protein		36.36	0.00
group_6271	UPI00053BE8EB		<i>DSD43_08455</i>	Uncharacterized protein		36.36	0.00
group_6276	A0A3A7EN18		<i>AFX46_00136</i>	XRE family transcriptional regulator		36.36	0.00
group_938	Q8YAG9		<i>lmo0157</i>	Lmo0157 protein	3.2.0	36.36	0.00
hsdM	A0A3A7RFF8		<i>hsdM</i>	SAM-dependent DNA methyltransferase (Type I restriction enzyme EcoKI M protein) (EC 2.1.1.72)		36.36	0.00
group_6253	UPI000BE1046E			relaxase		36.36	0.00
group_6255	E6EXY6	<i>Enterococcus faecium</i>	<i>HMPREF9511_0168</i> 3	Uncharacterized protein		36.36	0.00
group_6254	UPI00098E5223			plasmid mobilization relaxosome protein MobC		36.36	0.00
group_6256	UPI0004D69275		<i>ARJ20_16365</i>	LPXTG cell wall anchor domain-containing protein		36.36	0.00
group_6258	UPI000BE07A8C			CHAP domain-containing protein		36.36	0.00
group_3878	A0A393A2Z5		<i>DOZ93_04615</i>	XRE family transcriptional regulator		36.36	0.00
group_3876	UPI00074D51A1		<i>LM800396_140057</i>	Uncharacterized protein		36.36	0.00
group_3874	A0A0V7YCU8		<i>AOY33_09325</i>	Uncharacterized protein		36.36	0.00
group_3875	A0A3A7Q520		<i>AEZ78_00963</i>	Uncharacterized protein		36.36	0.00
group_6264	A0A0H3GD71		<i>LMRG_02934</i>	Uncharacterized protein		36.36	0.00
group_6266	A0A3A7MCD0		<i>AF821_01506</i>	Uncharacterized protein		36.36	0.00

group_6267	A0A0H3G912	<i>LMRG_02574</i>	GNAT family acetyltransferase		36.36	0.00
group_6260	Q2V4W9	<i>pCT0002</i>	Uncharacterized protein		36.36	0.00
group_6261	UPI00074D5B8B	<i>LM800396_140058</i>	Uncharacterized protein		36.36	0.00
group_6262	A0A3A7YC45	<i>AF821_01500</i>	Uncharacterized protein		36.36	0.00
group_6268	A0A3A7URE0	<i>ID87_02064</i>	Uncharacterized protein		36.36	0.00
hsdR	A0A3A7Y0A7	<i>hsdR</i>	Type I restriction endonuclease subunit R (Type-I restriction enzyme R protein) (EC 3.1.21.3)		36.36	0.00
yofA	A0A393QJ60	<i>yofA</i>	HTH-type transcriptional regulator YofA (LysR family transcriptional regulator)		36.36	0.00
group_294	UPI000BE003A6		helicase SNF2		36.36	0.00
group_3877	A0A3A7UV92	<i>ID87_02058</i>	Uncharacterized protein		36.36	0.00
group_6284	A0A0H3GFH8	<i>LMRG_02220</i>	Uncharacterized protein	6.0.0	36.36	0.00
group_6280	A0A3A7NSF4	<i>AFX80_00023</i>	Uncharacterized protein		36.36	0.00
group_6281	A0A3A7NH96	<i>AFX80_00025</i>	Uncharacterized protein		36.36	0.00
group_3873	UPI0004D8BD21	<i>ARJ20_16270</i>	Uncharacterized protein		36.36	0.00
group_6272	A0A3A7V8A6	<i>AF252_02435</i>	Sugar-phosphate nucleotidyltransferase		36.36	0.00
group_6270	UPI000678F014	<i>KO07_03320</i>	Uncharacterized protein		36.36	0.00
group_6277	A0A393A7N5	<i>DOZ93_04605</i>	Phage antirepressor		36.36	0.00
group_2760	UPI00086F2DD0		DUF1738 domain-containing protein		36.36	0.00
group_2742	A0A3A7TM14	<i>AF856_01591</i>	AP2 domain-containing protein	4.3.0	59.09	11.43
copB	UPI000E76FAAA		copper-translocating P-type ATPase		54.55	8.57
group_2752	A0A0H3GD86	<i>LMRG_02933</i>	Uncharacterized protein		40.91	2.86
group_5994	A0A0H3GDM5	<i>LMRG_00003</i>	Uncharacterized protein	6.0.0	40.91	2.86
group_3869	A0A394RPA7	<i>AF242_15480</i>	Uncharacterized protein		40.91	2.86
group_6291	UPI000BDFECA9		DUF262 domain-containing protein	5.2.0	40.91	2.86
group_3827	A0A392XHQ2	<i>pduM</i>	Microcompartment protein PduM	6.0.0	63.64	17.14
group_6269	A0A3A7V3E1	<i>immR_3</i>	HTH-type transcriptional regulator ImmR		31.82	0.00
group_295	UPI00042E7F14	<i>ARK89_15370</i>	Uncharacterized protein		31.82	0.00
group_6278	A0A393AES1	<i>DOZ93_04600</i>	Uncharacterized protein		31.82	0.00
group_5722	UPI0009853537		hypothetical protein		36.36	2.86
group_2750	A0A0H3GCJ6	<i>LMRG_02892</i>	Uncharacterized protein		36.36	2.86
group_488	A0A3A7U2K0	<i>AF856_02018</i>	Carbohydrate deacetylase (EC 3.5.1.-) (ChbG/HpnK family deacetylase)	5.2.0	36.36	2.86
group_3812	A0A2A6AA43	<i>CDR86_02440</i>	N-acetyltransferase		36.36	2.86
group_5916	A0A0H3GCIY0	<i>LMRG_02891</i>	Uncharacterized protein		36.36	2.86
group_5915	A0A0H3G8Y5	<i>LMRG_02330</i>	Uncharacterized protein	6.0.0	36.36	2.86
group_397	A0A0B8R5D0	<i>LmNIHS28_00068</i>	Uncharacterized protein	5.1.0	63.64	97.14
group_6074	A0A3A7NHD5	<i>AFX80_00024</i>	Uncharacterized protein		36.36	2.86
group_1884	UPI000E718624		hypothetical protein	5.2.0	36.36	2.86
group_3841	UPI000E6B9871		hypothetical protein		36.36	2.86

group_6011	A0A3A7NYZ5	<i>Xanthomonas citri</i>	<i>AFX80_00022</i>	Uncharacterized protein		36.36	2.86
group_6283	A0A393KIZ1		<i>AFX44_02360</i>	Uncharacterized protein		36.36	2.86
group_6240	A0A2H1SK93		<i>C</i>	C protein		36.36	2.86
group_194	A0A394YAU8		<i>AF255_15365</i>	Uncharacterized protein		90.91	48.57
npr	UPI000D735513			oxidoreductase		63.64	20.00
group_1990	A0A3A7UE98		<i>AF951_02473</i>	Uncharacterized protein		40.91	5.71
group_2751	UPI0000F3E668		<i>LMRG_00004</i>	Uncharacterized protein	6.0.0	40.91	5.71
group_3681	A0A3A7KXY9		<i>AF818_02931</i>	Uncharacterized protein		40.91	5.71
znuC_4	A0A3A7NPD6		<i>znuC_2</i>	ABC transporter ATP-binding protein (Zinc import ATP-binding protein ZnuC) (EC 3.6.3.-)		40.91	5.71
group_6068	A0A3A7VX21		<i>AF951_02474</i>	Uncharacterized protein		40.91	5.71
group_3850	A0A0H3GHG8	<i>Acidithiobacillus ferrivorans</i>	<i>LMRG_00005</i>	Uncharacterized protein		40.91	5.71
group_3864	A0A3A7IJW5		<i>AB922_01480</i>	Uncharacterized protein		40.91	5.71
hin_1	A0A1D2IUR0		<i>CDR86_15065</i>	Transposon DNA-invertase		50.00	11.43
parC	A0A3A7I7R9		<i>parc</i>	DNA topoisomerase 4 subunit A (EC 5.99.1.3) (Topoisomerase IV subunit A)	3.4.0	72.73	100.00
group_1672	A0A0H3GJX6		<i>parC</i>	DNA topoisomerase 4 subunit A (EC 5.99.1.3) (Topoisomerase IV subunit A)	3.4.0	27.27	0.00
group_846	A0A0B8R577		<i>hflX</i>	GTPase HflX (GTP-binding protein HflX)	4.5.0	27.27	0.00
tkf_3	A0A0D8X574		<i>CDR86_05070</i>	Uncharacterized protein	5.2.0	27.27	0.00
group_1811	A0A393U2U6		<i>codB</i>	Cytosine permease	1.2.0	54.55	14.29
group_4897	A0A0H3GA10		<i>LMRG_02887</i>	Uncharacterized protein		54.55	14.29
group_4896	A0A0H3GHU1		<i>LMRG_00151</i>	Uncharacterized protein		54.55	14.29
group_4470	A0A1D2IWI5	<i>Acidithiobacillus ferrivorans</i>	<i>pduM</i>	Microcompartment protein PduM	6.0.0	13.64	54.29
group_229	Q8Y9Q9		<i>lmo0464</i>	Lmo0464 protein	4.4.0	27.27	68.57
group_2757	A0A060UT12		<i>F</i>	Capsid protein F		31.82	2.86
group_487	A0A3A7GDL7		<i>AF264_00475</i>	Carbohydrate deacetylase (EC 3.5.1.-) (ChbG/HpnK family deacetylase)	5.2.0	68.18	97.14
group_6243	A0A060US63		<i>G</i>	Major spike protein G		31.82	2.86
mco	UPI000A1FFD33			copper oxidase		31.82	2.86
group_151	C1KYJ3		<i>rpoB</i>	DNA-directed RNA polymerase subunit beta (RNAP subunit beta) (EC 2.7.7.6)	3.5.3	31.82	2.86
group_1969	A0A0E0V124		<i>gidA</i>	tRNA uridine 5-carboxymethylaminomethyl modification enzyme MnmG (Glucose-inhibited division protein A)	1.7.0	59.09	20.00
gbuC_1	A0A142ECE5		<i>CDR86_15760</i>	Glycine betaine ABC transporter glycine betaine-binding protein (Glycine/betaine ABC transporter substrate-binding protein)		59.09	20.00

group_2545	UPI000BDFF9DB		hypothetical protein		59.09	20.00
group_377	UPI00074D6BC6	<i>LM83088_80034</i>	Uncharacterized protein	5.2.0	63.64	22.86
group_3519	Q8YA40	<i>lmo0324</i>	Lmo0324 protein	6.0.0	0.00	28.57
group_2657	A0A2Z5C560	<i>RK57_09450</i>	Endonuclease	5.2.0	0.00	28.57
group_2556	Q8YAP6	<i>lmo0071</i>	Lmo0071 protein	6.0.0	4.55	37.14
group_1843	A0A1S7FP06	<i>DC57_14095</i>	6-phospho-beta-glucosidase	2.1.1	77.27	37.14
codB	A0A3A7YB48	<i>codB</i>	Cytosine permease	1.2.0	50.00	85.71
group_1346	A0A3A7FZC8	<i>AF951_02536</i>	Uncharacterized protein		50.00	14.29
group_1144	A0A0E1RCC6	<i>yneQ</i>	Uncharacterized protein yneQ	5.2.0	77.27	100.00
group_1241	Q723T1	<i>iolA</i>	Malonate-semialdehyde dehydrogenase (MSA dehydrogenase) (EC 1.2.1.27)	2.1.1	22.73	0.00
hflX_1	Q8Y8Y0	<i>hflX</i>	GTPase HflX (GTP-binding protein HflX)	4.5.0	77.27	100.00
group_401	A0A394XJ12	<i>AF264_14015</i>	Uncharacterized protein		40.91	8.57
group_3733	A0A393N9I6	<i>D3C41_12950</i>	Uncharacterized protein		40.91	8.57
group_3700	UPI000984B87F		hypothetical protein		40.91	8.57
group_3858	A0A0H3GDJ9	<i>LMRG_02591</i>	Uncharacterized protein		40.91	8.57
group_6040	A0A3A7RS18	<i>AF818_02929</i>	Uncharacterized protein		40.91	8.57
group_2721	A0A142ECB6	<i>pA144_0059</i>	Uncharacterized protein		54.55	17.14
group_3748	A0A142ECB7	<i>pA144_0060</i>	Uncharacterized protein		54.55	17.14
group_3040	A0A3A7GE33	<i>AF264_08870</i>	Glycoside transferase	5.2.0	90.91	57.14
group_4590	Q8Y5Z0	<i>lmo1913</i>	Lmo1913 protein	5.2.0	9.09	42.86
group_6039	A0A393Q6N1	<i>AF951_01447</i>	Uncharacterized protein		36.36	5.71
group_3810	UPI000679072E		DUF4352 domain-containing protein		36.36	5.71
gltR_1	A0A0B8QZ17	<i>LmNIHS28_01096</i>	LysR family transcriptional regulator	3.5.2	63.64	94.29
group_4677	A0A393QPI9	<i>AF238_05485</i>	VRR-NUC domain-containing protein		36.36	5.71
nfrA1_1	A0A3A7H264	<i>nfrA1_2</i>	FMN reductase (NADPH) (EC 1.5.1.38) (NADPH-dependent oxidoreductase)	1.4.0	63.64	94.29
group_3705	A0A3A7DYA1	<i>AF249_03765</i>	DUF1541 domain-containing protein		36.36	5.71
group_4329	Q8YAN5	<i>lmo0082</i>	Lmo0082 protein	6.0.0	0.00	25.71
group_4328	Q8YAN7	<i>lmo0080</i>	Lmo0080 protein	6.0.0	0.00	25.71
group_2557	UPI0009B0B9A0		hypothetical protein	6.0.0	0.00	25.71
group_5655	UPI000BE0F385		hypothetical protein		45.45	11.43
group_2040	A0A3A7F101	<i>AF264_14455</i>	Ribonuclease (EC 3.1.-.-)	5.2.0	45.45	80.00
mmnG	A0A0E0V124	<i>gidA</i>	tRNA uridine 5-carboxymethylaminomethyl modification enzyme MnmG (Glucose-inhibited division protein A)	1.7.0	45.45	80.00
group_474	A0A393CRL8	<i>AF264_01650</i>	Putative sulfate transporter (SulP family inorganic anion transporter)	1.2.0	54.55	20.00
zosA_1	T1YRD8	<i>cada</i>	Heavy metal translocating P-type ATPase (Heavy metal-transporting ATPase Pli0048-like protein)		54.55	20.00
group_14	A0A0F5Z6U3	<i>UQ68_03245</i>	Holin	4.3.0	27.27	2.86

group_6242	A0A2I2M4I9	<i>Tenacibaculum dicentrarchi</i>	<i>J</i>	DNA-binding protein J		27.27	2.86
group_3871	A0A060UXK7	<i>Acidithiobacillus ferrivorans</i>	<i>H</i>	Minor spike protein H		27.27	2.86
nifS	Q8Y5N5		<i>lmo2022</i>	Lmo2022 protein	2.5.0	18.18	54.29
group_3446	A0A394Y6J8		<i>AF243_01275</i>	Uncharacterized protein	6.0.0	36.36	71.43
group_5435	A0A3A2KJM7		<i>AF255_07855</i>	Uncharacterized protein		45.45	14.29
group_1977	A0A3A7MNP5		<i>ssbA_1</i>	Single-stranded DNA-binding protein (SSB)	3.1.0	45.45	14.29
group_5443	A0A2A6A333		<i>CDR86_14125</i>	Uncharacterized protein		45.45	14.29
group_5442	A0A2A6A373		<i>CDR86_14120</i>	Uncharacterized protein		45.45	14.29
group_3806	A0A3A2LE02		<i>AEZ78_01356</i>	Uncharacterized protein		45.45	14.29
group_94	UPI00083E5C54		<i>AF252_11575</i>	Class I SAM-dependent methyltransferase (Fragment)		45.45	14.29
group_3778	A0A2A6A3S0		<i>CDR86_14100</i>	Uncharacterized protein		45.45	14.29
group_3769	UPI000984CE83			hypothetical protein		45.45	14.29
group_3779	A0A3A2R2K3		<i>AF847_01792</i>	Uncharacterized protein		45.45	14.29
group_3636	A0A3A2YAK1		<i>cas5b</i>	Type I-B CRISPR-associated protein Cas5		27.27	62.86
group_1963	UPI00098E7CD3			superoxide dismutase	6.0.0	72.73	37.14
cas1	UPI00092E4084		<i>B0X19_02870</i>	CRISPR-associated endonuclease Cas1		27.27	62.86
cas3	UPI00083D7946			CRISPR-associated helicase/endonuclease Cas3		27.27	62.86
group_1845	Q9EXF8		<i>bglA</i>	Beta-glucosidase (EC 3.2.1.21) (Glycoside hydrolase family 1 protein)	2.1.1	27.27	62.86
cas2	A0A0E0UTU7		<i>cas2</i>	CRISPR-associated endoribonuclease Cas2 (EC 3.1.-.-)		27.27	62.86
group_2659	A0A3A7SZG9		<i>cas6</i>	CRISPR-associated endoribonuclease Cas6		27.27	62.86
group_1422	A0A3A2RW22		<i>AF251_13400</i>	DUF1310 domain-containing protein (DUF1310 family protein)	5.1.0	22.73	57.14
group_1374	UPI000990612F			hypothetical protein	6.0.0	77.27	42.86
group_1855	UPI000BDFDF92			DUF1310 family protein	5.1.0	9.09	40.00
group_7000	A0A2Z5Z219	<i>Lactococcus lactis</i>	<i>E05_32090</i>	Uncharacterized protein		9.09	40.00
group_3809	A0A3A7AEP5		<i>DYZ48_00767</i>	Uncharacterized protein		36.36	8.57
group_307	UPI00027E8422		<i>D3B99_03045</i>	Uncharacterized protein		36.36	8.57
group_3773	A0A2A6A3R8		<i>CDR86_14045</i>	Uncharacterized protein		50.00	17.14
group_5438	A0A2A6A383		<i>CDR86_14065</i>	Phage major capsid protein		50.00	17.14
group_5436	A0A2A6A494		<i>CDR86_14040</i>	Phage tail protein		50.00	17.14
group_5437	A0A2A6A2S9		<i>CDR86_14060</i>	Uncharacterized protein		50.00	17.14
group_5450	A0A3A2JSK3		<i>AF847_01777</i>	Uncharacterized protein		50.00	17.14
group_2743	A0A3A2VA08		<i>D3B30_06385</i>	Cysteine desulfurase	2.5.0	50.00	17.14
group_5441	A0A2A6A2T7		<i>CDR86_14110</i>	Site-specific integrase		50.00	17.14
group_5440	A0A3A2Q1E8		<i>AF847_01796</i>	Phage portal protein		50.00	17.14
group_2732	A0A393U4Y6		<i>AF255_14330</i>	DUF2974 domain-containing protein	6.0.0	50.00	17.14

group_2724	A0A2A6A2X1	<i>CDR86_14035</i>	Uncharacterized protein		50.00	17.14
group_3870	A0A2A6A392	<i>CDR86_14115</i>	RNA polymerase subunit sigma		50.00	17.14
group_3781	A0A3A7A859	<i>AF847_01778</i>	Uncharacterized protein		50.00	17.14
smc_5	A0A3A2L5G2	<i>AF249_02565</i>	Phage tail tape measure protein		50.00	17.14
group_3776	A0A2A5ZK62	<i>CDR86_14085</i>	Terminase large subunit		50.00	17.14
group_3771	A0A2A6A353	<i>CDR86_14020</i>	Uncharacterized protein		50.00	17.14
group_1980	A0A392WP24	<i>AF255_14340</i>	DUF1310 domain-containing protein (DUF1310 family protein)	5.1.0	50.00	17.14
group_3775	A0A2A5ZJU3	<i>CDR86_14055</i>	Head-tail adaptor protein		50.00	17.14
group_3774	A0A2A5ZKW1	<i>CDR86_14050</i>	Uncharacterized protein		50.00	17.14
group_2723	A0A2A6A314	<i>CDR86_14025</i>	Phage tail protein		50.00	17.14
group_5515	UPI000BE047C1		DUF1310 family protein	5.1.0	50.00	17.14
group_5452	A0A2A5ZM51	<i>CDR86_09880</i>	DUF771 domain-containing protein		50.00	17.14
group_5455	A0A2A6A624	<i>CDR86_09860</i>	Uncharacterized protein		50.00	17.14
group_2698	A0A3A2JNT0	<i>D3C46_16425</i>	Uncharacterized protein		50.00	17.14
group_893	Q8Y802	<i>lmo1117</i>	Lmo1117 protein	6.0.0	68.18	34.29
group_1233	A0A0B8R4N6	<i>LmNIHS28_01797</i>	Uncharacterized protein	6.0.0	68.18	34.29
group_51	A0A393IDA4	<i>DN830_06205</i>	LPXTG cell wall anchor domain-containing protein	6.0.0	0.00	22.86
group_4200	A0A3A2WRU5	<i>AF241_01120</i>	Uncharacterized protein		18.18	0.00
group_4201	UPI00098E5B68	<i>DOV17_10730</i>	Uncharacterized protein		18.18	0.00
group_4202	A0A0B8RHX0	<i>LmNIHS28_01805</i>	Uncharacterized protein		18.18	0.00
group_4203	A0A0B8R119	<i>LmNIHS28_01806</i>	Uncharacterized protein		18.18	0.00
group_4204	A0A0B8RAJ2	<i>LmNIHS28_01807</i>	Uncharacterized protein		18.18	0.00
group_4205	A0A0B8RA54	<i>LmNIHS28_01808</i>	Uncharacterized protein		18.18	0.00
group_4206	UPI000873BE8A		hypothetical protein		18.18	0.00
araQ_4	Q8Y8X5	<i>lmo0767</i>	Lmo0767 protein	1.2.0	81.82	100.00
group_4199	A0A0B8RG01	<i>LmNIHS28_01804</i>	Uncharacterized protein		18.18	0.00
group_4211	A0A0B8QZH0	<i>LmNIHS28_01814</i>	Uncharacterized protein		18.18	0.00
group_4210	A0A0B8RA58	<i>LmNIHS28_01813</i>	Uncharacterized protein		18.18	0.00
ugpB	Q8Y8X4	<i>lmo0768</i>	Lmo0768 protein	1.2.0	81.82	100.00
group_4207	A0A0B8RHX3	<i>LmNIHS28_01810</i>	Membrane protein		18.18	0.00
araR	A0A3A8C7S0	<i>araR</i>	Arabinose metabolism transcriptional repressor	3.5.2	81.82	100.00
group_1809	UPI00073B1B95	<i>AN945_2724c</i>	Uncharacterized protein		18.18	0.00
group_2489	UPI000254880C	<i>AJZ74_11435</i>	PBS lyase		18.18	0.00
group_3545	A0A3A7QRH6	<i>AF249_03255</i>	Glycoside hydrolase family 125 protein	5.2.0	81.82	100.00
group_6259	UPI000B8EE202		hypothetical protein		18.18	0.00
group_3549	Q8Y8X1	<i>lmo0771</i>	Lmo0771 protein	6.0.0	81.82	100.00
group_4163	A0A0E0UTX3	<i>LMM7_0796</i>	Uncharacterized protein	6.0.0	18.18	0.00
ugpA	A0A3A8CAJ6	<i>ugpA</i>	sn-glycerol-3-phosphate transport system permease protein UgpA	1.2.0	81.82	100.00
iolA	A0A1D2IYM0	<i>mmsA</i>	Malonate-semialdehyde dehydrogenase (MSA dehydrogenase) (EC 1.2.1.27)	2.1.1	81.82	100.00
group_4208	A0A394XPH6	<i>AF241_01080</i>	Uncharacterized protein		18.18	0.00

group_1214	UPI000E72BE72	<i>AFX66_02803</i>	Uncharacterized protein	6.0.0	18.18	0.00
group_4209	A0A0B8R4P7	<i>LmNIHS28_01812</i>	Uncharacterized protein		18.18	0.00
lptB	A0A3A7JHL1	<i>natA_1</i>	ABC transporter ATP-binding protein NatA (ATP-binding cassette domain-containing protein) (DUF4162 domain-containing protein)	1.2.0	81.82	100.00
group_1873	Q8Y8X3	<i>lmo0769</i>	Lmo0769 protein	2.1.1	81.82	100.00
group_609	A0A1S7FLU5	<i>DC57_10100</i>	Uncharacterized protein	6.0.0	95.45	68.57
group_1332	UPI00057F741C	<i>OJ14_05160</i>	Uncharacterized protein		40.91	11.43
group_1987	A0A394RZ82	<i>AF240_05480</i>	Uncharacterized protein		40.91	11.43
group_3528	Q8Y9P6	<i>lmo0478</i>	Putative secreted protein	5.2.0	54.55	22.86
group_3917	A0A0H3G8X1	<i>LMRG_02492</i>	Uncharacterized protein		50.00	20.00
group_2056	A0A3A6WUY8	<i>AF251_14005</i>	Uncharacterized protein		50.00	20.00
group_4273	UPI0008759A67		XRE family transcriptional regulator		59.09	25.71
group_2656	UPI000766639A	<i>ERS409650_01636</i>	Uncharacterized protein		59.09	25.71
group_1260	S5XI65		Transposase Pli0049		22.73	2.86
group_692	A0A3A7SVH6	<i>AFX76_01934</i>	Transcriptional regulator		22.73	2.86
group_396	UPI00086EB4E1		hypothetical protein		77.27	45.71
group_2560	UPI000BE05954		hypothetical protein	5.1.0	22.73	54.29
group_312	UPI00083CE8C5		DNA primase		63.64	31.43
group_1232	A0A0B8R4N6	<i>LmNIHS28_01797</i>	Uncharacterized protein	6.0.0	36.36	68.57
group_1343	A0A394ZJX3	<i>AF243_05235</i>	DNA-binding protein		63.64	31.43
group_4686	A0A393MBE2	<i>cas7i</i>	Type I-B CRISPR-associated protein Cas7/Cst2/DevR		27.27	60.00
group_2660	A0A3A7IMJ8	<i>cas8a1</i>	Type I-B CRISPR-associated protein Cas8b1/Cst1		27.27	60.00
group_2547	Q8Y403	<i>lmo2675</i>	Lmo2675 protein	6.0.0	40.91	71.43
group_1933	A0A3A2P3J3	<i>D3B70_02255</i>	Phage tail protein		59.09	28.57
ibpA	A0A1B2LR36	<i>pLM-C-273_00100</i>	Protein involved in cell division		59.09	28.57
group_2195	A0A393SL84	<i>coia</i>	Competence protein CoiA	1.10.0	59.09	28.57
group_1396	A0A0H3GGU0	<i>LMRG_02850</i>	Uncharacterized protein		90.91	62.86
group_2729	A0A392X2X8	<i>AF238_14485</i>	Uncharacterized protein		9.09	37.14
group_3915	A0A0H3G8X6	<i>LMRG_02849</i>	Uncharacterized protein		90.91	62.86
group_2684	A0A393U116	<i>AF273_04990</i>	XRE family transcriptional regulator		9.09	37.14
group_3822	A0A3A2WJJ9	<i>AE233_01825</i>	SMI1/KNR4 family protein		40.91	14.29
inIJ_13	UPI00098DF5C5		hypothetical protein	1.8.0	59.09	85.71
group_3679	UPI00074D6382	<i>CJV36_07565</i>	Uncharacterized protein		40.91	14.29
group_2474	UPI000D72D1E5		DHA2 family efflux MFS transporter permease subunit	1.2.0	68.18	37.14
group_1423	A0A393L0Q4	<i>AF264_13385</i>	DUF1310 domain-containing protein (DUF1310 family protein)	5.1.0	31.82	62.86
dinB_3	D7PCE7		Putative DNA-directed DNA polymerase		72.73	42.86
group_2567	Q7AP83	<i>lmo0320</i>	Lmo0320 protein	1.8.0	27.27	57.14
Int-Tn	A0A2A6A695	<i>CDR86_09855</i>	Site-specific integrase		45.45	17.14
group_5439	A0A2A5ZKF2	<i>CDR86_14070</i>	HK97 family phage prohead protease		45.45	17.14
group_1497	A0A1D2IPP6	<i>CDR86_15840</i>	Uncharacterized protein		45.45	17.14
group_3616	A0A3A7VZK0	<i>AF947_03065</i>	DUF1642 domain-containing protein	4.3.0	45.45	17.14

group_1837	A0A241SLH2	<i>tkt</i>	Transketolase (EC 2.2.1.1)	2.1.2	45.45	17.14
smc_3	A0A393FGI0	<i>D3B68_15130</i>	Phage tail tape measure protein		45.45	17.14
group_3777	A0A2A5ZK31	<i>CDR86_14090</i>	Phage terminase small subunit P27 family		45.45	17.14
group_2697	A0A3A7Q910	<i>AF818_02415</i>	Uncharacterized protein		45.45	17.14
group_4230	A0A1S7FP22	<i>DC57_13960</i>	Uncharacterized protein		45.45	17.14
group_13	A0A0H3GF06	<i>LMRG_01553</i>	Phage holin	4.3.0	31.82	8.57
group_3527	UPI000E751432		hypothetical protein		0.00	20.00
group_4377	UPI00076678C4	<i>ERS409627_00120</i>	Preprotein translocase subunit SecB		0.00	20.00
group_4379	A0A1D2INM9	<i>CDR86_13980</i>	Uncharacterized protein		0.00	20.00
group_4378	Q8Y995	<i>lmo0638</i>	Lmo0638 protein	6.0.0	0.00	20.00
draG	Q8YAQ0	<i>lmo0067</i>	Lmo0067 protein	3.8.0	0.00	20.00
group_143	A0A3A2J7V9	<i>AF247_01180</i>	BspA family leucine-rich repeat surface protein	1.8.0	4.55	28.57
group_877	UPI000D65622D	<i>DF271_11275</i>	Uncharacterized protein (Fragment)	6.0.0	4.55	28.57
group_3647	A0A393KDI4	<i>AF247_14610</i>	Uncharacterized protein		4.55	28.57
group_3691	A0A3A2TPS8	<i>D3B72_03010</i>	DUF4274 domain-containing protein		4.55	28.57
group_697	A0A1T1YBY4	<i>DC57_15090</i>	Type VII secretion effector	5.1.0	86.36	60.00
group_2559	UPI000B54942D		DUF3130 family protein	5.1.0	13.64	40.00
group_2658	A0A2Z5C293	<i>RK57_09780</i>	Uncharacterized protein	6.0.0	13.64	40.00
group_2664	A0A392YE54	<i>AF247_14605</i>	Uncharacterized protein		13.64	40.00
group_1313	A0A3A7QYQ0	<i>AF249_11635</i>	Uncharacterized protein		36.36	11.43
group_4802	A0A0H3GNH6	<i>LMRG_02134</i>	Uncharacterized protein	6.0.0	36.36	11.43
group_920	A0A3A2NXX2	<i>D3B69_00475</i>	LPXTG cell wall anchor domain-containing protein		50.00	22.86
group_2648	A0A394T3U8	<i>AF252_05595</i>	DUF669 domain-containing protein		50.00	22.86
group_3626	A0A3A2TXX4	<i>AF238_05490</i>	Uncharacterized protein		50.00	22.86
group_3916	A0A3A7D3S5	<i>AF251_14010</i>	Uncharacterized protein		50.00	22.86
group_80	Q8YAQ1	<i>lmo0066</i>	Lmo0066 protein	4.5.0	18.18	45.71
group_241	A0A393CUH9	<i>AF264_04515</i>	DUF3130 family protein (TIGR04197 family type VII secretion effector)		81.82	54.29
group_679	A0A393MQP5	<i>AF237_14490</i>	Phage head-tail adapter protein		54.55	25.71
group_2655	UPI00070C5611		hypothetical protein		54.55	25.71
group_4274	A0A142EC60	<i>pA144_0003</i>	Uncharacterized protein		54.55	25.71
group_3633	UPI00074D6868	<i>LM801457_60030</i>	Phage protein		54.55	25.71
group_1932	A0A393D0P3	<i>AF261_15130</i>	Phage major capsid protein		54.55	25.71
group_681	A0A394U433	<i>AF237_14485</i>	Uncharacterized protein		54.55	25.71
group_4678	UPI00074D6276	<i>LM7423_400013</i>	Uncharacterized protein		54.55	25.71

‡ Non *L. monocytogenes* species

† Description for each functional category code is presented below

[1.1.0] Cell envelope and cellular processes > Cell wall

[1.2.0] Cell envelope and cellular processes > Transport/binding proteins and lipoproteins

[1.3.0] Cell envelope and cellular processes > Sensors (signal transduction)

[1.4.0] Cell envelope and cellular processes > Membrane bioenergetics

- [1.5.0] Cell envelope and cellular processes > Mobility and chemotaxis
- [1.6.0] Cell envelope and cellular processes > Protein secretion
- [1.7.0] Cell envelope and cellular processes > Cell division
- [1.8.0] Cell envelope and cellular processes > Cell surface proteins
- [1.9.0] Cell envelope and cellular processes > Soluble internalin
- [1.10.0] Cell envelope and cellular processes > Transformation/competence
- [2.1.0] Intermediary metabolism > Metabolism of carbohydrates and related molecule
- [2.1.1] Intermediary metabolism > Metabolism of carbohydrates and related molecule > Specific pathways
- [2.1.2] Intermediary metabolism > Metabolism of carbohydrates and related molecule > Main glycolytic pathways
- [2.1.3] Intermediary metabolism > Metabolism of carbohydrates and related molecule > TCA cycle
- [2.2.0] Intermediary metabolism > Metabolism of amino acids and related molecules
- [2.3.0] Intermediary metabolism > Metabolism of nucleotides and nucleic acids
- [2.4.0] Intermediary metabolism > Metabolism of lipids
- [2.5.0] Intermediary metabolism > Metabolism of coenzymes and prosthetic groups
- [2.6.0] Intermediary metabolism > Metabolism of phosphate
- [3.1.0] Information pathways > DNA replication
- [3.2.0] Information pathways > DNA restriction/modification and repair
- [3.3.0] Information pathways > DNA recombination
- [3.4.0] Information pathways > DNA packaging and segregation
- [3.5.1] Information pathways > RNA synthesis > Initiation
- [3.5.2] Information pathways > RNA synthesis > Regulation
- [3.5.3] Information pathways > RNA synthesis > Elongation
- [3.5.4] Information pathways > RNA synthesis > Termination
- [3.6.0] Information pathways > RNA modification
- [3.7.1] Information pathways > Protein synthesis > Ribosomal proteins
- [3.7.2] Information pathways > Protein synthesis > Aminoacyl-tRNA synthetases
- [3.7.3] Information pathways > Protein synthesis > Initiation
- [3.7.4] Information pathways > Protein synthesis > Elongation
- [3.7.5] Information pathways > Protein synthesis > Termination
- [3.8.0] Information pathways > Protein modification
- [3.9.0] Information pathways > Protein folding
- [4.1.0] Other functions > Adaptation to atypical conditions
- [4.2.0] Other functions > Detoxification
- [4.3.0] Other functions > Phage-related functions
- [4.4.0] Other functions > Transposon and IS
- [4.5.0] Other functions > Miscellaneous
- [5.1.0] Similar to unknown proteins > From *Listeria*
- [5.2.0] Similar to unknown proteins > From other organisms
- [6.0.0] No similarity

Supplementary Table 8. List of genes associated with biofilm production in dBHI media supplemented with 0.85% NaCl at 10°C after pan-GWAS (p < 0.05).

GWAS name	Uniprot Entry	Organism ¥	Gene name	Protein names	Function al category †	% in weak biofilm formers	% in strong biofilm formers
group_1915	A0A394U8V3		<i>AF237_14705</i>	Uncharacterized protein		35.71	2.33
group_4208	A0A394XPH6		<i>AF241_01080</i>	Uncharacterized protein		28.57	0.00
group_4209	A0A0B8R4P7		<i>LmNIHS28_01812</i>	Uncharacterized protein		28.57	0.00
group_4200	A0A3A2WRU5		<i>AF241_01120</i>	Uncharacterized protein		28.57	0.00
group_4201	UPI00098E5B68		<i>DOV17_10730</i>	Uncharacterized protein		28.57	0.00
group_4202	A0A0B8RHX0		<i>LmNIHS28_01805</i>	Uncharacterized protein		28.57	0.00
group_4203	A0A0B8R119		<i>LmNIHS28_01806</i>	Uncharacterized protein		28.57	0.00
group_4204	A0A0B8RAJ2		<i>LmNIHS28_01807</i>	Uncharacterized protein		28.57	0.00
group_4205	A0A0B8RA54		<i>LmNIHS28_01808</i>	Uncharacterized protein		28.57	0.00
group_4206	UPI000873BE8A			hypothetical protein		28.57	0.00
group_4207	A0A0B8RHX3		<i>LmNIHS28_01810</i>	Membrane protein		28.57	0.00
group_3545	A0A3A7QRH6		<i>AF249_03255</i>	Glycoside hydrolase family 125 protein	5.2.0	71.43	100.00
group_4163	A0A0E0UTX3		<i>LMM7_0796</i>	Uncharacterized protein	6.0.0	28.57	0.00
group_4210	A0A0B8RA58		<i>LmNIHS28_01813</i>	Uncharacterized protein		28.57	0.00
group_3549	Q8Y8X1		<i>lmo0771</i>	Lmo0771 protein	6.0.0	71.43	100.00
group_2489	UPI000254880C		<i>AJZ74_11435</i>	PBS lyase		28.57	0.00
iolA	A0A1D2IYM0		<i>mmsA</i>	Malonate-semialdehyde dehydrogenase (MSA dehydrogenase) (EC 1.2.1.27)	2.1.1	71.43	100.00
araR	A0A3A8C7S0		<i>araR</i>	Arabinose metabolism transcriptional repressor	3.5.2	71.43	100.00
araQ_4	Q8Y8X5		<i>lmo0767</i>	Lmo0767 protein	1.2.0	71.43	100.00
group_4211	A0A0B8QZH0		<i>LmNIHS28_01814</i>	Uncharacterized protein		28.57	0.00
ugpA	A0A3A8CAJ6		<i>ugpA</i>	sn-glycerol-3-phosphate transport system permease protein UgpA	1.2.0	71.43	100.00
group_4199	A0A0B8RG01		<i>LmNIHS28_01804</i>	Uncharacterized protein		28.57	0.00
ugpB	Q8Y8X4		<i>lmo0768</i>	Lmo0768 protein	1.2.0	71.43	100.00
group_1873	Q8Y8X3		<i>lmo0769</i>	Lmo0769 protein	2.1.1	71.43	100.00
group_4648	A0A393Q5I5		<i>AF238_11265</i>	Uncharacterized protein	4.3.0	35.71	4.65
group_1916	UPI000C83A576			hypothetical protein		35.71	4.65
group_4197	UPI00098E3EF0			hypothetical protein		71.43	27.91
group_2640	UPI000771882E			hypothetical protein		42.86	9.30
group_1920	UPI000B68876C		<i>CEQ29_000650</i>	Uncharacterized protein		50.00	13.95
group_3007	A0A0E1R7X6		<i>BN389_20550</i>	Uncharacterized protein		28.57	2.33
hflX_1	Q8Y8Y0		<i>hflX</i>	GTPase HflX (GTP-binding protein HflX)	4.5.0	71.43	97.67
group_3582	UPI000D72A586			XRE family transcriptional regulator		28.57	2.33
group_1241	Q723T1		<i>iolA</i>	Malonate-semialdehyde dehydrogenase (MSA dehydrogenase) (EC 1.2.1.27)	2.1.1	28.57	2.33
lacC_2	Q8Y4U5		<i>fruB</i>	Tagatose-6-phosphate kinase (EC 2.7.1.144)	2.1.1	28.57	2.33

group_4651	A0A241SSP0	<i>A410_2479</i>	Uncharacterized protein		28.57	2.33
group_4650	A0A3A2YIH6	<i>AE052_02493</i>	Uncharacterized protein		28.57	2.33
group_876	A0A1D2IYH2	<i>CDR86_08530</i>	Uncharacterized protein	6.0.0	7.14	44.19
group_194	A0A394YAU8	<i>AF255_15365</i>	Uncharacterized protein		92.86	55.81
group_5793	A0A3A7RNF5	<i>AF238_14525</i>	Uncharacterized protein		21.43	0.00
group_5794	A0A394V4F9	<i>AF238_14520</i>	Uncharacterized protein		21.43	0.00
group_5823	A0A393P7G5	<i>ssbA_2</i>	Single-stranded DNA-binding protein (SSB)	3.1.0	21.43	0.00
group_3581	A0A3A7YDK2	<i>AF821_00725</i>	ImmA/IrrE family metallo-endopeptidase		35.71	6.98
group_1150	A0A394RBJ1	<i>AF239_04485</i>	Uncharacterized protein		42.86	11.63
group_2638	A0A1D2J2T1	<i>CDR86_02640</i>	Uncharacterized protein	6.0.0	57.14	23.26
group_1919	A0A393FFS4	<i>AF249_11805</i>	Uncharacterized protein	4.3.0	57.14	23.26
group_2488	UPI000869A2AF		HEAT repeat domain-containing protein		28.57	4.65
group_4354	A0A0E0UTH3	<i>LMM7_0407</i>	Uncharacterized protein	6.0.0	71.43	95.35
group_4212	A0A0E1R3F0	<i>BN389_04600</i>	Uncharacterized protein		28.57	4.65
group_2641	A0A394UVY7	<i>AEZ78_03023</i>	Uncharacterized protein	4.3.0	28.57	4.65
group_3452	A0A0B8RG05	<i>LmNIHS28_01809</i>	Uncharacterized protein		28.57	4.65
group_846	A0A0B8R577	<i>hflX</i>	GTPase HflX (GTP-binding protein HflX)	4.5.0	28.57	4.65
group_4474	A0A2A6A4V8	<i>CDR86_11955</i>	Uncharacterized protein		35.71	9.30
group_1810	UPI000E6BA985	<i>D3C26_06200</i>	Uncharacterized protein		35.71	9.30
group_180	UPI000BDFE765		hypothetical protein		35.71	9.30
group_226	UPI000CD94099	<i>inlJ_17</i>	Internalin-J	1.8.0	21.43	2.33
group_2185	A0A241SS83	<i>fruB</i>	Tagatose-6-phosphate kinase (EC 2.7.1.144)	2.1.1	78.57	97.67
group_1809	UPI00073B1B95	<i>AN945_2724c</i>	Uncharacterized protein		21.43	2.33
group_907	A0A3A7F8U2	<i>DYZ75_01282</i>	Uncharacterized protein	3.5.2	21.43	2.33
group_3832	A0A3A2XE84	<i>AF238_11270</i>	Uncharacterized protein		21.43	2.33
group_2702	A0A0S4KTT7	<i>Candidatus Nitrospira inopinata</i> <i>NITINOP_1625</i>	Uncharacterized protein		21.43	2.33
group_664	A0A394VEJ2	<i>AF261_05390</i>	Site-specific integrase		21.43	2.33
group_388	UPI0009870563		DnaD domain protein		50.00	20.93
group_877	UPI000D65622D	<i>DF271_11275</i>	Uncharacterized protein (Fragment)	6.0.0	0.00	25.58
group_2178	A0A3A7KNB4	<i>gadB_1</i>	Glutamate decarboxylase (EC 4.1.1.15)	2.2.0	0.00	25.58
group_143	A0A3A2J7V9	<i>AF247_01180</i>	BspA family leucine-rich repeat surface protein	1.8.0	0.00	25.58

‡ Non *L. monocytogenes* species

† Description for each functional category code is presented below

[1.1.0] Cell envelope and cellular processes > Cell wall

[1.2.0] Cell envelope and cellular processes > Transport/binding proteins and lipoproteins

[1.3.0] Cell envelope and cellular processes > Sensors (signal transduction)

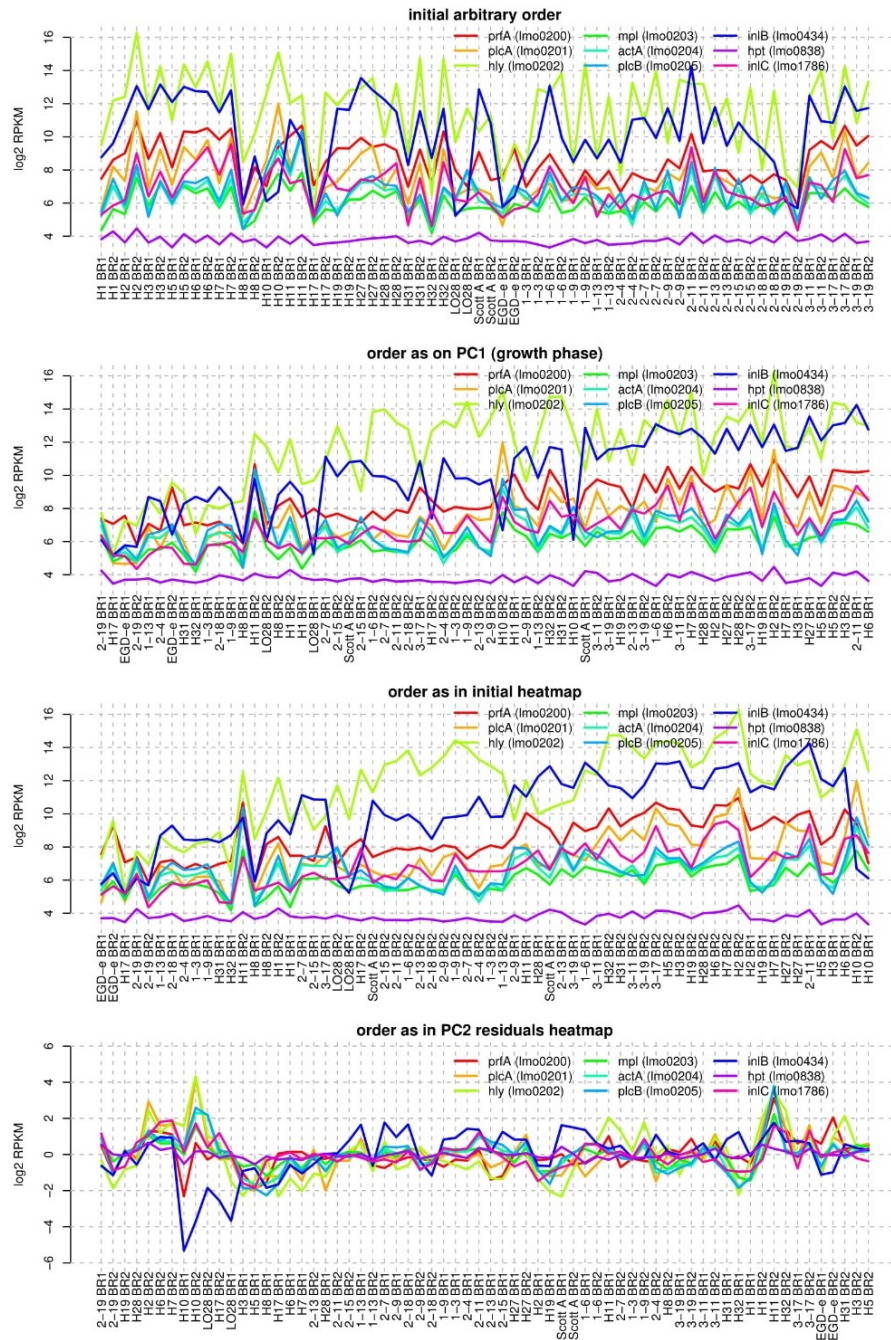
[1.4.0] Cell envelope and cellular processes > Membrane bioenergetics

[1.5.0] Cell envelope and cellular processes > Mobility and chemotaxis

[1.6.0] Cell envelope and cellular processes > Protein secretion

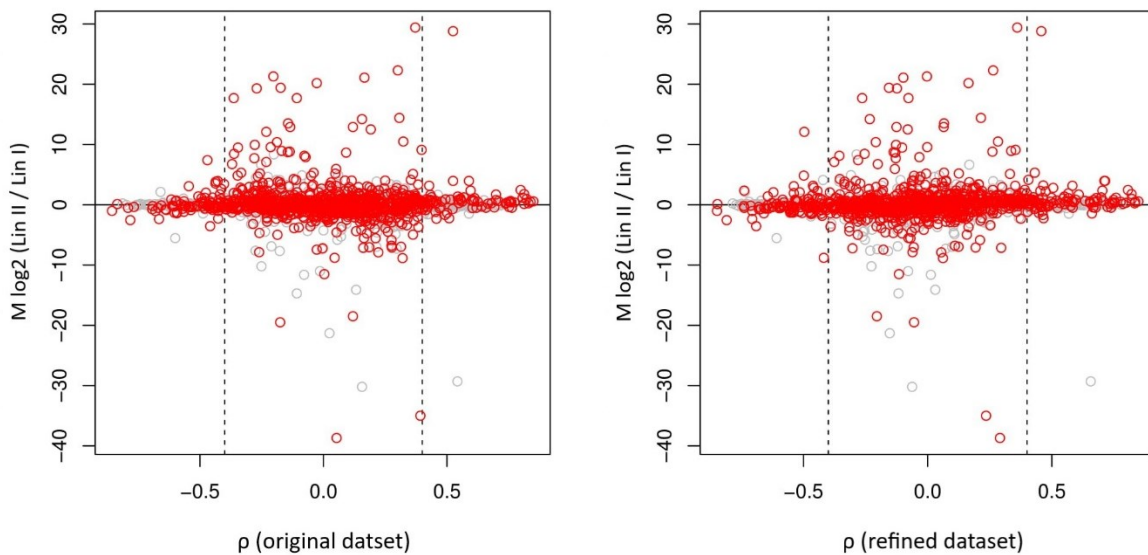
- [1.7.0] Cell envelope and cellular processes > Cell division
- [1.8.0] Cell envelope and cellular processes > Cell surface proteins
- [1.9.0] Cell envelope and cellular processes > Soluble internalin
- [1.10.0] Cell envelope and cellular processes > Transformation/competence
- [2.1.0] Intermediary metabolism > Metabolism of carbohydrates and related molecule
- [2.1.1] Intermediary metabolism > Metabolism of carbohydrates and related molecule > Specific pathways
- [2.1.2] Intermediary metabolism > Metabolism of carbohydrates and related molecule > Main glycolytic pathways
- [2.1.3] Intermediary metabolism > Metabolism of carbohydrates and related molecule > TCA cycle
- [2.2.0] Intermediary metabolism > Metabolism of amino acids and related molecules
- [2.3.0] Intermediary metabolism > Metabolism of nucleotides and nucleic acids
- [2.4.0] Intermediary metabolism > Metabolism of lipids
- [2.5.0] Intermediary metabolism > Metabolism of coenzymes and prosthetic groups
- [2.6.0] Intermediary metabolism > Metabolism of phosphate
- [3.1.0] Information pathways > DNA replication
- [3.2.0] Information pathways > DNA restriction/modification and repair
- [3.3.0] Information pathways > DNA recombination
- [3.4.0] Information pathways > DNA packaging and segregation
- [3.5.1] Information pathways > RNA synthesis > Initiation
- [3.5.2] Information pathways > RNA synthesis > Regulation
- [3.5.3] Information pathways > RNA synthesis > Elongation
- [3.5.4] Information pathways > RNA synthesis > Termination
- [3.6.0] Information pathways > RNA modification
- [3.7.1] Information pathways > Protein synthesis > Ribosomal proteins
- [3.7.2] Information pathways > Protein synthesis > Aminoacyl-tRNA synthetases
- [3.7.3] Information pathways > Protein synthesis > Initiation
- [3.7.4] Information pathways > Protein synthesis > Elongation
- [3.7.5] Information pathways > Protein synthesis > Termination
- [3.8.0] Information pathways > Protein modification
- [3.9.0] Information pathways > Protein folding
- [4.1.0] Other functions > Adaptation to atypical conditions
- [4.2.0] Other functions > Detoxification
- [4.3.0] Other functions > Phage-related functions
- [4.4.0] Other functions > Transposon and IS
- [4.5.0] Other functions > Miscellaneous
- [5.1.0] Similar to unknown proteins > From *Listeria*
- [5.2.0] Similar to unknown proteins > From other organisms
- [6.0.0] No similarity

Chapter V



Supplementary Figure 1. Comparison of transcript levels of core PrfA virulon. Levels of transcripts are expressed in log2 values from original and refined datasets. Samples are arranged in arbitrary order (first graph), ordered as expressed in principal component axis 1 (second graph), and ordered as shown in Figure 3A (third graph) from original dataset. Last graph shows transcript patterns from the improved dataset by removing variations captured by PC1 and PC2 with samples ordered as shown in Figure 6A.

In a previous study, differential expression of 1,034 genes discriminated lineages among 6 *L. monocytogenes* isolates (Severino et al., 2007) of which 943 genes were included in the list of 2,456 conserved single copy genes whose expression levels were analysed here. They decomposed into 462 genes with higher expression in lineage I as represented by four isolates (one of serotype 1/2b and three of serotype 4b) and 481 genes with higher expression in lineage II as represented by two isolates (both of serotype 1/2a). These lists of genes were compared to those established in the current study and the congruency between the results of the two analyses was found to be limited (Supplementary Fig. 2). Among the 261 genes whose expression was the most specific of lineage I in this study ($\rho \leq -0.4$), only 73 (28%) were included in the list of 462 reported by the previous study. Similarly, among the 222 genes found here as most specific of lineage II ($\rho \geq 0.4$), 71 (32%) were included in the list of 481 reported by the previous study. For some genes a contradiction was found between the two studies, this concerned 13% of the genes with $\rho \leq -0.4$ and 10% of the genes with $\rho \geq 0.4$ (details can be found in Table 2).



Supplementary Figure 2. Comparison of transcript pattern of genes between lineage I and II to the data from Severino et al. (2007). X-axis showing ρ value from the present correlation analysis is compared to y-axis showing M value, \log_2 (lineage II / lineage I), from Severino et al. Graphs on left used original transcriptomes and right refined transcriptomes (residual of PC1 and PC2). Differentially expressed genes according to Severino et al. are expressed in red circle.

Supplementary Table 1. List of genes in 12 clusters and corresponding transcription factors

Cluster 1				Cluster 3			
Locus tag	Regulator	Locus tag	Regulator	Locus tag	Regulator	Locus tag	Regulator
<i>lmo0019</i>	PrfA	<i>lmo0894</i>	SigB	<i>lmo2387</i>	SigB	<i>lmo0675</i>	NA
<i>lmo0043</i>	SigB	<i>lmo0895</i>	SigB	<i>lmo2389</i>	SigB	<i>lmo0676</i>	SigB
<i>lmo0169</i>	SigB	<i>lmo0896</i>	SigB	<i>lmo2434</i>	SigB	<i>lmo0677</i>	NA
<i>lmo0170</i>	SigB	<i>lmo0913</i>	SigB	<i>lmo2454</i>	SigB	<i>lmo0678</i>	NA
<i>lmo0274</i>	SigB	<i>lmo0929</i>	SigB	<i>lmo2463</i>	SigB	<i>lmo0679</i>	NA
<i>lmo0405</i>	SigB	<i>lmo0937</i>	SigB	<i>lmo2484</i>	SigB	<i>lmo0680</i>	NA
<i>lmo0406</i>	SigB	<i>lmo0994</i>	SigB	<i>lmo2485</i>	SigB	<i>lmo0681</i>	NA
<i>lmo0407</i>	SigB	<i>lmo0995</i>	SigB	<i>lmo2494</i>	SigB	<i>lmo0682</i>	NA
<i>lmo0408</i>	SigB	<i>lmo1027</i>	SigB	<i>lmo2495</i>	NA	<i>lmo0683</i>	NA
<i>lmo0434</i>	PrfA	<i>lmo1028</i>	SigB	<i>lmo2570</i>	SigB	<i>lmo0684</i>	NA
<i>lmo0439</i>	SigB	<i>lmo1140</i>	SigB	<i>lmo2571</i>	SigB	<i>lmo0685</i>	NA
<i>lmo0524</i>	SigB	<i>lmo1241</i>	SigB	<i>lmo2572</i>	SigB	<i>lmo0686</i>	CodY
<i>lmo0539</i>	SigB	<i>lmo1261</i>	SigB	<i>lmo2573</i>	SigB	<i>lmo0687</i>	CodY
<i>lmo0554</i>	SigB	<i>lmo1295</i>	SigB	<i>lmo2602</i>	SigB	<i>lmo0688</i>	NA
<i>lmo0555</i>	SigB	<i>lmo1340</i>	SigB	<i>lmo2603</i>	SigB	<i>lmo0689</i>	CodY
<i>lmo0579</i>	SigB	<i>lmo1421</i>	SigB	<i>lmo2724</i>	SigB	<i>lmo0690</i>	CodY
<i>lmo0580</i>	SigB	<i>lmo1422</i>	SigB	<i>lmo2748</i>	SigB	<i>lmo0691</i>	NA
<i>lmo0593</i>	SigB	<i>lmo1432</i>	SigB			<i>lmo0692</i>	NA
<i>lmo0602</i>	SigB	<i>lmo1433</i>	SigB			<i>lmo0693</i>	NA
<i>lmo0610</i>	SigB	<i>lmo1452</i>	NA			<i>lmo0694</i>	NA
<i>lmo0626</i>	SigB	<i>lmo1453</i>	SigB			<i>lmo0695</i>	NA
<i>lmo0628</i>	SigB	<i>lmo1454</i>	SigB			<i>lmo0696</i>	NA
<i>lmo0629</i>	SigB	<i>lmo1526</i>	SigB			<i>lmo0697</i>	NA
<i>lmo0642</i>	NA*	<i>lmo1601</i>	SigB			<i>lmo0698</i>	NA
<i>lmo0648</i>	SigB	<i>lmo1602</i>	SigB			<i>lmo0699</i>	CodY
<i>lmo0649</i>	SigB	<i>lmo1694</i>	SigB			<i>lmo0700</i>	NA
<i>lmo0650</i>	SigB	<i>lmo1708</i>	NA			<i>lmo0701</i>	CodY
<i>lmo0651</i>	SigB	<i>lmo1830</i>	SigB			<i>lmo0702</i>	CodY
<i>lmo0654</i>	SigB	<i>lmo1883</i>	NagR			<i>lmo0703</i>	NA
<i>lmo0655</i>	SigB	<i>lmo1911</i>	NA			<i>lmo0704</i>	NA
<i>lmo0669</i>	SigB	<i>lmo1912</i>	NA			<i>lmo0705</i>	NA
<i>lmo0670</i>	SigB	<i>lmo1913</i>	NA			<i>lmo0706</i>	NA
<i>lmo0722</i>	SigB	<i>lmo1914</i>	NA			<i>lmo0707</i>	CodY
<i>lmo0781</i>	SigB	<i>lmo2092</i>	NA			<i>lmo0708</i>	CodY
<i>lmo0782</i>	SigB	<i>lmo2130</i>	SigB			<i>lmo0709</i>	CodY
<i>lmo0783</i>	SigB	<i>lmo2132</i>	SigB			<i>lmo0710</i>	CodY
<i>lmo0784</i>	SigB	<i>lmo2157</i>	SigB			<i>lmo0711</i>	CodY
<i>lmo0794</i>	SigB	<i>lmo2158</i>	SigB			<i>lmo0712</i>	CodY
<i>lmo0820</i>	NA	<i>lmo2174</i>	SigB			<i>lmo0713</i>	CodY
<i>lmo0821</i>	NA	<i>lmo2213</i>	SigB			<i>lmo0714</i>	CodY
<i>lmo0869</i>	SigB	<i>lmo2230</i>	SigB			<i>lmo0715</i>	CodY
<i>lmo0870</i>	SigB	<i>lmo2231</i>	SigB			<i>lmo0716</i>	CodY

*information not available

Cluster 4		Cluster 7		Cluster 9		Cluster 11		Cluster 14	
Locus tag	Regulator	Locus tag	Regulator	Locus tag	Regulator	Locus tag	Regulator	Locus tag	Regulator
<i>lmo0133</i>	SigB	<i>lmo0113</i>	NA	<i>lmo1152</i>	SigB	<i>lmo1149</i>	NA	<i>lmo0643</i>	NA
<i>lmo0134</i>	SigB	<i>lmo0114</i>	NA	<i>lmo1153</i>	NA	<i>lmo1171</i>	NA	<i>lmo2065</i>	NA
<i>lmo0265</i>	SigB	<i>lmo0115</i>	NA	<i>lmo1154</i>	SigB	<i>lmo1174</i>	NA	<i>lmo2066</i>	NA
<i>lmo0321</i>	SigB	<i>lmo0116</i>	NA	<i>lmo1155</i>	NA	<i>lmo1175</i>	NA	<i>lmo2659</i>	CodY
<i>lmo0515</i>	SigB	<i>lmo0117</i>	NA	<i>lmo1156</i>	NA	<i>lmo1176</i>	NA	<i>lmo2660</i>	CodY
<i>lmo0584</i>	SigB	<i>lmo0118</i>	SigB	<i>lmo1157</i>	NA	<i>lmo1177</i>	NA	<i>lmo2661</i>	CodY
<i>lmo0911</i>	SigB	<i>lmo0119</i>	PrfA	<i>lmo1158</i>	NA	<i>lmo1178</i>	NA	<i>lmo2662</i>	CodY
<i>lmo0953</i>	SigB	<i>lmo0120</i>	NA	<i>lmo1160</i>	NA	<i>lmo1179</i>	NA	<i>lmo2663</i>	CodY
<i>lmo1267</i>	NA	<i>lmo0121</i>	NA	<i>lmo1161</i>	NA	<i>lmo1181</i>	NA	<i>lmo2664</i>	CodY
<i>lmo1375</i>	SigB	<i>lmo0122</i>	SigB	<i>lmo1162</i>	NA	<i>lmo1182</i>	NA	<i>lmo2665</i>	SigL
<i>lmo1376</i>	SigB	<i>lmo0123</i>	NA	<i>lmo1163</i>	NA	<i>lmo1183</i>	NA	<i>lmo2666</i>	CodY
<i>lmo1788</i>	SigB	<i>lmo0124</i>	NA	<i>lmo1164</i>	NA	<i>lmo1184</i>	NA	<i>lmo2667</i>	NA
<i>lmo1789</i>	SigB	<i>lmo0125</i>	NA	<i>lmo1165</i>	NA	<i>lmo1185</i>	NA	<i>lmo2668</i>	NA
<i>lmo1790</i>	SigB	<i>lmo0126</i>	NA	<i>lmo1166</i>	NA	<i>lmo1186</i>	NA		
<i>lmo1931</i>	NA	<i>lmo0127</i>	NA	<i>lmo1167</i>	NA	<i>lmo1187</i>	NA		
<i>lmo1932</i>	SigB	<i>lmo0128</i>	NA	<i>lmo1168</i>	SigB				
<i>lmo1933</i>	SigB	<i>lmo0129</i>	NA						
<i>lmo2067</i>	PrfA								
<i>lmo2085</i>	SigB								
<i>lmo2391</i>	SigB								
<i>lmo2398</i>	SigB								
<i>lmo2670</i>	SigB								
<i>lmo2671</i>	SigB								
<i>lmo2672</i>	SigB								
<i>lmo2673</i>	SigB								
<i>lmo2674</i>	SigB								

Cluster 15		Cluster 26		Cluster 30		Cluster 41		Cluster 45	
Locus tag	Regulator	Locus tag	Regulator	Locus tag	Regulator	Locus tag	Regulator	Locus tag	Regulator
<i>lmo0264</i>	NA	<i>lmo1587</i>	ArgR	<i>lmo0343</i>	SigB	<i>lmo0201</i>	PrfA	<i>lmo1997</i>	CodY
<i>lmo0481</i>	NA	<i>lmo1588</i>	ArgR	<i>lmo0344</i>	CodY	<i>lmo0202</i>	PrfA	<i>lmo1998</i>	CodY
<i>lmo0527</i>	NA	<i>lmo1589</i>	ArgR	<i>lmo0345</i>	CodY	<i>lmo0203</i>	PrfA	<i>lmo1999</i>	CodY
<i>lmo0528</i>	NA	<i>lmo1590</i>	ArgR	<i>lmo0346</i>	SigB	<i>lmo0204</i>	PrfA	<i>lmo2000</i>	SigB
<i>lmo0529</i>	SigB	<i>lmo1591</i>	ArgR	<i>lmo0347</i>	SigB	<i>lmo0205</i>	PrfA	<i>lmo2001</i>	CodY
<i>lmo0530</i>	NA	<i>lmo2090</i>	ArgR	<i>lmo0348</i>	SigB	<i>lmo0206</i>	NA	<i>lmo2002</i>	SigB
<i>lmo0531</i>	CtsR	<i>lmo2091</i>	ArgR	<i>lmo0349</i>	SigB	<i>lmo0207</i>	NA	<i>lmo2003</i>	SigB
<i>lmo1505</i>	NA	<i>lmo2250</i>	NA	<i>lmo0350</i>	NA	<i>lmo1786</i>	PrfA	<i>lmo2004</i>	SigB
<i>lmo1506</i>	NA	<i>lmo2251</i>	NA	<i>lmo0351</i>	SigB				
<i>lmo2831</i>	NA	<i>lmo2252</i>	NA						
<i>lmo2832</i>	SigB								
<i>lmo2833</i>	YcjW								

Supplementary Table 2. List of genes whose transcript levels are correlated with phylogenetic divergence (lineage II versus I)

Locus tag	Product	Coefficient †	q-value	Functional category ‡
<i>lmo1050</i>	hypothetical protein	-0.85	0.000	5.2.0
<i>lmo0832</i>	transposase	-0.85	0.000	4.4.0
<i>lmo0540</i>	penicillin-binding protein	-0.81	0.000	1.1.0
<i>lmo1283</i>	LacX protein	-0.79	0.000	5.2.0
<i>lmo1779</i>	hypothetical protein	-0.77	0.000	6.0.0
<i>lmo2728</i>	MerR family transcriptional regulator	-0.76	0.000	3.5.2
<i>lmo0264</i>	internalin E	-0.75	0.000	1.8.0
<i>lmo2527</i>	hypothetical protein	-0.75	0.000	5.2.0
<i>lmo2587</i>	hypothetical protein	-0.74	0.000	5.2.0
<i>lmo0531</i>	hypothetical protein	-0.74	0.000	6.0.0
<i>lmo1127</i>	hypothetical protein	-0.74	0.000	6.0.0
<i>lmo1308</i>	hypothetical protein	-0.74	0.000	3.8.0
<i>lmo0975</i>	ribose-5-phosphate isomerase A	-0.74	0.000	2.1.1
<i>lmo2376</i>	peptidyl-prolyl cis-trans isomerase	-0.74	0.000	3.9.0
<i>lmo0853</i>	SugE protein	-0.73	0.000	3.9.0
<i>lmo1826</i>	DNA-directed RNA polymerase subunit omega	-0.73	0.000	5.2.0
<i>lmo1689</i>	A/G-specific adenine glycosylase	-0.73	0.000	3.2.0
<i>lmo1817</i>	hypothetical protein	-0.72	0.000	2.5.0
<i>lmo0852</i>	TetR family transcriptional regulator	-0.71	0.000	3.5.2
<i>lmo1944</i>	ferredoxin	-0.71	0.000	1.4.0
<i>lmo1243</i>	hypothetical protein	-0.71	0.000	5.2.0
<i>lmo1274</i>	polypeptide deformylase	-0.71	0.000	3.8.0
<i>lmo0530</i>	hypothetical protein	-0.71	0.000	5.2.0
<i>lmo2366</i>	DeoR family transcriptional regulator	-0.71	0.000	3.5.2
<i>lmo1312</i>	hypothetical protein	-0.70	0.000	6.0.0
<i>lmo2117</i>	hypothetical protein	-0.70	0.000	5.2.0
<i>lmo0839</i>	tetracycline resistance protein	-0.70	0.000	1.2.0
<i>lmo2032</i>	cell division protein FtsZ	-0.69	0.000	1.7.0
<i>lmo1217</i>	endo-1,4-beta-glucanase and to aminopeptidase	-0.69	0.000	2.2.0
<i>lmo0618</i>	protein kinase	-0.69	0.000	3.8.0
<i>lmo0652</i>	hypothetical protein	-0.68	0.000	5.2.0
<i>lmo0617</i>	hypothetical protein	-0.68	0.000	5.1.0
<i>lmo2729</i>	hypothetical protein	-0.68	0.000	5.2.0
<i>lmo0529</i>	glucosaminyltransferase	-0.68	0.000	2.1.1
<i>lmo0528</i>	hypothetical protein	-0.67	0.000	1.8.0
<i>lmo1078</i>	UDP-glucose pyrophosphorylase	-0.67	0.000	1.1.0
<i>lmo1126</i>	hypothetical protein	-0.67	0.000	5.2.0
<i>lmo2833</i>	maltose phosphorylase	-0.66	0.000	2.1.1
<i>lmo2334</i>	transcriptional regulator	-0.66	0.000	3.5.2
<i>lmo0187</i>	hypothetical protein	-0.66	0.000	5.2.0
<i>lmo1347</i>	competence protein ComGA	-0.66	0.000	1.10.0
<i>lmo0629</i>	hypothetical protein	-0.65	0.000	5.2.0
<i>lmo1056</i>	hypothetical protein	-0.65	0.000	6.0.0
<i>lmo1213</i>	hypothetical protein	-0.65	0.000	5.2.0
<i>lmo1413</i>	peptidoglycan binding protein	-0.65	0.000	1.8.0
<i>lmo1800</i>	protein-tyrosine phosphatase	-0.65	0.000	3.8.0
<i>lmo1258</i>	hypothetical protein	-0.64	0.000	5.2.0

<i>lmo0213</i>	peptidyl-tRNA hydrolase	-0.64	0.000	3.7.5
<i>lmo1670</i>	hypothetical protein	-0.63	0.000	5.2.0
<i>lmo0158</i>	hypothetical protein	-0.63	0.000	5.2.0
<i>lmo2793</i>	hypothetical protein	-0.63	0.000	6.0.0
<i>lmo1218</i>	rRNA methylase	-0.63	0.000	3.6.0
<i>lmo2523</i>	single-strand DNA-binding protein	-0.63	0.000	3.1.0
<i>lmo2377</i>	multidrug transporter	-0.62	0.000	1.2.0
<i>lmo1500</i>	hypothetical protein	-0.62	0.000	5.2.0
<i>lmo2019</i>	isoleucyl-tRNA synthetase	-0.62	0.000	3.7.2
<i>lmo2557</i>	lipid kinase	-0.62	0.000	5.2.0
<i>lmo1282</i>	hypothetical protein	-0.61	0.000	5.2.0
<i>lmo0854</i>	SugE protein	-0.61	0.000	3.9.0
<i>lmo1049</i>	molybdopterin biosynthesis protein MoeB	-0.61	0.000	2.5.0
<i>lmo2370</i>	aminotransferase	-0.61	0.000	2.2.0
<i>lmo2750</i>	para-aminobenzoate synthase subunit I	-0.61	0.000	2.2.0
<i>lmo2078</i>	hypothetical protein	-0.61	0.000	5.2.0
<i>lmo2832</i>	hypothetical protein	-0.61	0.000	5.2.0
<i>lmo0772</i>	transcriptional regulator	-0.60	0.000	3.5.2
<i>lmo0800</i>	hypothetical protein	-0.60	0.000	5.2.0
<i>lmo1505</i>	ABC transporter ATP-binding protein	-0.60	0.000	1.2.0
<i>lmo1485</i>	hypothetical protein	-0.60	0.000	5.2.0
<i>lmo0322</i>	hypothetical protein	-0.59	0.000	5.2.0
<i>lmo0527</i>	transmembrane protein	-0.59	0.000	6.0.0
<i>lmo2092</i>	glycine betaine transporter BetL	-0.59	0.000	1.2.0
<i>lmo2551</i>	transcription termination factor Rho	-0.59	0.000	3.5.4
<i>lmo1525</i>	recombination protein RecJ	-0.58	0.000	3.3.0
<i>lmo1877</i>	formyl-tetrahydrofolate synthetase	-0.58	0.000	2.5.0
<i>lmo1005</i>	3-hydroxyisobutyrate dehydrogenase	-0.58	0.000	2.4.0
<i>lmo1965</i>	hypothetical protein	-0.58	0.000	5.2.0
<i>lmo1935</i>	protein-tyrosine/serine phosphatase	-0.58	0.000	3.8.0
<i>lmo1946</i>	acyl-CoA hydrolase	-0.58	0.000	2.4.0
<i>lmo0522</i>	transcriptional regulator	-0.58	0.000	3.5.2
<i>lmo2070</i>	hypothetical protein	-0.58	0.000	5.2.0
<i>lmo0623</i>	hypothetical protein	-0.58	0.000	5.1.0
<i>lmo1223</i>	ABC transporter ATP-binding proteins	-0.58	0.000	1.2.0
<i>lmo2338</i>	aminopeptidase	-0.57	0.000	2.2.0
<i>lmo1506</i>	transporter	-0.57	0.000	1.2.0
<i>lmo1575</i>	hypothetical protein	-0.56	0.000	5.2.0
<i>lmo2201</i>	3-oxoacyl-ACP synthase	-0.56	0.000	2.4.0
<i>lmo1332</i>	GTPase EngC	-0.56	0.000	5.2.0
<i>lmo1149</i>	alpha-ribazole-5'-phosphatase	-0.56	0.000	2.5.0
<i>lmo0406</i>	hypothetical protein	-0.56	0.001	5.2.0
<i>lmo0628</i>	hypothetical protein	-0.56	0.000	5.1.0
<i>lmo1309</i>	hypothetical protein	-0.56	0.000	5.2.0
<i>lmo2239</i>	hypothetical protein	-0.56	0.000	5.2.0
<i>lmo1880</i>	RNase HI	-0.55	0.000	3.1.0
<i>lmo2560</i>	DNA-directed RNA polymerase subunit delta	-0.55	0.001	3.5.3
<i>lmo1587</i>	ornithine carbamoyltransferase	-0.55	0.000	2.2.0
<i>lmo1281</i>	hypothetical protein	-0.55	0.000	5.2.0
<i>lmo2706</i>	hypothetical protein	-0.55	0.001	6.0.0
<i>lmo0485</i>	hypothetical protein	-0.55	0.001	5.2.0

<i>lmo2427</i>	cell division protein FtsW	-0.55	0.001	1.7.0
<i>lmo2005</i>	oxidoreductase	-0.55	0.000	2.1.1
<i>lmo1214</i>	hypothetical protein	-0.54	0.002	6.0.0
<i>lmo1390</i>	ABC transporter permease	-0.54	0.000	1.2.0
<i>lmo1299</i>	glutamine synthetase	-0.54	0.000	2.2.0
<i>lmo2715</i>	ABC transporter ATP-binding protein	-0.54	0.000	1.2.0
<i>lmo0610</i>	internalin	-0.54	0.001	1.8.0
<i>lmo0755</i>	hypothetical protein	-0.54	0.000	5.2.0
<i>lmo1761</i>	sodium-dependent transporter	-0.54	0.001	1.2.0
<i>lmo2024</i>	nicotinate-nucleotide pyrophosphorylase	-0.54	0.000	2.5.0
<i>lmo2641</i>	heptaprenyl diphosphate synthase subunit II	-0.54	0.001	2.5.0
<i>lmo1391</i>	sugar ABC transporter permease	-0.54	0.000	1.2.0
<i>lmo2207</i>	hypothetical protein	-0.54	0.000	5.2.0
<i>lmo0840</i>	hypothetical protein	-0.53	0.000	5.2.0
<i>lmo2021</i>	hypothetical protein	-0.53	0.000	5.2.0
<i>lmo1978</i>	glucose-6-phosphate 1-dehydrogenase	-0.53	0.000	2.1.1
<i>lmo2079</i>	hypothetical protein	-0.53	0.002	5.1.0
<i>lmo0008</i>	cardiolipin synthase	-0.53	0.000	2.4.0
<i>lmo1358</i>	hypothetical protein	-0.53	0.001	5.2.0
<i>lmo1908</i>	hypothetical protein	-0.53	0.000	5.2.0
<i>lmo1921</i>	hypothetical protein	-0.53	0.000	5.2.0
<i>lmo2400</i>	acetyltransferase	-0.53	0.000	2.2.0
<i>lmo0664</i>	acetyl transferase	-0.52	0.000	2.1.1
<i>lmo1319</i>	prolyl-tRNA synthetase	-0.52	0.000	3.7.2
<i>lmo0161</i>	hypothetical protein	-0.52	0.003	5.2.0
<i>lmo2388</i>	hypothetical protein	-0.52	0.002	5.2.0
<i>lmo0095</i>	hypothetical protein	-0.52	0.001	5.1.0
<i>lmo0549</i>	internalin	-0.52	0.001	1.9.0
<i>lmo2836</i>	alcohol dehydrogenase	-0.52	0.000	2.1.1
<i>lmo1346</i>	competence protein ComGB	-0.52	0.000	1.10.0
<i>lmo1389</i>	sugar ABC transporter ATP-binding protein	-0.52	0.001	1.2.0
<i>lmo0216</i>	hypothetical protein	-0.51	0.002	5.2.0
<i>lmo0526</i>	transcriptional regulator	-0.51	0.001	3.5.2
<i>lmo1939</i>	cytidylate kinase	-0.51	0.000	2.3.0
<i>lmo1653</i>	cellsurface protein	-0.51	0.003	6.0.0
<i>lmo2583</i>	DNA-binding response regulator	-0.51	0.002	3.5.2
<i>lmo0003</i>	hypothetical protein	-0.51	0.001	5.2.0
<i>lmo1697</i>	hypothetical protein	-0.51	0.001	5.2.0
<i>lmo0481</i>	hypothetical protein	-0.51	0.003	5.2.0
<i>lmo1813</i>	phosphoglycerate dehydrogenase	-0.51	0.000	2.2.0
<i>lmo0184</i>	oligo-1,6-glucosidase	-0.50	0.004	2.1.1
<i>lmo0948</i>	transcriptional regulator	-0.50	0.000	3.5.2
<i>lmo1310</i>	hypothetical protein	-0.50	0.000	5.2.0
<i>lmo1682</i>	transporter	-0.50	0.000	1.2.0
<i>lmo2025</i>	quinolinate synthetase	-0.50	0.003	2.5.0
<i>lmo2106</i>	hypothetical protein	-0.50	0.004	5.2.0
<i>lmo1430</i>	hypothetical protein	-0.50	0.003	5.2.0
<i>lmo1770</i>	phosphoribosylformylglycinamide synthase I	-0.50	0.001	2.3.0
<i>lmo0267</i>	hypothetical protein	-0.49	0.001	5.2.0
<i>lmo0991</i>	hypothetical protein	-0.49	0.000	5.2.0
<i>lmo1477</i>	oxidoreductase	-0.49	0.000	2.1.1

<i>lmo2424</i>	thioredoxin	-0.49	0.001	1.4.0
<i>lmo1729</i>	beta-glucosidase	-0.49	0.001	2.1.1
<i>lmo0455</i>	hypothetical protein	-0.49	0.003	5.2.0
<i>lmo1000</i>	phytoene dehydrogenase	-0.49	0.000	2.1.1
<i>lmo2033</i>	cell division protein FtsA	-0.48	0.001	1.7.0
<i>lmo0083</i>	MerR family transcriptional regulator	-0.48	0.005	3.5.2
<i>lmo0457</i>	hypothetical protein	-0.48	0.005	5.2.0
<i>lmo0756</i>	ABC transporter ATP-binding protein	-0.48	0.000	1.2.0
<i>lmo1259</i>	gamma-glutamyl phosphate reductase	-0.48	0.004	2.2.0
<i>lmo1668</i>	hypothetical protein	-0.48	0.000	5.2.0
<i>lmo0194</i>	ABC transporter ATP-binding protein	-0.48	0.004	1.2.0
<i>lmo0635</i>	hypothetical protein	-0.48	0.001	5.2.0
<i>lmo0733</i>	transcriptional regulator	-0.48	0.002	3.5.2
<i>lmo1573</i>	acetyl-CoA carboxylase subunit beta	-0.48	0.003	2.4.0
<i>lmo1688</i>	enoyl-ACP reductase	-0.48	0.003	2.1.1
<i>lmo1851</i>	carboxy-terminal processing proteinase	-0.48	0.002	2.2.0
<i>lmo1249</i>	hypothetical protein	-0.48	0.005	5.1.0
<i>lmo1738</i>	amino acid ABC transporter substrate-binding protein	-0.48	0.008	1.2.0
<i>lmo0487</i>	hypothetical protein	-0.48	0.005	5.2.0
<i>lmo2705</i>	hypothetical protein	-0.48	0.006	5.2.0
<i>lmo1868</i>	hypothetical protein	-0.47	0.000	5.2.0
<i>lmo2831</i>	phosphoglucomutase	-0.47	0.008	2.1.1
<i>lmo0928</i>	3-methyladenine DNA glycosylase	-0.47	0.004	3.2.0
<i>lmo2582</i>	histidine kinase	-0.47	0.004	1.3.0
<i>lmo2857</i>	hypothetical protein	-0.47	0.006	na
<i>lmo0458</i>	hydantoinase	-0.47	0.008	2.2.0
<i>lmo0612</i>	MarR family transcriptional evidence	-0.47	0.000	3.5.2
<i>lmo0883</i>	hypothetical protein	-0.47	0.005	5.2.0
<i>lmo0937</i>	hypothetical protein	-0.47	0.002	6.0.0
<i>lmo1781</i>	hypothetical protein	-0.47	0.003	5.2.0
<i>lmo2537</i>	UDP-N-acetylglucosamine 2-epimerase	-0.47	0.005	2.1.1
<i>lmo1435</i>	dihydrodipicolinate synthase	-0.47	0.004	2.2.0
<i>lmo2780</i>	PTS cellbiose transporter subunit IIA	-0.47	0.002	1.2.0
<i>lmo2707</i>	hypothetical protein	-0.47	0.007	6.0.0
<i>lmo2737</i>	LacI family transcriptional regulator	-0.47	0.004	3.5.2
<i>lmo0199</i>	ribose-phosphate pyrophosphokinase	-0.47	0.004	na
<i>lmo2634</i>	hypothetical protein	-0.47	0.005	5.2.0
<i>lmo1147</i>	cobalamin biosynthesis protein CopB	-0.46	0.006	2.5.0
<i>lmo0491</i>	3-dehydroquinone hydratase	-0.46	0.007	2.2.0
<i>lmo1446</i>	metal (zinc) transport protein (ABC transporter permease)	-0.46	0.004	1.2.0
<i>lmo2023</i>	L-aspartate oxidase	-0.46	0.001	2.5.0
<i>lmo2593</i>	MerR family transcriptional regulator	-0.46	0.007	3.5.2
<i>lmo0084</i>	oxidoreductase	-0.46	0.010	2.1.1
<i>lmo1919</i>	hypothetical protein	-0.46	0.002	5.2.0
<i>lmo0557</i>	phosphoglycerate mutase	-0.46	0.005	2.1.2
<i>lmo1434</i>	hypothetical protein	-0.46	0.003	5.2.0
<i>lmo1701</i>	hypothetical protein	-0.46	0.006	6.0.0
<i>lmo2393</i>	hypothetical protein	-0.46	0.007	5.2.0
<i>lmo2716</i>	ABC transporter	-0.46	0.003	1.2.0
<i>lmo0613</i>	oxidoreductase	-0.46	0.000	2.1.1
<i>lmo1667</i>	L-lactate dehydrogenase	-0.45	0.001	2.1.0

<i>lmo0405</i>	phosphate transporter	-0.45	0.007	1.2.0
<i>lmo1576</i>	hypothetical protein	-0.45	0.009	5.2.0
<i>lmo0511</i>	hypothetical protein	-0.45	0.008	5.2.0
<i>lmo0653</i>	hypothetical protein	-0.45	0.004	5.2.0
<i>lmo0156</i>	hypothetical protein	-0.45	0.001	5.1.0
<i>lmo0622</i>	hypothetical protein	-0.45	0.003	6.0.0
<i>lmo0637</i>	hypothetical protein	-0.45	0.009	3.6.0
<i>lmo0198</i>	bifunctional N-acetylglucosamine-1-phosphate uridyltransferase/glucosamine-1-phosphate acetyltransferase	-0.45	0.011	1.1.0
<i>lmo0556</i>	phosphoglycerate mutase	-0.44	0.008	2.1.2
<i>lmo0835</i>	peptidoglycan binding protein	-0.44	0.002	1.8.0
<i>lmo0935</i>	rRNA methylase	-0.44	0.003	3.6.0
<i>lmo0982</i>	peptidase	-0.44	0.004	2.1.1
<i>lmo1445</i>	ZurR family transcriptional regulator	-0.44	0.003	3.5.2
<i>lmo1869</i>	hypothetical protein	-0.44	0.001	5.2.0
<i>lmo1419</i>	hypothetical protein	-0.44	0.003	5.2.0
<i>lmo2658</i>	acyltransferase	-0.44	0.004	2.2.0
<i>lmo0903</i>	hypothetical protein	-0.44	0.014	5.2.0
<i>lmo1827</i>	guanylate kinase	-0.44	0.007	2.3.0
<i>lmo2038</i>	UDP-N-acetylmuramoylalanyl-D-glutamate--2,6-diaminopimelate ligase	-0.44	0.001	1.1.0
<i>lmo2392</i>	hypothetical protein	-0.44	0.009	5.2.0
<i>lmo2217</i>	hypothetical protein	-0.44	0.001	5.2.0
<i>lmo2796</i>	transcriptional regulator	-0.44	0.002	3.5.2
<i>lmo2657</i>	deoxyguanosinetriphosphate triphosphohydrolase	-0.44	0.007	2.3.0
<i>lmo0407</i>	hypothetical protein	-0.43	0.009	5.2.0
<i>lmo0983</i>	glutathione peroxidase	-0.43	0.004	4.1.0
<i>lmo1232</i>	recombination and DNA strand exchange inhibitor protein	-0.43	0.004	3.2.0
<i>lmo2062</i>	copper transporter	-0.43	0.002	1.2.0
<i>lmo1336</i>	5-formyltetrahydrofolate cyclo-ligase	-0.43	0.002	2.5.0
<i>lmo2127</i>	hypothetical protein	-0.43	0.013	5.2.0
<i>lmo0655</i>	phosphoprotein phosphatase	-0.43	0.011	3.8.0
<i>lmo1566</i>	isocitrate dehydrogenase	-0.43	0.012	2.1.3
<i>lmo1524</i>	adenine phosphoribosyltransferase	-0.42	0.013	2.3.0
<i>lmo2519</i>	teichoic acid linkage unit synthesis protein	-0.42	0.009	1.1.0
<i>lmo2164</i>	AraC family transcriptional regulator	-0.42	0.003	3.5.2
<i>lmo2428</i>	cell division protein FtsW	-0.42	0.003	1.7.0
<i>lmo0026</i>	copper homeostasis protein CutC	-0.42	0.007	4.2.0
<i>lmo1298</i>	glutamine synthetase repressor	-0.42	0.008	3.5.2
<i>lmo2744</i>	Crp/Fnr family transcriptional regulator	-0.42	0.012	3.5.2
<i>lmo2262</i>	hypothetical protein	-0.42	0.000	5.2.0
<i>lmo0844</i>	hypothetical protein	-0.42	0.003	5.2.0
<i>lmo1025</i>	hypothetical protein	-0.42	0.002	5.2.0
<i>lmo1096</i>	GMP synthase	-0.42	0.001	2.3.0
<i>lmo0787</i>	amino acid transporter	-0.42	0.016	1.2.0
<i>lmo1527</i>	preprotein translocase SecDF	-0.42	0.005	1.6.0
<i>lmo0034</i>	PTS cellbiose transporter subunit IIC	-0.42	0.011	1.2.0
<i>lmo1567</i>	citrate synthase	-0.42	0.007	2.1.3
<i>lmo1698</i>	ribosomal-protein-alanine N-acetyltransferase	-0.41	0.011	3.8.0
<i>lmo2569</i>	peptide ABC transporter substrate-binding protein	-0.41	0.014	1.2.0
<i>lmo2712</i>	gluconate kinase	-0.41	0.001	2.1.1
<i>lmo0947</i>	hypothetical protein	-0.41	0.005	1.2.0

<i>lmo1047</i>	molybdenum cofactor biosynthesis protein A	-0.41	0.015	2.5.0
<i>lmo2151</i>	hypothetical protein	-0.41	0.006	5.2.0
<i>lmo0346</i>	triosephosphate isomerase	-0.41	0.012	2.1.2
<i>lmo1619</i>	D-amino acid aminotransferase	-0.41	0.008	2.2.0
<i>lmo1739</i>	amino acid ABC transporter ATP-binding protein	-0.41	0.018	1.2.0
<i>lmo1512</i>	tRNA-specific 2-thiouridylase	-0.41	0.006	3.6.0
<i>lmo1730</i>	sugar ABC transporter substrate-binding protein	-0.41	0.014	1.2.0
<i>lmo2089</i>	lipase	-0.40	0.016	2.4.0
<i>lmo0879</i>	hypothetical protein	-0.40	0.018	5.2.0
<i>lmo2592</i>	aldo/keto reductase	-0.40	0.020	2.1.1
<i>lmo1224</i>	hypothetical protein	-0.40	0.003	5.2.0
<i>lmo0077</i>	hypothetical protein	0.40	0.022	5.2.0
<i>lmo0659</i>	transcriptional regulator	0.40	0.009	3.5.2
<i>lmo0443</i>	LytR family transcriptional regulator	0.40	0.011	3.5.2
<i>lmo2503</i>	cardiolipin synthase	0.40	0.014	2.4.0
<i>lmo1545</i>	septum formation inhibitor MinC	0.40	0.006	1.7.0
<i>lmo0090</i>	ATP synthase F0F1 subunit alpha	0.41	0.012	1.4.0
<i>lmo0742</i>	ABC transporter ATP-binding protein	0.41	0.001	1.2.0
<i>lmo1376</i>	6-phosphogluconate dehydrogenase	0.41	0.015	2.1.1
<i>lmo1470</i>	16S ribosomal RNA methyltransferase RsmE	0.41	0.016	5.2.0
<i>lmo0449</i>	hypothetical protein	0.41	0.003	5.1.0
<i>lmo0871</i>	hypothetical protein	0.41	0.004	5.2.0
<i>lmo0371</i>	GntR family transcriptional regulator	0.41	0.019	3.5.2
<i>lmo1242</i>	hypothetical protein	0.41	0.007	5.2.0
<i>lmo1638</i>	hypothetical protein	0.41	0.020	5.2.0
<i>lmo0507</i>	PTS galactitol transporter subunit IIB	0.41	0.011	1.2.0
<i>lmo0744</i>	ABC transporter ATP-binding protein	0.41	0.008	1.2.0
<i>lmo1208</i>	cobalamin synthase CbiP	0.41	0.011	2.5.0
<i>lmo1399</i>	phosphodiesterase	0.41	0.008	5.2.0
<i>lmo0911</i>	hypothetical protein	0.42	0.016	5.2.0
<i>lmo1436</i>	aspartate kinase	0.42	0.012	2.2.0
<i>lmo0031</i>	LacI family transcription regulator	0.42	0.007	3.5.2
<i>lmo1227</i>	uracil-DNA glycosylase	0.42	0.004	3.2.0
<i>lmo1510</i>	hypothetical protein	0.42	0.004	5.2.0
<i>lmo2355</i>	multidrug resistance protein	0.42	0.013	1.2.0
<i>lmo0728</i>	riboflavin kinase / FAD synthase	0.42	0.011	2.5.0
<i>lmo1532</i>	Holliday junction DNA helicase RuvB	0.42	0.011	3.3.0
<i>lmo2701</i>	hypothetical protein	0.42	0.009	5.2.0
<i>lmo0510</i>	hypothetical protein	0.43	0.008	6.0.0
<i>lmo0743</i>	hypothetical protein	0.43	0.003	6.0.0
<i>lmo1032</i>	transketolase	0.43	0.006	2.1.1
<i>lmo1031</i>	hypothetical protein	0.43	0.006	5.2.0
<i>lmo0858</i>	LacI family transcriptional regulator	0.43	0.001	3.5.2
<i>lmo2364</i>	hypothetical protein	0.43	0.005	6.0.0
<i>lmo1257</i>	hypothetical protein	0.43	0.015	6.0.0
<i>lmo1897</i>	aspartate aminotransferase	0.43	0.001	2.2.0
<i>lmo2173</i>	sigma-54-dependent transcriptional regulator	0.43	0.004	3.5.2
<i>lmo2577</i>	hypothetical protein	0.43	0.006	5.2.0
<i>lmo2166</i>	hypothetical protein	0.43	0.004	5.1.0
<i>lmo0546</i>	NAD(P)-dependent oxidoreductase	0.43	0.012	1.4.0
<i>lmo1033</i>	transketolase	0.43	0.007	2.1.1

<i>lmo1488</i>	nicotinic acid mononucleotide adenylyltransferase	0.44	0.008	5.2.0
<i>lmo2544</i>	thymidine kinase	0.44	0.002	2.3.0
<i>lmo2264</i>	hypothetical protein	0.44	0.007	5.2.0
<i>lmo0508</i>	PTS galactitol transporter subunit IIC	0.44	0.004	1.2.0
<i>lmo0217</i>	DivIC protein	0.44	0.001	1.7.0
<i>lmo2703</i>	hypothetical protein	0.44	0.010	5.2.0
<i>lmo2820</i>	amino-terminal domain-containing protein	0.44	0.006	3.5.2
<i>lmo1841</i>	hypothetical protein	0.45	0.002	6.0.0
<i>lmo0616</i>	glycerophosphoryl diester phosphodiesterase	0.45	0.004	2.1.1
<i>lmo0764</i>	lipoate-protein ligase	0.45	0.009	3.8.0
<i>lmo1790</i>	hypothetical protein	0.45	0.009	5.2.0
<i>lmo2502</i>	hypothetical protein	0.45	0.001	5.2.0
<i>lmo1949</i>	hypothetical protein	0.45	0.005	5.2.0
<i>lmo0999</i>	hypothetical protein	0.45	0.005	6.0.0
<i>lmo2266</i>	hypothetical protein	0.45	0.006	5.2.0
<i>lmo2490</i>	CsbA protein	0.45	0.005	5.2.0
<i>lmo1563</i>	dephospho-CoA kinase	0.46	0.004	5.2.0
<i>lmo2445</i>	internalin	0.46	0.004	1.8.0
<i>lmo0727</i>	glucosamine--fructose-6-phosphate aminotransferase	0.46	0.000	2.1.1
<i>lmo1484</i>	competence protein ComEA	0.46	0.005	1.10.0
<i>lmo1509</i>	exodeoxyribonuclease V	0.46	0.001	3.3.0
<i>lmo1821</i>	phosphoprotein phosphatase	0.46	0.006	3.8.0
<i>lmo0572</i>	hypothetical protein	0.46	0.004	6.0.0
<i>lmo2083</i>	hypothetical protein	0.46	0.007	5.2.0
<i>lmo0370</i>	hypothetical protein	0.46	0.001	5.2.0
<i>lmo0520</i>	transcriptional regulator	0.46	0.005	3.5.2
<i>lmo1721</i>	transcriptional regulator	0.46	0.003	3.5.2
<i>lmo2177</i>	hypothetical protein	0.46	0.003	5.2.0
<i>lmo2398</i>	hypothetical protein	0.47	0.010	4.1.0
<i>lmo1343</i>	competence protein ComGE	0.47	0.003	1.10.0
<i>lmo2504</i>	cell wall-binding protein	0.47	0.009	1.8.0
<i>lmo0317</i>	phosphomethylpyrimidine kinase	0.47	0.003	2.5.0
<i>lmo0600</i>	hypothetical protein	0.47	0.000	5.2.0
<i>lmo1341</i>	competence protein ComG	0.47	0.000	1.10.0
<i>lmo1873</i>	dihydrofolate reductase	0.47	0.000	2.5.0
<i>lmo1344</i>	competence protein ComGD	0.47	0.006	1.10.0
<i>lmo0133</i>	hypothetical protein	0.47	0.008	5.2.0
<i>lmo1743</i>	hypothetical protein	0.47	0.004	6.0.0
<i>lmo2049</i>	hypothetical protein	0.47	0.006	5.2.0
<i>lmo0321</i>	hypothetical protein	0.47	0.008	5.2.0
<i>lmo2580</i>	ABC transporter ATP-binding protein	0.47	0.000	1.2.0
<i>lmo2190</i>	adaptor protein	0.48	0.002	1.10.0
<i>lmo0953</i>	hypothetical protein	0.48	0.003	6.0.0
<i>lmo2178</i>	peptidoglycan binding protein	0.48	0.008	1.8.0
<i>lmo1584</i>	hypothetical protein	0.48	0.000	5.2.0
<i>lmo2143</i>	hypothetical protein	0.48	0.002	2.1.1
<i>lmo2444</i>	glycosidase	0.48	0.004	2.1.1
<i>lmo1408</i>	hypothetical protein	0.49	0.001	5.2.0
<i>lmo2245</i>	hypothetical protein	0.49	0.001	5.2.0
<i>lmo1012</i>	N-acyl-L-amino acid amidohydrolase	0.49	0.000	2.2.0
<i>lmo0036</i>	putrescine carbamoyltransferase	0.50	0.003	2.2.0

<i>lmo2672</i>	AraC family transcriptional regulator	0.50	0.002	3.5.2
<i>lmo0212</i>	hypothetical protein	0.50	0.001	6.0.0
<i>lmo2085</i>	peptidoglycan binding protein	0.51	0.007	1.8.0
<i>lmo2255</i>	hypothetical protein	0.51	0.000	6.0.0
<i>lmo2564</i>	4-oxalocrotonate isomerase	0.51	0.002	2.1.1
<i>lmo0029</i>	hypothetical protein	0.51	0.000	5.2.0
<i>lmo1593</i>	iron-sulfur cofactor synthesis protein NifS	0.51	0.000	2.5.0
<i>lmo1626</i>	hypothetical protein	0.51	0.001	6.0.0
<i>lmo0385</i>	IolC protein	0.52	0.001	2.1.1
<i>lmo1742</i>	adenine deaminase	0.52	0.000	2.3.0
<i>lmo2010</i>	two-component response regulator	0.52	0.000	3.5.2
<i>lmo0415</i>	endo-1,4-beta-xylanase	0.52	0.000	2.1.1
<i>lmo2525</i>	rod shape-determining protein MreB	0.52	0.002	1.1.0
<i>lmo0845</i>	hypothetical protein	0.52	0.000	5.2.0
<i>lmo0959</i>	undecaprenyl-phosphate N-acetylglucosaminyltransferase	0.52	0.002	1.1.0
<i>lmo1339</i>	glucose kinase	0.52	0.000	2.1.1
<i>lmo1398</i>	recombinase A	0.52	0.000	3.3.0
<i>lmo0774</i>	hypothetical protein	0.53	0.000	5.2.0
<i>lmo1679</i>	cystathionine beta-lyase	0.53	0.002	2.2.0
<i>lmo2462</i>	dipeptidase	0.53	0.001	2.2.0
<i>lmo1645</i>	ATP-dependent dsDNA exonuclease SbcC	0.53	0.001	3.3.0
<i>lmo0075</i>	carboxyphosphoenolpyruvate phosphonmutase	0.53	0.004	2.1.1
<i>lmo0532</i>	hypothetical protein	0.53	0.001	6.0.0
<i>lmo0318</i>	thiamine-phosphate pyrophosphorylase	0.54	0.001	2.5.0
<i>lmo1860</i>	methionine sulfoxide reductase A	0.54	0.001	3.8.0
<i>lmo0082</i>	hypothetical protein	0.54	0.001	6.0.0
<i>lmo2268</i>	ATP-dependent deoxyribonuclease subunit B	0.54	0.002	3.3.0
<i>lmo1013</i>	hypothetical protein	0.55	0.002	5.2.0
<i>lmo1874</i>	thymidylate synthase	0.55	0.000	2.3.0
<i>lmo1956</i>	Fur family transcriptional regulator	0.55	0.000	3.5.2
<i>lmo2385</i>	hypothetical protein	0.55	0.000	5.2.0
<i>lmo2680</i>	potassium-transporting ATPase subunit C	0.56	0.000	1.2.0
<i>lmo1342</i>	competence protein ComGF	0.56	0.000	1.10.0
<i>lmo2767</i>	hypothetical protein	0.56	0.000	5.2.0
<i>lmo1135</i>	hypothetical protein	0.56	0.000	6.0.0
<i>lmo2267</i>	ATP-dependent deoxyribonuclease subunit A	0.56	0.001	3.3.0
<i>lmo1400</i>	N-acetyltransferase	0.57	0.000	4.2.0
<i>lmo2679</i>	histidine kinase	0.57	0.000	1.3.0
<i>lmo1267</i>	trigger factor	0.57	0.000	3.9.0
<i>lmo1744</i>	hypothetical protein	0.57	0.000	5.2.0
<i>lmo1411</i>	hypothetical protein	0.57	0.000	5.2.0
<i>lmo2055</i>	hypothetical protein	0.57	0.000	5.2.0
<i>lmo0900</i>	hypothetical protein	0.58	0.000	5.2.0
<i>lmo0829</i>	pyruvate-flavodoxin oxidoreductase	0.58	0.000	1.4.0
<i>lmo1639</i>	DNA-3-methyladenine glycosidase	0.58	0.002	3.2.0
<i>lmo2356</i>	hypothetical protein	0.58	0.000	6.0.0
<i>lmo0930</i>	hypothetical protein	0.58	0.000	5.2.0
<i>lmo2067</i>	bile acid hydrolase	0.58	0.000	4.2.0
<i>lmo1996</i>	DeoR family transcriptional regulator	0.58	0.000	3.5.2
<i>lmo1460</i>	DNA repair protein RecO	0.59	0.001	3.3.0
<i>lmo2471</i>	NADPH dehydrogenase	0.59	0.000	1.4.0

<i>lmo1461</i>	hypothetical protein	0.59	0.000	6.0.0
<i>lmo2171</i>	MFS transporter	0.59	0.000	1.2.0
<i>lmo0516</i>	encapsulation protein CapA	0.60	0.000	1.1.0
<i>lmo1607</i>	phenylalanyl-tRNA synthetase subunit beta	0.60	0.000	na
<i>lmo1678</i>	bifunctional homocysteine S-methyltransferase/5,10-methylenetetrahydrofolate reductase	0.60	0.000	2.2.0
<i>lmo0872</i>	antibiotic resistance protein	0.60	0.000	1.2.0
<i>lmo0571</i>	methyltransferase	0.60	0.000	3.2.0
<i>lmo1514</i>	recombination factor protein RarA	0.60	0.000	5.2.0
<i>lmo0383</i>	methylmalonate-semialdehyde dehydrogenase	0.61	0.000	2.1.1
<i>lmo1386</i>	DNA translocase	0.61	0.000	3.4.0
<i>lmo1401</i>	hypothetical protein	0.61	0.000	5.2.0
<i>lmo0386</i>	IolD protein	0.61	0.000	2.1.1
<i>lmo1681</i>	5-methyltetrahydropteroyltriglutamate-- homocysteine S-methyltransferase	0.62	0.000	2.2.0
<i>lmo2671</i>	hypothetical protein	0.62	0.000	6.0.0
<i>lmo0037</i>	amino acid transporter	0.62	0.000	1.2.0
<i>lmo2016</i>	cold-shock protein	0.62	0.000	4.1.0
<i>lmo1745</i>	two-component response regulator	0.63	0.000	3.5.2
<i>lmo0419</i>	hypothetical protein	0.63	0.000	5.2.0
<i>lmo1483</i>	competence protein ComEB	0.65	0.000	1.10.0
<i>lmo1535</i>	hypothetical protein	0.65	0.000	5.2.0
<i>lmo0038</i>	agmatine deiminase	0.65	0.000	5.2.0
<i>lmo2222</i>	hypothetical protein	0.65	0.000	5.2.0
<i>lmo2845</i>	MFS transporter	0.66	0.000	1.2.0
<i>lmo2011</i>	two-component sensor histidine kinase	0.66	0.000	1.3.0
<i>lmo2425</i>	glycine cleavage system protein H	0.66	0.000	2.2.0
<i>lmo2670</i>	hypothetical protein	0.66	0.000	5.2.0
<i>lmo0614</i>	hypothetical protein	0.67	0.000	5.2.0
<i>lmo2540</i>	phosphatase	0.67	0.000	2.6.0
<i>lmo0396</i>	pyrroline-5-carboxylate reductase	0.67	0.000	2.2.0
<i>lmo0160</i>	peptidoglycan binding protein	0.67	0.000	1.8.0
<i>lmo0451</i>	hypothetical protein	0.67	0.000	6.0.0
<i>lmo0831</i>	hypothetical protein	0.68	0.000	5.2.0
<i>lmo0397</i>	hypothetical protein	0.68	0.000	5.2.0
<i>lmo2043</i>	MFS transporter	0.68	0.000	5.2.0
<i>lmo2146</i>	LysR family transcriptional regulator	0.69	0.000	3.5.2
<i>lmo2014</i>	sugar hydrolase	0.70	0.000	2.1.1
<i>lmo1533</i>	Holliday junction DNA helicase RuvA	0.70	0.000	3.3.0
<i>lmo2501</i>	two-component response phosphate regulator	0.70	0.000	3.5.2
<i>lmo0360a</i>	hypothetical protein	0.70	0.000	na
<i>lmo0931</i>	lipoate protein ligase A	0.70	0.000	2.4.0
<i>lmo2709</i>	hypothetical protein	0.70	0.000	6.0.0
<i>lmo0390</i>	uracil-DNA glycosylase	0.71	0.000	3.2.0
<i>lmo1875</i>	ABC transporter ATP-binding protein	0.71	0.000	1.2.0
<i>lmo1457</i>	hypothetical protein	0.71	0.000	5.2.0
<i>lmo1780</i>	aminotripeptidase	0.71	0.000	2.2.0
<i>lmo2013</i>	hypothetical protein	0.71	0.000	5.2.0
<i>lmo2170</i>	hypothetical protein	0.72	0.000	5.2.0
<i>lmo0104</i>	hypothetical protein	0.73	0.000	6.0.0
<i>lmo1397</i>	competence damage-inducible protein CinA	0.74	0.000	1.10.0
<i>lmo2500</i>	two-component sensor histidine kinase	0.74	0.000	1.3.0

<i>lmo2541</i>	tRNA threonylcarbamoyladenosine biosynthesis protein	0.74	0.000	3.7.3
<i>lmo0941</i>	hypothetical protein	0.74	0.000	5.2.0
<i>lmo1846</i>	multidrug transporter	0.75	0.000	5.2.0
<i>lmo0603</i>	hypothetical protein	0.75	0.000	6.0.0
<i>lmo1950</i>	hypothetical protein	0.75	0.000	5.2.0
<i>lmo2339</i>	hypothetical protein	0.75	0.000	5.2.0
<i>lmo0039</i>	carbamate kinase	0.75	0.000	2.2.0
<i>lmo0368</i>	hypothetical protein	0.75	0.000	na
<i>lmo1778</i>	ABC transporter ATP-binding protein	0.76	0.000	1.2.0
<i>lmo1609</i>	thioredoxin	0.78	0.000	1.4.0
<i>lmo0645</i>	amino acid transporter	0.78	0.000	1.2.0
<i>lmo2189</i>	competence protein CoiA	0.79	0.000	1.10.0
<i>lmo0763</i>	Ser/Thr protein phosphatase family protein	0.80	0.000	5.2.0
<i>lmo1608</i>	hypothetical protein	0.81	0.000	5.2.0
<i>lmo0356</i>	oxidoreductase	0.82	0.000	2.1.1
<i>lmo0866a</i>	hypothetical protein	0.82	0.000	na
<i>lmo1611</i>	aminopeptidase	0.82	0.000	2.2.0
<i>lmo0942</i>	heat shock protein 90	0.83	0.000	4.1.0
<i>lmo0752</i>	hypothetical protein	0.84	0.000	4.2.0
<i>lmo1534</i>	L-lactate dehydrogenase	0.85	0.000	2.1.1

† Spearman correlation coefficient

‡ Functional classification is retrieved from ListiList (<http://genolist.pasteur.fr/ListiList/>).

Description for each functional category code is presented below;

[1.1.0] Cell envelope and cellular processes > Cell wall

[1.2.0] Cell envelope and cellular processes > Transport/binding proteins and lipoproteins

[1.3.0] Cell envelope and cellular processes > Sensors (signal transduction)

[1.4.0] Cell envelope and cellular processes > Membrane bioenergetics

[1.5.0] Cell envelope and cellular processes > Mobility and chemotaxis

[1.6.0] Cell envelope and cellular processes > Protein secretion

[1.7.0] Cell envelope and cellular processes > Cell division

[1.8.0] Cell envelope and cellular processes > Cell surface proteins

[1.9.0] Cell envelope and cellular processes > Soluble internalin

[1.10.0] Cell envelope and cellular processes > Transformation/competence

[2.1.0] Intermediary metabolism > Metabolism of carbohydrates and related molecule

[2.1.1] Intermediary metabolism > Metabolism of carbohydrates and related molecule > Specific pathways

[2.1.2] Intermediary metabolism > Metabolism of carbohydrates and related molecule > Main glycolytic pathways

[2.1.3] Intermediary metabolism > Metabolism of carbohydrates and related molecule > TCA cycle

[2.2.0] Intermediary metabolism > Metabolism of amino acids and related molecules

[2.3.0] Intermediary metabolism > Metabolism of nucleotides and nucleic acids

[2.4.0] Intermediary metabolism > Metabolism of lipids

[2.5.0] Intermediary metabolism > Metabolism of coenzymes and prosthetic groups

[2.6.0] Intermediary metabolism > Metabolism of phosphate

[3.1.0] Information pathways > DNA replication

[3.2.0] Information pathways > DNA restriction/modification and repair

[3.3.0] Information pathways > DNA recombination

[3.4.0] Information pathways > DNA packaging and segregation

[3.5.1] Information pathways > RNA synthesis > Initiation

[3.5.2] Information pathways > RNA synthesis > Regulation

[3.5.3] Information pathways > RNA synthesis > Elongation

[3.5.4] Information pathways > RNA synthesis > Termination

[3.6.0] Information pathways > RNA modification

[3.7.1] Information pathways > Protein synthesis > Ribosomal proteins
[3.7.2] Information pathways > Protein synthesis > Aminoacyl-tRNA synthetases
[3.7.3] Information pathways > Protein synthesis > Initiation
[3.7.4] Information pathways > Protein synthesis > Elongation
[3.7.5] Information pathways > Protein synthesis > Termination
[3.8.0] Information pathways > Protein modification
[3.9.0] Information pathways > Protein folding
[4.1.0] Other functions > Adaptation to atypical conditions
[4.2.0] Other functions > Detoxification
[4.3.0] Other functions > Phage-related functions
[4.4.0] Other functions > Transposon and IS
[4.5.0] Other functions > Miscellaneous
[5.1.0] Similar to unknown proteins > From Listeria
[5.2.0] Similar to unknown proteins > From other organisms
[6.0.0] No similarity
[na] No information available

Supplementary Table 3. List of genes whose transcript levels are correlated with genotype classification with regard to virulence (hypo- versus hypervirulence)

Locus tag	Product	Coefficient †	q-value	Functional category ‡
<i>lmo0752</i>	hypothetical protein	-0.68	0.000	4.2.0
<i>lmo1780</i>	aminotripeptidase	-0.68	0.000	2.2.0
<i>lmo0104</i>	hypothetical protein	-0.65	0.000	6.0.0
<i>lmo2014</i>	sugar hydrolase	-0.65	0.000	2.1.1
<i>lmo0532</i>	hypothetical protein	-0.63	0.000	6.0.0
<i>lmo0397</i>	hypothetical protein	-0.62	0.000	5.2.0
<i>lmo2170</i>	hypothetical protein	-0.62	0.000	5.2.0
<i>lmo2013</i>	hypothetical protein	-0.60	0.000	5.2.0
<i>lmo1457</i>	hypothetical protein	-0.59	0.000	5.2.0
<i>lmo1611</i>	aminopeptidase	-0.57	0.008	2.2.0
<i>lmo2845</i>	MFS transporter	-0.57	0.005	1.2.0
<i>lmo1534</i>	L-lactate dehydrogenase	-0.56	0.006	2.1.1
<i>lmo0942</i>	heat shock protein 90	-0.55	0.006	4.1.0
<i>lmo0645</i>	amino acid transporter	-0.55	0.011	1.2.0
<i>lmo0153</i>	zinc ABC transporter substrate-binding protein	-0.55	0.000	1.2.0
<i>lmo2549</i>	wall teichoic acid glycosylation protein GtcA	-0.55	0.006	1.1.0
<i>lmo0396</i>	pyrroline-5-carboxylate reductase	-0.54	0.008	2.2.0
<i>lmo2339</i>	hypothetical protein	-0.54	0.009	5.2.0
<i>lmo2011</i>	two-component sensor histidine kinase	-0.54	0.000	1.3.0
<i>lmo2189</i>	competence protein CoiA	-0.53	0.013	1.10.0
<i>lmo2146</i>	LysR family transcriptional regulator	-0.53	0.006	3.5.2
<i>lmo0941</i>	hypothetical protein	-0.52	0.007	5.2.0
<i>lmo0360a</i>	hypothetical protein	-0.52	0.011	na
<i>lmo1257</i>	hypothetical protein	-0.52	0.010	6.0.0
<i>lmo1135</i>	hypothetical protein	-0.52	0.005	6.0.0
<i>lmo2171</i>	MFS transporter	-0.51	0.009	1.2.0
<i>lmo0212</i>	hypothetical protein	-0.51	0.000	6.0.0
<i>lmo1744</i>	hypothetical protein	-0.51	0.007	5.2.0
<i>lmo0390</i>	uracil-DNA glycosylase	-0.51	0.008	3.2.0
<i>lmo1551</i>	folyl-polyglutamate synthetase	-0.51	0.003	2.5.0
<i>lmo0763</i>	Ser/Thr protein phosphatase family protein	-0.50	0.014	5.2.0
<i>lmo1609</i>	thioredoxin	-0.50	0.015	1.4.0
<i>lmo1950</i>	hypothetical protein	-0.50	0.011	5.2.0
<i>lmo0415</i>	endo-1,4-beta-xylanase	-0.49	0.007	2.1.1
<i>lmo1470</i>	16S ribosomal RNA methyltransferase RsmE	-0.49	0.008	5.2.0
<i>lmo0866a</i>	hypothetical protein	-0.49	0.017	na
<i>lmo1875</i>	ABC transporter ATP-binding protein	-0.49	0.021	1.2.0
<i>lmo0358</i>	PTS fructose transporter subunit IIBC	-0.49	0.015	1.2.0
<i>lmo1679</i>	cystathionine beta-lyase	-0.48	0.011	2.2.0
<i>lmo1397</i>	competence damage-inducible protein CinA	-0.48	0.020	1.10.0
<i>lmo2444</i>	glycosidase	-0.48	0.014	2.1.1
<i>lmo2500</i>	two-component sensor histidine kinase	-0.48	0.012	1.3.0
<i>lmo1504</i>	alanyl-tRNA synthetase	-0.48	0.009	3.7.2
<i>lmo2553</i>	hypothetical protein	-0.48	0.000	5.2.0
<i>lmo2068</i>	molecular chaperone GroEL	-0.48	0.005	3.9.0
<i>lmo1533</i>	Holliday junction DNA helicase RuvA	-0.47	0.021	3.3.0
<i>lmo0981</i>	transporter	-0.47	0.009	1.2.0

<i>lmo1471</i>	ribosomal protein L11 methyltransferase	-0.47	0.008	3.8.0
<i>lmo1411</i>	hypothetical protein	-0.47	0.013	5.2.0
<i>lmo2069</i>	co-chaperonin GroES	-0.47	0.006	3.9.0
<i>lmo1535</i>	hypothetical protein	-0.47	0.015	5.2.0
<i>lmo0419</i>	hypothetical protein	-0.47	0.012	5.2.0
<i>lmo2268</i>	ATP-dependent deoxyribonuclease subunit B	-0.47	0.022	3.3.0
<i>lmo1681</i>	5-methyltetrahydropteroyltriglutamate-- homocysteine S-methyltransferase	-0.46	0.022	2.2.0
<i>lmo1742</i>	adenine deaminase	-0.46	0.011	2.3.0
<i>lmo2442</i>	hypothetical protein	-0.46	0.003	5.2.0
<i>lmo1608</i>	hypothetical protein	-0.46	0.025	5.2.0
<i>lmo2425</i>	glycine cleavage system protein H	-0.46	0.009	2.2.0
<i>lmo1874</i>	thymidylate synthase	-0.46	0.014	2.3.0
<i>lmo1242</i>	hypothetical protein	-0.46	0.011	5.2.0
<i>lmo0931</i>	lipoate protein ligase A	-0.46	0.018	2.4.0
<i>lmo1519</i>	aspartyl-tRNA synthetase	-0.46	0.008	3.7.2
<i>lmo2501</i>	two-component response phosphate regulator	-0.46	0.015	3.5.2
<i>lmo1846</i>	multidrug transporter	-0.46	0.025	5.2.0
<i>lmo1778</i>	ABC transporter ATP-binding protein	-0.46	0.021	1.2.0
<i>lmo0510</i>	hypothetical protein	-0.46	0.014	6.0.0
<i>lmo1678</i>	bifunctional homocysteine S-methyltransferase/5,10-methylenetetrahydrofolate reductase	-0.45	0.012	2.2.0
<i>lmo2043</i>	MFS transporter	-0.45	0.024	5.2.0
<i>lmo0451</i>	hypothetical protein	-0.45	0.024	6.0.0
<i>lmo2222</i>	hypothetical protein	-0.45	0.024	5.2.0
<i>lmo0829</i>	pyruvate-flavodoxin oxidoreductase	-0.45	0.011	1.4.0
<i>lmo1460</i>	DNA repair protein RecO	-0.44	0.034	3.3.0
<i>lmo0959</i>	undecaprenyl-phosphate N-acetylglucosaminyltransferase	-0.44	0.023	1.1.0
<i>lmo0039</i>	carbamate kinase	-0.44	0.026	2.2.0
<i>lmo0136</i>	peptide ABC transporter permease	-0.43	0.003	1.2.0
<i>lmo1745</i>	two-component response regulator	-0.43	0.029	3.5.2
<i>lmo2462</i>	dipeptidase	-0.43	0.018	2.2.0
<i>lmo0498</i>	5-phosphate isomerase	-0.43	0.022	2.1.1
<i>lmo2267</i>	ATP-dependent deoxyribonuclease subunit A	-0.43	0.029	3.3.0
<i>lmo0317</i>	phosphomethylpyrimidine kinase	-0.43	0.017	2.5.0
<i>lmo0614</i>	hypothetical protein	-0.43	0.029	5.2.0
<i>lmo0900</i>	hypothetical protein	-0.43	0.022	5.2.0
<i>lmo0831</i>	hypothetical protein	-0.42	0.034	5.2.0
<i>lmo0571</i>	methyltransferase	-0.42	0.020	3.2.0
<i>lmo2373</i>	PTS beta-glucoside transporter subunit IIB	-0.42	0.032	1.2.0
<i>lmo0371</i>	GntR family transcriptional regulator	-0.42	0.038	3.5.2
<i>lmo1170</i>	PduX protein	-0.42	0.021	5.2.0
<i>lmo0833</i>	transcriptional regulator	-0.42	0.009	3.5.2
<i>lmo2172</i>	propionate CoA-transferase	-0.42	0.018	2.1.1
<i>lmo0383</i>	methylmalonate-semialdehyde dehydrogenase	-0.42	0.029	2.1.1
<i>lmo1639</i>	DNA-3-methyladenine glycosidase	-0.42	0.043	3.2.0
<i>lmo1017</i>	PTS glucose transporter subunit IIA	-0.42	0.028	1.2.0
<i>lmo0370</i>	hypothetical protein	-0.42	0.021	5.2.0
<i>lmo0356</i>	oxidoreductase	-0.42	0.045	2.1.1
<i>lmo2767</i>	hypothetical protein	-0.41	0.036	5.2.0
<i>lmo0167</i>	hypothetical protein	-0.41	0.005	5.2.0
<i>lmo1743</i>	hypothetical protein	-0.41	0.031	6.0.0

<i>lmo2083</i>	hypothetical protein	-0.41	0.040	5.2.0
<i>lmo0516</i>	encapsulation protein CapA	-0.41	0.018	1.1.0
<i>lmo0368</i>	hypothetical protein	-0.41	0.051	na
<i>lmo1483</i>	competence protein ComEB	-0.41	0.027	1.10.0
<i>lmo0318</i>	thiamine-phosphate pyrophosphorylase	-0.41	0.037	2.5.0
<i>lmo0872</i>	antibiotic resistance protein	-0.41	0.036	1.2.0
<i>lmo2709</i>	hypothetical protein	-0.41	0.034	6.0.0
<i>lmo2580</i>	ABC transporter ATP-binding protein	-0.41	0.006	1.2.0
<i>lmo1996</i>	DeoR family transcriptional regulator	-0.40	0.024	3.5.2
<i>lmo0508</i>	PTS galactitol transporter subunit IIC	-0.40	0.027	1.2.0
<i>lmo0154</i>	zinc ABC transporter ATP-binding protein	-0.40	0.022	1.2.0
<i>lmo2010</i>	two-component response regulator	-0.40	0.028	3.5.2
<i>lmo2525</i>	rod shape-determining protein MreB	-0.40	0.036	1.1.0
<i>lmo0357</i>	PTS sugar transporter subunit IIA	-0.40	0.018	1.2.0
<i>lmo2814</i>	TetR family transcriptional regulator	0.40	0.031	3.5.2
<i>lmo0853</i>	SugE protein	0.40	0.035	3.9.0
<i>lmo1445</i>	ZurR family transcriptional regulator	0.40	0.021	3.5.2
<i>lmo0617</i>	hypothetical protein	0.40	0.045	5.1.0
<i>lmo0733</i>	transcriptional regulator	0.40	0.033	3.5.2
<i>lmo0622</i>	hypothetical protein	0.40	0.018	6.0.0
<i>lmo0970</i>	enoyl-ACP reductase	0.41	0.030	2.4.0
<i>lmo1573</i>	acetyl-CoA carboxylase subunit beta	0.41	0.026	2.4.0
<i>lmo2201</i>	3-oxoacyl-ACP synthase	0.41	0.037	2.4.0
<i>lmo0480</i>	transcriptional regulator	0.41	0.029	3.5.2
<i>lmo0187</i>	hypothetical protein	0.41	0.033	5.2.0
<i>lmo1599</i>	catabolite control protein A	0.41	0.024	3.5.2
<i>lmo1877</i>	formyl-tetrahydrofolate synthetase	0.41	0.034	2.5.0
<i>lmo0623</i>	hypothetical protein	0.41	0.013	5.1.0
<i>lmo1527</i>	preprotein translocase SecDF	0.41	0.020	1.6.0
<i>lmo1827</i>	guanylate kinase	0.41	0.029	2.3.0
<i>lmo1908</i>	hypothetical protein	0.41	0.022	5.2.0
<i>lmo2729</i>	hypothetical protein	0.41	0.024	5.2.0
<i>lmo2025</i>	quinolinate synthetase	0.42	0.035	2.5.0
<i>lmo0724</i>	hypothetical protein	0.42	0.010	5.2.0
<i>lmo1247</i>	hypothetical protein	0.42	0.013	5.1.0
<i>lmo1447</i>	metal (zinc) transport protein(ABC transporter ATP-binding protein)	0.42	0.026	1.2.0
<i>lmo0613</i>	oxidoreductase	0.42	0.003	2.1.1
<i>lmo2023</i>	L-aspartate oxidase	0.42	0.013	2.5.0
<i>lmo0305</i>	L-allo-threonine aldolase	0.42	0.025	2.2.0
<i>lmo2739</i>	NAD-dependent deacetylase	0.42	0.030	3.5.2
<i>lmo0529</i>	glucosaminyltransferase	0.42	0.033	2.1.1
<i>lmo2078</i>	hypothetical protein	0.43	0.024	5.2.0
<i>lmo2092</i>	glycine betaine transporter BetL	0.43	0.030	1.2.0
<i>lmo1946</i>	acyl-CoA hydrolase	0.43	0.015	2.4.0
<i>lmo0612</i>	MarR family transcriptional evidence	0.43	0.000	3.5.2
<i>lmo1939</i>	cytidylate kinase	0.43	0.009	2.3.0
<i>lmo1149</i>	alpha-ribazole-5'-phosphatase	0.43	0.020	2.5.0
<i>lmo2793</i>	hypothetical protein	0.43	0.018	6.0.0
<i>lmo1308</i>	hypothetical protein	0.43	0.029	3.8.0
<i>lmo1485</i>	hypothetical protein	0.43	0.019	5.2.0
<i>lmo1812</i>	L-serine dehydratase	0.44	0.015	2.2.0

<i>lmo2641</i>	heptaprenyl diphosphate synthase subunit II	0.44	0.026	2.5.0
<i>lmo0755</i>	hypothetical protein	0.44	0.007	5.2.0
<i>lmo2523</i>	single-strand DNA-binding protein	0.44	0.015	3.1.0
<i>lmo2480</i>	acetyltransferase	0.44	0.013	2.1.1
<i>lmo1486</i>	hypothetical protein	0.44	0.015	5.2.0
<i>lmo2058</i>	heme O oxygenase	0.44	0.024	2.5.0
<i>lmo1446</i>	metal (zinc) transport protein (ABC transporter permease)	0.44	0.015	1.2.0
<i>lmo1005</i>	3-hydroxyisobutyrate dehydrogenase	0.44	0.009	2.4.0
<i>lmo0223</i>	cysteine synthase	0.44	0.018	2.2.0
<i>lmo2127</i>	hypothetical protein	0.44	0.026	5.2.0
<i>lmo1214</i>	hypothetical protein	0.44	0.028	6.0.0
<i>lmo1274</i>	polypeptide deformylase	0.44	0.016	3.8.0
<i>lmo2366</i>	DeoR family transcriptional regulator	0.44	0.026	3.5.2
<i>lmo1347</i>	competence protein ComGA	0.45	0.021	1.10.0
<i>lmo2728</i>	MerR family transcriptional regulator	0.45	0.024	3.5.2
<i>lmo0530</i>	hypothetical protein	0.45	0.025	5.2.0
<i>lmo1761</i>	sodium-dependent transporter	0.45	0.020	1.2.0
<i>lmo0983</i>	glutathione peroxidase	0.45	0.011	4.1.0
<i>lmo1890</i>	hypothetical protein	0.45	0.012	5.2.0
<i>lmo1878</i>	manganese transport transcriptional regulator	0.46	0.005	3.5.2
<i>lmo0528</i>	hypothetical protein	0.46	0.023	1.8.0
<i>lmo1127</i>	hypothetical protein	0.46	0.025	6.0.0
<i>lmo0531</i>	hypothetical protein	0.47	0.022	6.0.0
<i>lmo1419</i>	hypothetical protein	0.47	0.005	5.2.0
<i>lmo1283</i>	LacX protein	0.47	0.027	5.2.0
<i>lmo0522</i>	transcriptional regulator	0.47	0.014	3.5.2
<i>lmo1817</i>	hypothetical protein	0.47	0.022	2.5.0
<i>lmo0928</i>	3-methyladenine DNA glycosylase	0.47	0.016	3.2.0
<i>lmo0653</i>	hypothetical protein	0.48	0.012	5.2.0
<i>lmo1275</i>	DNA topoisomerase I	0.48	0.004	3.4.0
<i>lmo2377</i>	multidrug transporter	0.48	0.015	1.2.0
<i>lmo1212</i>	hypothetical protein	0.48	0.012	5.2.0
<i>lmo2587</i>	hypothetical protein	0.48	0.015	5.2.0
<i>lmo1670</i>	hypothetical protein	0.48	0.015	5.2.0
<i>lmo1291</i>	acyltransferase	0.48	0.015	1.1.0
<i>lmo1701</i>	hypothetical protein	0.48	0.011	6.0.0
<i>lmo1826</i>	DNA-directed RNA polymerase subunit omega	0.48	0.019	5.2.0
<i>lmo1312</i>	hypothetical protein	0.48	0.009	6.0.0
<i>lmo2033</i>	cell division protein FtsA	0.48	0.008	1.7.0
<i>lmo1049</i>	molybdopterin biosynthesis protein MoeB	0.48	0.016	2.5.0
<i>lmo0527</i>	transmembrane protein	0.48	0.009	6.0.0
<i>lmo2024</i>	nicotinate-nucleotide pyrophosphorylase	0.48	0.009	2.5.0
<i>lmo0003</i>	hypothetical protein	0.49	0.008	5.2.0
<i>lmo1870</i>	alkaline phosphatase	0.49	0.010	2.6.0
<i>lmo1644</i>	helicase SNF2	0.49	0.014	3.5.3
<i>lmo1688</i>	enoyl-ACP reductase	0.49	0.006	2.1.1
<i>lmo1371</i>	dihydrolipoamide dehydrogenase	0.50	0.003	2.4.0
<i>lmo2520</i>	O-succinylbenzoate-CoA synthase	0.50	0.000	2.5.0
<i>lmo0975</i>	ribose-5-phosphate isomerase A	0.50	0.007	2.1.1
<i>lmo2719</i>	hypothetical protein	0.51	0.003	5.2.0
<i>lmo0839</i>	tetracycline resistance protein	0.51	0.009	1.2.0

<i>lmo0652</i>	hypothetical protein	0.52	0.009	5.2.0
<i>lmo1800</i>	protein-tyrosine phosphatase	0.52	0.007	3.8.0
<i>lmo1050</i>	hypothetical protein	0.53	0.010	5.2.0
<i>lmo1213</i>	hypothetical protein	0.54	0.003	5.2.0
<i>lmo1370</i>	butyrate kinase	0.56	0.000	2.4.0
<i>lmo0540</i>	penicillin-binding protein	0.56	0.009	1.1.0
<i>lmo1089</i>	glycerol-3-phosphate cytidyltransferase	0.56	0.005	1.1.0
<i>lmo2117</i>	hypothetical protein	0.57	0.000	5.2.0
<i>lmo2032</i>	cell division protein FtsZ	0.57	0.005	1.7.0
<i>lmo0832</i>	transposase	0.57	0.005	4.4.0
<i>lmo2519</i>	teichoic acid linkage unit synthesis protein	0.57	0.000	1.1.0
<i>lmo1944</i>	ferredoxin	0.59	0.003	1.4.0
<i>lmo1779</i>	hypothetical protein	0.59	0.000	6.0.0
<i>lmo2557</i>	lipid kinase	0.59	0.000	5.2.0
<i>lmo0772</i>	transcriptional regulator	0.59	0.000	3.5.2
<i>lmo1430</i>	hypothetical protein	0.60	0.000	5.2.0
<i>lmo0322</i>	hypothetical protein	0.61	0.000	5.2.0
<i>lmo1500</i>	hypothetical protein	0.62	0.000	5.2.0
<i>lmo2551</i>	transcription termination factor Rho	0.62	0.000	3.5.4
<i>lmo1413</i>	peptidoglycan binding protein	0.64	0.000	1.8.0
<i>lmo2527</i>	hypothetical protein	0.65	0.000	5.2.0
<i>lmo1689</i>	A/G-specific adenine glycosylase	0.67	0.000	3.2.0
<i>lmo1078</i>	UDP-glucose pyrophosphorylase	0.67	0.000	1.1.0

† Spearman correlation coefficient

‡ Functional classification is retrieved from ListiList (<http://genolist.pasteur.fr/ListiList/>).

Description for each functional category code is presented below;

- [1.1.0] Cell envelope and cellular processes > Cell wall
- [1.2.0] Cell envelope and cellular processes > Transport/binding proteins and lipoproteins
- [1.3.0] Cell envelope and cellular processes > Sensors (signal transduction)
- [1.4.0] Cell envelope and cellular processes > Membrane bioenergetics
- [1.5.0] Cell envelope and cellular processes > Mobility and chemotaxis
- [1.6.0] Cell envelope and cellular processes > Protein secretion
- [1.7.0] Cell envelope and cellular processes > Cell division
- [1.8.0] Cell envelope and cellular processes > Cell surface proteins
- [1.9.0] Cell envelope and cellular processes > Soluble internalin
- [1.10.0] Cell envelope and cellular processes > Transformation/competence
- [2.1.0] Intermediary metabolism > Metabolism of carbohydrates and related molecule
 - [2.1.1] Intermediary metabolism > Metabolism of carbohydrates and related molecule > Specific pathways
 - [2.1.2] Intermediary metabolism > Metabolism of carbohydrates and related molecule > Main glycolytic pathways
 - [2.1.3] Intermediary metabolism > Metabolism of carbohydrates and related molecule > TCA cycle
- [2.2.0] Intermediary metabolism > Metabolism of amino acids and related molecules
- [2.3.0] Intermediary metabolism > Metabolism of nucleotides and nucleic acids
- [2.4.0] Intermediary metabolism > Metabolism of lipids
- [2.5.0] Intermediary metabolism > Metabolism of coenzymes and prosthetic groups
- [2.6.0] Intermediary metabolism > Metabolism of phosphate
- [3.1.0] Information pathways > DNA replication
- [3.2.0] Information pathways > DNA restriction/modification and repair
- [3.3.0] Information pathways > DNA recombination
- [3.4.0] Information pathways > DNA packaging and segregation
 - [3.5.1] Information pathways > RNA synthesis > Initiation
 - [3.5.2] Information pathways > RNA synthesis > Regulation

[3.5.3] Information pathways > RNA synthesis > Elongation
[3.5.4] Information pathways > RNA synthesis > Termination
[3.6.0] Information pathways > RNA modification
[3.7.1] Information pathways > Protein synthesis > Ribosomal proteins
[3.7.2] Information pathways > Protein synthesis > Aminoacyl-tRNA synthetases
[3.7.3] Information pathways > Protein synthesis > Initiation
[3.7.4] Information pathways > Protein synthesis > Elongation
[3.7.5] Information pathways > Protein synthesis > Termination
[3.8.0] Information pathways > Protein modification
[3.9.0] Information pathways > Protein folding
[4.1.0] Other functions > Adaptation to atypical conditions
[4.2.0] Other functions > Detoxification
[4.3.0] Other functions > Phage-related functions
[4.4.0] Other functions > Transposon and IS
[4.5.0] Other functions > Miscellaneous
[5.1.0] Similar to unknown proteins > From Listeria
[5.2.0] Similar to unknown proteins > From other organisms
[6.0.0] No similarity
[na] No information available

Supplementary Table 4. Comparison of q-values in Spearman's rank correlation analyses between original and refined datasets

Locus tag	product	Lineage		Maury's		LT50	
		Orig nal	Refin ed	Orig nal	Refin ed	Orig nal	Refin ed
<i>lmo0001</i>	chromosome replication initiator DnaA	0.24	0.12	0.13	0.10	0.75	0.14
<i>lmo0002</i>	DNA polymerase III subunit beta	0.19	0.11	0.13	0.14	0.74	0.24
<i>lmo0003</i>	hypothetical protein	0.37	0.00	0.33	0.01	0.76	0.35
<i>lmo0004</i>	hypothetical protein	0.12	0.38	0.02	0.43	0.80	0.58
<i>lmo0005</i>	recombination protein F	0.24	0.39	0.12	0.55	0.87	0.61
<i>lmo0006</i>	DNA gyrase subunit B	0.17	0.44	0.13	0.48	0.90	0.40
<i>lmo0007</i>	DNA gyrase subunit A	0.02	0.02	0.05	0.19	0.87	0.46
<i>lmo0008</i>	cardiolipin synthase	0.01	0.00	0.04	0.05	0.69	0.38
<i>lmo0009</i>	spermidine acetyltransferase	0.12	0.42	0.04	0.43	0.89	0.67
<i>lmo0010</i>	mevalonate kinase	0.40	0.08	0.12	0.50	0.89	0.55
<i>lmo0011</i>	mevalonate diphosphate decarboxylase	0.17	0.40	0.04	0.36	0.91	0.47
<i>lmo0012</i>	mevalonate kinase	0.36	0.01	0.08	0.33	0.88	0.69
<i>lmo0013</i>	AA3-600 quinol oxidase subunit II	0.03	0.17	0.01	0.08	0.85	0.64
<i>lmo0014</i>	AA3-600 quinol oxidase subunit I	0.04	0.11	0.02	0.08	0.80	0.54
<i>lmo0015</i>	AA3-600 quinol oxidase subunit III	0.03	0.12	0.01	0.09	0.76	0.49
<i>lmo0016</i>	quinol oxidase aa3-600 subunit IV	0.03	0.08	0.02	0.16	0.82	0.58
<i>lmo0017</i>	capsule biosynthesis protein CapA	0.10	0.41	0.01	0.30	0.85	0.68
<i>lmo0018</i>	beta-glucosidase	0.02	0.11	0.02	0.22	0.84	0.52
<i>lmo0019</i>	hypothetical protein	0.24	0.38	0.07	0.48	0.74	0.29
<i>lmo0020</i>	GntR family transcriptional regulator	0.19	0.34	0.05	0.53	0.84	0.40
<i>lmo0021</i>	PTS fructose transporter subunit IIA	0.27	0.34	0.09	0.48	0.88	0.39
<i>lmo0022</i>	PTS fructose transporter subunit IIB	0.30	0.30	0.09	0.45	0.88	0.50
<i>lmo0023</i>	PTS fructose transporter subunit IIC	0.20	0.35	0.07	0.31	0.84	0.36
<i>lmo0024</i>	PTS mannose transporter subunit IID	0.07	0.13	0.03	0.26	0.85	0.36
<i>lmo0025</i>	phosphoheptose isomerase	0.12	0.40	0.02	0.27	0.92	0.26
<i>lmo0026</i>	copper homeostasis protein CutC	0.01	0.01	0.01	0.04	0.79	0.28
<i>lmo0027</i>	PTS beta-glucoside transporter subunit IIABC	0.10	0.39	0.02	0.24	0.92	0.62
<i>lmo0029</i>	hypothetical protein	0.00	0.00	0.07	0.11	0.74	0.41
<i>lmo0030</i>	hypothetical protein	0.14	0.06	0.17	0.17	0.83	0.47
<i>lmo0031</i>	LacI family transcription regulator	0.10	0.01	0.17	0.08	0.91	0.60
<i>lmo0032</i>	xylose repressor	0.00	0.02	0.01	0.16	0.74	0.20
<i>lmo0033</i>	endoglucanase	0.03	0.03	0.02	0.25	0.71	0.15
<i>lmo0034</i>	PTS cellbiose transporter subunit IIC	0.01	0.01	0.03	0.41	0.66	0.13
<i>lmo0035</i>	glucosamine--fructose-6-phosphate aminotransferase	0.01	0.04	0.02	0.24	0.66	0.09
<i>lmo0036</i>	putrescine carbamoyltransferase	0.28	0.00	0.29	0.06	0.92	0.68
<i>lmo0037</i>	amino acid transporter	0.05	0.00	0.26	0.09	0.85	0.43
<i>lmo0038</i>	agmatine deiminase	0.15	0.00	0.28	0.10	0.76	0.30
<i>lmo0039</i>	carbamate kinase	0.07	0.00	0.26	0.03	0.72	0.23
<i>lmo0040</i>	agmatine deiminase	0.30	0.49	0.13	0.48	0.86	0.66
<i>lmo0041</i>	hypothetical protein	0.00	0.01	0.01	0.21	0.88	0.56
<i>lmo0042</i>	DedA protein	0.25	0.03	0.09	0.09	0.74	0.10
<i>lmo0043</i>	arginine deiminase	0.15	0.50	0.06	0.46	0.75	0.33
<i>lmo0044</i>	30S ribosomal protein S6	0.05	0.16	0.01	0.14	0.91	0.60
<i>lmo0045</i>	single-strand binding protein	0.04	0.32	0.02	0.26	0.91	0.66
<i>lmo0046</i>	30S ribosomal protein S18	0.09	0.42	0.03	0.36	0.91	0.65
<i>lmo0047</i>	hypothetical protein	0.04	0.13	0.00	0.03	0.75	0.40
<i>lmo0048</i>	sensor histidine kinase AgrB	0.09	0.14	0.08	0.19	0.90	0.69
<i>lmo0051</i>	response regulator	0.12	0.12	0.24	0.37	0.83	0.53
<i>lmo0052</i>	hypothetical protein	0.39	0.26	0.26	0.52	0.85	0.53
<i>lmo0053</i>	50S ribosomal protein L9	0.40	0.50	0.29	0.52	0.85	0.54
<i>lmo0054</i>	replicative DNA helicase	0.18	0.19	0.24	0.48	0.74	0.38
<i>lmo0055</i>	adenylosuccinate synthetase	0.33	0.03	0.09	0.37	0.89	0.55
<i>lmo0056</i>	heat shock protein	0.07	0.15	0.06	0.20	0.72	0.28
<i>lmo0057</i>	hypothetical protein	0.01	0.03	0.02	0.10	0.72	0.23
<i>lmo0059</i>	hypothetical protein	0.18	0.44	0.05	0.36	0.92	0.69

<i>lmo0060</i>	hypothetical protein	0.14	0.34	0.05	0.20	0.92	0.49
<i>lmo0075</i>	carboxyphosphoenolpyruvate phosphonmutase	0.01	0.00	0.04	0.10	0.75	0.37
<i>lmo0076</i>	O6-methylguanine-DNA methyltransferase	0.20	0.18	0.24	0.54	0.77	0.42
<i>lmo0077</i>	hypothetical protein	0.06	0.02	0.27	0.46	0.69	0.33
<i>lmo0078</i>	phosphoglycerate dehydrogenase	0.03	0.25	0.03	0.52	0.87	0.17
<i>lmo0082</i>	hypothetical protein	0.00	0.00	0.02	0.16	0.68	0.20
<i>lmo0083</i>	MerR family transcriptional regulator	0.01	0.01	0.08	0.35	0.76	0.27
<i>lmo0084</i>	oxidoreductase	0.02	0.01	0.16	0.44	0.73	0.38
<i>lmo0085</i>	hypothetical protein	0.10	0.10	0.16	0.29	0.86	0.49
<i>lmo0087</i>	hypothetical protein	0.32	0.44	0.17	0.55	0.87	0.52
<i>lmo0088</i>	ATP synthase subunit C	0.26	0.35	0.26	0.41	0.82	0.52
<i>lmo0089</i>	ATP synthase subunit delta	0.12	0.01	0.29	0.26	0.74	0.23
<i>lmo0090</i>	ATP synthase F0F1 subunit alpha	0.23	0.01	0.24	0.32	0.70	0.21
<i>lmo0091</i>	ATP synthase subunit gamma	0.22	0.02	0.32	0.17	0.70	0.21
<i>lmo0092</i>	ATP synthase F0F1 subunit beta	0.11	0.02	0.30	0.34	0.64	0.20
<i>lmo0093</i>	ATP synthase subunit epsilon	0.14	0.18	0.16	0.47	0.92	0.65
<i>lmo0094</i>	hypothetical protein	0.28	0.41	0.11	0.16	0.83	0.42
<i>lmo0095</i>	hypothetical protein	0.00	0.00	0.02	0.10	0.90	0.47
<i>lmo0096</i>	PTS mannose transporter subunit IIAB	0.39	0.25	0.16	0.48	0.90	0.58
<i>lmo0097</i>	PTS mannose transporter subunit IIC	0.42	0.17	0.21	0.55	0.91	0.61
<i>lmo0098</i>	PTS mannose transporter subunit IID	0.31	0.11	0.27	0.54	0.88	0.64
<i>lmo0099</i>	hypothetical protein	0.33	0.36	0.08	0.46	0.92	0.41
<i>lmo0100</i>	hypothetical protein	0.13	0.44	0.01	0.18	0.73	0.45
<i>lmo0101</i>	transcriptional regulator	0.11	0.32	0.01	0.25	0.91	0.65
<i>lmo0102</i>	hypothetical protein	0.13	0.43	0.00	0.04	0.88	0.41
<i>lmo0103</i>	NADH oxidase	0.23	0.45	0.01	0.07	0.91	0.52
<i>lmo0104</i>	hypothetical protein	0.00	0.00	0.00	0.00	0.56	0.20
<i>lmo0107</i>	ABC transporter ATP-binding protein	0.28	0.31	0.10	0.20	0.61	0.17
<i>lmo0109</i>	AraC family transcriptional regulator	0.11	0.41	0.01	0.34	0.89	0.39
<i>lmo0110</i>	lipase	0.13	0.36	0.01	0.33	0.90	0.57
<i>lmo0111</i>	hypothetical protein	0.09	0.32	0.07	0.45	0.92	0.56
<i>lmo0112</i>	Fnr/Crp family transcriptional regulator	0.17	0.06	0.23	0.44	0.92	0.65
<i>lmo0113</i>	hypothetical protein	0.25	0.09	0.19	0.08	0.88	0.58
<i>lmo0114</i>	repressor C1	0.36	0.04	0.26	0.05	0.88	0.67
<i>lmo0115</i>	hypothetical protein	0.32	0.21	0.24	0.19	0.86	0.57
<i>lmo0116</i>	hypothetical protein	0.42	0.31	0.31	0.28	0.88	0.59
<i>lmo0117</i>	antigen B	0.34	0.21	0.25	0.18	0.91	0.68
<i>lmo0118</i>	antigen A	0.32	0.22	0.25	0.20	0.90	0.66
<i>lmo0119</i>	hypothetical protein	0.35	0.26	0.25	0.23	0.92	0.67
<i>lmo0120</i>	hypothetical protein	0.29	0.23	0.21	0.22	0.92	0.69
<i>lmo0121</i>	phage tail protein	0.32	0.22	0.24	0.22	0.92	0.69
<i>lmo0122</i>	hypothetical protein	0.36	0.27	0.26	0.27	0.93	0.69
<i>lmo0123</i>	hypothetical protein	0.33	0.23	0.25	0.23	0.93	0.70
<i>lmo0124</i>	hypothetical protein	0.34	0.24	0.23	0.20	0.92	0.70
<i>lmo0125</i>	hypothetical protein	0.34	0.25	0.25	0.22	0.92	0.66
<i>lmo0126</i>	hypothetical protein	0.35	0.23	0.29	0.25	0.92	0.69
<i>lmo0127</i>	hypothetical protein	0.38	0.27	0.29	0.25	0.92	0.67
<i>lmo0128</i>	hypothetical protein	0.37	0.37	0.28	0.37	0.92	0.66
<i>lmo0129</i>	N-acetylmuramoyl-L-alanine amidase	0.43	0.31	0.29	0.26	0.92	0.65
<i>lmo0130</i>	5'-nucleotidase	0.27	0.44	0.13	0.54	0.63	0.22
<i>lmo0131</i>	hypothetical protein	0.18	0.37	0.24	0.12	0.91	0.67
<i>lmo0132</i>	inosine 5-monophosphate dehydrogenase	0.01	0.22	0.02	0.42	0.88	0.69
<i>lmo0133</i>	hypothetical protein	0.37	0.01	0.11	0.47	0.64	0.16
<i>lmo0134</i>	hypothetical protein	0.39	0.04	0.09	0.51	0.67	0.18
<i>lmo0135</i>	peptide ABC transporter substrate-binding protein	0.01	0.10	0.01	0.12	0.67	0.36
<i>lmo0136</i>	peptide ABC transporter permease	0.02	0.06	0.00	0.00	0.72	0.56
<i>lmo0137</i>	peptide ABC transporter permease	0.04	0.14	0.00	0.01	0.68	0.52
<i>lmo0139</i>	hypothetical protein	0.39	0.45	0.24	0.24	0.92	0.64
<i>lmo0152</i>	peptide ABC transporter substrate-binding protein	0.02	0.28	0.06	0.49	0.70	0.52
<i>lmo0153</i>	zinc ABC transporter substrate-binding protein	0.00	0.02	0.00	0.00	0.90	0.61
<i>lmo0154</i>	zinc ABC transporter ATP-binding protein	0.02	0.08	0.00	0.02	0.82	0.46

<i>lmo0155</i>	zinc ABC transporter permease	0.09	0.21	0.00	0.04	0.67	0.27
<i>lmo0156</i>	hypothetical protein	0.01	0.00	0.10	0.05	0.74	0.36
<i>lmo0157</i>	ATP-dependent helicase	0.11	0.05	0.21	0.53	0.89	0.56
<i>lmo0158</i>	hypothetical protein	0.04	0.00	0.32	0.14	0.74	0.36
<i>lmo0160</i>	peptidoglycan binding protein	0.00	0.00	0.02	0.09	0.70	0.30
<i>lmo0161</i>	hypothetical protein	0.00	0.00	0.02	0.36	0.89	0.29
<i>lmo0162</i>	DNA polymerase III subunit delta'	0.07	0.05	0.03	0.13	0.92	0.59
<i>lmo0163</i>	hypothetical protein	0.14	0.44	0.07	0.50	0.88	0.61
<i>lmo0164</i>	DNA replication initiation control protein YabA	0.18	0.31	0.11	0.36	0.74	0.48
<i>lmo0165</i>	hypothetical protein	0.06	0.47	0.02	0.25	0.75	0.43
<i>lmo0166</i>	GIY-YIG nuclease	0.02	0.12	0.01	0.07	0.84	0.67
<i>lmo0167</i>	hypothetical protein	0.01	0.00	0.00	0.00	0.83	0.70
<i>lmo0168</i>	AbrB family transcriptional regulator	0.37	0.11	0.27	0.18	0.70	0.33
<i>lmo0169</i>	glucose transporter	0.08	0.39	0.03	0.40	0.83	0.43
<i>lmo0170</i>	hypothetical protein	0.08	0.28	0.02	0.16	0.81	0.40
<i>lmo0175</i>	peptidoglycan-binding protein	0.22	0.10	0.25	0.27	0.66	0.23
<i>lmo0176</i>	glucose transporter	0.01	0.03	0.01	0.03	0.92	0.50
<i>lmo0177</i>	methionyl-tRNA synthetase	0.02	0.13	0.01	0.02	0.81	0.52
<i>lmo0178</i>	xylose repressor	0.16	0.46	0.15	0.29	0.86	0.33
<i>lmo0179</i>	sugar ABC transporter permease	0.09	0.37	0.09	0.51	0.74	0.34
<i>lmo0180</i>	sugar ABC transporter permease	0.18	0.22	0.22	0.55	0.69	0.40
<i>lmo0182</i>	alpha-glucosidase	0.14	0.10	0.31	0.54	0.74	0.51
<i>lmo0183</i>	alpha-glucosidase	0.18	0.05	0.31	0.51	0.68	0.46
<i>lmo0184</i>	oligo-16-glucosidase	0.02	0.00	0.24	0.39	0.58	0.23
<i>lmo0185</i>	hypothetical protein	0.35	0.10	0.16	0.21	0.89	0.58
<i>lmo0186</i>	hypothetical protein	0.24	0.15	0.08	0.45	0.91	0.59
<i>lmo0187</i>	hypothetical protein	0.11	0.00	0.25	0.03	0.78	0.35
<i>lmo0188</i>	dimethyladenosine transferase	0.21	0.30	0.08	0.44	0.90	0.67
<i>lmo0189</i>	Veg protein	0.08	0.32	0.02	0.19	0.86	0.66
<i>lmo0191</i>	phospho-beta-glucosidase	0.16	0.35	0.30	0.17	0.86	0.62
<i>lmo0192</i>	PurR family transcriptional regulator	0.25	0.34	0.05	0.21	0.89	0.69
<i>lmo0193</i>	hypothetical protein	0.31	0.04	0.10	0.54	0.75	0.40
<i>lmo0194</i>	ABC transporter ATP-binding protein	0.17	0.00	0.18	0.34	0.71	0.31
<i>lmo0195</i>	ABC transporter permease	0.32	0.02	0.08	0.53	0.59	0.20
<i>lmo0196</i>	regulatory protein SpoVG	0.23	0.48	0.26	0.23	0.89	0.50
<i>lmo0197</i>	regulatory protein SpoVG	0.22	0.22	0.09	0.15	0.87	0.56
<i>lmo0198</i>	bifunctional N-acetylglucosamine-1-phosphate uridyltransferase/glucosamine-1-phosphate acetyltransferase	0.40	0.01	0.12	0.25	0.92	0.66
<i>lmo0199</i>	ribose-phosphate pyrophosphokinase	0.42	0.00	0.18	0.13	0.88	0.47
<i>lmo0200</i>	listeriolysin positive regulatory protein	0.20	0.38	0.21	0.22	0.90	0.29
<i>lmo0201</i>	phosphatidylinositol-specific phospholipase c	0.12	0.49	0.06	0.41	0.91	0.52
<i>lmo0202</i>	listeriolysin O precursor	0.16	0.04	0.05	0.28	0.74	0.63
<i>lmo0203</i>	Zinc metalloproteinase precursor	0.12	0.33	0.11	0.55	0.85	0.48
<i>lmo0204</i>	actin-assembly inducing protein precursor	0.18	0.31	0.16	0.46	0.92	0.69
<i>lmo0205</i>	phospholipase C	0.11	0.16	0.15	0.39	0.90	0.58
<i>lmo0206</i>	hypothetical protein	0.16	0.47	0.02	0.23	0.78	0.38
<i>lmo0207</i>	hypothetical protein	0.05	0.24	0.03	0.21	0.91	0.37
<i>lmo0208</i>	hypothetical protein	0.04	0.06	0.08	0.36	0.90	0.57
<i>lmo0209</i>	hypothetical protein	0.12	0.07	0.21	0.36	0.91	0.63
<i>lmo0210</i>	L-lactate dehydrogenase	0.08	0.23	0.08	0.44	0.86	0.39
<i>lmo0211</i>	50S ribosomal protein L25	0.09	0.20	0.06	0.10	0.81	0.54
<i>lmo0212</i>	hypothetical protein	0.02	0.00	0.01	0.00	0.91	0.68
<i>lmo0213</i>	peptidyl-tRNA hydrolase	0.00	0.00	0.05	0.03	0.75	0.21
<i>lmo0214</i>	transcription-repair coupling factor	0.14	0.38	0.01	0.18	0.75	0.55
<i>lmo0215</i>	hypothetical protein	0.10	0.48	0.02	0.12	0.76	0.58
<i>lmo0216</i>	hypothetical protein	0.07	0.00	0.30	0.36	0.67	0.31
<i>lmo0217</i>	DivIC protein	0.07	0.00	0.23	0.10	0.59	0.22
<i>lmo0218</i>	hypothetical protein	0.13	0.49	0.04	0.31	0.91	0.59
<i>lmo0219</i>	hypothetical protein	0.35	0.01	0.14	0.09	0.90	0.65
<i>lmo0220</i>	cell division protein FtsH	0.33	0.03	0.18	0.09	0.85	0.66
<i>lmo0221</i>	pantothenate kinase	0.10	0.10	0.06	0.21	0.70	0.16

<i>lmo0222</i>	heat shock protein 33	0.32	0.20	0.12	0.47	0.84	0.37
<i>lmo0223</i>	cysteine synthase	0.33	0.03	0.16	0.02	0.58	0.23
<i>lmo0224</i>	dihydropteroate synthases	0.07	0.16	0.24	0.48	0.85	0.32
<i>lmo0225</i>	dihydroneopterin aldolase	0.31	0.31	0.13	0.33	0.90	0.68
<i>lmo0226</i>	78-dihydro-6-hydroxymethylpterin pyrophosphokinase	0.01	0.08	0.01	0.14	0.88	0.61
<i>lmo0227</i>	hypothetical protein	0.02	0.02	0.01	0.04	0.91	0.69
<i>lmo0228</i>	lysyl-tRNA synthetase	0.04	0.28	0.01	0.07	0.80	0.53
<i>lmo0229</i>	CtsR family transcriptional regulator	0.07	0.24	0.10	0.55	0.87	0.59
<i>lmo0230</i>	hypothetical protein	0.13	0.47	0.11	0.48	0.83	0.63
<i>lmo0231</i>	ATP:guanido phosphotransferase	0.06	0.34	0.05	0.55	0.87	0.69
<i>lmo0232</i>	endopeptidase Clp ATP-binding chain C	0.12	0.45	0.08	0.32	0.88	0.59
<i>lmo0233</i>	DNA repair protein RadA	0.12	0.23	0.02	0.12	0.92	0.67
<i>lmo02333</i>	hypothetical protein	0.42	0.43	0.22	0.48	0.75	0.45
<i>lmo0234</i>	hypothetical protein	0.32	0.16	0.30	0.12	0.73	0.44
<i>lmo0235</i>	2-C-methyl-D-erythritol 4-phosphate cytidyltransferase	0.42	0.02	0.26	0.02	0.62	0.30
<i>lmo0236</i>	2-C-methyl-D-erythritol 24-cyclodiphosphate synthase	0.25	0.14	0.19	0.16	0.61	0.28
<i>lmo0237</i>	glutamyl-tRNA synthetase	0.02	0.10	0.02	0.24	0.75	0.66
<i>lmo0238</i>	serine O-acetyltransferase	0.01	0.11	0.02	0.43	0.92	0.67
<i>lmo0239</i>	cysteinyl-tRNA synthetase	0.09	0.46	0.12	0.33	0.74	0.56
<i>lmo0240</i>	hypothetical protein	0.05	0.42	0.10	0.41	0.74	0.70
<i>lmo0241</i>	hypothetical protein	0.01	0.20	0.04	0.51	0.80	0.60
<i>lmo0242</i>	hypothetical protein	0.03	0.47	0.07	0.38	0.75	0.69
<i>lmo0243</i>	RNA polymerase factor sigma-70	0.01	0.10	0.03	0.55	0.83	0.54
<i>lmo0244</i>	50S ribosomal protein L33 type II	0.21	0.42	0.18	0.24	0.92	0.55
<i>lmo0245</i>	preprotein translocase subunit SecE	0.21	0.47	0.18	0.17	0.92	0.62
<i>lmo0246</i>	transcription antitermination protein NusG	0.17	0.44	0.06	0.54	0.92	0.70
<i>lmo0247</i>	hypothetical protein	0.10	0.35	0.02	0.19	0.89	0.62
<i>lmo0248</i>	50S ribosomal protein L11	0.10	0.32	0.01	0.11	0.88	0.53
<i>lmo0249</i>	50S ribosomal protein L1	0.10	0.28	0.01	0.10	0.83	0.53
<i>lmo0250</i>	50S ribosomal protein L10	0.10	0.22	0.06	0.19	0.88	0.63
<i>lmo0251</i>	50S ribosomal protein L7/L12	0.04	0.07	0.03	0.10	0.90	0.55
<i>lmo0256</i>	hypothetical protein	0.15	0.04	0.11	0.55	0.74	0.30
<i>lmo0257</i>	hypothetical protein	0.37	0.44	0.26	0.49	0.81	0.53
<i>lmo0258</i>	DNA-directed RNA polymerase subunit beta	0.31	0.10	0.14	0.25	0.72	0.35
<i>lmo0259</i>	DNA-directed RNA polymerase subunit beta'	0.14	0.36	0.05	0.37	0.71	0.41
<i>lmo0260</i>	hypothetical protein	0.26	0.03	0.11	0.12	0.89	0.65
<i>lmo0261</i>	phospho-beta-glucosidase	0.05	0.43	0.02	0.41	0.91	0.26
<i>lmo0264</i>	internalin E	0.00	0.00	0.02	0.10	0.87	0.24
<i>lmo0265</i>	succinyl-diaminopimelate desuccinylase	0.28	0.03	0.13	0.17	0.72	0.20
<i>lmo0266</i>	transcriptional regulator	0.08	0.45	0.15	0.11	0.87	0.58
<i>lmo0267</i>	hypothetical protein	0.00	0.00	0.01	0.26	0.89	0.18
<i>lmo0268</i>	phosphoglycerate mutase	0.00	0.02	0.03	0.36	0.85	0.24
<i>lmo0269</i>	transporter	0.02	0.08	0.06	0.36	0.70	0.16
<i>lmo0270</i>	hypothetical protein	0.00	0.01	0.02	0.15	0.88	0.33
<i>lmo0271</i>	phospho-beta-glucosidase	0.01	0.03	0.01	0.18	0.91	0.32
<i>lmo0272</i>	hypothetical protein	0.41	0.04	0.18	0.13	0.89	0.65
<i>lmo0273</i>	hypothetical protein	0.12	0.26	0.03	0.21	0.82	0.38
<i>lmo0274</i>	hypothetical protein	0.03	0.11	0.02	0.23	0.90	0.46
<i>lmo0276</i>	hypothetical protein	0.15	0.38	0.09	0.44	0.60	0.27
<i>lmo0277</i>	oxidoreductase	0.34	0.02	0.10	0.23	0.85	0.50
<i>lmo0278</i>	sugar ABC transporter ATP-binding protein	0.18	0.48	0.13	0.38	0.73	0.32
<i>lmo0279</i>	anaerobic ribonucleoside triphosphate reductase	0.33	0.43	0.26	0.26	0.78	0.32
<i>lmo0280</i>	anaerobic ribonucleotide reductase activator protein	0.28	0.39	0.25	0.42	0.89	0.40
<i>lmo0281</i>	hypothetical protein	0.01	0.05	0.02	0.48	0.92	0.36
<i>lmo0282</i>	hypothetical protein	0.18	0.09	0.14	0.16	0.60	0.26
<i>lmo0283</i>	ABC transporter permease	0.06	0.37	0.02	0.41	0.71	0.24
<i>lmo0284</i>	ABC transporter ATP-binding protein	0.04	0.24	0.05	0.50	0.75	0.34
<i>lmo0285</i>	lipoprotein	0.03	0.16	0.04	0.49	0.87	0.44
<i>lmo0286</i>	aminotransferase	0.13	0.43	0.04	0.29	0.90	0.64
<i>lmo0287</i>	two-component response regulator	0.35	0.07	0.30	0.12	0.88	0.51
<i>lmo0288</i>	two-component sensor histidine kinase	0.01	0.01	0.01	0.08	0.91	0.40

<i>lmo0289</i>	hypothetical protein	0.00	0.06	0.01	0.34	0.74	0.57
<i>lmo0290</i>	hypothetical protein	0.05	0.28	0.03	0.23	0.62	0.30
<i>lmo0291</i>	hypothetical protein	0.13	0.25	0.04	0.54	0.74	0.31
<i>lmo0292</i>	heat-shock protein htrA serine protease	0.07	0.45	0.02	0.43	0.80	0.62
<i>lmo0293</i>	rRNA large subunit methyltransferase	0.01	0.09	0.00	0.05	0.75	0.19
<i>lmo0296</i>	hypothetical protein	0.07	0.04	0.30	0.42	0.84	0.52
<i>lmo0297</i>	transcriptional antiterminator BglG	0.11	0.21	0.05	0.29	0.88	0.47
<i>lmo0298</i>	PTS beta-glucoside transporter subunit IIC	0.35	0.10	0.25	0.09	0.67	0.28
<i>lmo0299</i>	PTS beta-glucoside transporter subunit IIB	0.29	0.18	0.23	0.17	0.65	0.27
<i>lmo0300</i>	phospho-beta-galactosidase	0.41	0.07	0.29	0.07	0.60	0.21
<i>lmo0301</i>	PTS beta-glucoside transporter subunit IIA	0.43	0.07	0.32	0.07	0.61	0.27
<i>lmo0305</i>	L-allo-threonine aldolase	0.01	0.03	0.00	0.03	0.88	0.35
<i>lmo0314</i>	hypothetical protein	0.22	0.31	0.03	0.09	0.89	0.65
<i>lmo0315</i>	thiamin biosynthesis protein	0.37	0.47	0.27	0.47	0.75	0.39
<i>lmo0316</i>	hydroxyethylthiazole kinase	0.39	0.34	0.27	0.23	0.75	0.31
<i>lmo0317</i>	phosphomethylpyrimidine kinase	0.06	0.00	0.07	0.02	0.89	0.59
<i>lmo0318</i>	thiamine-phosphate pyrophosphorylase	0.02	0.00	0.07	0.04	0.76	0.40
<i>lmo0319</i>	phospho-beta-glucosidase	0.14	0.35	0.10	0.52	0.88	0.66
<i>lmo0321</i>	hypothetical protein	0.29	0.01	0.15	0.38	0.69	0.19
<i>lmo0322</i>	hypothetical protein	0.00	0.00	0.00	0.00	0.76	0.25
<i>lmo0334</i>	hypothetical protein	0.27	0.06	0.21	0.08	0.76	0.50
<i>lmo0343</i>	translaldolase	0.01	0.03	0.01	0.18	0.91	0.28
<i>lmo0344</i>	short chain dehydrogenase	0.01	0.03	0.01	0.19	0.92	0.25
<i>lmo0345</i>	sugar-phosphate isomerase	0.01	0.01	0.01	0.16	0.91	0.24
<i>lmo0346</i>	triosephosphate isomerase	0.00	0.01	0.01	0.13	0.92	0.23
<i>lmo0347</i>	dihydroxyacetone kinase	0.00	0.02	0.01	0.14	0.92	0.24
<i>lmo0348</i>	dihydroxyacetone kinase	0.01	0.06	0.01	0.25	0.92	0.23
<i>lmo0349</i>	hypothetical protein	0.01	0.03	0.01	0.26	0.92	0.23
<i>lmo0350</i>	hypothetical protein	0.01	0.03	0.01	0.22	0.92	0.24
<i>lmo0351</i>	phosphotransferase mannanose-specific family component IIA	0.02	0.16	0.02	0.35	0.91	0.32
<i>lmo0352</i>	DeoR family transcriptional regulator	0.04	0.19	0.05	0.50	0.91	0.21
<i>lmo0353</i>	hypothetical protein	0.13	0.24	0.04	0.47	0.91	0.52
<i>lmo0354</i>	fatty-acid--CoA ligase	0.00	0.02	0.01	0.07	0.88	0.57
<i>lmo0355</i>	fumarate reductase subunit A	0.13	0.42	0.05	0.43	0.87	0.55
<i>lmo0356</i>	oxidoreductase	0.00	0.00	0.01	0.05	0.50	0.18
<i>lmo0357</i>	PTS sugar transporter subunit IIA	0.35	0.01	0.24	0.02	0.75	0.48
<i>lmo0358</i>	PTS fructose transporter subunit IIBC	0.32	0.20	0.22	0.02	0.90	0.67
<i>lmo0359</i>	D-fructose-16-biphosphate aldolase	0.09	0.36	0.13	0.13	0.92	0.58
<i>lmo0360</i>	DeoR family transcriptional regulator	0.24	0.28	0.16	0.21	0.89	0.25
<i>lmo0360a</i>	hypothetical protein	0.00	0.00	0.00	0.01	0.58	0.15
<i>lmo0368</i>	hypothetical protein	0.00	0.00	0.01	0.05	0.57	0.16
<i>lmo0369</i>	hypothetical protein	0.04	0.05	0.01	0.06	0.86	0.51
<i>lmo0370</i>	hypothetical protein	0.00	0.00	0.00	0.02	0.86	0.53
<i>lmo0371</i>	GntR family transcriptional regulator	0.03	0.02	0.03	0.04	0.91	0.67
<i>lmo0372</i>	beta-glucosidase	0.17	0.43	0.19	0.18	0.70	0.09
<i>lmo0373</i>	PTS beta-glucoside transporter subunit IIC	0.20	0.42	0.20	0.21	0.70	0.10
<i>lmo0374</i>	PTS beta-glucoside transporter subunit IIB	0.14	0.48	0.15	0.24	0.72	0.09
<i>lmo0375</i>	hypothetical protein	0.35	0.03	0.18	0.08	0.50	0.12
<i>lmo0376</i>	transcriptional regulator	0.03	0.24	0.01	0.17	0.92	0.64
<i>lmo0377</i>	hypothetical protein	0.09	0.40	0.02	0.40	0.73	0.57
<i>lmo0382</i>	transcriptional regulator	0.33	0.28	0.20	0.40	0.92	0.65
<i>lmo0383</i>	methylmalonate-semialdehyde dehydrogenase	0.33	0.00	0.25	0.03	0.76	0.56
<i>lmo0384</i>	IolB protein	0.39	0.01	0.14	0.13	0.75	0.54
<i>lmo0385</i>	IolC protein	0.42	0.00	0.17	0.07	0.74	0.42
<i>lmo0386</i>	IolD protein	0.34	0.00	0.26	0.04	0.74	0.42
<i>lmo0387</i>	hypothetical protein	0.08	0.49	0.06	0.49	0.86	0.58
<i>lmo0388</i>	hypothetical protein	0.25	0.30	0.17	0.31	0.90	0.68
<i>lmo0389</i>	low temperature requirement protein A	0.00	0.01	0.01	0.20	0.88	0.59
<i>lmo0390</i>	uracil-DNA glycosylase	0.00	0.00	0.00	0.01	0.60	0.14
<i>lmo0391</i>	hypothetical protein	0.04	0.32	0.05	0.34	0.92	0.30
<i>lmo0392</i>	hypothetical protein	0.05	0.50	0.05	0.21	0.91	0.48

<i>lmo0393</i>	hypothetical protein	0.05	0.43	0.05	0.16	0.91	0.51
<i>lmo0394</i>	P60 protein	0.17	0.47	0.08	0.42	0.90	0.56
<i>lmo0395</i>	blasticidin S-acetyltransferase	0.41	0.26	0.22	0.47	0.92	0.68
<i>lmo0396</i>	pyrroline-5-carboxylate reductase	0.16	0.00	0.22	0.01	0.69	0.35
<i>lmo0397</i>	hypothetical protein	0.05	0.00	0.05	0.00	0.40	0.13
<i>lmo0398</i>	PTS sugar transporter subunit IIA	0.08	0.31	0.07	0.29	0.79	0.59
<i>lmo0399</i>	PTS fructose transporter subunit IIB	0.05	0.48	0.04	0.36	0.82	0.69
<i>lmo0400</i>	PTS fructose transporter subunit IIC	0.06	0.49	0.04	0.42	0.82	0.68
<i>lmo0401</i>	alpha-mannosidase	0.09	0.30	0.06	0.27	0.76	0.55
<i>lmo0402</i>	transcriptional antiterminator BglG	0.16	0.09	0.09	0.17	0.72	0.41
<i>lmo0403</i>	hypothetical protein	0.11	0.06	0.17	0.28	0.60	0.18
<i>lmo0404</i>	hypothetical protein	0.20	0.27	0.20	0.52	0.72	0.23
<i>lmo0405</i>	phosphate transporter	0.01	0.01	0.02	0.09	0.89	0.55
<i>lmo0406</i>	hypothetical protein	0.01	0.00	0.02	0.04	0.91	0.36
<i>lmo0407</i>	hypothetical protein	0.03	0.01	0.03	0.17	0.91	0.36
<i>lmo0408</i>	hypothetical protein	0.12	0.44	0.05	0.48	0.89	0.55
<i>lmo0412</i>	hypothetical protein	0.15	0.39	0.03	0.27	0.76	0.50
<i>lmo0413</i>	hypothetical protein	0.28	0.17	0.19	0.24	0.86	0.66
<i>lmo0414</i>	hypothetical protein	0.30	0.03	0.30	0.19	0.81	0.56
<i>lmo0415</i>	endo-14-beta-xylanase	0.00	0.00	0.00	0.01	0.93	0.48
<i>lmo0416</i>	transcriptional regulator	0.01	0.07	0.03	0.41	0.88	0.24
<i>lmo0417</i>	hypothetical protein	0.01	0.05	0.01	0.23	0.88	0.21
<i>lmo0418</i>	hypothetical protein	0.36	0.38	0.31	0.47	0.91	0.66
<i>lmo0419</i>	hypothetical protein	0.00	0.00	0.00	0.01	0.90	0.35
<i>lmo0420</i>	hypothetical protein	0.01	0.00	0.01	0.08	0.83	0.21
<i>lmo0424</i>	glucose uptake protein	0.01	0.05	0.01	0.06	0.88	0.57
<i>lmo0425</i>	transcriptional antiterminator BglG	0.08	0.49	0.03	0.47	0.87	0.64
<i>lmo0426</i>	PTS fructose transporter subunit IIA	0.06	0.35	0.03	0.36	0.90	0.67
<i>lmo0427</i>	PTS fructose transporter subunit IIB	0.07	0.36	0.03	0.36	0.88	0.69
<i>lmo0428</i>	PTS fructose transporter subunit IIC	0.13	0.34	0.06	0.49	0.86	0.62
<i>lmo0429</i>	sugar hydrolase	0.14	0.29	0.05	0.46	0.85	0.62
<i>lmo0430</i>	LysR family transcriptional regulator	0.02	0.05	0.10	0.41	0.79	0.45
<i>lmo0431</i>	acetyltransferase	0.36	0.23	0.21	0.30	0.87	0.59
<i>lmo0432</i>	oxidoreductase	0.33	0.36	0.22	0.34	0.89	0.67
<i>lmo0434</i>	internalin B	0.12	0.46	0.04	0.46	0.71	0.19
<i>lmo0436</i>	hypothetical protein	0.03	0.18	0.01	0.14	0.90	0.35
<i>lmo0437</i>	hypothetical protein	0.39	0.07	0.13	0.31	0.91	0.60
<i>lmo0438</i>	hypothetical protein	0.25	0.19	0.32	0.45	0.81	0.52
<i>lmo0439</i>	hypothetical protein	0.25	0.26	0.08	0.52	0.73	0.33
<i>lmo0441</i>	D-alanyl-D-alanine carboxypeptidase	0.12	0.34	0.06	0.34	0.65	0.22
<i>lmo0442</i>	hypothetical protein	0.04	0.12	0.09	0.41	0.86	0.62
<i>lmo0443</i>	LytR family transcriptional regulator	0.00	0.01	0.01	0.06	0.71	0.23
<i>lmo0449</i>	hypothetical protein	0.00	0.00	0.01	0.03	0.62	0.15
<i>lmo0450</i>	hypothetical protein	0.01	0.10	0.02	0.31	0.90	0.60
<i>lmo0451</i>	hypothetical protein	0.00	0.00	0.00	0.02	0.76	0.42
<i>lmo0452</i>	hypothetical protein	0.10	0.41	0.02	0.31	0.85	0.48
<i>lmo0453</i>	hypothetical protein	0.37	0.05	0.17	0.18	0.91	0.55
<i>lmo0454</i>	hypothetical protein	0.29	0.03	0.32	0.12	0.82	0.32
<i>lmo0455</i>	hypothetical protein	0.05	0.00	0.22	0.12	0.45	0.20
<i>lmo0456</i>	permease	0.25	0.08	0.12	0.51	0.71	0.31
<i>lmo0457</i>	hypothetical protein	0.03	0.00	0.24	0.24	0.55	0.18
<i>lmo0458</i>	hydantoinase	0.07	0.01	0.30	0.29	0.54	0.27
<i>lmo0480</i>	transcriptional regulator	0.17	0.13	0.03	0.03	0.85	0.53
<i>lmo0481</i>	hypothetical protein	0.00	0.00	0.01	0.09	0.87	0.38
<i>lmo0482</i>	ribosomal RNA large subunit methyltransferase N	0.03	0.05	0.02	0.20	0.92	0.68
<i>lmo0483</i>	hypothetical protein	0.15	0.47	0.18	0.20	0.92	0.67
<i>lmo0484</i>	heme-degrading monooxygenase IsdG	0.25	0.24	0.15	0.23	0.85	0.56
<i>lmo0485</i>	hypothetical protein	0.00	0.00	0.02	0.11	0.93	0.69
<i>lmo0486</i>	50S ribosomal protein L32	0.15	0.03	0.21	0.48	0.87	0.57
<i>lmo0487</i>	hypothetical protein	0.00	0.01	0.08	0.42	0.80	0.25
<i>lmo0488</i>	LysR family transcriptional regulator	0.14	0.33	0.09	0.19	0.90	0.60

<i>lmo0489</i>	NADH:flavin oxidoreductase	0.02	0.27	0.01	0.15	0.85	0.65
<i>lmo0490</i>	shikimate 5-dehydrogenase	0.38	0.10	0.32	0.20	0.74	0.60
<i>lmo0491</i>	3-dehydroquinase dehydratase	0.13	0.01	0.28	0.15	0.71	0.40
<i>lmo0494</i>	hypothetical protein	0.14	0.03	0.30	0.21	0.61	0.20
<i>lmo0495</i>	hypothetical protein	0.39	0.21	0.09	0.53	0.89	0.59
<i>lmo0496</i>	hypothetical protein	0.08	0.42	0.07	0.31	0.82	0.65
<i>lmo0498</i>	5-phosphate isomerase	0.42	0.02	0.30	0.02	0.84	0.67
<i>lmo0499</i>	ribulose-5-phosphate 3 epimerase	0.40	0.04	0.31	0.04	0.91	0.42
<i>lmo0500</i>	transaldolase	0.42	0.02	0.29	0.03	0.92	0.36
<i>lmo0502</i>	sugar-phosphate isomerase	0.19	0.21	0.11	0.18	0.91	0.28
<i>lmo0503</i>	PTS fructose transporter subunit IIA	0.11	0.38	0.06	0.35	0.92	0.24
<i>lmo0504</i>	hypothetical protein	0.17	0.22	0.09	0.23	0.92	0.24
<i>lmo0505</i>	ribulose-5-phosphate 3-epimerase	0.08	0.47	0.06	0.39	0.91	0.23
<i>lmo0506</i>	sorbitol dehydrogenase	0.20	0.27	0.16	0.17	0.90	0.20
<i>lmo0507</i>	PTS galactitol transporter subunit IIB	0.34	0.01	0.31	0.05	0.85	0.63
<i>lmo0508</i>	PTS galactitol transporter subunit IIC	0.43	0.00	0.29	0.03	0.92	0.59
<i>lmo0509</i>	phosphoribosyl pyrophosphate synthetase	0.00	0.02	0.01	0.10	0.89	0.41
<i>lmo0510</i>	hypothetical protein	0.02	0.01	0.01	0.01	0.91	0.63
<i>lmo0511</i>	hypothetical protein	0.02	0.01	0.24	0.55	0.69	0.24
<i>lmo0512</i>	hypothetical protein	0.17	0.19	0.30	0.49	0.91	0.61
<i>lmo0513</i>	hypothetical protein	0.09	0.07	0.08	0.10	0.77	0.34
<i>lmo0514</i>	internalin	0.25	0.27	0.26	0.06	0.92	0.65
<i>lmo0515</i>	hypothetical protein	0.11	0.19	0.05	0.38	0.75	0.38
<i>lmo0516</i>	encapsulation protein CapA	0.00	0.00	0.01	0.02	0.72	0.31
<i>lmo0517</i>	phosphoglycerate mutase	0.14	0.34	0.04	0.34	0.88	0.59
<i>lmo0518</i>	hypothetical protein	0.03	0.14	0.00	0.02	0.92	0.52
<i>lmo0519</i>	multidrug resistance protein	0.26	0.16	0.09	0.42	0.88	0.66
<i>lmo0520</i>	transcriptional regulator	0.12	0.00	0.14	0.07	0.87	0.51
<i>lmo0521</i>	6-phospho-beta-glucosidase	0.10	0.25	0.06	0.27	0.92	0.45
<i>lmo0522</i>	transcriptional regulator	0.01	0.00	0.03	0.01	0.84	0.40
<i>lmo0523</i>	hypothetical protein	0.21	0.24	0.07	0.37	0.88	0.56
<i>lmo0524</i>	sulfate transporter	0.09	0.36	0.03	0.32	0.82	0.50
<i>lmo0526</i>	transcriptional regulator	0.00	0.00	0.03	0.25	0.83	0.32
<i>lmo0527</i>	transmembrane protein	0.00	0.00	0.01	0.01	0.87	0.47
<i>lmo0528</i>	hypothetical protein	0.00	0.00	0.01	0.02	0.74	0.37
<i>lmo0529</i>	glucosaminyltransferase	0.00	0.00	0.01	0.03	0.71	0.37
<i>lmo0530</i>	hypothetical protein	0.00	0.00	0.00	0.02	0.62	0.31
<i>lmo0531</i>	hypothetical protein	0.00	0.00	0.00	0.02	0.62	0.29
<i>lmo0532</i>	hypothetical protein	0.00	0.00	0.00	0.00	0.91	0.63
<i>lmo0533</i>	hypothetical protein	0.09	0.50	0.01	0.19	0.79	0.69
<i>lmo0534</i>	hypothetical protein	0.08	0.45	0.01	0.26	0.75	0.56
<i>lmo0535</i>	LacI family transcriptional regulator	0.03	0.34	0.01	0.38	0.91	0.44
<i>lmo0536</i>	6-phospho-beta-glucosidase	0.03	0.27	0.02	0.31	0.92	0.32
<i>lmo0537</i>	allantoate amidohydrolase	0.09	0.26	0.12	0.55	0.87	0.40
<i>lmo0538</i>	N-acyl-L-amino acid amidohydrolase	0.08	0.47	0.08	0.43	0.91	0.56
<i>lmo0539</i>	tagatose 16-diphosphate aldolase	0.06	0.41	0.04	0.47	0.77	0.36
<i>lmo0540</i>	penicillin-binding protein	0.00	0.00	0.00	0.01	0.67	0.16
<i>lmo0541</i>	ABC transporter substrate-binding protein	0.07	0.10	0.12	0.30	0.74	0.34
<i>lmo0542</i>	PTS sorbitol transporter subunit IIA	0.18	0.05	0.27	0.44	0.88	0.50
<i>lmo0543</i>	PTS sorbitol transporter subunit IIBC	0.37	0.19	0.09	0.54	0.91	0.63
<i>lmo0544</i>	PTS sorbitol transporter subunit IIC	0.38	0.03	0.19	0.27	0.86	0.47
<i>lmo0545</i>	hypothetical protein	0.29	0.02	0.22	0.22	0.75	0.37
<i>lmo0546</i>	NAD(P)-dependent oxidoreductase	0.36	0.01	0.29	0.08	0.79	0.36
<i>lmo0547</i>	DeoR family transcriptional regulator	0.06	0.02	0.11	0.12	0.75	0.53
<i>lmo0548</i>	hypothetical protein	0.29	0.42	0.11	0.48	0.91	0.62
<i>lmo0549</i>	internalin	0.00	0.00	0.01	0.07	0.79	0.43
<i>lmo0550</i>	pepidoglycan-bound protein	0.28	0.47	0.17	0.51	0.91	0.66
<i>lmo0551</i>	hypothetical protein	0.06	0.16	0.06	0.47	0.87	0.65
<i>lmo0552</i>	hypothetical protein	0.06	0.09	0.10	0.48	0.89	0.64
<i>lmo0553</i>	hypothetical protein	0.08	0.31	0.07	0.07	0.85	0.64
<i>lmo0554</i>	NADH-dependent butanol dehydrogenase	0.06	0.18	0.02	0.13	0.82	0.50

<i>lmo0555</i>	di-tripeptide transporter	0.06	0.04	0.02	0.04	0.78	0.53
<i>lmo0556</i>	phosphoglycerate mutase	0.00	0.01	0.02	0.14	0.72	0.17
<i>lmo0557</i>	phosphoglycerate mutase	0.00	0.00	0.02	0.17	0.61	0.15
<i>lmo0558</i>	hypothetical protein	0.42	0.50	0.21	0.33	0.90	0.69
<i>lmo0559</i>	hypothetical protein	0.05	0.18	0.02	0.22	0.87	0.50
<i>lmo0560</i>	glutamate dehydrogenase	0.02	0.04	0.02	0.08	0.71	0.22
<i>lmo0561</i>	phosphoribosyl-ATP pyrophosphatase	0.32	0.45	0.10	0.28	0.76	0.60
<i>lmo0562</i>	phosphoribosyl-AMP cyclohydrolase	0.05	0.10	0.03	0.11	0.91	0.40
<i>lmo0563</i>	imidazole glycerol phosphate synthase subunit HisF	0.15	0.29	0.02	0.07	0.93	0.63
<i>lmo0564</i>	1-(5-phosphoribosyl)-5-[(5- phosphoribosylamino)methylideneamino]imidazole-4-carboxamide isomerase	0.15	0.07	0.11	0.10	0.83	0.36
<i>lmo0565</i>	imidazole glycerol phosphate synthase subunit HisH	0.07	0.06	0.08	0.13	0.85	0.44
<i>lmo0566</i>	imidazoleglycerol-phosphate dehydratase	0.16	0.29	0.05	0.17	0.91	0.44
<i>lmo0567</i>	histidinol dehydrogenase	0.07	0.25	0.03	0.19	0.92	0.45
<i>lmo0568</i>	ATP phosphoribosyltransferase	0.25	0.16	0.24	0.49	0.90	0.66
<i>lmo0569</i>	ATP phosphoribosyltransferase	0.33	0.49	0.07	0.28	0.76	0.37
<i>lmo0570</i>	histidinol-phosphatase	0.03	0.04	0.01	0.05	0.91	0.59
<i>lmo0571</i>	methyltransferase	0.00	0.00	0.00	0.02	0.74	0.19
<i>lmo0572</i>	hypothetical protein	0.00	0.00	0.00	0.07	0.92	0.34
<i>lmo0573</i>	hypothetical protein	0.02	0.30	0.03	0.49	0.76	0.42
<i>lmo0574</i>	beta-glucosidase	0.03	0.10	0.04	0.54	0.92	0.22
<i>lmo0575</i>	GntR family transcriptional regulator	0.15	0.45	0.15	0.34	0.91	0.38
<i>lmo0577</i>	hypothetical protein	0.15	0.30	0.03	0.49	0.88	0.66
<i>lmo0578</i>	hypothetical protein	0.12	0.45	0.02	0.31	0.92	0.50
<i>lmo0579</i>	hypothetical protein	0.04	0.08	0.04	0.33	0.84	0.65
<i>lmo0580</i>	hypothetical protein	0.07	0.34	0.06	0.54	0.81	0.61
<i>lmo0581</i>	hypothetical protein	0.12	0.48	0.14	0.39	0.81	0.69
<i>lmo0582</i>	invasion associated secreted endopeptidase	0.15	0.23	0.07	0.19	0.83	0.52
<i>lmo0583</i>	preprotein translocase subunit SecA	0.28	0.14	0.32	0.31	0.91	0.60
<i>lmo0584</i>	hypothetical protein	0.23	0.03	0.08	0.26	0.74	0.36
<i>lmo0585</i>	secreted protein	0.10	0.20	0.04	0.19	0.92	0.53
<i>lmo0586</i>	hypothetical protein	0.04	0.13	0.02	0.17	0.90	0.56
<i>lmo0587</i>	secreted protein	0.18	0.50	0.06	0.35	0.92	0.66
<i>lmo0588</i>	DNA photolyase	0.16	0.06	0.20	0.15	0.74	0.42
<i>lmo0589</i>	hypothetical protein	0.13	0.24	0.08	0.28	0.88	0.62
<i>lmo0590</i>	hypothetical protein	0.10	0.25	0.05	0.22	0.86	0.51
<i>lmo0591</i>	hypothetical protein	0.41	0.41	0.25	0.42	0.76	0.41
<i>lmo0592</i>	hypothetical protein	0.36	0.49	0.30	0.43	0.86	0.61
<i>lmo0593</i>	formate transporter	0.06	0.20	0.05	0.31	0.80	0.49
<i>lmo0594</i>	homoserine O-acetyltransferase	0.34	0.36	0.27	0.11	0.90	0.53
<i>lmo0595</i>	O-acetylhomoserine sulfhydrylase	0.40	0.15	0.29	0.09	0.92	0.54
<i>lmo0597</i>	Crp/Fnr family transcriptional regulator	0.39	0.44	0.22	0.33	0.66	0.24
<i>lmo0597a</i>	hypothetical protein	0.25	0.34	0.07	0.52	0.78	0.49
<i>lmo0599</i>	hypothetical protein	0.01	0.03	0.04	0.34	0.91	0.56
<i>lmo0600</i>	hypothetical protein	0.00	0.00	0.01	0.16	0.91	0.55
<i>lmo0601</i>	cell surface protein	0.30	0.10	0.23	0.23	0.58	0.22
<i>lmo0602</i>	transcriptonal regulator	0.13	0.40	0.04	0.48	0.71	0.21
<i>lmo0603</i>	hypothetical protein	0.00	0.00	0.03	0.07	0.75	0.32
<i>lmo0604</i>	hypothetical protein	0.26	0.38	0.32	0.40	0.88	0.52
<i>lmo0605</i>	hypothetical protein	0.13	0.34	0.04	0.53	0.75	0.46
<i>lmo0606</i>	MarR family transcriptional regulator	0.35	0.12	0.14	0.47	0.60	0.29
<i>lmo0607</i>	ABC transporter ATP-binding protein	0.22	0.50	0.05	0.29	0.74	0.43
<i>lmo0608</i>	ABC transporter ATP-binding protein	0.21	0.06	0.26	0.38	0.72	0.33
<i>lmo0609</i>	phage shock protein E	0.03	0.02	0.08	0.05	0.92	0.47
<i>lmo0610</i>	internalin	0.00	0.00	0.01	0.09	0.91	0.58
<i>lmo0611</i>	azoreductase	0.35	0.08	0.31	0.11	0.87	0.41
<i>lmo0612</i>	MarR family transcriptional evidence	0.00	0.00	0.00	0.00	0.91	0.52
<i>lmo0613</i>	oxidoreductase	0.00	0.00	0.00	0.00	0.87	0.59
<i>lmo0614</i>	hypothetical protein	0.00	0.00	0.01	0.03	0.85	0.43
<i>lmo0615</i>	hypothetical protein	0.02	0.22	0.08	0.31	0.91	0.61

<i>lmo0616</i>	glycerophosphoryl diester phosphodiesterase	0.00	0.00	0.03	0.15	0.90	0.66
<i>lmo0617</i>	hypothetical protein	0.00	0.00	0.01	0.05	0.57	0.16
<i>lmo0618</i>	protein kinase	0.00	0.00	0.00	0.06	0.89	0.29
<i>lmo0619</i>	hypothetical protein	0.06	0.08	0.27	0.52	0.86	0.54
<i>lmo0620</i>	hypothetical protein	0.36	0.39	0.29	0.42	0.83	0.40
<i>lmo0621</i>	hypothetical protein	0.32	0.43	0.15	0.27	0.92	0.62
<i>lmo0622</i>	hypothetical protein	0.00	0.00	0.00	0.02	0.89	0.69
<i>lmo0623</i>	hypothetical protein	0.00	0.00	0.00	0.01	0.92	0.54
<i>lmo0624</i>	hypothetical protein	0.04	0.46	0.05	0.26	0.90	0.53
<i>lmo0625</i>	hypothetical protein	0.09	0.33	0.08	0.12	0.90	0.55
<i>lmo0626</i>	hypothetical protein	0.06	0.13	0.08	0.49	0.89	0.60
<i>lmo0627</i>	pepdidoglycan bound protein	0.41	0.15	0.22	0.41	0.92	0.70
<i>lmo0628</i>	hypothetical protein	0.01	0.00	0.02	0.14	0.89	0.38
<i>lmo0629</i>	hypothetical protein	0.01	0.00	0.01	0.06	0.91	0.22
<i>lmo0635</i>	hypothetical protein	0.31	0.00	0.09	0.10	0.76	0.13
<i>lmo0636</i>	hypothetical protein	0.25	0.07	0.17	0.48	0.74	0.35
<i>lmo0637</i>	hypothetical protein	0.11	0.01	0.32	0.20	0.57	0.22
<i>lmo0639</i>	transcriptonal regulator	0.02	0.08	0.02	0.20	0.88	0.24
<i>lmo0640</i>	oxidoreductase	0.02	0.36	0.02	0.42	0.92	0.43
<i>lmo0641</i>	heavy metal-transporting ATPase	0.06	0.09	0.03	0.08	0.85	0.57
<i>lmo0642</i>	hypothetical protein	0.05	0.16	0.02	0.15	0.91	0.58
<i>lmo0643</i>	transaldolase	0.04	0.34	0.02	0.34	0.91	0.20
<i>lmo0644</i>	hypothetical protein	0.29	0.04	0.11	0.18	0.89	0.59
<i>lmo0645</i>	amino acid transporter	0.00	0.00	0.00	0.01	0.89	0.36
<i>lmo0646</i>	hypothetical protein	0.24	0.44	0.09	0.37	0.71	0.28
<i>lmo0647</i>	hypothetical protein	0.09	0.28	0.05	0.25	0.82	0.58
<i>lmo0648</i>	hypothetical protein	0.10	0.14	0.05	0.27	0.80	0.68
<i>lmo0649</i>	transcriptional regulator	0.12	0.29	0.07	0.44	0.86	0.64
<i>lmo0650</i>	hypothetical protein	0.12	0.35	0.07	0.37	0.82	0.59
<i>lmo0651</i>	transcriptional regulator	0.27	0.38	0.12	0.54	0.72	0.31
<i>lmo0652</i>	hypothetical protein	0.00	0.00	0.00	0.01	0.86	0.40
<i>lmo0653</i>	hypothetical protein	0.01	0.00	0.00	0.01	0.81	0.61
<i>lmo0654</i>	hypothetical protein	0.03	0.24	0.02	0.19	0.83	0.61
<i>lmo0655</i>	phosphoprotein phosphatase	0.00	0.01	0.01	0.09	0.89	0.66
<i>lmo0656</i>	hypothetical protein	0.42	0.06	0.32	0.05	0.92	0.63
<i>lmo0657</i>	hypothetical protein	0.01	0.02	0.02	0.26	0.91	0.21
<i>lmo0658</i>	hypothetical protein	0.01	0.06	0.02	0.22	0.80	0.22
<i>lmo0659</i>	transcriptional regulator	0.03	0.01	0.10	0.12	0.76	0.44
<i>lmo0660</i>	transposase	0.00	0.06	0.01	0.42	0.69	0.08
<i>lmo0661</i>	hypothetical protein	0.01	0.04	0.03	0.20	0.90	0.39
<i>lmo0662</i>	phosphomethylpyrimidine kinase	0.42	0.04	0.18	0.18	0.91	0.65
<i>lmo0663</i>	hypothetical protein	0.42	0.03	0.25	0.04	0.92	0.64
<i>lmo0664</i>	acetyl transferase	0.00	0.00	0.05	0.09	0.86	0.33
<i>lmo0665</i>	hypothetical protein	0.01	0.04	0.00	0.04	0.91	0.55
<i>lmo0666</i>	hypothetical protein	0.12	0.42	0.01	0.18	0.92	0.67
<i>lmo0669</i>	oxidoreductase	0.31	0.20	0.11	0.49	0.74	0.22
<i>lmo0670</i>	hypothetical protein	0.37	0.06	0.20	0.33	0.67	0.19
<i>lmo0671</i>	hypothetical protein	0.21	0.37	0.14	0.44	0.79	0.53
<i>lmo0672</i>	hypothetical protein	0.01	0.04	0.04	0.45	0.85	0.23
<i>lmo0673</i>	hypothetical protein	0.36	0.45	0.10	0.43	0.92	0.67
<i>lmo0674</i>	hypothetical protein	0.34	0.35	0.08	0.43	0.92	0.64
<i>lmo0675</i>	hypothetical protein	0.35	0.31	0.21	0.16	0.84	0.50
<i>lmo0676</i>	flagellar biosynthesis protein FliP	0.35	0.32	0.16	0.13	0.85	0.51
<i>lmo0677</i>	flagellar biosynthesis protein FliQ	0.38	0.22	0.15	0.15	0.80	0.49
<i>lmo0678</i>	flagellar biosynthesis protein FliR	0.26	0.31	0.26	0.14	0.88	0.62
<i>lmo0679</i>	flagellar biosynthesis protein FlhB	0.17	0.37	0.31	0.19	0.90	0.67
<i>lmo0680</i>	flagellar biosynthesis protein FlhA	0.21	0.48	0.20	0.23	0.92	0.69
<i>lmo0681</i>	flagellar biosynthesis regulator FlhF	0.42	0.44	0.10	0.19	0.89	0.62
<i>lmo0682</i>	flagellar basal body rod protein FlgG	0.08	0.02	0.04	0.04	0.71	0.37
<i>lmo0683</i>	chemotaxis protein CheR	0.20	0.06	0.08	0.09	0.80	0.52
<i>lmo0684</i>	hypothetical protein	0.08	0.03	0.03	0.05	0.70	0.38

<i>lmo0685</i>	flagellar motor protein MotA	0.10	0.04	0.05	0.08	0.71	0.37
<i>lmo0686</i>	flagellar motor rotation MotB	0.12	0.02	0.05	0.05	0.73	0.42
<i>lmo0687</i>	hypothetical protein	0.31	0.19	0.10	0.12	0.75	0.50
<i>lmo0688</i>	hypothetical protein	0.17	0.05	0.06	0.06	0.74	0.41
<i>lmo0689</i>	chemotaxis protein CheV	0.37	0.29	0.09	0.13	0.89	0.66
<i>lmo0690</i>	flagellin	0.06	0.11	0.07	0.27	0.77	0.39
<i>lmo0691</i>	chemotaxis response regulator CheY	0.36	0.39	0.18	0.18	0.80	0.51
<i>lmo0692</i>	two-component sensor histidine kinase CheA	0.39	0.46	0.15	0.21	0.83	0.57
<i>lmo0693</i>	flagellar motor switch protein FliY	0.40	0.42	0.13	0.17	0.88	0.69
<i>lmo0694</i>	hypothetical protein	0.37	0.37	0.15	0.12	0.87	0.65
<i>lmo0695</i>	hypothetical protein	0.41	0.27	0.16	0.11	0.83	0.60
<i>lmo0696</i>	flagellar basal body rod modification protein	0.42	0.36	0.10	0.11	0.86	0.57
<i>lmo0697</i>	flagellar hook protein FlgE	0.41	0.42	0.13	0.17	0.85	0.61
<i>lmo0698</i>	flagellar motor switch protein	0.37	0.41	0.19	0.19	0.88	0.68
<i>lmo0699</i>	flagellar motor switch protein FliM	0.41	0.37	0.15	0.16	0.89	0.68
<i>lmo0700</i>	flagellar motor switch protein FliY	0.36	0.41	0.18	0.17	0.87	0.64
<i>lmo0701</i>	hypothetical protein	0.38	0.33	0.20	0.18	0.86	0.63
<i>lmo0702</i>	hypothetical protein	0.35	0.26	0.07	0.08	0.82	0.58
<i>lmo0703</i>	hypothetical protein	0.37	0.50	0.15	0.21	0.88	0.68
<i>lmo0704</i>	hypothetical protein	0.42	0.46	0.11	0.16	0.84	0.65
<i>lmo0705</i>	flagellar hook-associated protein FlgK	0.41	0.48	0.11	0.18	0.84	0.64
<i>lmo0706</i>	flagellar hook-associated protein FlgL	0.41	0.41	0.09	0.12	0.85	0.63
<i>lmo0707</i>	flagellar capping protein FliD	0.35	0.44	0.15	0.16	0.85	0.60
<i>lmo0708</i>	flagellar protein	0.42	0.35	0.11	0.15	0.80	0.60
<i>lmo0709</i>	hypothetical protein	0.40	0.33	0.08	0.12	0.78	0.56
<i>lmo0710</i>	flagellar basal-body rod protein FlgB	0.19	0.17	0.04	0.07	0.81	0.63
<i>lmo0711</i>	flagellar basal body rod protein FlgC	0.31	0.30	0.06	0.12	0.80	0.63
<i>lmo0712</i>	flagellar hook-basal body protein FliE	0.42	0.35	0.19	0.28	0.89	0.64
<i>lmo0713</i>	flagellar MS-ring protein FliF	0.41	0.24	0.16	0.12	0.81	0.63
<i>lmo0714</i>	flagellar motor switch protein FliG	0.41	0.31	0.18	0.18	0.86	0.66
<i>lmo0715</i>	flagellar assembly protein H	0.32	0.19	0.10	0.13	0.82	0.61
<i>lmo0716</i>	flagellum-specific ATP synthase	0.41	0.26	0.14	0.14	0.82	0.60
<i>lmo0717</i>	transglycosylase	0.42	0.23	0.16	0.11	0.80	0.55
<i>lmo0718</i>	hypothetical protein	0.37	0.31	0.16	0.12	0.82	0.59
<i>lmo0719</i>	hypothetical protein	0.18	0.31	0.16	0.11	0.90	0.33
<i>lmo0720</i>	hypothetical protein	0.23	0.24	0.20	0.10	0.90	0.34
<i>lmo0721</i>	fibronectin-binding protein	0.41	0.24	0.16	0.06	0.69	0.42
<i>lmo0722</i>	pyruvate oxidase	0.34	0.30	0.08	0.50	0.69	0.29
<i>lmo0723</i>	methyl-accepting chemotaxis protein	0.26	0.33	0.04	0.08	0.91	0.66
<i>lmo0724</i>	hypothetical protein	0.04	0.02	0.01	0.01	0.85	0.56
<i>lmo0727</i>	glucosamine--fructose-6-phosphate aminotransferase	0.00	0.00	0.00	0.01	0.87	0.65
<i>lmo0728</i>	riboflavin kinase / FAD synthase	0.16	0.01	0.17	0.45	0.61	0.35
<i>lmo0729</i>	hypothetical protein	0.02	0.04	0.02	0.12	0.83	0.69
<i>lmo0730</i>	hypothetical protein	0.04	0.09	0.05	0.28	0.72	0.51
<i>lmo0731</i>	hypothetical protein	0.28	0.35	0.03	0.22	0.74	0.65
<i>lmo0733</i>	transcriptional regulator	0.00	0.00	0.01	0.03	0.82	0.20
<i>lmo0740</i>	transcriptional regulator	0.12	0.42	0.11	0.34	0.82	0.70
<i>lmo0741</i>	GntR family transcriptional regulator	0.03	0.10	0.01	0.10	0.70	0.23
<i>lmo0742</i>	ABC transporter ATP-binding protein	0.00	0.00	0.01	0.02	0.60	0.23
<i>lmo0743</i>	hypothetical protein	0.00	0.00	0.08	0.19	0.69	0.23
<i>lmo0744</i>	ABC transporter ATP-binding protein	0.05	0.01	0.22	0.19	0.63	0.21
<i>lmo0745</i>	hypothetical protein	0.01	0.01	0.09	0.21	0.74	0.38
<i>lmo0752</i>	hypothetical protein	0.00	0.00	0.00	0.00	0.73	0.29
<i>lmo0753</i>	Crp/Fnr family transcriptional regulator	0.19	0.24	0.19	0.36	0.72	0.57
<i>lmo0754</i>	hypothetical protein	0.05	0.05	0.16	0.33	0.68	0.49
<i>lmo0755</i>	hypothetical protein	0.00	0.00	0.00	0.01	0.81	0.38
<i>lmo0756</i>	ABC transporter ATP-binding protein	0.00	0.00	0.06	0.08	0.76	0.42
<i>lmo0757</i>	hypothetical protein	0.42	0.09	0.11	0.48	0.90	0.35
<i>lmo0758</i>	hypothetical protein	0.22	0.04	0.13	0.07	0.70	0.26
<i>lmo0760</i>	hypothetical protein	0.19	0.01	0.11	0.03	0.72	0.21
<i>lmo0762</i>	ATP/GTP-binding protein	0.01	0.12	0.04	0.40	0.92	0.60

<i>lmo0763</i>	Ser/Thr protein phosphatase family protein	0.00	0.00	0.00	0.01	0.66	0.16
<i>lmo0764</i>	lipoate-protein ligase	0.00	0.01	0.01	0.10	0.90	0.22
<i>lmo0772</i>	transcriptional regulator	0.01	0.00	0.01	0.00	0.75	0.21
<i>lmo0773</i>	alcohol dehydrogenase	0.37	0.33	0.15	0.31	0.88	0.53
<i>lmo0774</i>	hypothetical protein	0.17	0.00	0.28	0.07	0.72	0.42
<i>lmo0775</i>	hypothetical protein	0.27	0.00	0.19	0.17	0.85	0.68
<i>lmo0776</i>	transcriptional regulator	0.01	0.03	0.01	0.11	0.72	0.16
<i>lmo0777</i>	hypothetical protein	0.20	0.30	0.06	0.18	0.92	0.59
<i>lmo0778</i>	hypothetical protein	0.38	0.35	0.18	0.43	0.90	0.60
<i>lmo0779</i>	hypothetical protein	0.22	0.01	0.26	0.34	0.49	0.21
<i>lmo0781</i>	PTS mannose transporter subunit IID	0.01	0.04	0.01	0.10	0.87	0.67
<i>lmo0782</i>	PTS mannose transporter subunit IIC	0.03	0.10	0.02	0.14	0.86	0.64
<i>lmo0783</i>	PTS mannose transporter subunit IIB	0.09	0.30	0.03	0.27	0.85	0.55
<i>lmo0784</i>	PTS mannose transporter subunit IIB	0.08	0.30	0.03	0.26	0.85	0.56
<i>lmo0786</i>	ACP phosphodiesterase	0.03	0.10	0.01	0.07	0.74	0.37
<i>lmo0787</i>	amino acid transporter	0.40	0.02	0.29	0.07	0.74	0.34
<i>lmo0788</i>	hypothetical protein	0.06	0.33	0.02	0.24	0.86	0.62
<i>lmo0790</i>	transcriptional regulator	0.01	0.07	0.28	0.32	0.76	0.28
<i>lmo0791</i>	hypothetical protein	0.23	0.35	0.06	0.46	0.92	0.64
<i>lmo0793</i>	hypothetical protein	0.19	0.44	0.04	0.36	0.87	0.67
<i>lmo0794</i>	hypothetical protein	0.05	0.26	0.04	0.36	0.79	0.51
<i>lmo0795</i>	hypothetical protein	0.34	0.21	0.05	0.47	0.89	0.67
<i>lmo0796</i>	hypothetical protein	0.15	0.48	0.03	0.37	0.69	0.22
<i>lmo0797</i>	hypothetical protein	0.30	0.22	0.12	0.45	0.92	0.40
<i>lmo0798</i>	lysine-specific permease	0.12	0.47	0.05	0.47	0.60	0.22
<i>lmo0799</i>	hypothetical protein	0.01	0.01	0.04	0.17	0.89	0.45
<i>lmo0800</i>	hypothetical protein	0.00	0.00	0.00	0.07	0.91	0.18
<i>lmo0802</i>	hypothetical protein	0.39	0.21	0.08	0.53	0.78	0.21
<i>lmo0803</i>	Na ⁺ /H ⁺ antiporter	0.41	0.35	0.28	0.24	0.74	0.44
<i>lmo0806</i>	transcriptional regulator	0.12	0.48	0.04	0.41	0.59	0.19
<i>lmo0807</i>	spermidine/putrescine ABC transporter ATP-binding protein	0.07	0.33	0.01	0.13	0.69	0.23
<i>lmo0808</i>	spermidine/putrescine ABC transporter permease	0.04	0.15	0.01	0.15	0.74	0.52
<i>lmo0809</i>	spermidine/putrescine ABC transporter permease	0.00	0.02	0.01	0.09	0.84	0.61
<i>lmo0810</i>	spermidine/putrescine ABC transporter substrate-binding protein	0.02	0.09	0.02	0.14	0.73	0.53
<i>lmo0811</i>	carbonic anhydrase	0.22	0.39	0.31	0.49	0.84	0.59
<i>lmo0812</i>	hypothetical protein	0.22	0.02	0.06	0.20	0.58	0.16
<i>lmo0813</i>	fructokinase	0.35	0.20	0.20	0.22	0.90	0.61
<i>lmo0814</i>	oxidoreductase	0.05	0.28	0.01	0.12	0.86	0.67
<i>lmo0817</i>	PhnB protein	0.39	0.25	0.11	0.51	0.68	0.40
<i>lmo0818</i>	cation-transporting ATPase	0.14	0.32	0.02	0.19	0.75	0.41
<i>lmo0819</i>	hypothetical protein	0.10	0.43	0.01	0.08	0.74	0.44
<i>lmo0820</i>	acetyltransferase	0.27	0.29	0.13	0.24	0.77	0.39
<i>lmo0821</i>	hypothetical protein	0.28	0.47	0.27	0.39	0.71	0.26
<i>lmo0822</i>	transcriptional regulator	0.22	0.02	0.06	0.36	0.71	0.45
<i>lmo0823</i>	oxidoreductase	0.14	0.26	0.04	0.11	0.76	0.34
<i>lmo0824</i>	hypothetical protein	0.08	0.47	0.04	0.49	0.92	0.56
<i>lmo0825</i>	3-hydroxy-3-methylglutaryl-CoA reductase	0.04	0.18	0.04	0.35	0.80	0.32
<i>lmo0826</i>	transporter	0.17	0.05	0.14	0.11	0.74	0.55
<i>lmo0829</i>	pyruvate-flavodoxin oxidoreductase	0.10	0.00	0.19	0.01	0.75	0.37
<i>lmo0830</i>	fructose-1,6-bisphosphatase	0.43	0.29	0.28	0.20	0.88	0.60
<i>lmo0831</i>	hypothetical protein	0.00	0.00	0.00	0.03	0.67	0.09
<i>lmo0832</i>	transposase	0.00	0.00	0.00	0.00	0.69	0.17
<i>lmo0833</i>	transcriptional regulator	0.03	0.05	0.01	0.01	0.92	0.58
<i>lmo0834</i>	hypothetical protein	0.12	0.44	0.02	0.40	0.82	0.64
<i>lmo0835</i>	peptidoglycan binding protein	0.03	0.00	0.19	0.14	0.61	0.24
<i>lmo0836</i>	phosphate-starvation-inducible protein PsiE	0.01	0.05	0.01	0.07	0.90	0.48
<i>lmo0837</i>	hypothetical protein	0.03	0.08	0.01	0.04	0.93	0.20
<i>lmo0838</i>	sugar:phosphate antiporter	0.05	0.06	0.03	0.13	0.78	0.44
<i>lmo0839</i>	tetracycline resistance protein	0.00	0.00	0.00	0.01	0.69	0.22
<i>lmo0840</i>	hypothetical protein	0.00	0.00	0.06	0.33	0.80	0.30
<i>lmo0841</i>	calcium-transporting ATPase	0.34	0.25	0.23	0.32	0.77	0.21

<i>lmo0843</i>	hypothetical protein	0.17	0.28	0.03	0.13	0.71	0.21
<i>lmo0844</i>	hypothetical protein	0.00	0.00	0.04	0.28	0.85	0.37
<i>lmo0845</i>	hypothetical protein	0.00	0.00	0.02	0.07	0.80	0.40
<i>lmo0846</i>	excinuclease ABC subunit C	0.29	0.38	0.07	0.47	0.91	0.63
<i>lmo0847</i>	glutamine ABC transporter	0.18	0.11	0.03	0.54	0.66	0.27
<i>lmo0848</i>	amino acid ABC transporter ATP-binding protein	0.17	0.24	0.03	0.35	0.67	0.36
<i>lmo0850</i>	hypothetical protein	0.01	0.12	0.01	0.21	0.84	0.65
<i>lmo0851</i>	hypothetical protein	0.14	0.44	0.06	0.12	0.90	0.47
<i>lmo0852</i>	TetR family transcriptional regulator	0.00	0.00	0.02	0.05	0.52	0.20
<i>lmo0853</i>	SugE protein	0.00	0.00	0.03	0.04	0.48	0.21
<i>lmo0854</i>	SugE protein	0.00	0.00	0.06	0.09	0.60	0.31
<i>lmo0855</i>	D-alanyl-alanine synthetase A	0.03	0.07	0.02	0.23	0.90	0.56
<i>lmo0856</i>	UDP-N-acetylmuramoylalanyl-D-glutamyl-2 6-diamino pimelate-D-alanyl-D-alanyl ligase	0.03	0.34	0.01	0.28	0.82	0.54
<i>lmo0857</i>	carboxylesterase	0.15	0.45	0.04	0.36	0.92	0.64
<i>lmo0858</i>	LacI family transcriptional regulator	0.36	0.00	0.16	0.03	0.89	0.60
<i>lmo0860</i>	sugar ABC transporter permease	0.10	0.17	0.02	0.12	0.81	0.22
<i>lmo0861</i>	sugar ABC transporter permease	0.14	0.27	0.02	0.07	0.81	0.23
<i>lmo0862</i>	oligo-16-glucosidase	0.14	0.18	0.02	0.07	0.82	0.22
<i>lmo0863</i>	hypothetical protein	0.21	0.30	0.04	0.16	0.69	0.22
<i>lmo0864</i>	hypothetical protein	0.15	0.23	0.02	0.13	0.73	0.19
<i>lmo0865</i>	phosphomannomutase	0.23	0.28	0.04	0.16	0.76	0.37
<i>lmo0866</i>	ATP-dependent RNA helicase	0.25	0.07	0.10	0.25	0.92	0.68
<i>lmo0866a</i>	hypothetical protein	0.00	0.00	0.02	0.02	0.65	0.23
<i>lmo0867</i>	hypothetical protein	0.19	0.23	0.07	0.48	0.90	0.64
<i>lmo0868</i>	hypothetical protein	0.01	0.01	0.01	0.03	0.92	0.64
<i>lmo0869</i>	hypothetical protein	0.05	0.12	0.05	0.47	0.80	0.66
<i>lmo0870</i>	hypothetical protein	0.08	0.31	0.06	0.53	0.79	0.62
<i>lmo0871</i>	hypothetical protein	0.32	0.00	0.28	0.06	0.68	0.45
<i>lmo0872</i>	antibiotic resistance protein	0.00	0.00	0.02	0.04	0.64	0.27
<i>lmo0873</i>	transcriptional regulator	0.39	0.27	0.20	0.32	0.73	0.20
<i>lmo0874</i>	PTS sugar transporter subunit IIA	0.23	0.46	0.06	0.37	0.73	0.16
<i>lmo0875</i>	PTS beta-glucoside transporter subunit IIB	0.10	0.36	0.10	0.53	0.68	0.11
<i>lmo0876</i>	PTS sugar transporter subunit IIC	0.08	0.07	0.05	0.25	0.76	0.18
<i>lmo0877</i>	glucosamine-6-phosphate isomerase	0.09	0.14	0.06	0.38	0.75	0.20
<i>lmo0878</i>	oxidoreductase	0.07	0.15	0.06	0.40	0.76	0.16
<i>lmo0879</i>	hypothetical protein	0.02	0.02	0.07	0.36	0.71	0.13
<i>lmo0881</i>	hypothetical protein	0.14	0.35	0.21	0.20	0.75	0.22
<i>lmo0882</i>	hypothetical protein	0.14	0.17	0.22	0.42	0.74	0.39
<i>lmo0883</i>	hypothetical protein	0.01	0.00	0.15	0.18	0.40	0.17
<i>lmo0884</i>	protoporphyrinogen oxidase	0.02	0.15	0.01	0.18	0.87	0.16
<i>lmo0885</i>	4'-phosphopantetheinyl transferase	0.01	0.12	0.01	0.25	0.93	0.25
<i>lmo0886</i>	alanine racemase	0.03	0.43	0.03	0.45	0.92	0.24
<i>lmo0887</i>	hypothetical protein	0.26	0.31	0.28	0.54	0.88	0.65
<i>lmo0889</i>	positive regulator of sigma-B activity	0.40	0.25	0.27	0.25	0.92	0.70
<i>lmo0890</i>	negative regulation of sigma-B activity	0.30	0.28	0.17	0.30	0.90	0.70
<i>lmo0891</i>	positive regulation of sigma-B activity	0.25	0.30	0.16	0.33	0.88	0.70
<i>lmo0894</i>	serine-protein kinase RsbW	0.40	0.17	0.30	0.32	0.93	0.60
<i>lmo0895</i>	RNA polymerase sigma factor SigB	0.24	0.45	0.28	0.41	0.72	0.27
<i>lmo0896</i>	indirect negative regulation of sigma B dependant gene expression (serine phosphatase)	0.12	0.30	0.26	0.51	0.62	0.17
<i>lmo0897</i>	transporter	0.10	0.43	0.04	0.53	0.82	0.60
<i>lmo0898</i>	hypothetical protein	0.06	0.44	0.02	0.36	0.92	0.31
<i>lmo0899</i>	hypothetical protein	0.41	0.04	0.27	0.10	0.84	0.68
<i>lmo0900</i>	hypothetical protein	0.07	0.00	0.12	0.02	0.55	0.18
<i>lmo0901</i>	PTS cellbiose transporter subunit IIC	0.31	0.16	0.18	0.16	0.73	0.26
<i>lmo0902</i>	GntR family transcriptional regulator	0.05	0.37	0.05	0.51	0.91	0.53
<i>lmo0903</i>	hypothetical protein	0.03	0.01	0.05	0.07	0.42	0.15
<i>lmo0904</i>	hypothetical protein	0.31	0.19	0.07	0.46	0.81	0.56
<i>lmo0905</i>	hypothetical protein	0.12	0.23	0.05	0.33	0.62	0.20
<i>lmo0906</i>	glutathione reductase	0.05	0.33	0.03	0.40	0.71	0.29

<i>lmo0907</i>	phosphoglycerate mutase	0.01	0.03	0.01	0.11	0.89	0.67
<i>lmo0908</i>	hypothetical protein	0.22	0.32	0.15	0.29	0.92	0.59
<i>lmo0909</i>	GntR family transcriptional regulator	0.15	0.18	0.07	0.31	0.89	0.65
<i>lmo0910</i>	hypothetical protein	0.23	0.07	0.11	0.22	0.83	0.54
<i>lmo0911</i>	hypothetical protein	0.28	0.02	0.11	0.18	0.78	0.57
<i>lmo0912</i>	formate transporter	0.14	0.41	0.09	0.42	0.87	0.69
<i>lmo0913</i>	succinate semialdehyde dehydrogenase	0.10	0.49	0.03	0.38	0.71	0.20
<i>lmo0914</i>	PTS sugar transporter subunit IIB	0.09	0.36	0.08	0.33	0.85	0.61
<i>lmo0915</i>	PTS sugar transporter subunit IIC	0.11	0.24	0.09	0.26	0.81	0.53
<i>lmo0916</i>	PTS sugar transporter subunit IIA	0.11	0.28	0.08	0.27	0.81	0.53
<i>lmo0917</i>	beta-glucosidase	0.11	0.27	0.09	0.22	0.79	0.54
<i>lmo0918</i>	transcription antiterminator BglG	0.14	0.14	0.11	0.21	0.74	0.39
<i>lmo0919</i>	antibiotic ABC transporter ATP-binding protein	0.40	0.13	0.08	0.53	0.92	0.63
<i>lmo0920</i>	hypothetical protein	0.11	0.29	0.03	0.09	0.91	0.32
<i>lmo0921</i>	hypothetical protein	0.09	0.45	0.02	0.26	0.90	0.66
<i>lmo0922</i>	pantothenate kinase	0.06	0.09	0.10	0.51	0.77	0.22
<i>lmo0923</i>	ABC transporter ATP-binding protein	0.17	0.11	0.10	0.19	0.74	0.52
<i>lmo0925</i>	hypothetical protein	0.15	0.15	0.05	0.30	0.85	0.63
<i>lmo0926</i>	TetR family transcriptional regulator	0.07	0.37	0.03	0.49	0.90	0.53
<i>lmo0927</i>	hypothetical protein	0.14	0.04	0.14	0.05	0.92	0.68
<i>lmo0928</i>	3-methyladenine DNA glycosylase	0.00	0.00	0.00	0.02	0.88	0.61
<i>lmo0929</i>	sortase	0.08	0.27	0.03	0.15	0.74	0.46
<i>lmo0930</i>	hypothetical protein	0.02	0.00	0.06	0.04	0.69	0.24
<i>lmo0931</i>	lipoate protein ligase A	0.00	0.00	0.02	0.02	0.69	0.21
<i>lmo0932</i>	hypothetical protein	0.42	0.03	0.27	0.03	0.61	0.24
<i>lmo0934</i>	hypothetical protein	0.31	0.12	0.10	0.38	0.76	0.17
<i>lmo0935</i>	rRNA methylase	0.29	0.00	0.10	0.14	0.76	0.20
<i>lmo0936</i>	nitroflavin reductase	0.09	0.40	0.03	0.47	0.74	0.21
<i>lmo0937</i>	hypothetical protein	0.00	0.00	0.01	0.05	0.86	0.70
<i>lmo0938</i>	protein-tyrosine-phosphatase	0.00	0.03	0.01	0.19	0.93	0.57
<i>lmo0939</i>	hypothetical protein	0.09	0.28	0.03	0.32	0.91	0.59
<i>lmo0941</i>	hypothetical protein	0.00	0.00	0.00	0.01	0.91	0.41
<i>lmo0942</i>	heat shock protein 90	0.00	0.00	0.00	0.01	0.81	0.30
<i>lmo0943</i>	non-heme iron-binding ferritin	0.22	0.16	0.04	0.41	0.85	0.62
<i>lmo0944</i>	hypothetical protein	0.09	0.31	0.05	0.38	0.59	0.20
<i>lmo0945</i>	competence protein ComEC	0.39	0.26	0.14	0.51	0.91	0.69
<i>lmo0946</i>	hypothetical protein	0.20	0.48	0.06	0.33	0.92	0.60
<i>lmo0947</i>	hypothetical protein	0.33	0.00	0.16	0.29	0.62	0.30
<i>lmo0948</i>	transcriptional regulator	0.06	0.00	0.24	0.10	0.62	0.25
<i>lmo0949</i>	hypothetical protein	0.16	0.27	0.29	0.53	0.91	0.57
<i>lmo0950</i>	hypothetical protein	0.06	0.17	0.05	0.53	0.88	0.34
<i>lmo0951</i>	hypothetical protein	0.21	0.48	0.17	0.36	0.78	0.54
<i>lmo0952</i>	hypothetical protein	0.10	0.40	0.03	0.42	0.86	0.50
<i>lmo0953</i>	hypothetical protein	0.40	0.00	0.14	0.22	0.60	0.21
<i>lmo0954</i>	hypothetical protein	0.05	0.49	0.09	0.28	0.89	0.39
<i>lmo0955</i>	hypothetical protein	0.05	0.47	0.07	0.35	0.91	0.38
<i>lmo0956</i>	N-acetylglucosamine-6P-phosphate deacetylase	0.07	0.13	0.01	0.11	0.74	0.50
<i>lmo0957</i>	glucosamine-6-phosphate isomerase	0.07	0.07	0.01	0.06	0.74	0.55
<i>lmo0958</i>	GntR family transcripational regulator	0.06	0.05	0.01	0.05	0.73	0.50
<i>lmo0959</i>	undecaprenyl-phosphate N-acetylglucosaminyltransferase	0.00	0.00	0.00	0.02	0.79	0.39
<i>lmo0960</i>	protease	0.01	0.04	0.01	0.07	0.86	0.58
<i>lmo0961</i>	protease	0.00	0.05	0.02	0.16	0.90	0.64
<i>lmo0962</i>	LemA protein	0.39	0.30	0.19	0.41	0.69	0.38
<i>lmo0963</i>	heat shock protein HtpX	0.05	0.06	0.03	0.09	0.87	0.68
<i>lmo0964</i>	hypothetical protein	0.20	0.06	0.06	0.40	0.74	0.40
<i>lmo0965</i>	hypothetical protein	0.12	0.29	0.07	0.39	0.90	0.42
<i>lmo0966</i>	hypothetical protein	0.02	0.22	0.04	0.49	0.89	0.65
<i>lmo0967</i>	hypothetical protein	0.37	0.21	0.10	0.43	0.77	0.60
<i>lmo0968</i>	inorganic polyphosphate/ATP-NAD kinase	0.10	0.05	0.29	0.50	0.82	0.58
<i>lmo0969</i>	ribosomal large subunit pseudouridine synthetase	0.22	0.47	0.31	0.36	0.90	0.67
<i>lmo0970</i>	enoyl-ACP reductase	0.23	0.03	0.17	0.03	0.75	0.29

<i>lmo0971</i>	DltD protein for D-alanine esterification of lipoteichoic acid and wall teichoic acid	0.21	0.38	0.17	0.49	0.88	0.67
<i>lmo0972</i>	D-alanine--poly(phosphoribitol) ligase subunit 2	0.34	0.50	0.28	0.49	0.87	0.63
<i>lmo0973</i>	DltB protein for D-alanine esterification of lipoteichoic acid and wall teichoic acid	0.42	0.48	0.27	0.45	0.91	0.67
<i>lmo0974</i>	D-alanine--poly(phosphoribitol) ligase subunit 1	0.23	0.44	0.13	0.45	0.90	0.69
<i>lmo0975</i>	ribose-5-phosphate isomerase A	0.00	0.00	0.00	0.01	0.72	0.21
<i>lmo0976</i>	hypothetical protein	0.03	0.04	0.01	0.02	0.74	0.49
<i>lmo0977</i>	hypothetical protein	0.12	0.29	0.02	0.10	0.70	0.35
<i>lmo0978</i>	branched-chain amino acid aminotransferase	0.42	0.04	0.25	0.12	0.71	0.33
<i>lmo0979</i>	daunorubicin resistance ATP-binding protein	0.31	0.12	0.32	0.26	0.92	0.70
<i>lmo0980</i>	ABC transporter permease	0.25	0.03	0.31	0.12	0.91	0.69
<i>lmo0981</i>	transporter	0.01	0.01	0.00	0.01	0.92	0.42
<i>lmo0982</i>	peptidase	0.01	0.00	0.01	0.03	0.89	0.48
<i>lmo0983</i>	glutathione peroxidase	0.01	0.00	0.01	0.01	0.91	0.50
<i>lmo0984</i>	hypothetical protein	0.02	0.26	0.02	0.38	0.91	0.52
<i>lmo0985</i>	hypothetical protein	0.00	0.05	0.01	0.18	0.92	0.57
<i>lmo0986</i>	antibiotic ABC transporter ATP-binding protein	0.11	0.46	0.04	0.54	0.92	0.64
<i>lmo0987</i>	CylB protein	0.11	0.05	0.15	0.12	0.91	0.63
<i>lmo0988</i>	peptide chain release factor 3	0.06	0.21	0.02	0.20	0.91	0.57
<i>lmo0989</i>	MarR family transcriptional regulator	0.32	0.11	0.20	0.37	0.84	0.65
<i>lmo0991</i>	hypothetical protein	0.30	0.00	0.20	0.11	0.88	0.67
<i>lmo0992</i>	hypothetical protein	0.26	0.07	0.17	0.03	0.91	0.37
<i>lmo0993</i>	Na ⁺ -transporting ATP synthase subunit J	0.12	0.13	0.06	0.08	0.90	0.55
<i>lmo0994</i>	hypothetical protein	0.04	0.40	0.03	0.42	0.77	0.30
<i>lmo0995</i>	hypothetical protein	0.37	0.37	0.07	0.38	0.65	0.26
<i>lmo0996</i>	methylated-DNA-protein-cysteine methyltransferase	0.37	0.37	0.03	0.10	0.90	0.66
<i>lmo0997</i>	ATP-dependent protease	0.05	0.44	0.10	0.22	0.91	0.51
<i>lmo0998</i>	hypothetical protein	0.26	0.22	0.08	0.51	0.90	0.58
<i>lmo0999</i>	hypothetical protein	0.02	0.00	0.03	0.12	0.87	0.47
<i>lmo1000</i>	phytoene dehydrogenase	0.01	0.00	0.05	0.10	0.92	0.52
<i>lmo1001</i>	hypothetical protein	0.31	0.47	0.32	0.54	0.75	0.45
<i>lmo1002</i>	phosphocarrier protein HPr	0.39	0.20	0.26	0.48	0.79	0.59
<i>lmo1003</i>	phosphotransferase system enzyme I	0.27	0.06	0.27	0.38	0.70	0.51
<i>lmo1005</i>	3-hydroxyisobutyrate dehydrogenase	0.13	0.00	0.21	0.01	0.81	0.38
<i>lmo1006</i>	aminotransferase	0.20	0.43	0.08	0.53	0.90	0.52
<i>lmo1007</i>	hypothetical protein	0.34	0.47	0.24	0.54	0.86	0.61
<i>lmo1008</i>	hypothetical protein	0.10	0.01	0.27	0.12	0.92	0.67
<i>lmo1009</i>	hypothetical protein	0.01	0.11	0.02	0.18	0.74	0.50
<i>lmo1010</i>	LysR family transcriptional regulator	0.01	0.05	0.01	0.08	0.73	0.46
<i>lmo1011</i>	tetrahydrodipicolinate succinylase	0.28	0.33	0.14	0.42	0.92	0.62
<i>lmo1012</i>	N-acyl-L-amino acid amidohydrolase	0.00	0.00	0.00	0.02	0.77	0.31
<i>lmo1013</i>	hypothetical protein	0.00	0.00	0.01	0.09	0.92	0.32
<i>lmo1014</i>	glycine/betaine ABC transporter ATP-binding protein	0.17	0.48	0.03	0.23	0.92	0.40
<i>lmo1015</i>	glycine/betaine ABC transporter permease	0.22	0.30	0.04	0.44	0.87	0.58
<i>lmo1016</i>	glycine/betaine ABC transporter substrate-binding protein	0.07	0.22	0.01	0.09	0.89	0.40
<i>lmo1017</i>	PTS glucose transporter subunit IIA	0.01	0.05	0.00	0.03	0.87	0.37
<i>lmo1018</i>	copper homeostasis protein CutC	0.31	0.09	0.10	0.25	0.78	0.66
<i>lmo1019</i>	hypothetical protein	0.28	0.50	0.09	0.36	0.66	0.33
<i>lmo1020</i>	hypothetical protein	0.24	0.27	0.19	0.44	0.85	0.57
<i>lmo1021</i>	two-component sensor histidine kinase	0.39	0.47	0.07	0.25	0.85	0.65
<i>lmo1022</i>	two-component response regulator	0.25	0.43	0.28	0.38	0.79	0.43
<i>lmo1023</i>	potassium transporter	0.25	0.17	0.02	0.02	0.86	0.45
<i>lmo1025</i>	hypothetical protein	0.01	0.00	0.09	0.07	0.57	0.19
<i>lmo1026</i>	LytR protein	0.32	0.45	0.08	0.40	0.75	0.24
<i>lmo1027</i>	hypothetical protein	0.05	0.29	0.19	0.41	0.74	0.27
<i>lmo1028</i>	hypothetical protein	0.14	0.16	0.05	0.13	0.87	0.53
<i>lmo1029</i>	hypothetical protein	0.01	0.01	0.01	0.05	0.73	0.33
<i>lmo1030</i>	LacI family transcriptional regulator	0.34	0.48	0.17	0.47	0.70	0.40
<i>lmo1031</i>	hypothetical protein	0.26	0.01	0.33	0.08	0.80	0.61
<i>lmo1032</i>	transketolase	0.24	0.01	0.31	0.07	0.79	0.60

<i>lmo1033</i>	transketolase	0.33	0.01	0.25	0.09	0.83	0.62
<i>lmo1034</i>	glycerol kinase	0.32	0.06	0.12	0.18	0.90	0.63
<i>lmo1035</i>	PTS beta-glucoside transporter subunit IIABC	0.43	0.03	0.19	0.12	0.91	0.53
<i>lmo1036</i>	hypothetical protein	0.37	0.03	0.26	0.12	0.90	0.58
<i>lmo1037</i>	hypothetical protein	0.38	0.25	0.23	0.37	0.90	0.59
<i>lmo1038</i>	hypothetical protein	0.36	0.27	0.08	0.33	0.90	0.57
<i>lmo1039</i>	ABC transporter ATP-binding protein	0.33	0.37	0.09	0.41	0.91	0.62
<i>lmo1040</i>	molybdenum ABC transporter permease	0.22	0.49	0.09	0.39	0.91	0.52
<i>lmo1041</i>	molybdate ABC transporter substrate-binding protein	0.03	0.07	0.02	0.19	0.89	0.43
<i>lmo1042</i>	molybdopterin biosynthesis protein MoeA	0.05	0.46	0.02	0.27	0.91	0.52
<i>lmo1043</i>	molybdopterin-guanine dinucleotide biosynthesis MobB	0.04	0.46	0.02	0.29	0.92	0.56
<i>lmo1044</i>	molybdopterin converting factor subunit 2	0.07	0.40	0.02	0.41	0.92	0.63
<i>lmo1045</i>	molybdopterin converting factor subunit 1	0.01	0.04	0.01	0.11	0.92	0.43
<i>lmo1046</i>	molybdenum cofactor biosynthesis protein MoaC	0.01	0.06	0.01	0.11	0.91	0.37
<i>lmo1047</i>	molybdenum cofactor biosynthesis protein A	0.01	0.01	0.01	0.09	0.91	0.31
<i>lmo1048</i>	molybdenum cofactor biosynthesis protein B	0.10	0.27	0.04	0.53	0.88	0.59
<i>lmo1049</i>	molybdopterin biosynthesis protein MoeB	0.00	0.00	0.01	0.02	0.93	0.17
<i>lmo1050</i>	hypothetical protein	0.00	0.00	0.00	0.01	0.57	0.15
<i>lmo1051</i>	peptide deformylase	0.01	0.11	0.02	0.39	0.91	0.38
<i>lmo1052</i>	pyruvate dehydrogenase subunit E1 alpha	0.04	0.41	0.05	0.50	0.74	0.50
<i>lmo1053</i>	pyruvate dehydrogenase subunit E1 beta	0.14	0.25	0.05	0.54	0.70	0.32
<i>lmo1054</i>	dihydrolipoamide acetyltransferase	0.09	0.45	0.06	0.51	0.83	0.56
<i>lmo1055</i>	dihydrolipoamide dehydrogenase	0.22	0.13	0.14	0.21	0.79	0.35
<i>lmo1056</i>	hypothetical protein	0.00	0.00	0.04	0.07	0.90	0.50
<i>lmo1057</i>	L-lactate dehydrogenase	0.01	0.01	0.01	0.07	0.81	0.56
<i>lmo1058</i>	hypothetical protein	0.01	0.12	0.01	0.32	0.85	0.70
<i>lmo1059</i>	hypothetical protein	0.01	0.05	0.01	0.10	0.87	0.70
<i>lmo1064</i>	transporter	0.09	0.34	0.05	0.52	0.91	0.69
<i>lmo1065</i>	hypothetical protein	0.26	0.29	0.15	0.32	0.87	0.50
<i>lmo1066</i>	myo-inositol-1(or 4)-monophosphatase	0.29	0.25	0.06	0.49	0.90	0.66
<i>lmo1067</i>	GTP-binding elongation factor	0.41	0.01	0.15	0.25	0.91	0.69
<i>lmo1069</i>	hypothetical protein	0.23	0.06	0.12	0.11	0.72	0.29
<i>lmo1070</i>	hypothetical protein	0.26	0.37	0.06	0.47	0.89	0.68
<i>lmo1071</i>	cell division protein FtsW	0.06	0.04	0.03	0.33	0.91	0.38
<i>lmo1072</i>	pyruvate carboxylase	0.16	0.09	0.08	0.19	0.83	0.70
<i>lmo1073</i>	metal ABC transporter substrate-binding protein	0.08	0.28	0.02	0.50	0.74	0.44
<i>lmo1074</i>	teichoic acid translocation permease TagG	0.16	0.09	0.06	0.34	0.79	0.32
<i>lmo1075</i>	teichoic acid ABC transporter ATP-binding protein	0.03	0.13	0.01	0.03	0.84	0.67
<i>lmo1078</i>	UDP-glucose pyrophosphorylase	0.13	0.00	0.14	0.00	0.88	0.19
<i>lmo1089</i>	glycerol-3-phosphate cytidyltransferase	0.15	0.08	0.02	0.00	0.80	0.57
<i>lmo1092</i>	nicotinate phosphoribosyltransferase	0.31	0.42	0.21	0.24	0.60	0.18
<i>lmo1093</i>	NAD synthetase	0.16	0.06	0.10	0.10	0.89	0.56
<i>lmo1094</i>	hypothetical protein	0.16	0.04	0.10	0.09	0.92	0.63
<i>lmo1095</i>	PTS cellbiose transporter subunit IIB	0.40	0.15	0.31	0.23	0.74	0.39
<i>lmo1096</i>	GMP synthase	0.36	0.00	0.22	0.02	0.77	0.51
<i>lmo1126</i>	hypothetical protein	0.00	0.00	0.01	0.05	0.68	0.19
<i>lmo1127</i>	hypothetical protein	0.00	0.00	0.01	0.02	0.73	0.23
<i>lmo1128</i>	hypothetical protein	0.19	0.18	0.13	0.26	0.92	0.67
<i>lmo1129</i>	hypothetical protein	0.10	0.15	0.05	0.17	0.91	0.62
<i>lmo1131</i>	ABC transporter ATP-binding protein	0.03	0.37	0.07	0.51	0.89	0.34
<i>lmo1132</i>	ABC transporter ATP-binding protein	0.08	0.47	0.20	0.26	0.91	0.37
<i>lmo1133</i>	hypothetical protein	0.21	0.36	0.25	0.29	0.90	0.61
<i>lmo1135</i>	hypothetical protein	0.00	0.00	0.01	0.00	0.60	0.21
<i>lmo1137</i>	hypothetical protein	0.34	0.19	0.22	0.27	0.70	0.43
<i>lmo1138</i>	ATP-dependent Clp protease proteolytic subunit	0.01	0.18	0.05	0.53	0.92	0.43
<i>lmo1140</i>	hypothetical protein	0.24	0.11	0.10	0.43	0.69	0.21
<i>lmo1142</i>	PduS protein	0.10	0.47	0.03	0.31	0.87	0.33
<i>lmo1143</i>	PduT protein	0.34	0.18	0.08	0.55	0.88	0.55
<i>lmo1144</i>	PduU protein	0.04	0.24	0.06	0.46	0.76	0.25
<i>lmo1145</i>	PduV protein	0.13	0.42	0.08	0.49	0.87	0.39
<i>lmo1146</i>	hypothetical protein	0.04	0.19	0.05	0.37	0.73	0.20

<i>lmo1147</i>	cobalamin biosynthesis protein CopB	0.00	0.01	0.01	0.14	0.62	0.09
<i>lmo1148</i>	cobalamin (5'-phosphatase) synthetase	0.01	0.04	0.02	0.21	0.70	0.20
<i>lmo1149</i>	alpha-ribazole-5'-phosphatase	0.00	0.00	0.00	0.02	0.66	0.15
<i>lmo1150</i>	transcriptional regulator PocR	0.12	0.34	0.03	0.33	0.90	0.36
<i>lmo1152</i>	PduB protein	0.40	0.34	0.30	0.36	0.84	0.38
<i>lmo1153</i>	propanediol dehydratase subunit alpha	0.42	0.34	0.32	0.42	0.90	0.41
<i>lmo1154</i>	diol dehydratase subunit gamma	0.43	0.46	0.15	0.34	0.87	0.28
<i>lmo1155</i>	diol dehydratase subunit gamma	0.36	0.45	0.28	0.40	0.89	0.43
<i>lmo1156</i>	diol dehydratase-reactivating factor large subunit	0.41	0.36	0.21	0.48	0.81	0.33
<i>lmo1157</i>	diol dehydratase-reactivating factor small subunit	0.32	0.29	0.32	0.44	0.91	0.56
<i>lmo1158</i>	PduK protein	0.37	0.40	0.28	0.40	0.84	0.32
<i>lmo1160</i>	PduL protein	0.33	0.41	0.33	0.40	0.91	0.54
<i>lmo1161</i>	ethanolamine utilization protein EutJ	0.36	0.27	0.29	0.31	0.92	0.41
<i>lmo1162</i>	hypothetical protein	0.32	0.33	0.22	0.36	0.91	0.56
<i>lmo1163</i>	carbon dioxide concentrating mechanism protein	0.37	0.40	0.18	0.18	0.92	0.58
<i>lmo1164</i>	ATP:cob(I)alamin adenosyltransferase PduO	0.24	0.50	0.19	0.54	0.86	0.36
<i>lmo1165</i>	ethanolamine utilization protein EutE	0.06	0.32	0.10	0.55	0.79	0.21
<i>lmo1166</i>	NADPH-dependent butanol dehydrogenase	0.30	0.42	0.31	0.28	0.89	0.48
<i>lmo1167</i>	glycerol uptake facilitator protein	0.42	0.41	0.26	0.29	0.86	0.41
<i>lmo1168</i>	acetate kinase	0.15	0.27	0.01	0.05	0.86	0.56
<i>lmo1169</i>	threonine-phosphate decarboxylase	0.32	0.04	0.07	0.37	0.78	0.39
<i>lmo1170</i>	PduX protein	0.03	0.18	0.00	0.02	0.81	0.59
<i>lmo1171</i>	NADPH-dependent butanol dehydrogenase	0.01	0.08	0.01	0.15	0.82	0.29
<i>lmo1172</i>	two-component response regulator	0.03	0.14	0.01	0.12	0.87	0.29
<i>lmo1173</i>	two-component sensor histidine kinase	0.02	0.07	0.01	0.07	0.85	0.26
<i>lmo1174</i>	ethanolamine utilization protein EutA	0.05	0.26	0.01	0.36	0.86	0.39
<i>lmo1175</i>	ethanolamine ammonia-lyase large subunit	0.05	0.24	0.01	0.22	0.92	0.39
<i>lmo1176</i>	ethanolamine ammonia-lyase small subunit	0.05	0.24	0.01	0.21	0.91	0.39
<i>lmo1177</i>	carboxysome structural protein EutL	0.13	0.27	0.04	0.21	0.84	0.36
<i>lmo1178</i>	carboxysome structural protein	0.11	0.32	0.03	0.27	0.81	0.41
<i>lmo1179</i>	alcohol dehydrogenase	0.08	0.25	0.02	0.17	0.92	0.47
<i>lmo1181</i>	cobalamin adenosyl transferase	0.08	0.22	0.02	0.22	0.83	0.34
<i>lmo1182</i>	PduL protein	0.14	0.25	0.04	0.28	0.80	0.33
<i>lmo1183</i>	hypothetical protein	0.08	0.28	0.02	0.22	0.87	0.39
<i>lmo1184</i>	carbon dioxide concentrating mechanism protein	0.02	0.14	0.01	0.18	0.92	0.50
<i>lmo1185</i>	PduT protein	0.01	0.11	0.01	0.22	0.88	0.31
<i>lmo1186</i>	ethanolamine utilization protein EutH	0.12	0.25	0.04	0.23	0.70	0.23
<i>lmo1187</i>	ethanolamine utilization protein EutQ	0.14	0.34	0.06	0.36	0.92	0.66
<i>lmo1189</i>	transcriptional regulator	0.23	0.12	0.10	0.29	0.92	0.61
<i>lmo1190</i>	hypothetical protein	0.30	0.12	0.11	0.39	0.90	0.63
<i>lmo1191</i>	cobyric acid ac-diamide synthase	0.13	0.36	0.07	0.54	0.91	0.42
<i>lmo1192</i>	cobalamin biosynthesis protein	0.30	0.41	0.14	0.52	0.85	0.38
<i>lmo1193</i>	cobalt-precorrin-8X methylmutase	0.18	0.44	0.13	0.48	0.74	0.29
<i>lmo1194</i>	cobalt-precorrin-6A synthase	0.17	0.48	0.09	0.49	0.76	0.31
<i>lmo1195</i>	cobalt-precorrin-6Y C(5)-methyltransferase	0.08	0.34	0.07	0.45	0.75	0.23
<i>lmo1196</i>	cobalt-precorrin-6Y C(15)-methyltransferase	0.17	0.48	0.11	0.52	0.82	0.40
<i>lmo1197</i>	precorrin-3 methylase	0.08	0.24	0.12	0.49	0.72	0.20
<i>lmo1198</i>	cobalamin biosynthesis protein CbiG	0.05	0.21	0.08	0.40	0.75	0.30
<i>lmo1199</i>	precorrin-3B C17-methyltransferase	0.04	0.15	0.10	0.45	0.73	0.28
<i>lmo1200</i>	cobalamin biosynthesis protein CbiJ	0.09	0.19	0.06	0.24	0.75	0.30
<i>lmo1201</i>	uroporphyrinogen-III methyltransferase/uroporphyrinogen-III synthase	0.11	0.19	0.09	0.31	0.72	0.23
<i>lmo1202</i>	cobalt chelatase	0.22	0.36	0.15	0.40	0.72	0.33
<i>lmo1203</i>	cobalt-precorrin-2 C(20)-methyltransferase	0.10	0.16	0.11	0.27	0.57	0.17
<i>lmo1204</i>	cobalamin biosynthesis protein CbiM	0.38	0.42	0.18	0.38	0.74	0.31
<i>lmo1205</i>	cobalamin biosynthesis protein CbiN	0.40	0.46	0.19	0.39	0.83	0.54
<i>lmo1206</i>	cobalamin biosynthesis protein CbiQ	0.32	0.40	0.21	0.37	0.81	0.51
<i>lmo1207</i>	cobalt transporter ATP-binding protein CbiO	0.15	0.09	0.31	0.46	0.92	0.69
<i>lmo1208</i>	cobyric acid synthase CbiP	0.20	0.01	0.32	0.21	0.64	0.31
<i>lmo1209</i>	hypothetical protein	0.14	0.01	0.32	0.26	0.69	0.32
<i>lmo1210</i>	hypothetical protein	0.16	0.27	0.05	0.52	0.87	0.69

<i>lmo1211</i>	hypothetical protein	0.15	0.23	0.06	0.45	0.87	0.56
<i>lmo1212</i>	hypothetical protein	0.01	0.02	0.00	0.01	0.90	0.55
<i>lmo1213</i>	hypothetical protein	0.00	0.00	0.00	0.00	0.78	0.24
<i>lmo1214</i>	hypothetical protein	0.00	0.00	0.00	0.03	0.80	0.22
<i>lmo1215</i>	N-acetylmuramoyl-L-alanine amidase	0.23	0.44	0.12	0.47	0.90	0.29
<i>lmo1216</i>	N-acetylmuramoyl-L-alanine amidase	0.34	0.14	0.09	0.54	0.91	0.40
<i>lmo1217</i>	endo-1,4-beta-glucanase and to aminopeptidase	0.00	0.00	0.14	0.17	0.64	0.30
<i>lmo1218</i>	rRNA methylase	0.01	0.00	0.27	0.28	0.67	0.33
<i>lmo1219</i>	hypothetical protein	0.09	0.46	0.07	0.46	0.88	0.69
<i>lmo1220</i>	hypothetical protein	0.14	0.19	0.06	0.39	0.73	0.36
<i>lmo1221</i>	phenylalanyl-tRNA synthetase subunit alpha	0.15	0.19	0.03	0.54	0.80	0.45
<i>lmo1222</i>	phenylalanyl-tRNA synthetase subunit beta	0.23	0.02	0.04	0.53	0.68	0.37
<i>lmo1223</i>	ABC transporter ATP-binding proteins	0.00	0.00	0.01	0.03	0.84	0.52
<i>lmo1224</i>	hypothetical protein	0.25	0.00	0.27	0.18	0.73	0.63
<i>lmo1225</i>	MarR family transcriptional regulator	0.10	0.16	0.10	0.27	0.84	0.58
<i>lmo1226</i>	transporter	0.38	0.24	0.12	0.48	0.75	0.36
<i>lmo1227</i>	uracil-DNA glycosylase	0.04	0.00	0.10	0.06	0.88	0.46
<i>lmo1228</i>	ribonuclease HIII	0.12	0.33	0.04	0.48	0.91	0.67
<i>lmo1229</i>	hypothetical protein	0.28	0.29	0.11	0.54	0.61	0.33
<i>lmo1230</i>	hypothetical protein	0.14	0.31	0.05	0.14	0.68	0.30
<i>lmo1231</i>	DNA polymerase beta	0.40	0.06	0.30	0.10	0.89	0.52
<i>lmo1232</i>	recombination and DNA strand exchange inhibitor protein	0.39	0.00	0.17	0.13	0.89	0.67
<i>lmo1233</i>	thioredoxin	0.37	0.20	0.14	0.53	0.55	0.22
<i>lmo1234</i>	excinuclease ABC subunit C	0.11	0.29	0.03	0.37	0.72	0.23
<i>lmo1235</i>	aspartate kinase	0.13	0.19	0.06	0.24	0.74	0.19
<i>lmo1236</i>	hypothetical protein	0.04	0.10	0.07	0.20	0.91	0.46
<i>lmo1237</i>	glutamate racemase	0.06	0.10	0.03	0.30	0.88	0.40
<i>lmo1238</i>	ribonuclease PH	0.15	0.44	0.09	0.28	0.92	0.66
<i>lmo1239</i>	nucleoside-triphosphatase	0.20	0.08	0.14	0.09	0.89	0.49
<i>lmo1240</i>	hypothetical protein	0.05	0.40	0.05	0.44	0.90	0.56
<i>lmo1241</i>	hypothetical protein	0.16	0.39	0.05	0.50	0.72	0.26
<i>lmo1242</i>	hypothetical protein	0.01	0.01	0.00	0.01	0.59	0.23
<i>lmo1243</i>	hypothetical protein	0.00	0.00	0.01	0.06	0.89	0.45
<i>lmo1244</i>	phosphoglycerate mutase	0.29	0.24	0.27	0.19	0.82	0.66
<i>lmo1245</i>	hypothetical protein	0.16	0.04	0.17	0.09	0.90	0.67
<i>lmo1246</i>	ATP-dependent RNA helicase	0.35	0.06	0.20	0.02	0.90	0.63
<i>lmo1247</i>	hypothetical protein	0.40	0.07	0.23	0.01	0.88	0.40
<i>lmo1248</i>	hypothetical protein	0.02	0.18	0.01	0.09	0.92	0.52
<i>lmo1249</i>	hypothetical protein	0.06	0.00	0.21	0.12	0.90	0.63
<i>lmo1250</i>	antibiotic resistance protein	0.41	0.06	0.15	0.30	0.92	0.57
<i>lmo1251</i>	Fnr/Crp family transcriptional regulator	0.03	0.17	0.01	0.15	0.89	0.30
<i>lmo1252</i>	hypothetical protein	0.32	0.48	0.25	0.46	0.60	0.13
<i>lmo1253</i>	GntR family transcriptional regulator	0.42	0.08	0.30	0.14	0.80	0.58
<i>lmo1254</i>	alphaalpha-phosphotrehalase	0.10	0.48	0.03	0.44	0.88	0.43
<i>lmo1255</i>	PTS trehalose transporter subunit IIBC	0.10	0.44	0.04	0.50	0.90	0.50
<i>lmo1257</i>	hypothetical protein	0.37	0.02	0.30	0.01	0.65	0.23
<i>lmo1258</i>	hypothetical protein	0.00	0.00	0.01	0.08	0.92	0.20
<i>lmo1259</i>	gamma-glutamyl phosphate reductase	0.22	0.00	0.31	0.10	0.74	0.41
<i>lmo1260</i>	gamma-glutamyl kinase	0.13	0.41	0.06	0.53	0.91	0.48
<i>lmo1261</i>	hypothetical protein	0.03	0.09	0.01	0.07	0.88	0.61
<i>lmo1262</i>	transcriptional regulator	0.30	0.25	0.14	0.36	0.90	0.48
<i>lmo1263</i>	transcriptional regulator	0.30	0.47	0.22	0.53	0.61	0.23
<i>lmo1264</i>	hypothetical protein	0.04	0.03	0.16	0.33	0.61	0.22
<i>lmo1265</i>	hypothetical protein	0.03	0.05	0.09	0.32	0.86	0.52
<i>lmo1266</i>	hypothetical protein	0.09	0.14	0.02	0.07	0.86	0.51
<i>lmo1267</i>	trigger factor	0.00	0.00	0.01	0.12	0.86	0.24
<i>lmo1268</i>	ATP-dependent protease ATP-binding subunit ClpX	0.01	0.01	0.03	0.12	0.71	0.39
<i>lmo1269</i>	type I signal peptidase	0.22	0.02	0.30	0.13	0.81	0.48
<i>lmo1270</i>	type I signal peptidase	0.23	0.01	0.22	0.04	0.78	0.41
<i>lmo1271</i>	type I signal peptidase	0.21	0.34	0.13	0.25	0.87	0.26
<i>lmo1272</i>	ribosomal biogenesis GTPase	0.20	0.32	0.10	0.32	0.89	0.21

<i>lmo1273</i>	ribonuclease HII	0.15	0.39	0.07	0.50	0.92	0.25
<i>lmo1274</i>	polypeptide deformylase	0.00	0.00	0.00	0.02	0.64	0.19
<i>lmo1275</i>	DNA topoisomerase I	0.28	0.03	0.17	0.00	0.84	0.47
<i>lmo1276</i>	tRNA (uracil-5-)-methyltransferase Gid	0.13	0.32	0.05	0.54	0.75	0.51
<i>lmo1277</i>	integrase/recombinase	0.01	0.01	0.04	0.32	0.88	0.23
<i>lmo1278</i>	ATP-dependent protease peptidase subunit	0.12	0.38	0.09	0.46	0.72	0.48
<i>lmo1279</i>	ATP-dependent protease ATP-binding subunit HslU	0.06	0.48	0.03	0.35	0.75	0.47
<i>lmo1280</i>	transcriptional repressor CodY	0.28	0.16	0.14	0.39	0.77	0.65
<i>lmo1281</i>	hypothetical protein	0.00	0.00	0.00	0.04	0.92	0.30
<i>lmo1282</i>	hypothetical protein	0.00	0.00	0.01	0.08	0.89	0.38
<i>lmo1283</i>	LacX protein	0.00	0.00	0.01	0.03	0.74	0.24
<i>lmo1284</i>	hypothetical protein	0.15	0.07	0.10	0.27	0.87	0.49
<i>lmo1285</i>	hypothetical protein	0.25	0.06	0.13	0.20	0.71	0.50
<i>lmo1286</i>	DNA topoisomerase IV subunit B	0.15	0.19	0.03	0.52	0.89	0.67
<i>lmo1287</i>	DNA topoisomerase IV subunit A	0.06	0.39	0.01	0.16	0.83	0.69
<i>lmo1288</i>	S-ribosylhomocysteinase	0.17	0.33	0.15	0.48	0.93	0.41
<i>lmo1290</i>	internalin	0.03	0.15	0.07	0.48	0.76	0.43
<i>lmo1291</i>	acyltransferase	0.18	0.07	0.08	0.01	0.85	0.67
<i>lmo1292</i>	glycerophosphodiester phosphodiesterase	0.03	0.10	0.03	0.17	0.90	0.70
<i>lmo1293</i>	glycerol-3-phosphate dehydrogenase	0.10	0.27	0.04	0.45	0.75	0.32
<i>lmo1294</i>	tRNA delta(2)-isopentenylpyrophosphate transferase	0.21	0.27	0.11	0.52	0.90	0.60
<i>lmo1295</i>	host factor-1 protein	0.08	0.28	0.03	0.18	0.87	0.62
<i>lmo1296</i>	hypothetical protein	0.17	0.14	0.05	0.47	0.86	0.56
<i>lmo1297</i>	aluminum resistance protein	0.22	0.05	0.10	0.28	0.75	0.35
<i>lmo1298</i>	glutamine synthetase repressor	0.10	0.01	0.25	0.08	0.78	0.29
<i>lmo1299</i>	glutamine synthetase	0.11	0.00	0.19	0.02	0.78	0.31
<i>lmo1301</i>	hypothetical protein	0.15	0.23	0.12	0.15	0.91	0.58
<i>lmo1302</i>	LexA family transcriptional regulator	0.05	0.35	0.05	0.37	0.92	0.36
<i>lmo1303</i>	cell division suppressor	0.30	0.30	0.24	0.30	0.90	0.67
<i>lmo1304</i>	hypothetical protein	0.02	0.01	0.04	0.13	0.67	0.28
<i>lmo1305</i>	transketolase	0.16	0.33	0.16	0.37	0.91	0.52
<i>lmo1306</i>	hypothetical protein	0.35	0.03	0.03	0.51	0.62	0.19
<i>lmo1308</i>	hypothetical protein	0.06	0.00	0.27	0.03	0.55	0.23
<i>lmo1309</i>	hypothetical protein	0.17	0.00	0.31	0.08	0.65	0.39
<i>lmo1310</i>	hypothetical protein	0.12	0.00	0.24	0.05	0.61	0.39
<i>lmo1312</i>	hypothetical protein	0.00	0.00	0.00	0.01	0.73	0.37
<i>lmo1313</i>	uridylate kinase	0.10	0.48	0.03	0.53	0.87	0.38
<i>lmo1314</i>	ribosome recycling factor	0.08	0.48	0.04	0.48	0.81	0.47
<i>lmo1315</i>	UDP pyrophosphate synthase	0.39	0.01	0.17	0.07	0.85	0.18
<i>lmo1316</i>	phosphatidate cytidyltransferase	0.30	0.03	0.19	0.04	0.88	0.37
<i>lmo1317</i>	1-deoxy-D-xylulose 5-phosphate reductoisomerase	0.24	0.03	0.10	0.18	0.74	0.19
<i>lmo1318</i>	hypothetical protein	0.21	0.03	0.10	0.07	0.75	0.19
<i>lmo1319</i>	prolyl-tRNA synthetase	0.38	0.00	0.12	0.07	0.60	0.20
<i>lmo1320</i>	DNA polymerase III PolC	0.38	0.03	0.07	0.45	0.60	0.34
<i>lmo1321</i>	hypothetical protein	0.23	0.07	0.10	0.10	0.85	0.51
<i>lmo1322</i>	transcription elongation factor NusA	0.13	0.35	0.06	0.41	0.88	0.63
<i>lmo1323</i>	hypothetical protein	0.09	0.48	0.05	0.54	0.88	0.61
<i>lmo1324</i>	hypothetical protein	0.06	0.41	0.03	0.51	0.84	0.67
<i>lmo1325</i>	translation initiation factor IF-2	0.08	0.42	0.03	0.54	0.77	0.61
<i>lmo1326</i>	hypothetical protein	0.17	0.21	0.06	0.49	0.74	0.48
<i>lmo1327</i>	ribosome-binding factor A	0.16	0.19	0.06	0.54	0.73	0.46
<i>lmo1328</i>	tRNA pseudouridine synthase B	0.03	0.37	0.02	0.55	0.85	0.68
<i>lmo1329</i>	riboflavin kinase	0.12	0.40	0.13	0.28	0.91	0.61
<i>lmo1330</i>	30S ribosomal protein S15	0.26	0.40	0.07	0.38	0.92	0.68
<i>lmo1331</i>	polynucleotide phosphorylase	0.14	0.45	0.10	0.26	0.86	0.41
<i>lmo1332</i>	GTPase EngC	0.00	0.00	0.01	0.19	0.92	0.37
<i>lmo1333</i>	hypothetical protein	0.03	0.06	0.01	0.10	0.92	0.65
<i>lmo1333a</i>	hypothetical protein	0.14	0.23	0.02	0.08	0.91	0.54
<i>lmo1334</i>	hypothetical protein	0.13	0.24	0.02	0.12	0.92	0.67
<i>lmo1335</i>	50S ribosomal protein L33	0.13	0.35	0.10	0.27	0.86	0.43
<i>lmo1336</i>	5-formyltetrahydrofolate cyclo-ligase	0.25	0.00	0.31	0.04	0.90	0.45

<i>lmo1337</i>	hypothetical protein	0.20	0.42	0.26	0.22	0.88	0.46
<i>lmo1338</i>	hypothetical protein	0.04	0.28	0.06	0.48	0.92	0.53
<i>lmo1339</i>	glucose kinase	0.00	0.00	0.00	0.07	0.91	0.46
<i>lmo1340</i>	hypothetical protein	0.10	0.28	0.07	0.52	0.85	0.48
<i>lmo1341</i>	competence protein ComG	0.08	0.00	0.21	0.07	0.86	0.52
<i>lmo1342</i>	competence protein ComGF	0.12	0.00	0.33	0.08	0.88	0.52
<i>lmo1343</i>	competence protein ComGE	0.10	0.00	0.24	0.14	0.75	0.35
<i>lmo1344</i>	competence protein ComGD	0.24	0.01	0.28	0.17	0.91	0.57
<i>lmo1345</i>	competence protein ComGC	0.19	0.25	0.15	0.36	0.80	0.45
<i>lmo1346</i>	competence protein ComGB	0.00	0.00	0.10	0.12	0.35	0.09
<i>lmo1347</i>	competence protein ComGA	0.00	0.00	0.01	0.02	0.61	0.21
<i>lmo1348</i>	glycine cleavage system aminomethyltransferase T	0.12	0.50	0.01	0.12	0.85	0.57
<i>lmo1349</i>	glycine dehydrogenase subunit 1	0.17	0.47	0.01	0.11	0.84	0.63
<i>lmo1350</i>	glycine dehydrogenase subunit 2	0.22	0.41	0.01	0.14	0.82	0.60
<i>lmo1351</i>	hypothetical protein	0.17	0.07	0.03	0.50	0.81	0.31
<i>lmo1352</i>	hypothetical protein	0.11	0.46	0.02	0.34	0.91	0.59
<i>lmo1353</i>	hypothetical protein	0.14	0.42	0.06	0.50	0.93	0.64
<i>lmo1354</i>	aminopeptidase P	0.14	0.38	0.08	0.51	0.76	0.37
<i>lmo1355</i>	elongation factor P	0.14	0.34	0.05	0.53	0.92	0.69
<i>lmo1356</i>	acetyl-CoA carboxylase subunit (biotin carboxyl carrier subunit)	0.40	0.01	0.27	0.05	0.92	0.48
<i>lmo1357</i>	acetyl-CoA carboxylase biotin carboxylase subunit	0.30	0.03	0.17	0.08	0.85	0.49
<i>lmo1358</i>	hypothetical protein	0.36	0.00	0.26	0.05	0.78	0.50
<i>lmo1359</i>	transcription antitermination protein NusB	0.41	0.01	0.24	0.08	0.80	0.58
<i>lmo1360</i>	bifunctional 510-methylene-tetrahydrofolate dehydrogenase/ 510-methylene-tetrahydrofolate cyclohydrolase	0.09	0.41	0.04	0.53	0.73	0.36
<i>lmo1361</i>	exodeoxyribonuclease VII large subunit	0.05	0.47	0.01	0.31	0.75	0.49
<i>lmo1362</i>	exodeoxyribonuclease VII small subunit	0.03	0.20	0.01	0.23	0.85	0.66
<i>lmo1363</i>	geranyltranstransferase	0.18	0.13	0.06	0.35	0.75	0.53
<i>lmo1364</i>	cold-shock protein	0.37	0.49	0.17	0.37	0.60	0.18
<i>lmo1365</i>	1-deoxy-D-xylulose-5-phosphate synthase	0.15	0.45	0.10	0.37	0.91	0.48
<i>lmo1366</i>	hypothetical protein	0.02	0.02	0.04	0.44	0.89	0.18
<i>lmo1367</i>	arginine repressor ArgR	0.08	0.40	0.03	0.44	0.92	0.27
<i>lmo1368</i>	DNA repair protein	0.40	0.15	0.12	0.55	0.93	0.56
<i>lmo1369</i>	phosphotransbutyrylase	0.18	0.10	0.09	0.12	0.92	0.51
<i>lmo1370</i>	butyrate kinase	0.25	0.03	0.10	0.00	0.89	0.53
<i>lmo1371</i>	dihydrolipoamide dehydrogenase	0.09	0.02	0.03	0.00	0.84	0.33
<i>lmo1372</i>	branched-chain alpha-keto acid dehydrogenase subunit E1	0.30	0.09	0.14	0.05	0.75	0.45
<i>lmo1373</i>	branched-chain alpha-keto acid dehydrogenase subunit E1	0.36	0.09	0.21	0.07	0.71	0.35
<i>lmo1374</i>	branched-chain alpha-keto acid dehydrogenase subunit E2	0.33	0.32	0.29	0.24	0.73	0.58
<i>lmo1375</i>	aminotripeptidase	0.39	0.25	0.06	0.36	0.80	0.55
<i>lmo1376</i>	6-phosphogluconate dehydrogenase	0.02	0.02	0.08	0.45	0.79	0.19
<i>lmo1377</i>	two-component response regulator	0.05	0.38	0.01	0.17	0.92	0.30
<i>lmo1378</i>	two-component sensor histidine kinase	0.17	0.48	0.02	0.21	0.90	0.47
<i>lmo1379</i>	sporulation protein SpoJ	0.09	0.37	0.04	0.52	0.90	0.64
<i>lmo1380</i>	hypothetical protein	0.09	0.36	0.05	0.44	0.85	0.60
<i>lmo1381</i>	acylphosphatase	0.05	0.32	0.04	0.55	0.90	0.36
<i>lmo1382</i>	hypothetical protein	0.22	0.18	0.07	0.40	0.60	0.23
<i>lmo1383</i>	isopentenyl pyrophosphate isomerase	0.10	0.00	0.26	0.15	0.39	0.16
<i>lmo1384</i>	hypothetical protein	0.24	0.36	0.18	0.37	0.87	0.63
<i>lmo1385</i>	hypothetical protein	0.07	0.08	0.31	0.55	0.75	0.39
<i>lmo1386</i>	DNA translocase	0.00	0.00	0.01	0.09	0.83	0.43
<i>lmo1387</i>	pyrroline-5-carboxylate reductase	0.12	0.20	0.26	0.55	0.87	0.67
<i>lmo1388</i>	CD4+ T cell-stimulating antigen lipoprotein	0.18	0.42	0.32	0.28	0.84	0.44
<i>lmo1389</i>	sugar ABC transporter ATP-binding protein	0.00	0.00	0.01	0.09	0.68	0.12
<i>lmo1390</i>	ABC transporter permease	0.00	0.00	0.00	0.07	0.60	0.09
<i>lmo1391</i>	sugar ABC transporter permease	0.00	0.00	0.01	0.11	0.58	0.09
<i>lmo1392</i>	peptidase	0.34	0.20	0.22	0.06	0.86	0.61
<i>lmo1393</i>	peptidase	0.42	0.42	0.23	0.18	0.91	0.69
<i>lmo1394</i>	3-ketoacyl-ACP reductase	0.41	0.49	0.11	0.10	0.87	0.50
<i>lmo1395</i>	hypothetical protein	0.24	0.46	0.30	0.11	0.87	0.33
<i>lmo1396</i>	phosphatidylglycerophosphate synthase	0.09	0.41	0.03	0.49	0.92	0.38

<i>lmo1397</i>	competence damage-inducible protein CinA	0.00	0.00	0.01	0.02	0.60	0.19
<i>lmo1398</i>	recombinase A	0.02	0.00	0.07	0.05	0.68	0.38
<i>lmo1399</i>	phosphodiesterase	0.13	0.01	0.21	0.34	0.48	0.16
<i>lmo1400</i>	N-acetyltransferase	0.00	0.00	0.00	0.05	0.81	0.22
<i>lmo1401</i>	hypothetical protein	0.00	0.00	0.00	0.03	0.85	0.16
<i>lmo1402</i>	hypothetical protein	0.01	0.01	0.02	0.28	0.92	0.35
<i>lmo1403</i>	DNA mismatch repair protein MutS	0.04	0.31	0.05	0.52	0.91	0.57
<i>lmo1404</i>	DNA mismatch repair protein	0.17	0.38	0.11	0.45	0.67	0.43
<i>lmo1405</i>	anti-terminator regulatory protein	0.09	0.49	0.06	0.49	0.70	0.50
<i>lmo1406</i>	pyruvate formate-lyase	0.08	0.40	0.03	0.31	0.91	0.45
<i>lmo1407</i>	pyruvate-formate lyase activating enzyme	0.05	0.25	0.02	0.28	0.91	0.42
<i>lmo1408</i>	hypothetical protein	0.38	0.00	0.25	0.04	0.62	0.24
<i>lmo1409</i>	multidrug transporter	0.21	0.19	0.06	0.48	0.86	0.59
<i>lmo1411</i>	hypothetical protein	0.01	0.00	0.03	0.01	0.92	0.64
<i>lmo1413</i>	peptidoglycan binding protein	0.01	0.00	0.01	0.00	0.74	0.48
<i>lmo1414</i>	acetyl-CoA:acetyltransferase	0.35	0.16	0.07	0.45	0.43	0.12
<i>lmo1415</i>	hydroxy-3-methylglutaryl-CoA synthase	0.25	0.41	0.19	0.41	0.60	0.20
<i>lmo1416</i>	hypothetical protein	0.02	0.28	0.05	0.49	0.81	0.53
<i>lmo1417</i>	hypothetical protein	0.02	0.21	0.02	0.35	0.83	0.51
<i>lmo1418</i>	hypothetical protein	0.17	0.29	0.12	0.18	0.89	0.64
<i>lmo1419</i>	hypothetical protein	0.41	0.00	0.29	0.00	0.91	0.50
<i>lmo1420</i>	UDP-N-acetylenolpyruvoylglucosamine reductase	0.35	0.18	0.27	0.08	0.92	0.35
<i>lmo1421</i>	glycine/betaine ABC transporter ATP-binding protein	0.35	0.38	0.06	0.10	0.79	0.43
<i>lmo1422</i>	glycine/betaine ABC transporter permease	0.41	0.28	0.10	0.06	0.86	0.47
<i>lmo1423</i>	hypothetical protein	0.05	0.39	0.04	0.53	0.83	0.65
<i>lmo1424</i>	manganese transporter	0.26	0.46	0.20	0.55	0.68	0.24
<i>lmo1425</i>	glycine/betaine ABC transporter permease	0.16	0.34	0.05	0.28	0.88	0.53
<i>lmo1426</i>	glycine/betaine ABC transporter substrate-binding protein	0.10	0.21	0.03	0.19	0.86	0.51
<i>lmo1427</i>	glycine/betaine ABC transporter permease	0.13	0.33	0.02	0.20	0.81	0.36
<i>lmo1428</i>	glycine/betaine ABC transporter ATP-binding protein	0.03	0.20	0.01	0.12	0.91	0.50
<i>lmo1430</i>	hypothetical protein	0.05	0.00	0.02	0.00	0.81	0.47
<i>lmo1431</i>	ABC transporter ATP-binding protein	0.31	0.03	0.16	0.07	0.90	0.59
<i>lmo1432</i>	hypothetical protein	0.07	0.16	0.02	0.10	0.74	0.36
<i>lmo1433</i>	glutathione reductase	0.09	0.38	0.03	0.24	0.75	0.40
<i>lmo1434</i>	hypothetical protein	0.01	0.00	0.01	0.05	0.72	0.28
<i>lmo1435</i>	dihydrodipicolinate synthase	0.02	0.00	0.02	0.04	0.75	0.23
<i>lmo1436</i>	aspartate kinase	0.00	0.01	0.04	0.43	0.91	0.57
<i>lmo1437</i>	aspartate-semialdehyde dehydrogenase	0.01	0.05	0.09	0.50	0.92	0.64
<i>lmo1438</i>	penicillin-binding protein	0.34	0.17	0.19	0.07	0.92	0.58
<i>lmo1439</i>	superoxide dismutase	0.01	0.05	0.00	0.05	0.82	0.41
<i>lmo1440</i>	hypothetical protein	0.13	0.17	0.07	0.45	0.91	0.68
<i>lmo1441</i>	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase	0.40	0.42	0.12	0.24	0.58	0.24
<i>lmo1442</i>	transporter	0.22	0.48	0.17	0.06	0.78	0.41
<i>lmo1443</i>	hypothetical protein	0.01	0.06	0.12	0.38	0.88	0.32
<i>lmo1444</i>	foldase	0.40	0.17	0.16	0.42	0.91	0.56
<i>lmo1445</i>	ZurR family transcriptional regulator	0.24	0.00	0.24	0.02	0.89	0.41
<i>lmo1446</i>	metal (zinc) transport protein (ABC transporter permease)	0.24	0.00	0.17	0.01	0.90	0.64
<i>lmo1447</i>	metal (zinc) transport protein(ABC transporter ATP-binding protein)	0.24	0.04	0.12	0.03	0.84	0.65
<i>lmo1448</i>	manganese-dependent inorganic pyrophosphatase	0.03	0.14	0.04	0.52	0.92	0.36
<i>lmo1449</i>	endonuclease IV	0.24	0.13	0.18	0.08	0.91	0.67
<i>lmo1450</i>	DEAD/DEAH box helicase	0.22	0.42	0.18	0.12	0.88	0.41
<i>lmo1451</i>	4-hydroxy-3-methylbut-2-enyl diphosphate reductase	0.25	0.21	0.21	0.51	0.92	0.69
<i>lmo1452</i>	hypothetical protein	0.18	0.25	0.07	0.12	0.91	0.62
<i>lmo1453</i>	hypothetical protein	0.32	0.46	0.09	0.14	0.88	0.65
<i>lmo1454</i>	RNA polymerase sigma factor RpoD	0.06	0.38	0.03	0.33	0.82	0.70
<i>lmo1455</i>	DNA primase	0.01	0.05	0.01	0.16	0.86	0.46
<i>lmo1456</i>	hypothetical protein	0.28	0.08	0.13	0.24	0.85	0.67
<i>lmo1457</i>	hypothetical protein	0.00	0.00	0.01	0.00	0.89	0.28
<i>lmo1458</i>	glycyl-tRNA synthetase subunit beta	0.09	0.37	0.04	0.12	0.75	0.65
<i>lmo1459</i>	glycyl-tRNA synthetase subunit alpha	0.21	0.11	0.07	0.53	0.72	0.53

<i>lmo1460</i>	DNA repair protein RecO	0.13	0.00	0.17	0.03	0.62	0.32
<i>lmo1461</i>	hypothetical protein	0.01	0.00	0.10	0.09	0.60	0.26
<i>lmo1462</i>	GTP-binding protein Era	0.22	0.06	0.16	0.13	0.90	0.64
<i>lmo1463</i>	cytidine deaminase	0.34	0.30	0.26	0.24	0.87	0.41
<i>lmo1464</i>	diacylglycerol kinase	0.31	0.45	0.07	0.13	0.58	0.16
<i>lmo1465</i>	metalloprotease	0.17	0.22	0.16	0.33	0.60	0.20
<i>lmo1466</i>	hypothetical protein	0.34	0.27	0.02	0.21	0.56	0.20
<i>lmo1468</i>	hypothetical protein	0.29	0.38	0.32	0.53	0.71	0.32
<i>lmo1469</i>	30S ribosomal protein S21	0.20	0.36	0.21	0.49	0.72	0.28
<i>lmo1470</i>	16S ribosomal RNA methyltransferase RsmE	0.01	0.02	0.01	0.01	0.76	0.67
<i>lmo1471</i>	ribosomal protein L11 methyltransferase	0.01	0.04	0.00	0.01	0.80	0.67
<i>lmo1472</i>	molecular chaperone DnaJ	0.32	0.40	0.05	0.21	0.76	0.57
<i>lmo1473</i>	molecular chaperone DnaK	0.35	0.41	0.18	0.14	0.75	0.35
<i>lmo1474</i>	heat shock protein GrpE	0.06	0.16	0.22	0.41	0.71	0.27
<i>lmo1475</i>	heat-inducible transcription repressor	0.41	0.31	0.12	0.06	0.85	0.45
<i>lmo1476</i>	coproporphyrinogen III oxidase	0.03	0.01	0.05	0.37	0.72	0.18
<i>lmo1477</i>	oxidoreductase	0.00	0.00	0.01	0.02	0.88	0.56
<i>lmo1478</i>	MerR family transcriptional regulator	0.02	0.02	0.07	0.20	0.88	0.68
<i>lmo1479</i>	GTP-binding protein LepA	0.12	0.39	0.06	0.54	0.90	0.56
<i>lmo1480</i>	30S ribosomal protein S20	0.11	0.45	0.03	0.45	0.92	0.67
<i>lmo1481</i>	DNA polymerase III subunit delta	0.18	0.36	0.08	0.16	0.92	0.46
<i>lmo1482</i>	competence protein ComEC	0.33	0.03	0.14	0.37	0.81	0.47
<i>lmo1483</i>	competence protein ComEB	0.00	0.00	0.01	0.03	0.92	0.37
<i>lmo1484</i>	competence protein ComEA	0.00	0.01	0.02	0.11	0.92	0.66
<i>lmo1485</i>	hypothetical protein	0.25	0.00	0.29	0.02	0.78	0.27
<i>lmo1486</i>	hypothetical protein	0.30	0.02	0.22	0.01	0.87	0.56
<i>lmo1487</i>	hypothetical protein	0.09	0.49	0.15	0.22	0.91	0.58
<i>lmo1488</i>	nicotinic acid mononucleotide adenylyltransferase	0.00	0.01	0.01	0.18	0.92	0.35
<i>lmo1489</i>	hypothetical protein	0.03	0.23	0.02	0.39	0.89	0.54
<i>lmo1490</i>	shikimate 5-dehydrogenase	0.03	0.11	0.02	0.28	0.90	0.42
<i>lmo1491</i>	GTP-binding protein	0.03	0.11	0.04	0.44	0.92	0.53
<i>lmo1492</i>	hypothetical protein	0.17	0.43	0.13	0.26	0.91	0.52
<i>lmo1493</i>	oligopeptidase	0.34	0.44	0.12	0.32	0.81	0.51
<i>lmo1494</i>	5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase	0.07	0.35	0.13	0.32	0.88	0.60
<i>lmo1495</i>	hypothetical protein	0.39	0.25	0.28	0.10	0.74	0.40
<i>lmo1496</i>	transcription elongation factor GreA	0.40	0.02	0.21	0.07	0.88	0.23
<i>lmo1497</i>	uridine kinase	0.08	0.42	0.02	0.48	0.81	0.30
<i>lmo1498</i>	O-methyltransferase	0.22	0.16	0.06	0.32	0.79	0.20
<i>lmo1499</i>	hypothetical protein	0.12	0.39	0.10	0.36	0.90	0.52
<i>lmo1500</i>	hypothetical protein	0.25	0.00	0.24	0.00	0.83	0.23
<i>lmo1501</i>	hypothetical protein	0.04	0.19	0.02	0.32	0.91	0.59
<i>lmo1502</i>	Holliday junction resolvase	0.12	0.35	0.05	0.42	0.88	0.60
<i>lmo1503</i>	hypothetical protein	0.17	0.14	0.07	0.25	0.88	0.66
<i>lmo1504</i>	alanyl-tRNA synthetase	0.01	0.02	0.00	0.01	0.84	0.63
<i>lmo1505</i>	ABC transporter ATP-binding protein	0.00	0.00	0.01	0.05	0.75	0.23
<i>lmo1506</i>	transporter	0.00	0.00	0.02	0.11	0.61	0.20
<i>lmo1507</i>	response regulator	0.00	0.00	0.01	0.08	0.89	0.53
<i>lmo1508</i>	histidine kinase	0.02	0.23	0.01	0.32	0.91	0.64
<i>lmo1509</i>	exodeoxyribonuclease V	0.00	0.00	0.01	0.11	0.90	0.50
<i>lmo1510</i>	hypothetical protein	0.00	0.00	0.01	0.18	0.90	0.54
<i>lmo1512</i>	tRNA-specific 2-thiouridylase	0.40	0.01	0.23	0.06	0.80	0.40
<i>lmo1513</i>	iron-sulfur cofactor synthesis protein	0.27	0.09	0.13	0.10	0.89	0.64
<i>lmo1514</i>	recombination factor protein RarA	0.04	0.00	0.23	0.12	0.59	0.29
<i>lmo1516</i>	ammonium transporter NrgA	0.08	0.02	0.26	0.10	0.85	0.54
<i>lmo1517</i>	nitrogen regulatory PII protein	0.40	0.14	0.20	0.23	0.91	0.66
<i>lmo1518</i>	hypothetical protein	0.03	0.08	0.15	0.42	0.85	0.20
<i>lmo1519</i>	aspartyl-tRNA synthetase	0.00	0.02	0.00	0.01	0.84	0.66
<i>lmo1520</i>	histidyl-tRNA synthetase	0.01	0.10	0.00	0.08	0.76	0.65
<i>lmo1521</i>	N-acetylmuramoyl-L-alanine amidase	0.39	0.32	0.09	0.41	0.92	0.58
<i>lmo1522</i>	D-tyrosyl-tRNA(Tyr) deacylase	0.14	0.05	0.04	0.02	0.71	0.36
<i>lmo1523</i>	(p)ppGpp synthetase	0.19	0.30	0.29	0.21	0.92	0.65

<i>lmo1524</i>	adenine phosphoribosyltransferase	0.26	0.01	0.07	0.23	0.81	0.34
<i>lmo1525</i>	recombination protein RecJ	0.18	0.00	0.32	0.07	0.82	0.37
<i>lmo1526</i>	hypothetical protein	0.12	0.49	0.04	0.40	0.67	0.21
<i>lmo1527</i>	preprotein translocase SecDF	0.25	0.01	0.17	0.02	0.73	0.25
<i>lmo1528</i>	hypothetical protein	0.42	0.01	0.27	0.03	0.91	0.58
<i>lmo1529</i>	hypothetical protein	0.16	0.32	0.09	0.34	0.84	0.67
<i>lmo1530</i>	queuine tRNA-ribosyltransferase	0.08	0.27	0.04	0.49	0.90	0.68
<i>lmo1531</i>	S-adenosylmethionine:tRNA ribosyltransferase-isomerase	0.03	0.16	0.02	0.46	0.84	0.64
<i>lmo1532</i>	Holliday junction DNA helicase RuvB	0.01	0.01	0.01	0.21	0.88	0.70
<i>lmo1533</i>	Holliday junction DNA helicase RuvA	0.00	0.00	0.00	0.02	0.92	0.51
<i>lmo1534</i>	L-lactate dehydrogenase	0.00	0.00	0.00	0.01	0.70	0.22
<i>lmo1535</i>	hypothetical protein	0.00	0.00	0.01	0.02	0.77	0.57
<i>lmo1536</i>	prephenate dehydratase	0.08	0.47	0.03	0.48	0.90	0.58
<i>lmo1537</i>	GTPase ObgE	0.05	0.22	0.06	0.48	0.90	0.41
<i>lmo1538</i>	glycerol kinase	0.10	0.25	0.03	0.48	0.74	0.25
<i>lmo1539</i>	glycerol transporter	0.15	0.01	0.04	0.27	0.72	0.21
<i>lmo1540</i>	50S ribosomal protein L27	0.28	0.33	0.04	0.40	0.76	0.39
<i>lmo1541</i>	hypothetical protein	0.23	0.38	0.03	0.31	0.78	0.49
<i>lmo1542</i>	50S ribosomal protein L21	0.18	0.49	0.03	0.29	0.85	0.63
<i>lmo1543</i>	ribonuclease G	0.02	0.11	0.01	0.26	0.81	0.54
<i>lmo1544</i>	septum formation inhibitor MinD	0.02	0.07	0.03	0.37	0.91	0.65
<i>lmo1545</i>	septum formation inhibitor MinC	0.01	0.01	0.01	0.13	0.91	0.63
<i>lmo1546</i>	cell-shape determining protein MreD	0.12	0.28	0.07	0.14	0.75	0.19
<i>lmo1547</i>	rod shape-determining protein MreC	0.18	0.11	0.11	0.07	0.82	0.32
<i>lmo1548</i>	rod shape-determining protein MreB	0.29	0.23	0.16	0.14	0.86	0.32
<i>lmo1550</i>	competence protein ComC	0.03	0.32	0.01	0.46	0.92	0.39
<i>lmo1551</i>	folyl-polyglutamate synthetase	0.01	0.01	0.00	0.00	0.80	0.63
<i>lmo1552</i>	valyl-tRNA synthetase	0.03	0.19	0.02	0.13	0.76	0.67
<i>lmo1553</i>	glutamate-1-semialdehyde aminotransferase	0.18	0.22	0.10	0.24	0.72	0.37
<i>lmo1554</i>	delta-aminolevulinic acid dehydratase	0.29	0.06	0.20	0.10	0.75	0.40
<i>lmo1555</i>	uroporphyrinogen-III synthase	0.28	0.10	0.23	0.07	0.86	0.61
<i>lmo1556</i>	porphobilinogen deaminase	0.37	0.05	0.30	0.02	0.92	0.67
<i>lmo1557</i>	glutamyl-tRNA reductase	0.33	0.28	0.30	0.04	0.85	0.52
<i>lmo1558</i>	GTP-binding protein EngB	0.24	0.40	0.17	0.14	0.89	0.54
<i>lmo1559</i>	threonyl-tRNA synthetase	0.08	0.42	0.02	0.48	0.90	0.49
<i>lmo1560</i>	primosomal protein DnaI	0.10	0.13	0.10	0.31	0.76	0.44
<i>lmo1561</i>	chromosome replication initiation / membrane attachment protein DnaB	0.22	0.27	0.22	0.29	0.75	0.44
<i>lmo1562</i>	transcriptional regulator NrdR	0.38	0.06	0.31	0.10	0.74	0.37
<i>lmo1563</i>	dephospho-CoA kinase	0.13	0.00	0.29	0.11	0.83	0.27
<i>lmo1564</i>	formamidopyrimidine-DNA glycosylase	0.41	0.03	0.15	0.35	0.77	0.23
<i>lmo1565</i>	DNA polymerase I	0.10	0.42	0.03	0.30	0.81	0.40
<i>lmo1566</i>	isocitrate dehydrogenase	0.00	0.01	0.00	0.05	0.92	0.66
<i>lmo1567</i>	citrate synthase	0.00	0.01	0.00	0.05	0.91	0.59
<i>lmo1568</i>	hypothetical protein	0.00	0.01	0.01	0.06	0.84	0.58
<i>lmo1569</i>	FxsA	0.01	0.05	0.01	0.11	0.75	0.58
<i>lmo1570</i>	pyruvate kinase	0.26	0.29	0.17	0.26	0.74	0.39
<i>lmo1571</i>	6-phosphofructokinase	0.40	0.02	0.14	0.22	0.73	0.51
<i>lmo1572</i>	acetyl-CoA carboxylase carboxyltransferase subunit alpha	0.16	0.19	0.11	0.16	0.78	0.62
<i>lmo1573</i>	acetyl-CoA carboxylase subunit beta	0.33	0.00	0.18	0.03	0.74	0.23
<i>lmo1574</i>	DNA polymerase III subunit alpha	0.03	0.46	0.02	0.53	0.74	0.35
<i>lmo1575</i>	hypothetical protein	0.00	0.00	0.01	0.06	0.86	0.50
<i>lmo1576</i>	hypothetical protein	0.00	0.01	0.01	0.15	0.90	0.47
<i>lmo1577</i>	metal-dependent hydrolase	0.01	0.10	0.03	0.40	0.90	0.69
<i>lmo1578</i>	X-Pro dipeptidase	0.01	0.03	0.04	0.48	0.91	0.68
<i>lmo1579</i>	alanine dehydrogenase	0.13	0.24	0.04	0.45	0.85	0.59
<i>lmo1580</i>	hypothetical protein	0.08	0.47	0.04	0.49	0.84	0.56
<i>lmo1581</i>	acetate kinase	0.06	0.34	0.07	0.34	0.76	0.30
<i>lmo1582</i>	hypothetical protein	0.13	0.34	0.15	0.32	0.87	0.52
<i>lmo1583</i>	thiol peroxidase	0.31	0.03	0.26	0.30	0.46	0.22
<i>lmo1584</i>	hypothetical protein	0.00	0.00	0.01	0.16	0.89	0.45

<i>lmo1586</i>	inorganic polyphosphate/ATP-NAD kinase	0.08	0.06	0.26	0.51	0.90	0.58
<i>lmo1587</i>	ornithine carbamoyltransferase	0.00	0.00	0.01	0.08	0.81	0.47
<i>lmo1588</i>	acetylornithine aminotransferase	0.02	0.01	0.11	0.28	0.91	0.67
<i>lmo1589</i>	acetylglutamate kinase	0.37	0.24	0.20	0.45	0.92	0.69
<i>lmo1590</i>	bifunctional ornithine acetyltransferase/N-acetylglutamate synthase	0.39	0.25	0.19	0.43	0.91	0.62
<i>lmo1591</i>	N-acetyl-gamma-glutamyl-phosphate reductase	0.24	0.16	0.09	0.43	0.90	0.69
<i>lmo1592</i>	thiamine biosynthesis protein ThiI	0.09	0.26	0.03	0.49	0.74	0.23
<i>lmo1593</i>	iron-sulfur cofactor synthesis protein NifS	0.01	0.00	0.01	0.07	0.91	0.68
<i>lmo1594</i>	septation ring formation regulator EzrA	0.10	0.14	0.23	0.38	0.91	0.70
<i>lmo1595</i>	hypothetical protein	0.23	0.23	0.18	0.19	0.84	0.56
<i>lmo1596</i>	30S ribosomal protein S4	0.05	0.29	0.01	0.21	0.85	0.58
<i>lmo1598</i>	tyrosyl-tRNA synthetase	0.17	0.23	0.05	0.46	0.64	0.33
<i>lmo1599</i>	catabolite control protein A	0.38	0.33	0.05	0.02	0.91	0.65
<i>lmo1600</i>	bifunctional 3-deoxy-7-phosphoheptulonate synthase/chorismate mutase	0.09	0.35	0.03	0.26	0.92	0.51
<i>lmo1601</i>	general stress protein	0.05	0.17	0.06	0.47	0.84	0.65
<i>lmo1602</i>	hypothetical protein	0.07	0.35	0.08	0.35	0.82	0.60
<i>lmo1603</i>	aminopeptidase	0.18	0.27	0.03	0.42	0.75	0.51
<i>lmo1604</i>	2-cys peroxiredoxin	0.02	0.13	0.05	0.49	0.82	0.44
<i>lmo1605</i>	UDP-N-acetylmuramate--L-alanine ligase	0.38	0.41	0.09	0.22	0.81	0.52
<i>lmo1606</i>	DNA translocase	0.30	0.42	0.04	0.22	0.74	0.49
<i>lmo1607</i>	phenylalanyl-tRNA synthetase subunit beta	0.00	0.00	0.02	0.15	0.77	0.31
<i>lmo1608</i>	hypothetical protein	0.00	0.00	0.01	0.02	0.70	0.26
<i>lmo1609</i>	thioredoxin	0.00	0.00	0.00	0.01	0.67	0.23
<i>lmo1611</i>	aminopeptidase	0.00	0.00	0.00	0.01	0.49	0.15
<i>lmo1612</i>	hypothetical protein	0.04	0.31	0.03	0.47	0.92	0.25
<i>lmo1613</i>	hypothetical protein	0.09	0.24	0.03	0.17	0.90	0.53
<i>lmo1614</i>	hypothetical protein	0.01	0.02	0.02	0.21	0.92	0.50
<i>lmo1615</i>	tRNA (guanine-N(7)-)-methyltransferase	0.20	0.30	0.10	0.17	0.89	0.54
<i>lmo1616</i>	hypothetical protein	0.10	0.18	0.06	0.49	0.90	0.60
<i>lmo1617</i>	multidrug transporter	0.15	0.43	0.05	0.40	0.92	0.52
<i>lmo1618</i>	MarR family transcriptional regulator	0.10	0.49	0.03	0.33	0.90	0.38
<i>lmo1619</i>	D-amino acid aminotransferase	0.14	0.01	0.18	0.41	0.73	0.40
<i>lmo1620</i>	dipeptidase PepV	0.10	0.01	0.32	0.52	0.65	0.42
<i>lmo1621</i>	hypothetical protein	0.01	0.01	0.02	0.16	0.74	0.21
<i>lmo1622</i>	hypothetical protein	0.04	0.15	0.04	0.43	0.75	0.32
<i>lmo1623</i>	hypothetical protein	0.20	0.28	0.28	0.04	0.71	0.36
<i>lmo1624</i>	transporter	0.06	0.18	0.19	0.25	0.91	0.60
<i>lmo1625</i>	transporter	0.00	0.02	0.00	0.08	0.93	0.40
<i>lmo1626</i>	hypothetical protein	0.00	0.00	0.00	0.07	0.83	0.30
<i>lmo1627</i>	tryptophan synthase subunit alpha	0.36	0.43	0.21	0.20	0.85	0.64
<i>lmo1628</i>	tryptophan synthase subunit beta	0.20	0.16	0.12	0.05	0.89	0.64
<i>lmo1629</i>	N-(5'-phosphoribosyl)anthranilate isomerase	0.26	0.28	0.29	0.26	0.84	0.57
<i>lmo1630</i>	indole-3-glycerol phosphate synthase	0.11	0.02	0.17	0.11	0.89	0.69
<i>lmo1631</i>	anthranilate phosphoribosyltransferase	0.37	0.23	0.26	0.38	0.89	0.59
<i>lmo1632</i>	anthranilate synthase subunit beta	0.31	0.22	0.30	0.32	0.84	0.52
<i>lmo1633</i>	anthranilate synthase subunit alpha	0.19	0.21	0.27	0.34	0.79	0.42
<i>lmo1634</i>	bifunctional acetaldehyde-CoA/alcohol dehydrogenase	0.24	0.46	0.07	0.24	0.85	0.58
<i>lmo1635</i>	hypothetical protein	0.31	0.04	0.31	0.11	0.92	0.66
<i>lmo1636</i>	ABC transporter ATP-binding protein	0.26	0.08	0.14	0.16	0.75	0.23
<i>lmo1637</i>	hypothetical protein	0.16	0.13	0.10	0.14	0.61	0.18
<i>lmo1638</i>	hypothetical protein	0.01	0.02	0.03	0.13	0.87	0.64
<i>lmo1639</i>	DNA-3-methyladenine glycosidase	0.00	0.00	0.01	0.04	0.79	0.54
<i>lmo1640</i>	hypothetical protein	0.06	0.07	0.02	0.10	0.82	0.61
<i>lmo1641</i>	aconitate hydratase	0.10	0.29	0.06	0.34	0.89	0.58
<i>lmo1642</i>	sigma factor regulator	0.01	0.02	0.22	0.51	0.84	0.36
<i>lmo1643</i>	hypothetical protein	0.34	0.40	0.07	0.05	0.90	0.68
<i>lmo1644</i>	helicase SNF2	0.15	0.29	0.29	0.01	0.85	0.64
<i>lmo1645</i>	ATP-dependent dsDNA exonuclease SbcC	0.00	0.00	0.02	0.14	0.92	0.30
<i>lmo1646</i>	exonuclease SbcD	0.10	0.04	0.30	0.35	0.62	0.21

<i>lmo1647</i>	1-acylglycerol-3-phosphate O-acyltransferase	0.12	0.21	0.05	0.28	0.92	0.63
<i>lmo1649</i>	hypothetical protein	0.39	0.08	0.16	0.30	0.91	0.65
<i>lmo1650</i>	hypothetical protein	0.29	0.15	0.27	0.06	0.78	0.27
<i>lmo1651</i>	ABC transporter ATP-binding protein	0.05	0.43	0.03	0.39	0.71	0.21
<i>lmo1652</i>	ABC transporter ATP-binding protein	0.10	0.38	0.03	0.50	0.74	0.21
<i>lmo1653</i>	cell surface protein	0.04	0.00	0.07	0.05	0.60	0.20
<i>lmo1654</i>	cell surface protein	0.22	0.06	0.31	0.26	0.68	0.27
<i>lmo1657</i>	elongation factor Ts	0.16	0.09	0.04	0.33	0.85	0.49
<i>lmo1658</i>	30S ribosomal protein S2	0.15	0.50	0.06	0.53	0.92	0.47
<i>lmo1660</i>	leucyl-tRNA synthetase	0.06	0.49	0.02	0.31	0.80	0.67
<i>lmo1661</i>	hypothetical protein	0.06	0.32	0.12	0.46	0.92	0.62
<i>lmo1662</i>	hypothetical protein	0.09	0.35	0.08	0.33	0.83	0.54
<i>lmo1663</i>	asparagine synthetase	0.09	0.46	0.03	0.50	0.88	0.53
<i>lmo1664</i>	S-adenosylmethionine synthetase	0.32	0.28	0.09	0.48	0.58	0.13
<i>lmo1665</i>	hypothetical protein	0.02	0.02	0.02	0.18	0.76	0.14
<i>lmo1667</i>	L-lactate dehydrogenase	0.00	0.00	0.01	0.07	0.73	0.21
<i>lmo1668</i>	hypothetical protein	0.00	0.00	0.01	0.08	0.86	0.23
<i>lmo1669</i>	hypothetical protein	0.16	0.21	0.09	0.09	0.92	0.68
<i>lmo1670</i>	hypothetical protein	0.00	0.00	0.01	0.02	0.88	0.61
<i>lmo1671</i>	ABC transporter	0.38	0.23	0.31	0.30	0.90	0.63
<i>lmo1672</i>	O-succinylbenzoic acid--CoA ligase	0.02	0.16	0.01	0.20	0.85	0.69
<i>lmo1673</i>	naphthoate synthase	0.15	0.47	0.16	0.45	0.90	0.61
<i>lmo1674</i>	prolyl aminopeptidase	0.33	0.28	0.25	0.31	0.87	0.62
<i>lmo1675</i>	2-succinyl-5-enolpyruvyl-6-hydroxy-3- cyclohexene-1-carboxylate synthase	0.42	0.41	0.25	0.23	0.88	0.61
<i>lmo1676</i>	menaquinone-specific isochorismate synthase	0.42	0.49	0.21	0.14	0.70	0.35
<i>lmo1677</i>	14-dihydroxy-2-naphthoate octaprenyltransferase	0.24	0.20	0.15	0.11	0.92	0.59
<i>lmo1678</i>	bifunctional homocysteine S-methyltransferase/510-methylenetetrahydrofolate reductase	0.00	0.00	0.02	0.01	0.75	0.30
<i>lmo1679</i>	cystathionine beta-lyase	0.02	0.00	0.02	0.01	0.85	0.40
<i>lmo1681</i>	5-methyltetrahydropteroyltriglutamate-- homocysteine S-methyltransferase	0.00	0.00	0.01	0.02	0.83	0.43
<i>lmo1682</i>	transporter	0.07	0.00	0.24	0.07	0.61	0.35
<i>lmo1683</i>	Fur family transcriptional regulator	0.01	0.04	0.01	0.11	0.92	0.31
<i>lmo1684</i>	glycerate dehydrogenase	0.08	0.38	0.04	0.37	0.89	0.51
<i>lmo1685</i>	glutamate-1-semialdehyde aminotransferase	0.04	0.25	0.01	0.19	0.86	0.61
<i>lmo1686</i>	hypothetical protein	0.24	0.42	0.04	0.17	0.75	0.57
<i>lmo1687</i>	hypothetical protein	0.23	0.30	0.05	0.51	0.58	0.22
<i>lmo1688</i>	enoyl-ACP reductase	0.25	0.00	0.18	0.01	0.73	0.31
<i>lmo1689</i>	A/G-specific adenine glycosylase	0.09	0.00	0.11	0.00	0.76	0.21
<i>lmo1690</i>	hypothetical protein	0.12	0.16	0.09	0.16	0.77	0.62
<i>lmo1691</i>	deoxyuridine triphosphate nucleotidohydrolase	0.29	0.12	0.31	0.25	0.91	0.69
<i>lmo1692</i>	hypothetical protein	0.28	0.34	0.19	0.45	0.91	0.62
<i>lmo1693</i>	recombination regulator RecX	0.22	0.49	0.25	0.44	0.73	0.52
<i>lmo1694</i>	CDP-abequose synthase	0.11	0.30	0.03	0.53	0.79	0.31
<i>lmo1695</i>	hypothetical protein	0.10	0.24	0.20	0.34	0.86	0.66
<i>lmo1696</i>	hypothetical protein	0.37	0.32	0.26	0.33	0.90	0.64
<i>lmo1697</i>	hypothetical protein	0.37	0.00	0.21	0.12	0.79	0.44
<i>lmo1698</i>	ribosomal-protein-alanine N-acetyltransferase	0.00	0.01	0.02	0.18	0.87	0.47
<i>lmo1699</i>	chemotaxis protein	0.18	0.06	0.10	0.10	0.73	0.41
<i>lmo1700</i>	hypothetical protein	0.24	0.11	0.10	0.07	0.75	0.48
<i>lmo1701</i>	hypothetical protein	0.01	0.01	0.00	0.01	0.89	0.53
<i>lmo1702</i>	glutathione transferase	0.08	0.19	0.01	0.06	0.92	0.59
<i>lmo1703</i>	RNA methyltransferase	0.13	0.15	0.02	0.51	0.87	0.40
<i>lmo1704</i>	hypothetical protein	0.12	0.26	0.03	0.54	0.86	0.65
<i>lmo1705</i>	deoxyguanosine kinase/deoxyadenosine kinase	0.18	0.46	0.07	0.50	0.91	0.47
<i>lmo1706</i>	transporter	0.25	0.22	0.05	0.47	0.70	0.27
<i>lmo1707</i>	hypothetical protein	0.42	0.02	0.17	0.18	0.82	0.28
<i>lmo1708</i>	aminoglycoside N3'-acetyltransferase	0.08	0.40	0.02	0.26	0.71	0.41
<i>lmo1709</i>	methionine aminopeptidase	0.13	0.39	0.08	0.53	0.91	0.53
<i>lmo1710</i>	flavodoxin	0.20	0.18	0.11	0.17	0.83	0.54

<i>lmo1711</i>	aminopeptidase	0.36	0.23	0.17	0.26	0.88	0.66
<i>lmo1712</i>	multidrug resistance protein	0.00	0.03	0.02	0.42	0.77	0.66
<i>lmo1713</i>	rod shape-determining protein MreB	0.24	0.08	0.21	0.18	0.76	0.34
<i>lmo1715</i>	hypothetical protein	0.23	0.09	0.16	0.15	0.92	0.70
<i>lmo1716</i>	transcriptional regulator	0.39	0.17	0.19	0.43	0.91	0.58
<i>lmo1718</i>	hypothetical protein	0.06	0.03	0.04	0.09	0.77	0.58
<i>lmo1720</i>	PTS lichenan transporter subunit IIB	0.08	0.03	0.11	0.13	0.86	0.62
<i>lmo1721</i>	transcriptional regulator	0.11	0.00	0.25	0.27	0.62	0.33
<i>lmo1722</i>	ATP-dependent RNA helicase	0.12	0.17	0.03	0.12	0.85	0.30
<i>lmo1726</i>	hypothetical protein	0.02	0.07	0.01	0.09	0.89	0.61
<i>lmo1727</i>	LacI family transcriptional regulator	0.12	0.32	0.08	0.28	0.87	0.70
<i>lmo1728</i>	cellobiose phosphorylase	0.02	0.01	0.01	0.07	0.93	0.21
<i>lmo1729</i>	beta-glucosidase	0.01	0.00	0.01	0.06	0.92	0.17
<i>lmo1730</i>	sugar ABC transporter substrate-binding protein	0.01	0.01	0.02	0.15	0.92	0.19
<i>lmo1731</i>	sugar ABC transporter permease	0.02	0.11	0.02	0.16	0.90	0.33
<i>lmo1732</i>	sugar ABC transporter permease	0.02	0.10	0.02	0.15	0.90	0.31
<i>lmo1733</i>	glutamate synthase subunit beta	0.30	0.36	0.28	0.23	0.91	0.51
<i>lmo1734</i>	glutamate synthase large subunit	0.13	0.48	0.06	0.41	0.88	0.62
<i>lmo1735</i>	transcription activator of glutamate synthase operon GltC	0.01	0.06	0.00	0.04	0.92	0.39
<i>lmo1736</i>	hypothetical protein	0.01	0.02	0.01	0.15	0.92	0.55
<i>lmo1737</i>	glycerol dehydrogenase	0.15	0.40	0.13	0.50	0.92	0.63
<i>lmo1738</i>	amino acid ABC transporter substrate-binding protein	0.14	0.01	0.28	0.25	0.84	0.60
<i>lmo1739</i>	amino acid ABC transporter ATP-binding protein	0.22	0.02	0.15	0.32	0.88	0.64
<i>lmo1740</i>	amino acid ABC transporter permease	0.30	0.07	0.13	0.49	0.85	0.56
<i>lmo1741</i>	histidine kinase	0.06	0.41	0.01	0.12	0.60	0.26
<i>lmo1742</i>	adenine deaminase	0.00	0.00	0.00	0.01	0.91	0.67
<i>lmo1743</i>	hypothetical protein	0.00	0.00	0.00	0.03	0.89	0.56
<i>lmo1744</i>	hypothetical protein	0.00	0.00	0.00	0.01	0.91	0.69
<i>lmo1745</i>	two-component response regulator	0.00	0.00	0.00	0.03	0.92	0.60
<i>lmo1746</i>	ABC transporter permease	0.04	0.25	0.03	0.50	0.72	0.31
<i>lmo1747</i>	ABC transporter ATP-binding protein	0.04	0.10	0.02	0.33	0.88	0.55
<i>lmo1748</i>	hypothetical protein	0.32	0.45	0.33	0.37	0.88	0.58
<i>lmo1749</i>	shikimate kinase	0.01	0.02	0.07	0.31	0.53	0.18
<i>lmo1750</i>	hypothetical protein	0.19	0.10	0.18	0.52	0.92	0.69
<i>lmo1751</i>	hypothetical protein	0.01	0.03	0.01	0.10	0.91	0.37
<i>lmo1752</i>	hypothetical protein	0.04	0.13	0.02	0.12	0.91	0.57
<i>lmo1753</i>	lipid kinase	0.11	0.08	0.06	0.35	0.89	0.46
<i>lmo1754</i>	aspartyl/glutamyl-tRNA amidotransferase subunit B	0.18	0.15	0.06	0.52	0.65	0.31
<i>lmo1755</i>	aspartyl/glutamyl-tRNA amidotransferase subunit A	0.13	0.10	0.04	0.41	0.61	0.15
<i>lmo1756</i>	aspartyl/glutamyl-tRNA amidotransferase subunit C	0.07	0.50	0.03	0.40	0.63	0.17
<i>lmo1757</i>	hypothetical protein	0.24	0.08	0.09	0.32	0.61	0.22
<i>lmo1758</i>	NAD-dependent DNA ligase LigA	0.07	0.36	0.04	0.34	0.65	0.21
<i>lmo1759</i>	ATP-dependent DNA helicase	0.08	0.43	0.04	0.53	0.72	0.29
<i>lmo1760</i>	geranylgeranyl glyceryl phosphate synthase-like protein	0.00	0.01	0.01	0.09	0.87	0.25
<i>lmo1761</i>	sodium-dependent transporter	0.38	0.00	0.26	0.02	0.82	0.48
<i>lmo1762</i>	hypothetical protein	0.40	0.49	0.28	0.49	0.88	0.40
<i>lmo1763</i>	hypothetical protein	0.42	0.42	0.19	0.54	0.83	0.29
<i>lmo1764</i>	phosphoribosylamine--glycine ligase	0.01	0.06	0.01	0.08	0.91	0.28
<i>lmo1765</i>	bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase	0.00	0.02	0.01	0.09	0.91	0.29
<i>lmo1766</i>	phosphoribosylglycinamide formyltransferase	0.07	0.32	0.04	0.55	0.86	0.61
<i>lmo1767</i>	phosphoribosylaminoimidazole synthetase	0.14	0.27	0.03	0.47	0.75	0.69
<i>lmo1768</i>	amidophosphoribosyltransferase	0.31	0.26	0.15	0.46	0.75	0.63
<i>lmo1769</i>	phosphoribosylformylglycinamide synthase II	0.23	0.27	0.05	0.46	0.77	0.66
<i>lmo1770</i>	phosphoribosylformylglycinamide synthase I	0.07	0.00	0.31	0.16	0.76	0.52
<i>lmo1771</i>	phosphoribosylformylglycinamide synthase subunit PurS	0.37	0.17	0.09	0.55	0.87	0.70
<i>lmo1772</i>	phosphoribosylaminoimidazole-succinocarboxamide synthase	0.13	0.06	0.21	0.24	0.91	0.62
<i>lmo1773</i>	adenylosuccinate lyase	0.32	0.45	0.07	0.19	0.73	0.39
<i>lmo1774</i>	phosphoribosylaminoimidazole carboxylase ATPase subunit	0.39	0.18	0.16	0.44	0.58	0.25
<i>lmo1775</i>	phosphoribosylaminoimidazole carboxylase catalytic subunit	0.34	0.49	0.12	0.50	0.92	0.67
<i>lmo1776</i>	hypothetical protein	0.02	0.05	0.06	0.38	0.89	0.54

<i>lmo1777</i>	hypothetical protein	0.36	0.12	0.13	0.51	0.81	0.65
<i>lmo1778</i>	ABC transporter ATP-binding protein	0.00	0.00	0.00	0.02	0.86	0.31
<i>lmo1779</i>	hypothetical protein	0.00	0.00	0.00	0.00	0.74	0.28
<i>lmo1780</i>	aminotripeptidase	0.00	0.00	0.00	0.00	0.71	0.22
<i>lmo1781</i>	hypothetical protein	0.00	0.00	0.00	0.07	0.90	0.30
<i>lmo1782</i>	3'-exo-deoxyribonuclease	0.00	0.03	0.02	0.19	0.80	0.49
<i>lmo1783</i>	50S ribosomal protein L20	0.15	0.38	0.03	0.20	0.86	0.65
<i>lmo1784</i>	50S ribosomal protein L35	0.11	0.42	0.02	0.22	0.90	0.63
<i>lmo1785</i>	translation initiation factor IF-3	0.15	0.49	0.03	0.28	0.91	0.68
<i>lmo1786</i>	internalin C	0.07	0.45	0.12	0.08	0.90	0.62
<i>lmo1787</i>	50S ribosomal protein L19	0.25	0.40	0.05	0.33	0.81	0.49
<i>lmo1788</i>	transcriptional regulator	0.30	0.05	0.08	0.46	0.72	0.30
<i>lmo1789</i>	hypothetical protein	0.34	0.02	0.09	0.37	0.69	0.22
<i>lmo1790</i>	hypothetical protein	0.39	0.01	0.11	0.31	0.65	0.18
<i>lmo1791</i>	hypothetical protein	0.12	0.22	0.03	0.52	0.75	0.37
<i>lmo1792</i>	tRNA (guanine-N(1)-)-methyltransferase	0.10	0.43	0.03	0.45	0.78	0.50
<i>lmo1793</i>	16S rRNA-processing protein RimM	0.26	0.18	0.14	0.33	0.83	0.46
<i>lmo1794</i>	hypothetical protein	0.17	0.26	0.12	0.31	0.87	0.56
<i>lmo1795</i>	hypothetical protein	0.23	0.03	0.09	0.17	0.74	0.52
<i>lmo1796</i>	hypothetical protein	0.16	0.43	0.03	0.25	0.92	0.67
<i>lmo1797</i>	30S ribosomal protein S16	0.19	0.43	0.05	0.28	0.91	0.70
<i>lmo1798</i>	hypothetical protein	0.34	0.25	0.17	0.03	0.75	0.52
<i>lmo1800</i>	protein-tyrosine phosphatase	0.00	0.00	0.00	0.01	0.76	0.30
<i>lmo1801</i>	signal recognition particle protein Ffh	0.03	0.11	0.00	0.05	0.88	0.62
<i>lmo1802</i>	DNA-binding protein	0.39	0.37	0.03	0.14	0.92	0.56
<i>lmo1803</i>	cell division protein FtsY	0.03	0.18	0.01	0.02	0.73	0.52
<i>lmo1804</i>	chromosome condensation protein Smc	0.05	0.33	0.01	0.07	0.72	0.37
<i>lmo1805</i>	ribonuclease III	0.25	0.13	0.04	0.55	0.75	0.24
<i>lmo1806</i>	acyl carrier protein	0.10	0.41	0.02	0.35	0.82	0.68
<i>lmo1807</i>	3-ketoacyl-ACP reductase	0.05	0.42	0.02	0.24	0.81	0.63
<i>lmo1808</i>	ACP S-malonyltransferase	0.05	0.33	0.02	0.29	0.83	0.65
<i>lmo1809</i>	glycerol-3-phosphate acyltransferase PlsX	0.06	0.33	0.03	0.48	0.82	0.56
<i>lmo1810</i>	fatty acid biosynthesis transcriptional regulator	0.12	0.48	0.05	0.55	0.87	0.51
<i>lmo1811</i>	ATP-dependent DNA helicase RecG	0.38	0.03	0.26	0.07	0.61	0.24
<i>lmo1812</i>	L-serine dehydratase	0.24	0.07	0.08	0.02	0.69	0.37
<i>lmo1813</i>	phosphoglycerate dehydrogenase	0.09	0.00	0.18	0.03	0.69	0.37
<i>lmo1815</i>	hypothetical protein	0.41	0.12	0.18	0.20	0.90	0.47
<i>lmo1816</i>	50S ribosomal protein L28	0.10	0.40	0.03	0.28	0.92	0.70
<i>lmo1817</i>	hypothetical protein	0.17	0.00	0.32	0.02	0.61	0.36
<i>lmo1818</i>	ribulose-phosphate 3-epimerase	0.07	0.30	0.12	0.49	0.84	0.61
<i>lmo1819</i>	ribosome-associated GTPase	0.03	0.10	0.08	0.35	0.90	0.38
<i>lmo1820</i>	serine/threonine protein kinase	0.02	0.05	0.06	0.29	0.85	0.55
<i>lmo1821</i>	phosphoprotein phosphatase	0.00	0.01	0.01	0.19	0.92	0.24
<i>lmo1822</i>	RNA-binding Sun protein	0.01	0.08	0.06	0.47	0.83	0.59
<i>lmo1823</i>	methionyl-tRNA formyltransferase	0.01	0.05	0.07	0.44	0.87	0.51
<i>lmo1824</i>	primosome assembly protein PriA	0.20	0.24	0.15	0.36	0.92	0.59
<i>lmo1825</i>	pantothenate metabolism flavoprotein	0.22	0.18	0.04	0.48	0.89	0.66
<i>lmo1826</i>	DNA-directed RNA polymerase subunit omega	0.32	0.00	0.22	0.02	0.76	0.21
<i>lmo1827</i>	guanylate kinase	0.25	0.01	0.10	0.03	0.82	0.20
<i>lmo1828</i>	hypothetical protein	0.23	0.18	0.11	0.15	0.83	0.23
<i>lmo1829</i>	fibronectin-binding proteins	0.26	0.48	0.27	0.19	0.80	0.29
<i>lmo1830</i>	short-chain dehydrogenase	0.09	0.49	0.06	0.45	0.77	0.32
<i>lmo1831</i>	orotate phosphoribosyltransferase	0.38	0.05	0.13	0.46	0.71	0.50
<i>lmo1832</i>	orotidine 5'-phosphate decarboxylase	0.19	0.41	0.06	0.31	0.75	0.64
<i>lmo1833</i>	dihydroorotate dehydrogenase	0.01	0.10	0.02	0.12	0.92	0.57
<i>lmo1834</i>	dihydroorotate dehydrogenase electron transfer subunit	0.00	0.03	0.00	0.04	0.92	0.62
<i>lmo1835</i>	carbamoyl-phosphate synthetase	0.21	0.42	0.04	0.37	0.72	0.45
<i>lmo1836</i>	carbamoyl phosphate synthase small subunit	0.09	0.32	0.09	0.41	0.84	0.57
<i>lmo1837</i>	dihydroorotase	0.03	0.25	0.02	0.22	0.85	0.66
<i>lmo1838</i>	aspartate carbamoyltransferase	0.20	0.20	0.25	0.47	0.75	0.45
<i>lmo1839</i>	uracil permease	0.11	0.48	0.04	0.52	0.88	0.53

<i>lmo1840</i>	bifunctional pyrimidine regulatory protein PyrR uracil phosphoribosyltransferase	0.11	0.46	0.03	0.49	0.86	0.49
<i>lmo1841</i>	hypothetical protein	0.00	0.00	0.02	0.12	0.71	0.28
<i>lmo1842</i>	hypothetical protein	0.36	0.07	0.12	0.36	0.90	0.57
<i>lmo1843</i>	hypothetical protein	0.04	0.05	0.02	0.22	0.90	0.68
<i>lmo1844</i>	lipoprotein signal peptidase	0.04	0.07	0.02	0.29	0.92	0.62
<i>lmo1845</i>	hypothetical protein	0.10	0.37	0.03	0.55	0.81	0.55
<i>lmo1846</i>	multidrug transporter	0.00	0.00	0.00	0.02	0.89	0.40
<i>lmo1847</i>	metal ABC transporter	0.14	0.35	0.07	0.29	0.92	0.64
<i>lmo1848</i>	metal ABC transporter permease	0.11	0.39	0.08	0.46	0.89	0.54
<i>lmo1849</i>	metal ABC transporter ATP-binding protein	0.05	0.14	0.04	0.19	0.87	0.49
<i>lmo1850</i>	MarR family transcriptional regulator	0.20	0.05	0.07	0.20	0.85	0.31
<i>lmo1851</i>	carboxy-terminal processing proteinase	0.41	0.00	0.21	0.03	0.87	0.37
<i>lmo1852</i>	mercury-binding protein	0.31	0.09	0.17	0.40	0.74	0.46
<i>lmo1853</i>	heavy metal-transporting ATPase	0.00	0.24	0.01	0.38	0.92	0.51
<i>lmo1854</i>	hypothetical protein	0.23	0.01	0.26	0.07	0.91	0.53
<i>lmo1855</i>	D-alanyl-D-alanine carboxypeptidase	0.00	0.02	0.02	0.26	0.87	0.63
<i>lmo1856</i>	purine nucleoside phosphorylase	0.02	0.10	0.06	0.44	0.86	0.63
<i>lmo1857</i>	hypothetical protein	0.10	0.42	0.12	0.47	0.67	0.26
<i>lmo1858</i>	dehydrogenase	0.27	0.12	0.23	0.09	0.61	0.19
<i>lmo1860</i>	methionine sulfoxide reductase A	0.06	0.00	0.28	0.14	0.72	0.35
<i>lmo1861</i>	hypothetical protein	0.34	0.21	0.32	0.30	0.72	0.26
<i>lmo1862</i>	hypothetical protein	0.09	0.12	0.03	0.11	0.40	0.10
<i>lmo1863</i>	hypothetical protein	0.37	0.03	0.27	0.16	0.39	0.13
<i>lmo1864</i>	hemolysin	0.30	0.08	0.26	0.35	0.60	0.24
<i>lmo1865</i>	hypothetical protein	0.32	0.45	0.05	0.32	0.89	0.53
<i>lmo1866</i>	hypothetical protein	0.22	0.42	0.04	0.21	0.73	0.36
<i>lmo1867</i>	pyruvate phosphate dikinase	0.12	0.05	0.11	0.08	0.83	0.55
<i>lmo1868</i>	hypothetical protein	0.00	0.00	0.01	0.05	0.85	0.40
<i>lmo1869</i>	hypothetical protein	0.00	0.00	0.01	0.06	0.75	0.31
<i>lmo1870</i>	alkaline phosphatase	0.20	0.02	0.07	0.01	0.74	0.32
<i>lmo1871</i>	phosphoglucomutase	0.03	0.09	0.18	0.52	0.88	0.57
<i>lmo1872</i>	methyltransferase	0.14	0.32	0.03	0.43	0.82	0.25
<i>lmo1873</i>	dihydrofolate reductase	0.00	0.00	0.01	0.07	0.86	0.54
<i>lmo1874</i>	thymidylate synthase	0.00	0.00	0.00	0.01	0.90	0.47
<i>lmo1875</i>	ABC transporter ATP-binding protein	0.00	0.00	0.01	0.02	0.91	0.37
<i>lmo1877</i>	formyl-tetrahydrofolate synthetase	0.00	0.00	0.00	0.03	0.82	0.29
<i>lmo1878</i>	manganese transport transcriptional regulator	0.02	0.01	0.02	0.00	0.88	0.70
<i>lmo1879</i>	cold-shock protein	0.09	0.46	0.05	0.44	0.92	0.53
<i>lmo1880</i>	RNase HI	0.00	0.00	0.02	0.06	0.82	0.29
<i>lmo1881</i>	5'-3' exonuclease	0.03	0.02	0.02	0.06	0.75	0.25
<i>lmo1882</i>	30S ribosomal protein S14	0.17	0.14	0.06	0.13	0.70	0.35
<i>lmo1883</i>	chitinase	0.03	0.12	0.02	0.16	0.89	0.65
<i>lmo1884</i>	xanthine permease	0.07	0.42	0.03	0.53	0.75	0.57
<i>lmo1885</i>	xanthine phosphoribosyltransferase	0.23	0.19	0.19	0.53	0.66	0.28
<i>lmo1886</i>	carboxypeptidase	0.35	0.20	0.27	0.22	0.87	0.63
<i>lmo1887</i>	hypothetical protein	0.01	0.06	0.01	0.08	0.85	0.54
<i>lmo1888</i>	hypothetical protein	0.12	0.06	0.04	0.29	0.81	0.51
<i>lmo1889</i>	hypothetical protein	0.09	0.31	0.01	0.08	0.71	0.36
<i>lmo1890</i>	hypothetical protein	0.03	0.04	0.01	0.01	0.72	0.37
<i>lmo1891</i>	Holliday junction-specific endonuclease	0.18	0.47	0.09	0.46	0.89	0.34
<i>lmo1892</i>	penicillin-binding protein 2A	0.31	0.00	0.09	0.07	0.75	0.19
<i>lmo1893</i>	hypothetical protein	0.40	0.11	0.20	0.30	0.75	0.59
<i>lmo1894</i>	endonuclease III (DNA repair)	0.37	0.03	0.24	0.22	0.72	0.46
<i>lmo1895</i>	chromosome replication initiation protein	0.41	0.03	0.23	0.12	0.73	0.52
<i>lmo1896</i>	asparaginyl-tRNA synthetase	0.15	0.25	0.04	0.49	0.68	0.25
<i>lmo1897</i>	aspartate aminotransferase	0.00	0.00	0.01	0.08	0.83	0.57
<i>lmo1898</i>	hypothetical protein	0.04	0.22	0.03	0.45	0.77	0.60
<i>lmo1899</i>	bifunctional ATP-dependent DNA helicase/DNA polymerase III subunit epsilon	0.14	0.41	0.09	0.43	0.75	0.53
<i>lmo1900</i>	aspartate alpha-decarboxylase	0.33	0.42	0.25	0.49	0.87	0.55

<i>lmo1901</i>	pantoate--beta-alanine ligase	0.34	0.41	0.17	0.48	0.91	0.66
<i>lmo1902</i>	3-methyl-2-oxobutanoate hydroxymethyltransferase	0.18	0.01	0.32	0.30	0.73	0.57
<i>lmo1903</i>	thioredoxin	0.18	0.01	0.31	0.15	0.59	0.31
<i>lmo1904</i>	transcriptional regulator	0.20	0.47	0.22	0.50	0.87	0.46
<i>lmo1905</i>	tRNA CCA-pyrophosphorylase	0.15	0.36	0.14	0.51	0.89	0.45
<i>lmo1906</i>	methylglyoxal synthase	0.12	0.28	0.11	0.44	0.85	0.35
<i>lmo1907</i>	dihydrodipicolinate reductase	0.36	0.47	0.20	0.47	0.92	0.57
<i>lmo1908</i>	hypothetical protein	0.04	0.00	0.09	0.02	0.54	0.17
<i>lmo1909</i>	hypothetical protein	0.05	0.07	0.04	0.28	0.89	0.43
<i>lmo1910</i>	oxidoreductase	0.09	0.36	0.04	0.41	0.91	0.49
<i>lmo1911</i>	histidine kinase	0.19	0.46	0.12	0.46	0.83	0.46
<i>lmo1912</i>	histidine kinase	0.15	0.31	0.03	0.12	0.75	0.45
<i>lmo1913</i>	hypothetical protein	0.15	0.32	0.03	0.11	0.81	0.48
<i>lmo1914</i>	hypothetical protein	0.11	0.22	0.02	0.09	0.75	0.40
<i>lmo1915</i>	malate dehydrogenase	0.11	0.19	0.14	0.42	0.80	0.40
<i>lmo1916</i>	peptidase	0.00	0.03	0.01	0.20	0.92	0.44
<i>lmo1917</i>	pyruvate formate-lyase	0.36	0.38	0.17	0.54	0.88	0.57
<i>lmo1918</i>	hypothetical protein	0.17	0.47	0.04	0.38	0.92	0.62
<i>lmo1919</i>	hypothetical protein	0.00	0.00	0.01	0.09	0.88	0.51
<i>lmo1920</i>	hypothetical protein	0.42	0.23	0.08	0.51	0.81	0.54
<i>lmo1921</i>	hypothetical protein	0.00	0.00	0.03	0.11	0.91	0.44
<i>lmo1922</i>	hypothetical protein	0.15	0.42	0.04	0.42	0.87	0.23
<i>lmo1923</i>	3-phosphoshikimate 1-carboxyvinyltransferase	0.01	0.06	0.01	0.08	0.89	0.36
<i>lmo1924</i>	prephenate dehydrogenase	0.01	0.23	0.00	0.08	0.82	0.50
<i>lmo1925</i>	histidinol-phosphate aminotransferase	0.03	0.43	0.01	0.32	0.80	0.42
<i>lmo1926</i>	chorismate mutase	0.38	0.02	0.20	0.11	0.82	0.67
<i>lmo1927</i>	3-dehydroquinate synthase	0.09	0.27	0.03	0.52	0.90	0.35
<i>lmo1928</i>	chorismate synthase	0.05	0.27	0.02	0.21	0.90	0.41
<i>lmo1929</i>	nucleoside diphosphate kinase	0.14	0.07	0.08	0.15	0.89	0.66
<i>lmo1930</i>	heptaprenyl diphosphate synthase subunit II	0.41	0.46	0.17	0.29	0.74	0.37
<i>lmo1931</i>	ubiquinone/menaquinone biosynthesis methyltransferase	0.06	0.01	0.28	0.30	0.64	0.22
<i>lmo1932</i>	heptaprenyl diphosphate synthase subunit I	0.20	0.01	0.20	0.37	0.62	0.22
<i>lmo1933</i>	GTP cyclohydrolase I	0.43	0.08	0.12	0.49	0.62	0.26
<i>lmo1934</i>	DNA-binding protein HU	0.08	0.29	0.06	0.50	0.92	0.70
<i>lmo1935</i>	protein-tyrosine/serine phosphatase	0.00	0.00	0.02	0.07	0.60	0.22
<i>lmo1936</i>	NAD(P)H-dependent glycerol-3-phosphate dehydrogenase	0.09	0.37	0.02	0.20	0.88	0.67
<i>lmo1937</i>	GTP-binding protein EngA	0.14	0.18	0.03	0.49	0.89	0.65
<i>lmo1938</i>	30S ribosomal protein S1	0.35	0.16	0.32	0.32	0.92	0.60
<i>lmo1939</i>	cytidylate kinase	0.00	0.00	0.02	0.01	0.61	0.27
<i>lmo1940</i>	asparaginase	0.14	0.06	0.09	0.09	0.85	0.51
<i>lmo1941</i>	hypothetical protein	0.01	0.00	0.01	0.30	0.92	0.44
<i>lmo1942</i>	ATP-dependent DNA helicase	0.05	0.22	0.07	0.35	0.84	0.49
<i>lmo1943</i>	hypothetical protein	0.31	0.41	0.31	0.55	0.76	0.41
<i>lmo1944</i>	ferredoxin	0.00	0.00	0.00	0.00	0.73	0.22
<i>lmo1945</i>	hypothetical protein	0.29	0.12	0.28	0.32	0.83	0.38
<i>lmo1946</i>	acyl-CoA hydrolase	0.08	0.00	0.14	0.01	0.70	0.30
<i>lmo1947</i>	two-component sensor histidine kinase	0.15	0.04	0.09	0.04	0.82	0.53
<i>lmo1948</i>	two-component response regulator ResD	0.18	0.22	0.06	0.10	0.92	0.52
<i>lmo1949</i>	hypothetical protein	0.00	0.01	0.01	0.05	0.85	0.56
<i>lmo1950</i>	hypothetical protein	0.00	0.00	0.00	0.01	0.91	0.34
<i>lmo1951</i>	segregation and condensation protein A	0.01	0.15	0.01	0.26	0.87	0.55
<i>lmo1952</i>	diaminopimelate decarboxylase	0.08	0.49	0.02	0.33	0.84	0.49
<i>lmo1953</i>	purine nucleoside phosphorylase	0.29	0.42	0.16	0.49	0.86	0.40
<i>lmo1954</i>	phosphopentomutase	0.22	0.49	0.10	0.49	0.91	0.55
<i>lmo1955</i>	integrase/recombinase	0.26	0.05	0.29	0.26	0.89	0.66
<i>lmo1956</i>	Fur family transcriptional regulator	0.00	0.00	0.01	0.14	0.91	0.66
<i>lmo1957</i>	ferrichrome ABC transporter permease	0.08	0.34	0.05	0.44	0.83	0.64
<i>lmo1958</i>	ferrichrome ABC transporter permease	0.30	0.39	0.24	0.35	0.86	0.66
<i>lmo1959</i>	ferrichrome-binding protein	0.25	0.44	0.08	0.50	0.92	0.53
<i>lmo1960</i>	ferrichrome ABC transporter ATP-binding protein	0.04	0.12	0.07	0.32	0.88	0.50
<i>lmo1961</i>	oxidoreductase	0.02	0.13	0.05	0.36	0.91	0.50

<i>lmo1962</i>	TetR family transcriptional regulator	0.00	0.03	0.02	0.36	0.74	0.12
<i>lmo1963</i>	hypothetical protein	0.01	0.04	0.02	0.28	0.72	0.09
<i>lmo1965</i>	hypothetical protein	0.00	0.00	0.01	0.06	0.79	0.20
<i>lmo1966</i>	hypothetical protein	0.01	0.05	0.01	0.35	0.88	0.15
<i>lmo1967</i>	toxic ion resistance protein	0.02	0.11	0.02	0.38	0.87	0.19
<i>lmo1975</i>	DNA polymerase IV	0.13	0.11	0.06	0.11	0.85	0.59
<i>lmo1976</i>	oxidoreductase	0.04	0.13	0.06	0.52	0.92	0.52
<i>lmo1977</i>	hypothetical protein	0.33	0.11	0.17	0.15	0.92	0.51
<i>lmo1978</i>	glucose-6-phosphate 1-dehydrogenase	0.00	0.00	0.03	0.03	0.85	0.40
<i>lmo1979</i>	hypothetical protein	0.37	0.31	0.13	0.33	0.71	0.33
<i>lmo1980</i>	hypothetical protein	0.34	0.42	0.32	0.39	0.85	0.60
<i>lmo1981</i>	hypothetical protein	0.06	0.06	0.08	0.24	0.92	0.66
<i>lmo1982</i>	hypothetical protein	0.01	0.01	0.01	0.07	0.91	0.45
<i>lmo1983</i>	dihydroxy-acid dehydratase	0.09	0.38	0.07	0.48	0.88	0.43
<i>lmo1984</i>	acetolactate synthase	0.29	0.37	0.13	0.52	0.90	0.47
<i>lmo1985</i>	acetolactate synthase small subunit	0.21	0.48	0.08	0.50	0.91	0.47
<i>lmo1986</i>	ketol-acid reductoisomerase	0.09	0.29	0.07	0.44	0.91	0.62
<i>lmo1987</i>	2-isopropylmalate synthase	0.26	0.46	0.16	0.53	0.89	0.46
<i>lmo1988</i>	3-isopropylmalate dehydrogenase	0.30	0.43	0.23	0.44	0.84	0.36
<i>lmo1989</i>	isopropylmalate isomerase large subunit	0.20	0.35	0.16	0.55	0.88	0.42
<i>lmo1990</i>	isopropylmalate isomerase small subunit	0.23	0.44	0.18	0.54	0.85	0.36
<i>lmo1991</i>	threonine dehydratase	0.15	0.38	0.15	0.55	0.92	0.65
<i>lmo1992</i>	alpha-acetolactate decarboxylase	0.01	0.03	0.01	0.16	0.90	0.38
<i>lmo1993</i>	pyrimidine-nucleoside phosphorylase	0.26	0.30	0.11	0.42	0.87	0.64
<i>lmo1994</i>	LacI family transcriptional regulator	0.37	0.40	0.31	0.50	0.88	0.61
<i>lmo1995</i>	deoxyribose-phosphate aldolase	0.07	0.24	0.08	0.38	0.89	0.64
<i>lmo1996</i>	DeoR family transcriptional regulator	0.00	0.00	0.00	0.02	0.67	0.20
<i>lmo1997</i>	PTS mannose transporter subunit IIA	0.14	0.46	0.14	0.30	0.93	0.55
<i>lmo1998</i>	opine catabolism protein	0.16	0.40	0.15	0.26	0.92	0.52
<i>lmo1999</i>	hypothetical protein	0.12	0.46	0.13	0.29	0.91	0.42
<i>lmo2000</i>	PTS mannose transporter subunit IID	0.13	0.42	0.13	0.26	0.92	0.40
<i>lmo2001</i>	PTS mannose transporter subunit IIC	0.11	0.44	0.09	0.31	0.91	0.33
<i>lmo2002</i>	PTS mannose transporter subunit IIB	0.11	0.40	0.08	0.23	0.91	0.26
<i>lmo2003</i>	GntR family transcriptional regulator	0.17	0.23	0.11	0.18	0.92	0.35
<i>lmo2004</i>	GntR family transcriptional regulator	0.19	0.27	0.13	0.25	0.92	0.40
<i>lmo2005</i>	oxidoreductase	0.00	0.00	0.02	0.16	0.90	0.55
<i>lmo2006</i>	acetolactate synthase	0.25	0.37	0.17	0.40	0.83	0.59
<i>lmo2007</i>	hypothetical protein	0.05	0.05	0.06	0.13	0.88	0.67
<i>lmo2008</i>	ABC transporter permease	0.03	0.06	0.06	0.18	0.74	0.49
<i>lmo2009</i>	sugar ABC transporter permease	0.09	0.25	0.10	0.41	0.75	0.45
<i>lmo2010</i>	two-component response regulator	0.00	0.00	0.01	0.03	0.92	0.65
<i>lmo2011</i>	two-component sensor histidine kinase	0.00	0.00	0.00	0.00	0.74	0.34
<i>lmo2012</i>	hypothetical protein	0.06	0.14	0.05	0.15	0.81	0.59
<i>lmo2013</i>	hypothetical protein	0.00	0.00	0.03	0.00	0.89	0.40
<i>lmo2014</i>	sugar hydrolase	0.01	0.00	0.02	0.00	0.73	0.33
<i>lmo2015</i>	alpha-mannosidase	0.03	0.04	0.03	0.10	0.92	0.50
<i>lmo2016</i>	cold-shock protein	0.04	0.00	0.28	0.05	0.55	0.21
<i>lmo2017</i>	hypothetical protein	0.01	0.06	0.00	0.06	0.90	0.63
<i>lmo2018</i>	diaminopimelate epimerase	0.03	0.39	0.01	0.28	0.89	0.64
<i>lmo2019</i>	isoleucyl-tRNA synthetase	0.27	0.00	0.18	0.16	0.60	0.26
<i>lmo2020</i>	chemotaxis protein CheY	0.19	0.47	0.15	0.32	0.93	0.69
<i>lmo2021</i>	hypothetical protein	0.00	0.00	0.02	0.08	0.88	0.39
<i>lmo2022</i>	carbon-sulfur lyase	0.03	0.12	0.08	0.45	0.80	0.58
<i>lmo2023</i>	L-aspartate oxidase	0.06	0.00	0.05	0.01	0.40	0.16
<i>lmo2024</i>	nicotinate-nucleotide pyrophosphorylase	0.02	0.00	0.03	0.01	0.39	0.11
<i>lmo2025</i>	quinolinate synthetase	0.03	0.00	0.05	0.03	0.75	0.44
<i>lmo2028</i>	hypothetical protein	0.00	0.02	0.01	0.06	0.89	0.38
<i>lmo2029</i>	hypothetical protein	0.02	0.06	0.01	0.05	0.92	0.68
<i>lmo2030</i>	hypothetical protein	0.10	0.32	0.01	0.08	0.91	0.67
<i>lmo2031</i>	hypothetical protein	0.14	0.33	0.02	0.08	0.83	0.68
<i>lmo2032</i>	cell division protein FtsZ	0.00	0.00	0.01	0.00	0.74	0.48

<i>lmo2033</i>	cell division protein FtsA	0.01	0.00	0.01	0.01	0.91	0.69
<i>lmo2034</i>	cell division protein FtsQ	0.00	0.01	0.01	0.06	0.79	0.64
<i>lmo2035</i>	UDP-diphospho-muramoylpentapeptide beta-N-acetylglucosaminyltransferase	0.01	0.02	0.01	0.08	0.81	0.66
<i>lmo2036</i>	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase	0.15	0.08	0.03	0.49	0.64	0.16
<i>lmo2037</i>	phospho-N-acetylmuramoyl-pentapeptide- transferase	0.01	0.01	0.01	0.16	0.89	0.61
<i>lmo2038</i>	UDP-N-acetylmuramoylalanyl-D-glutamate--2 6-diaminopimelate ligase	0.29	0.00	0.12	0.04	0.75	0.22
<i>lmo2039</i>	penicillin-binding protein 2B	0.10	0.29	0.04	0.49	0.81	0.59
<i>lmo2040</i>	cell division protein FtsL	0.32	0.18	0.25	0.12	0.82	0.39
<i>lmo2041</i>	S-adenosyl-methyltransferase MraW	0.31	0.22	0.18	0.11	0.88	0.69
<i>lmo2042</i>	cell division protein MraZ	0.09	0.13	0.09	0.12	0.89	0.69
<i>lmo2043</i>	MFS transporter	0.00	0.00	0.01	0.02	0.89	0.45
<i>lmo2044</i>	peptide ABC transporter substrate-binding protein	0.13	0.01	0.28	0.11	0.76	0.32
<i>lmo2045</i>	hypothetical protein	0.02	0.25	0.02	0.49	0.89	0.52
<i>lmo2046</i>	2-dehydropantoate 2-reductase	0.00	0.02	0.00	0.14	0.88	0.41
<i>lmo2047</i>	50S ribosomal protein L32	0.20	0.42	0.04	0.29	0.84	0.59
<i>lmo2048</i>	hypothetical protein	0.36	0.05	0.06	0.53	0.90	0.57
<i>lmo2049</i>	hypothetical protein	0.00	0.01	0.01	0.08	0.86	0.35
<i>lmo2050</i>	excinuclease ABC subunit A	0.20	0.29	0.01	0.22	0.80	0.66
<i>lmo2051</i>	hypothetical protein	0.29	0.13	0.10	0.35	0.91	0.63
<i>lmo2052</i>	phosphopantetheine adenylyltransferase	0.12	0.39	0.05	0.48	0.86	0.32
<i>lmo2053</i>	hypothetical protein	0.28	0.28	0.07	0.53	0.91	0.61
<i>lmo2054</i>	hypothetical protein	0.36	0.05	0.10	0.34	0.69	0.52
<i>lmo2055</i>	hypothetical protein	0.13	0.00	0.31	0.06	0.77	0.68
<i>lmo2056</i>	hypothetical protein	0.37	0.05	0.13	0.28	0.92	0.60
<i>lmo2057</i>	protoheme IX farnesyltransferase	0.09	0.20	0.03	0.45	0.59	0.16
<i>lmo2058</i>	heme O oxygenase	0.42	0.03	0.31	0.02	0.91	0.69
<i>lmo2059</i>	potassium channel protein	0.01	0.01	0.01	0.09	0.91	0.62
<i>lmo2060</i>	hypothetical protein	0.22	0.23	0.20	0.11	0.92	0.51
<i>lmo2061</i>	hypothetical protein	0.38	0.08	0.29	0.07	0.91	0.48
<i>lmo2062</i>	copper transporter	0.05	0.00	0.11	0.04	0.82	0.55
<i>lmo2063</i>	hypothetical protein	0.07	0.40	0.02	0.55	0.88	0.49
<i>lmo2064</i>	large-conductance mechanosensitive channel protein	0.06	0.03	0.08	0.14	0.66	0.22
<i>lmo2065</i>	hypothetical protein	0.12	0.13	0.05	0.21	0.82	0.65
<i>lmo2066</i>	hypothetical protein	0.13	0.07	0.05	0.17	0.82	0.68
<i>lmo2067</i>	bile acid hydrolase	0.36	0.00	0.16	0.14	0.68	0.20
<i>lmo2068</i>	molecular chaperone GroEL	0.37	0.10	0.14	0.00	0.91	0.68
<i>lmo2069</i>	co-chaperonin GroES	0.35	0.09	0.12	0.01	0.91	0.63
<i>lmo2070</i>	hypothetical protein	0.31	0.00	0.23	0.06	0.83	0.32
<i>lmo2071</i>	hypothetical protein	0.42	0.00	0.21	0.03	0.87	0.59
<i>lmo2073</i>	ABC transporter ATP-binding protein	0.05	0.14	0.15	0.44	0.92	0.65
<i>lmo2075</i>	DNA-binding/iron metalloprotein/AP endonuclease	0.22	0.48	0.27	0.33	0.83	0.70
<i>lmo2076</i>	alanine acetyltransferase	0.17	0.08	0.30	0.26	0.71	0.36
<i>lmo2077</i>	glycoprotease	0.05	0.09	0.06	0.15	0.88	0.40
<i>lmo2078</i>	hypothetical protein	0.00	0.00	0.02	0.02	0.59	0.14
<i>lmo2079</i>	hypothetical protein	0.27	0.00	0.17	0.11	0.75	0.55
<i>lmo2080</i>	hypothetical protein	0.06	0.29	0.02	0.38	0.87	0.53
<i>lmo2081</i>	camphor resistance protein CrcB	0.31	0.17	0.18	0.25	0.79	0.43
<i>lmo2082</i>	camphor resistance protein CrcB	0.40	0.13	0.23	0.32	0.80	0.39
<i>lmo2083</i>	hypothetical protein	0.01	0.01	0.02	0.04	0.91	0.59
<i>lmo2085</i>	peptidoglycan binding protein	0.38	0.01	0.19	0.16	0.61	0.15
<i>lmo2086</i>	hypothetical protein	0.16	0.23	0.22	0.37	0.69	0.25
<i>lmo2087</i>	hypothetical protein	0.00	0.03	0.02	0.16	0.65	0.26
<i>lmo2088</i>	transcriptional regulator	0.01	0.07	0.07	0.36	0.74	0.33
<i>lmo2089</i>	lipase	0.02	0.02	0.05	0.33	0.92	0.54
<i>lmo2090</i>	argininosuccinate synthase	0.40	0.36	0.13	0.35	0.90	0.68
<i>lmo2091</i>	argininosuccinate lyase	0.41	0.44	0.15	0.32	0.91	0.67
<i>lmo2092</i>	glycine betaine transporter BetL	0.00	0.00	0.01	0.03	0.87	0.54
<i>lmo2093</i>	hypothetical protein	0.06	0.41	0.07	0.45	0.92	0.23
<i>lmo2094</i>	L-fuculose-phosphate aldolase	0.08	0.48	0.11	0.45	0.92	0.22

<i>lmo2095</i>	phosphofructokinase	0.05	0.39	0.10	0.44	0.92	0.20
<i>lmo2096</i>	PTS galacticol transporter subunit IIC	0.05	0.36	0.08	0.52	0.93	0.18
<i>lmo2097</i>	PTS galacticol transporter subunit IIB	0.05	0.30	0.08	0.54	0.91	0.15
<i>lmo2098</i>	PTS galacticol transporter subunit IIA	0.07	0.40	0.09	0.52	0.92	0.19
<i>lmo2099</i>	transcriptional antiterminator	0.07	0.37	0.09	0.54	0.91	0.19
<i>lmo2100</i>	GntR family transcriptional regulator	0.35	0.13	0.10	0.41	0.83	0.51
<i>lmo2101</i>	pyridoxal biosynthesis lyase PdxS	0.37	0.13	0.14	0.45	0.61	0.36
<i>lmo2102</i>	glutamine amidotransferase subunit PdxT	0.37	0.29	0.08	0.53	0.63	0.37
<i>lmo2103</i>	phosphotransacetylase	0.38	0.43	0.30	0.51	0.75	0.39
<i>lmo2104</i>	hypothetical protein	0.26	0.24	0.21	0.52	0.74	0.38
<i>lmo2104a</i>	hypothetical protein	0.12	0.25	0.32	0.49	0.71	0.29
<i>lmo2105</i>	ferrous iron transport protein B	0.23	0.26	0.22	0.46	0.76	0.39
<i>lmo2106</i>	hypothetical protein	0.00	0.00	0.01	0.06	0.48	0.08
<i>lmo2107</i>	DeoR family transcriptional regulator	0.09	0.34	0.12	0.34	0.81	0.24
<i>lmo2108</i>	N-acetylglucosamine-6-phosphate deacetylase	0.16	0.44	0.15	0.30	0.88	0.27
<i>lmo2109</i>	hydrolase	0.06	0.13	0.11	0.44	0.78	0.18
<i>lmo2110</i>	mannnose-6 phosphate isomerase	0.12	0.10	0.08	0.10	0.85	0.57
<i>lmo2111</i>	nitroreductase	0.14	0.41	0.15	0.34	0.86	0.54
<i>lmo2112</i>	hypothetical protein	0.23	0.37	0.15	0.30	0.91	0.46
<i>lmo2113</i>	heme peroxidase	0.22	0.41	0.07	0.47	0.91	0.63
<i>lmo2114</i>	ABC transporter ATP-binding protein	0.14	0.35	0.14	0.47	0.91	0.68
<i>lmo2115</i>	ABC transporter permease	0.08	0.23	0.11	0.48	0.90	0.68
<i>lmo2116</i>	hypothetical protein	0.38	0.06	0.18	0.17	0.91	0.65
<i>lmo2117</i>	hypothetical protein	0.00	0.00	0.00	0.00	0.89	0.55
<i>lmo2118</i>	phosphoglucosamine mutase	0.12	0.48	0.07	0.29	0.90	0.42
<i>lmo2119</i>	hypothetical protein	0.13	0.46	0.00	0.05	0.92	0.59
<i>lmo2120</i>	hypothetical protein	0.11	0.47	0.00	0.04	0.85	0.61
<i>lmo2121</i>	maltose phosphorylase	0.24	0.08	0.06	0.33	0.86	0.56
<i>lmo2122</i>	maltodextrose utilization protein MalA	0.20	0.14	0.05	0.38	0.77	0.69
<i>lmo2123</i>	sugar ABC transporter permease	0.17	0.25	0.03	0.53	0.86	0.64
<i>lmo2124</i>	sugar ABC transporter permease	0.25	0.07	0.06	0.32	0.79	0.68
<i>lmo2125</i>	sugar ABC transporter substrate-binding protein	0.29	0.01	0.09	0.13	0.75	0.60
<i>lmo2126</i>	maltogenic amylase	0.40	0.33	0.06	0.54	0.88	0.42
<i>lmo2127</i>	hypothetical protein	0.11	0.01	0.06	0.03	0.60	0.09
<i>lmo2128</i>	LacI family transcriptional regulator	0.06	0.14	0.02	0.31	0.91	0.52
<i>lmo2129</i>	hypothetical protein	0.01	0.16	0.01	0.26	0.88	0.19
<i>lmo2130</i>	hypothetical protein	0.04	0.11	0.02	0.14	0.88	0.69
<i>lmo2131</i>	hypothetical protein	0.17	0.36	0.04	0.44	0.90	0.65
<i>lmo2132</i>	hypothetical protein	0.11	0.44	0.09	0.48	0.83	0.60
<i>lmo2133</i>	fructose-16-biphosphate aldolase type II	0.27	0.37	0.13	0.46	0.92	0.61
<i>lmo2134</i>	fructose-16-biphosphate aldolase type II	0.19	0.44	0.11	0.48	0.92	0.67
<i>lmo2135</i>	PTS fructose transporter subunit IIC	0.29	0.33	0.07	0.38	0.91	0.59
<i>lmo2136</i>	PTS fructose transporter subunit IIB	0.17	0.33	0.03	0.16	0.83	0.25
<i>lmo2137</i>	PTS fructose transporter subunit IIA	0.30	0.41	0.15	0.55	0.89	0.50
<i>lmo2138</i>	transcriptional regulator	0.15	0.32	0.04	0.44	0.91	0.33
<i>lmo2139</i>	ABC transporter ATP-binding protein	0.14	0.44	0.03	0.21	0.88	0.67
<i>lmo2140</i>	ABC transporter permease	0.04	0.11	0.01	0.03	0.92	0.58
<i>lmo2141</i>	hypothetical protein	0.03	0.08	0.01	0.03	0.89	0.67
<i>lmo2142</i>	hypothetical protein	0.38	0.27	0.25	0.36	0.72	0.37
<i>lmo2143</i>	hypothetical protein	0.42	0.00	0.23	0.03	0.82	0.40
<i>lmo2144</i>	GntR family transcriptional regulator	0.08	0.20	0.06	0.31	0.89	0.52
<i>lmo2145</i>	hypothetical protein	0.15	0.29	0.07	0.32	0.91	0.46
<i>lmo2146</i>	LysR family transcriptional regulator	0.00	0.00	0.00	0.01	0.92	0.58
<i>lmo2147</i>	hypothetical protein	0.33	0.46	0.30	0.33	0.84	0.54
<i>lmo2148</i>	hypothetical protein	0.01	0.03	0.01	0.10	0.91	0.39
<i>lmo2149</i>	hypothetical protein	0.02	0.03	0.02	0.19	0.76	0.30
<i>lmo2150</i>	hypothetical protein	0.10	0.29	0.05	0.26	0.89	0.57
<i>lmo2151</i>	hypothetical protein	0.14	0.01	0.20	0.08	0.78	0.53
<i>lmo2152</i>	thioredoxin	0.10	0.38	0.01	0.10	0.83	0.57
<i>lmo2153</i>	flavodoxin	0.22	0.44	0.10	0.31	0.74	0.47
<i>lmo2154</i>	ribonucleotide-diphosphate reductase subunit beta	0.05	0.14	0.02	0.10	0.80	0.46

<i>lmo2155</i>	ribonucleotide-diphosphate reductase subunit alpha	0.02	0.05	0.02	0.08	0.71	0.33
<i>lmo2156</i>	hypothetical protein	0.24	0.09	0.27	0.41	0.89	0.66
<i>lmo2157</i>	hypothetical protein	0.10	0.45	0.02	0.39	0.75	0.31
<i>lmo2158</i>	hypothetical protein	0.09	0.46	0.04	0.46	0.74	0.23
<i>lmo2159</i>	oxidoreductase	0.37	0.05	0.26	0.22	0.93	0.51
<i>lmo2160</i>	hypothetical protein	0.40	0.10	0.18	0.39	0.92	0.41
<i>lmo2161</i>	hypothetical protein	0.41	0.09	0.24	0.32	0.92	0.48
<i>lmo2162</i>	hypothetical protein	0.42	0.09	0.22	0.31	0.92	0.47
<i>lmo2163</i>	oxidoreductase	0.42	0.08	0.23	0.28	0.92	0.45
<i>lmo2164</i>	AraC family transcriptional regulator	0.00	0.00	0.02	0.22	0.90	0.59
<i>lmo2165</i>	Crp/Fnr family transcriptional regulator	0.02	0.09	0.02	0.33	0.91	0.62
<i>lmo2166</i>	hypothetical protein	0.01	0.00	0.05	0.26	0.75	0.46
<i>lmo2167</i>	hypothetical protein	0.22	0.49	0.11	0.31	0.87	0.64
<i>lmo2168</i>	glyoxalase	0.37	0.45	0.09	0.41	0.74	0.37
<i>lmo2169</i>	hypothetical protein	0.18	0.20	0.05	0.14	0.88	0.59
<i>lmo2170</i>	hypothetical protein	0.00	0.00	0.00	0.00	0.75	0.22
<i>lmo2171</i>	MFS transporter	0.00	0.00	0.00	0.01	0.86	0.34
<i>lmo2172</i>	propionate CoA-transferase	0.00	0.01	0.00	0.02	0.90	0.40
<i>lmo2173</i>	sigma-54-dependent transcriptional regulator	0.31	0.00	0.19	0.12	0.88	0.39
<i>lmo2174</i>	hypothetical protein	0.07	0.08	0.04	0.19	0.85	0.61
<i>lmo2175</i>	3-ketoacyl-ACP reductase	0.02	0.29	0.01	0.34	0.90	0.13
<i>lmo2177</i>	hypothetical protein	0.01	0.00	0.14	0.25	0.81	0.43
<i>lmo2178</i>	peptidoglycan binding protein	0.29	0.01	0.13	0.41	0.65	0.23
<i>lmo2179</i>	peptidoglycan binding protein	0.00	0.01	0.01	0.04	0.92	0.60
<i>lmo2180</i>	hypothetical protein	0.31	0.45	0.11	0.34	0.89	0.54
<i>lmo2181</i>	hypothetical protein	0.31	0.50	0.12	0.39	0.92	0.63
<i>lmo2182</i>	ferrichrome ABC transporter ATP-binding protein	0.14	0.25	0.04	0.17	0.89	0.52
<i>lmo2183</i>	ferrichrome ABC transporter permease	0.06	0.11	0.04	0.15	0.86	0.51
<i>lmo2184</i>	ferrichrome ABC transporter substrate-binding protein	0.11	0.13	0.09	0.22	0.82	0.49
<i>lmo2185</i>	hypothetical protein	0.24	0.27	0.20	0.36	0.83	0.51
<i>lmo2186</i>	hypothetical protein	0.36	0.36	0.28	0.44	0.90	0.62
<i>lmo2187</i>	hypothetical protein	0.09	0.10	0.11	0.29	0.58	0.17
<i>lmo2188</i>	oligoendopeptidase	0.10	0.40	0.03	0.31	0.88	0.52
<i>lmo2189</i>	competence protein CoiA	0.00	0.00	0.00	0.01	0.58	0.18
<i>lmo2190</i>	adaptor protein	0.27	0.00	0.09	0.07	0.74	0.26
<i>lmo2191</i>	ArsC family transcriptional regulator	0.07	0.44	0.02	0.36	0.70	0.31
<i>lmo2192</i>	peptide ABC transporter ATP-binding protein	0.12	0.27	0.02	0.17	0.75	0.61
<i>lmo2193</i>	peptide ABC transporter ATP-binding protein	0.05	0.35	0.01	0.03	0.74	0.68
<i>lmo2194</i>	peptide ABC transporter permease	0.05	0.39	0.01	0.11	0.83	0.69
<i>lmo2195</i>	peptide ABC transporter permease	0.04	0.37	0.02	0.23	0.87	0.57
<i>lmo2196</i>	hypothetical protein	0.17	0.40	0.02	0.16	0.62	0.36
<i>lmo2197</i>	hypothetical protein	0.35	0.01	0.14	0.19	0.86	0.52
<i>lmo2198</i>	tryptophanyl-tRNA synthetase	0.20	0.11	0.07	0.49	0.84	0.60
<i>lmo2199</i>	hypothetical protein	0.40	0.04	0.20	0.18	0.56	0.22
<i>lmo2200</i>	MarR family transcriptional regulator	0.38	0.04	0.23	0.16	0.44	0.20
<i>lmo2201</i>	3-oxoacyl-ACP synthase	0.30	0.00	0.11	0.04	0.77	0.29
<i>lmo2202</i>	3-oxoacyl-ACP synthase	0.23	0.04	0.11	0.14	0.92	0.67
<i>lmo2203</i>	N-acetylmuramoyl-L-alanine amidase	0.15	0.13	0.27	0.41	0.92	0.64
<i>lmo2204</i>	hypothetical protein	0.10	0.43	0.04	0.54	0.89	0.59
<i>lmo2205</i>	phosphoglyceromutase	0.04	0.32	0.03	0.47	0.90	0.35
<i>lmo2206</i>	Clp protease subunit B	0.03	0.31	0.09	0.20	0.92	0.40
<i>lmo2207</i>	hypothetical protein	0.00	0.00	0.00	0.02	0.82	0.24
<i>lmo2208</i>	hypothetical protein	0.39	0.03	0.19	0.17	0.92	0.67
<i>lmo2209</i>	hypothetical protein	0.20	0.36	0.02	0.10	0.81	0.37
<i>lmo2210</i>	hypothetical protein	0.07	0.40	0.16	0.28	0.73	0.59
<i>lmo2211</i>	ferrochelataase	0.30	0.02	0.30	0.15	0.80	0.47
<i>lmo2212</i>	uroporphyrinogen decarboxylase	0.35	0.03	0.31	0.08	0.92	0.63
<i>lmo2213</i>	hypothetical protein	0.10	0.29	0.05	0.48	0.79	0.35
<i>lmo2214</i>	ABC transporter permease	0.10	0.05	0.14	0.21	0.75	0.36
<i>lmo2215</i>	ABC transporter ATP-binding protein	0.21	0.44	0.19	0.45	0.88	0.53
<i>lmo2216</i>	histidine triad (HIT) protein	0.17	0.14	0.08	0.38	0.56	0.06

<i>lmo2217</i>	hypothetical protein	0.00	0.00	0.01	0.17	0.78	0.68
<i>lmo2218</i>	hypothetical protein	0.15	0.47	0.03	0.32	0.92	0.55
<i>lmo2219</i>	foldase	0.37	0.09	0.18	0.18	0.84	0.41
<i>lmo2220</i>	3'-5' exoribonuclease	0.15	0.03	0.09	0.04	0.91	0.56
<i>lmo2221</i>	hypothetical protein	0.07	0.11	0.08	0.25	0.88	0.68
<i>lmo2222</i>	hypothetical protein	0.00	0.00	0.00	0.02	0.74	0.37
<i>lmo2223</i>	hypothetical protein	0.27	0.02	0.22	0.27	0.89	0.47
<i>lmo2225</i>	fumarate hydratase	0.03	0.12	0.07	0.48	0.86	0.31
<i>lmo2226</i>	hypothetical protein	0.05	0.11	0.20	0.45	0.74	0.20
<i>lmo2227</i>	ABC transporter ATP-binding protein	0.04	0.05	0.15	0.53	0.74	0.20
<i>lmo2228</i>	hypothetical protein	0.07	0.11	0.15	0.53	0.74	0.20
<i>lmo2229</i>	penicillin-binding protein	0.09	0.20	0.01	0.09	0.92	0.67
<i>lmo2230</i>	arsenate reductase	0.05	0.40	0.04	0.51	0.84	0.49
<i>lmo2231</i>	hypothetical protein	0.23	0.38	0.07	0.53	0.78	0.38
<i>lmo2232</i>	hypothetical protein	0.11	0.19	0.22	0.49	0.40	0.12
<i>lmo2233</i>	LysR family transcriptional regulator	0.15	0.31	0.15	0.47	0.67	0.21
<i>lmo2234</i>	hypothetical protein	0.23	0.43	0.11	0.45	0.84	0.45
<i>lmo2235</i>	NADH oxidase	0.37	0.33	0.15	0.55	0.90	0.65
<i>lmo2236</i>	shikimate 5-dehydrogenase	0.30	0.42	0.26	0.43	0.83	0.60
<i>lmo2237</i>	MFS transporter permease	0.17	0.37	0.30	0.46	0.83	0.62
<i>lmo2238</i>	MFS transporter	0.41	0.31	0.21	0.30	0.71	0.23
<i>lmo2239</i>	hypothetical protein	0.00	0.00	0.01	0.03	0.74	0.15
<i>lmo2240</i>	ABC transporter ATP-binding protein	0.08	0.03	0.19	0.14	0.80	0.14
<i>lmo2241</i>	GntR family transcriptional regulator	0.03	0.00	0.12	0.08	0.79	0.16
<i>lmo2242</i>	O6-methylguanine-DNA methyltransferase	0.00	0.03	0.01	0.36	0.92	0.47
<i>lmo2243</i>	AraC family transcriptional regulator	0.23	0.45	0.03	0.28	0.86	0.49
<i>lmo2244</i>	ribosomal large subunit pseudouridine synthase	0.20	0.38	0.06	0.54	0.90	0.59
<i>lmo2245</i>	hypothetical protein	0.00	0.00	0.00	0.02	0.87	0.41
<i>lmo2246</i>	hypothetical protein	0.03	0.08	0.06	0.16	0.90	0.70
<i>lmo2247</i>	oxidoreductase	0.37	0.29	0.13	0.09	0.84	0.52
<i>lmo2248</i>	hypothetical protein	0.37	0.08	0.08	0.48	0.88	0.63
<i>lmo2249</i>	low-affinity inorganic phosphate transporter	0.38	0.06	0.06	0.52	0.85	0.57
<i>lmo2250</i>	amino acid ABC transporter permease	0.15	0.50	0.01	0.14	0.91	0.64
<i>lmo2251</i>	amino acid ABC transporter ATP-binding protein	0.19	0.45	0.02	0.25	0.88	0.68
<i>lmo2252</i>	aspartate aminotransferase	0.02	0.12	0.00	0.06	0.91	0.56
<i>lmo2253</i>	phosphoglucomutase	0.01	0.11	0.04	0.37	0.80	0.62
<i>lmo2254</i>	hypothetical protein	0.04	0.15	0.01	0.16	0.87	0.36
<i>lmo2255</i>	hypothetical protein	0.01	0.00	0.05	0.06	0.76	0.51
<i>lmo2256</i>	hypothetical protein	0.02	0.06	0.02	0.27	0.85	0.59
<i>lmo2257</i>	hypothetical protein	0.19	0.16	0.06	0.36	0.89	0.58
<i>lmo2258</i>	hypothetical protein	0.12	0.36	0.17	0.45	0.75	0.21
<i>lmo2259</i>	PTS beta-glucoside transporter subunit IIA	0.35	0.33	0.24	0.35	0.74	0.51
<i>lmo2261</i>	hypothetical protein	0.04	0.17	0.07	0.32	0.74	0.42
<i>lmo2262</i>	hypothetical protein	0.00	0.00	0.02	0.09	0.92	0.56
<i>lmo2263</i>	hypothetical protein	0.41	0.19	0.11	0.40	0.54	0.15
<i>lmo2264</i>	hypothetical protein	0.02	0.01	0.04	0.06	0.89	0.39
<i>lmo2265</i>	hypothetical protein	0.41	0.26	0.26	0.15	0.92	0.59
<i>lmo2266</i>	hypothetical protein	0.05	0.01	0.07	0.06	0.92	0.50
<i>lmo2267</i>	ATP-dependent deoxyribonuclease subunit A	0.02	0.00	0.05	0.03	0.89	0.45
<i>lmo2268</i>	ATP-dependent deoxyribonuclease subunit B	0.02	0.00	0.03	0.02	0.80	0.41
<i>lmo2269</i>	hypothetical protein	0.37	0.02	0.13	0.25	0.68	0.23
<i>lmo2334</i>	transcriptional regulator	0.00	0.00	0.01	0.07	0.88	0.19
<i>lmo2335</i>	PTS fructose transporter subunit IIABC	0.39	0.41	0.30	0.53	0.84	0.58
<i>lmo2337</i>	DeoR family transcriptional regulator	0.32	0.39	0.29	0.51	0.86	0.55
<i>lmo2338</i>	aminopeptidase	0.00	0.00	0.01	0.07	0.91	0.37
<i>lmo2339</i>	hypothetical protein	0.00	0.00	0.02	0.01	0.71	0.28
<i>lmo2340</i>	hypothetical protein	0.08	0.37	0.04	0.48	0.92	0.63
<i>lmo2341</i>	sugar kinase	0.11	0.46	0.05	0.50	0.92	0.66
<i>lmo2342</i>	16S pseudouridylylase synthase	0.09	0.44	0.05	0.50	0.90	0.66
<i>lmo2343</i>	nitrilotriacetate monooxygenase	0.16	0.40	0.08	0.35	0.90	0.50
<i>lmo2344</i>	hypothetical protein	0.05	0.21	0.07	0.37	0.90	0.52

<i>lmo2345</i>	hypothetical protein	0.13	0.46	0.14	0.55	0.92	0.64
<i>lmo2346</i>	amino acid ABC transporter ATP-binding protein	0.22	0.49	0.20	0.52	0.92	0.54
<i>lmo2347</i>	amino acid ABC transporter permease	0.10	0.46	0.06	0.46	0.92	0.52
<i>lmo2348</i>	amino acid ABC transporter permease	0.16	0.48	0.10	0.52	0.91	0.66
<i>lmo2349</i>	amino acid ABC transporter substrate-binding protein	0.06	0.24	0.04	0.28	0.89	0.50
<i>lmo2350</i>	hypothetical protein	0.06	0.26	0.01	0.11	0.92	0.56
<i>lmo2351</i>	FMN reductase	0.20	0.40	0.14	0.44	0.92	0.59
<i>lmo2352</i>	LysR family transcriptional regulator	0.01	0.06	0.03	0.31	0.89	0.68
<i>lmo2353</i>	Na ⁺ /H ⁺ antiporter	0.03	0.32	0.01	0.22	0.74	0.48
<i>lmo2354</i>	hypothetical protein	0.02	0.33	0.02	0.35	0.84	0.64
<i>lmo2355</i>	multidrug resistance protein	0.01	0.01	0.01	0.13	0.92	0.55
<i>lmo2356</i>	hypothetical protein	0.00	0.00	0.05	0.07	0.74	0.40
<i>lmo2357</i>	hypothetical protein	0.18	0.22	0.05	0.55	0.66	0.14
<i>lmo2358</i>	N-acetylglucosamine-6-phosphate isomerase	0.34	0.04	0.10	0.35	0.60	0.16
<i>lmo2359</i>	hypothetical protein	0.01	0.04	0.03	0.35	0.79	0.59
<i>lmo2360</i>	transmembrane protein	0.09	0.37	0.01	0.09	0.89	0.65
<i>lmo2361</i>	hypothetical protein	0.12	0.45	0.01	0.09	0.91	0.60
<i>lmo2362</i>	amino acid antiporter	0.38	0.36	0.08	0.45	0.74	0.56
<i>lmo2363</i>	glutamate decarboxylase	0.32	0.48	0.07	0.39	0.79	0.64
<i>lmo2364</i>	hypothetical protein	0.00	0.01	0.02	0.07	0.88	0.54
<i>lmo2366</i>	DeoR family transcriptional regulator	0.00	0.00	0.00	0.03	0.88	0.27
<i>lmo2367</i>	glucose-6-phosphate isomerase	0.32	0.16	0.02	0.31	0.66	0.40
<i>lmo2368</i>	hypothetical protein	0.10	0.02	0.08	0.04	0.62	0.28
<i>lmo2369</i>	general stress protein 13	0.40	0.47	0.02	0.10	0.90	0.67
<i>lmo2370</i>	aminotransferase	0.00	0.00	0.01	0.16	0.91	0.15
<i>lmo2371</i>	ABC transporter permease	0.27	0.03	0.07	0.18	0.74	0.43
<i>lmo2372</i>	ABC transporter ATP-binding protein	0.12	0.09	0.07	0.22	0.81	0.59
<i>lmo2373</i>	PTS beta-glucoside transporter subunit IIB	0.16	0.09	0.15	0.03	0.75	0.47
<i>lmo2374</i>	aspartate kinase	0.11	0.35	0.06	0.48	0.91	0.67
<i>lmo2376</i>	peptidyl-prolyl cis-trans isomerase	0.00	0.00	0.02	0.05	0.77	0.38
<i>lmo2377</i>	multidrug transporter	0.12	0.00	0.18	0.01	0.70	0.23
<i>lmo2378</i>	monovalent cation/H ⁺ antiporter subunit A	0.26	0.22	0.12	0.36	0.87	0.34
<i>lmo2379</i>	monovalent cation/H ⁺ antiporter subunit B	0.09	0.29	0.28	0.36	0.93	0.49
<i>lmo2380</i>	monovalent cation/H ⁺ antiporter subunit C	0.17	0.02	0.13	0.08	0.86	0.62
<i>lmo2381</i>	monovalent cation/H ⁺ antiporter subunit D	0.30	0.36	0.23	0.48	0.93	0.53
<i>lmo2382</i>	monovalent cation/H ⁺ antiporter subunit E	0.10	0.06	0.12	0.12	0.89	0.60
<i>lmo2383</i>	monovalent cation/H ⁺ antiporter subunit F	0.05	0.01	0.12	0.18	0.90	0.49
<i>lmo2384</i>	monovalent cation/H ⁺ antiporter subunit G	0.35	0.31	0.29	0.40	0.74	0.57
<i>lmo2385</i>	hypothetical protein	0.01	0.00	0.10	0.08	0.86	0.59
<i>lmo2386</i>	hypothetical protein	0.09	0.42	0.03	0.38	0.80	0.45
<i>lmo2387</i>	hypothetical protein	0.07	0.16	0.03	0.14	0.81	0.61
<i>lmo2388</i>	hypothetical protein	0.00	0.00	0.01	0.10	0.75	0.23
<i>lmo2389</i>	NADH dehydrogenase	0.01	0.05	0.01	0.09	0.74	0.48
<i>lmo2390</i>	hypothetical thioredoxine reductase	0.24	0.42	0.09	0.49	0.68	0.41
<i>lmo2391</i>	hypothetical protein	0.18	0.04	0.10	0.18	0.74	0.26
<i>lmo2392</i>	hypothetical protein	0.00	0.01	0.02	0.23	0.92	0.35
<i>lmo2393</i>	hypothetical protein	0.00	0.01	0.01	0.14	0.92	0.30
<i>lmo2397</i>	NifU protein	0.07	0.41	0.05	0.55	0.70	0.38
<i>lmo2398</i>	hypothetical protein	0.40	0.01	0.12	0.30	0.62	0.20
<i>lmo2399</i>	hypothetical protein	0.08	0.26	0.06	0.43	0.73	0.53
<i>lmo2400</i>	acetyltransferase	0.00	0.00	0.00	0.04	0.92	0.50
<i>lmo2401</i>	hypothetical protein	0.29	0.27	0.04	0.36	0.73	0.44
<i>lmo2402</i>	hypothetical protein	0.09	0.50	0.06	0.53	0.88	0.69
<i>lmo2403</i>	hypothetical protein	0.34	0.01	0.12	0.12	0.73	0.47
<i>lmo2404</i>	hypothetical protein	0.38	0.04	0.07	0.55	0.90	0.56
<i>lmo2405</i>	hypothetical protein	0.29	0.06	0.14	0.54	0.90	0.58
<i>lmo2406</i>	hypothetical protein	0.11	0.19	0.07	0.18	0.87	0.66
<i>lmo2411</i>	hypothetical protein	0.05	0.10	0.05	0.18	0.74	0.57
<i>lmo2412</i>	hypothetical protein	0.06	0.20	0.05	0.24	0.72	0.50
<i>lmo2413</i>	aminotransferase	0.05	0.20	0.08	0.44	0.75	0.56
<i>lmo2414</i>	aminotransferase	0.04	0.15	0.17	0.53	0.87	0.67

<i>lmo2415</i>	ABC transporter ATP-binding protein	0.20	0.35	0.26	0.36	0.74	0.40
<i>lmo2416</i>	hypothetical protein	0.30	0.38	0.14	0.45	0.88	0.56
<i>lmo2417</i>	ABC transporter substrate-binding protein	0.42	0.02	0.18	0.14	0.55	0.25
<i>lmo2418</i>	ABC transporter permease	0.04	0.30	0.05	0.50	0.75	0.44
<i>lmo2419</i>	ABC transporter ATP-binding protein	0.19	0.50	0.11	0.41	0.86	0.43
<i>lmo2420</i>	hypothetical protein	0.03	0.30	0.01	0.23	0.88	0.70
<i>lmo2421</i>	two-component sensor histidine kinase	0.03	0.05	0.03	0.24	0.88	0.29
<i>lmo2422</i>	two-component response regulator	0.12	0.15	0.05	0.26	0.74	0.22
<i>lmo2423</i>	hypothetical protein	0.10	0.39	0.02	0.32	0.92	0.69
<i>lmo2424</i>	thioredoxin	0.01	0.00	0.03	0.05	0.77	0.21
<i>lmo2425</i>	glycine cleavage system protein H	0.11	0.00	0.29	0.01	0.65	0.22
<i>lmo2426</i>	hypothetical protein	0.34	0.01	0.17	0.14	0.74	0.54
<i>lmo2427</i>	cell division protein FtsW	0.28	0.00	0.16	0.22	0.62	0.18
<i>lmo2428</i>	cell division protein FtsW	0.35	0.00	0.14	0.05	0.86	0.20
<i>lmo2429</i>	ferrichrome ABC transporter ATP-binding protein	0.34	0.06	0.12	0.31	0.77	0.66
<i>lmo2430</i>	ferrichrome ABC transporter permease	0.15	0.43	0.16	0.31	0.89	0.68
<i>lmo2431</i>	ferrichrome ABC transporter substrate-binding protein	0.22	0.24	0.28	0.46	0.72	0.34
<i>lmo2432</i>	hypothetical protein	0.14	0.18	0.17	0.06	0.86	0.61
<i>lmo2433</i>	acetylsterase	0.04	0.36	0.07	0.54	0.73	0.47
<i>lmo2434</i>	glutamate decarboxylase	0.08	0.46	0.02	0.32	0.84	0.54
<i>lmo2435</i>	hypothetical protein	0.15	0.50	0.08	0.49	0.90	0.66
<i>lmo2436</i>	transcription antiterminator	0.04	0.25	0.01	0.12	0.88	0.66
<i>lmo2437</i>	hypothetical protein	0.18	0.24	0.12	0.32	0.84	0.61
<i>lmo2438</i>	hypothetical protein	0.03	0.10	0.02	0.26	0.78	0.21
<i>lmo2439</i>	hypothetical protein	0.32	0.39	0.24	0.55	0.91	0.60
<i>lmo2440</i>	hypothetical protein	0.16	0.48	0.12	0.38	0.89	0.42
<i>lmo2441</i>	transcriptional regulator	0.07	0.23	0.07	0.46	0.92	0.44
<i>lmo2442</i>	hypothetical protein	0.00	0.01	0.00	0.00	0.75	0.33
<i>lmo2443</i>	hypothetical protein	0.13	0.28	0.04	0.55	0.89	0.53
<i>lmo2444</i>	glycosidase	0.07	0.00	0.07	0.01	0.80	0.31
<i>lmo2445</i>	internalin	0.03	0.00	0.09	0.09	0.77	0.41
<i>lmo2447</i>	transcriptional regulator	0.19	0.41	0.29	0.27	0.75	0.63
<i>lmo2448</i>	SsrA-binding protein	0.40	0.46	0.23	0.47	0.91	0.55
<i>lmo2449</i>	exoribonuclease RNase-R	0.42	0.45	0.16	0.38	0.91	0.57
<i>lmo2450</i>	carboxylesterase	0.01	0.16	0.03	0.40	0.78	0.36
<i>lmo2451</i>	preprotein translocase subunit SecG	0.36	0.29	0.22	0.49	0.92	0.67
<i>lmo2452</i>	carboxylesterase	0.03	0.49	0.07	0.24	0.79	0.59
<i>lmo2453</i>	epoxide hydrolase	0.11	0.10	0.06	0.13	0.85	0.66
<i>lmo2454</i>	hypothetical protein	0.03	0.44	0.03	0.36	0.82	0.54
<i>lmo2455</i>	phosphopyruvate hydratase	0.41	0.37	0.09	0.09	0.85	0.63
<i>lmo2456</i>	phosphoglyceromutase	0.43	0.30	0.09	0.19	0.80	0.61
<i>lmo2457</i>	triosephosphate isomerase	0.43	0.29	0.10	0.21	0.81	0.62
<i>lmo2458</i>	phosphoglycerate kinase	0.37	0.22	0.15	0.34	0.79	0.58
<i>lmo2459</i>	glyceraldehyde-3-phosphate dehydrogenase	0.26	0.30	0.20	0.24	0.92	0.70
<i>lmo2460</i>	transcriptional regulator	0.16	0.04	0.23	0.25	0.49	0.22
<i>lmo2461</i>	RNA polymerase factor sigma-54	0.23	0.10	0.10	0.25	0.84	0.68
<i>lmo2462</i>	dipeptidase	0.05	0.00	0.13	0.02	0.40	0.09
<i>lmo2463</i>	multidrug transporter	0.34	0.22	0.11	0.48	0.70	0.22
<i>lmo2464</i>	transcriptional regulator	0.02	0.14	0.02	0.24	0.75	0.23
<i>lmo2465</i>	hypothetical protein	0.06	0.28	0.04	0.35	0.90	0.46
<i>lmo2467</i>	chitin-binding protein	0.09	0.45	0.08	0.45	0.92	0.55
<i>lmo2468</i>	ATP-dependent Clp protease proteolytic subunit	0.03	0.30	0.05	0.43	0.88	0.55
<i>lmo2469</i>	amino acid transporter	0.19	0.04	0.12	0.06	0.74	0.60
<i>lmo2470</i>	internalin	0.01	0.02	0.01	0.05	0.85	0.42
<i>lmo2471</i>	NADPH dehydrogenase	0.07	0.00	0.33	0.12	0.82	0.39
<i>lmo2472</i>	hypothetical protein	0.25	0.04	0.17	0.43	0.74	0.35
<i>lmo2473</i>	hypothetical protein	0.04	0.20	0.03	0.16	0.74	0.51
<i>lmo2474</i>	hypothetical protein	0.01	0.12	0.01	0.11	0.90	0.67
<i>lmo2475</i>	phosphoglucomutase	0.04	0.24	0.01	0.12	0.75	0.61
<i>lmo2476</i>	aldose 1-epimerase	0.16	0.07	0.23	0.20	0.74	0.40
<i>lmo2477</i>	UDP-glucose 4-epimerase	0.14	0.27	0.16	0.36	0.82	0.46

<i>lmo2478</i>	thioredoxin reductase	0.01	0.02	0.00	0.01	0.72	0.48
<i>lmo2479</i>	hypothetical protein	0.23	0.47	0.08	0.45	0.75	0.45
<i>lmo2480</i>	acetyltransferase	0.25	0.09	0.28	0.01	0.82	0.30
<i>lmo2481</i>	pyrophosphatase PpaX	0.11	0.49	0.11	0.24	0.83	0.47
<i>lmo2482</i>	prolipoprotein diacylglyceryl transferase	0.04	0.03	0.07	0.46	0.91	0.68
<i>lmo2483</i>	HPr kinase/phosphorylase	0.06	0.01	0.06	0.25	0.87	0.58
<i>lmo2484</i>	hypothetical protein	0.04	0.10	0.02	0.15	0.89	0.60
<i>lmo2485</i>	hypothetical protein	0.15	0.38	0.05	0.49	0.84	0.67
<i>lmo2486</i>	hypothetical protein	0.09	0.16	0.18	0.55	0.47	0.08
<i>lmo2487</i>	hypothetical protein	0.06	0.23	0.18	0.46	0.61	0.12
<i>lmo2488</i>	excinuclease ABC subunit A	0.09	0.14	0.02	0.05	0.91	0.66
<i>lmo2489</i>	excinuclease ABC subunit B	0.16	0.17	0.08	0.15	0.86	0.52
<i>lmo2490</i>	CsbA protein	0.00	0.01	0.01	0.10	0.81	0.38
<i>lmo2491</i>	hypothetical protein	0.01	0.01	0.01	0.16	0.87	0.48
<i>lmo2492</i>	hypothetical protein	0.02	0.06	0.01	0.10	0.92	0.64
<i>lmo2493</i>	ArsR family transcriptional regulator	0.04	0.02	0.11	0.11	0.57	0.09
<i>lmo2494</i>	PhoU family transcriptional regulator	0.09	0.43	0.04	0.35	0.81	0.60
<i>lmo2495</i>	phosphate ABC transporter ATP-binding protein	0.07	0.35	0.03	0.30	0.82	0.66
<i>lmo2496</i>	phosphate ABC transporter ATP-binding protein	0.37	0.11	0.31	0.12	0.74	0.39
<i>lmo2497</i>	phosphate ABC transporter permease	0.40	0.04	0.25	0.26	0.83	0.55
<i>lmo2498</i>	phosphate ABC transporter permease	0.36	0.06	0.30	0.13	0.79	0.51
<i>lmo2499</i>	phosphate ABC transporter substrate-binding protein	0.39	0.01	0.24	0.13	0.82	0.53
<i>lmo2500</i>	two-component sensor histidine kinase	0.00	0.00	0.01	0.01	0.86	0.31
<i>lmo2501</i>	two-component response phosphate regulator	0.00	0.00	0.01	0.02	0.75	0.36
<i>lmo2502</i>	hypothetical protein	0.00	0.00	0.01	0.23	0.90	0.20
<i>lmo2503</i>	cardiolipin synthase	0.02	0.01	0.03	0.24	0.90	0.48
<i>lmo2504</i>	cell wall-binding protein	0.01	0.01	0.08	0.31	0.60	0.21
<i>lmo2505</i>	peptidoglycan lytic protein P45	0.12	0.34	0.07	0.39	0.84	0.46
<i>lmo2506</i>	cell division protein FtsX	0.32	0.09	0.20	0.14	0.86	0.35
<i>lmo2507</i>	cell division protein FtsE	0.35	0.09	0.22	0.14	0.90	0.40
<i>lmo2508</i>	hypothetical protein	0.00	0.04	0.01	0.06	0.85	0.68
<i>lmo2509</i>	peptide chain release factor 2	0.02	0.13	0.01	0.10	0.81	0.35
<i>lmo2510</i>	preprotein translocase subunit SecA	0.28	0.09	0.13	0.50	0.61	0.26
<i>lmo2511</i>	hypothetical protein	0.11	0.07	0.06	0.12	0.83	0.65
<i>lmo2512</i>	competence protein ComFC	0.42	0.21	0.04	0.31	0.64	0.27
<i>lmo2513</i>	competence protein comFA	0.16	0.44	0.02	0.19	0.90	0.66
<i>lmo2514</i>	hypothetical protein	0.03	0.24	0.01	0.19	0.65	0.23
<i>lmo2515</i>	two-component response regulator DegU	0.01	0.03	0.01	0.08	0.72	0.31
<i>lmo2516</i>	hypothetical protein	0.18	0.32	0.04	0.48	0.73	0.16
<i>lmo2517</i>	hypothetical protein	0.12	0.42	0.03	0.42	0.74	0.22
<i>lmo2518</i>	LytR family transcriptional regulator	0.18	0.43	0.06	0.50	0.91	0.52
<i>lmo2519</i>	teichoic acid linkage unit synthesis protein	0.39	0.01	0.27	0.00	0.78	0.37
<i>lmo2520</i>	O-succinylbenzoate-CoA synthase	0.10	0.01	0.03	0.00	0.72	0.29
<i>lmo2521</i>	polyglycerol phosphate biosynthesis protein TagA	0.40	0.31	0.05	0.21	0.77	0.47
<i>lmo2522</i>	cell wall-binding protein	0.41	0.18	0.08	0.45	0.88	0.53
<i>lmo2523</i>	single-strand DNA-binding protein	0.00	0.00	0.03	0.02	0.39	0.16
<i>lmo2524</i>	(3R)-hydroxymyristoyl-ACP dehydratase	0.01	0.02	0.01	0.10	0.76	0.33
<i>lmo2525</i>	rod shape-determining protein MreB	0.01	0.00	0.01	0.04	0.90	0.64
<i>lmo2526</i>	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	0.33	0.06	0.21	0.07	0.87	0.49
<i>lmo2527</i>	hypothetical protein	0.00	0.00	0.00	0.00	0.89	0.39
<i>lmo2528</i>	ATP synthase F0F1 subunit epsilon	0.08	0.32	0.04	0.09	0.85	0.58
<i>lmo2529</i>	ATP synthase F0F1 subunit beta	0.03	0.08	0.02	0.07	0.88	0.40
<i>lmo2530</i>	ATP synthase F0F1 subunit gamma	0.11	0.41	0.06	0.41	0.84	0.61
<i>lmo2531</i>	ATP synthase F0F1 subunit alpha	0.13	0.32	0.06	0.52	0.85	0.50
<i>lmo2532</i>	ATP synthase F0F1 subunit delta	0.10	0.39	0.04	0.49	0.89	0.40
<i>lmo2533</i>	ATP synthase F0F1 subunit B	0.07	0.46	0.06	0.54	0.90	0.30
<i>lmo2534</i>	ATP synthase F0F1 subunit C	0.21	0.20	0.09	0.42	0.88	0.37
<i>lmo2535</i>	ATP synthase F0F1 subunit A	0.01	0.18	0.04	0.41	0.90	0.20
<i>lmo2536</i>	ATP synthase subunit I	0.12	0.35	0.13	0.39	0.85	0.54
<i>lmo2536a</i>	hypothetical protein	0.11	0.48	0.05	0.44	0.82	0.64
<i>lmo2537</i>	UDP-N-acetylglucosamine 2-epimerase	0.36	0.01	0.06	0.37	0.74	0.37

<i>lmo2538</i>	uracil phosphoribosyltransferase	0.05	0.44	0.01	0.21	0.81	0.34
<i>lmo2539</i>	serine hydroxymethyltransferase	0.27	0.21	0.09	0.46	0.73	0.52
<i>lmo2540</i>	phosphatase	0.00	0.00	0.12	0.23	0.66	0.27
<i>lmo2541</i>	tRNA threonylcarbamoyladenine biosynthesis protein	0.00	0.00	0.13	0.13	0.52	0.20
<i>lmo2542</i>	protoporphyrinogen oxidase	0.01	0.03	0.01	0.12	0.72	0.33
<i>lmo2543</i>	peptide chain release factor 1	0.03	0.37	0.04	0.44	0.73	0.25
<i>lmo2544</i>	thymidine kinase	0.01	0.00	0.01	0.07	0.91	0.65
<i>lmo2545</i>	homoserine kinase	0.01	0.17	0.02	0.46	0.88	0.52
<i>lmo2546</i>	threonine synthase	0.02	0.20	0.02	0.40	0.88	0.60
<i>lmo2547</i>	homoserine dehydrogenase	0.04	0.32	0.02	0.37	0.91	0.55
<i>lmo2548</i>	50S ribosomal protein L31	0.11	0.35	0.02	0.18	0.89	0.67
<i>lmo2549</i>	wall teichoic acid glycosylation protein GtcA	0.00	0.04	0.00	0.01	0.91	0.63
<i>lmo2551</i>	transcription termination factor Rho	0.40	0.00	0.31	0.00	0.74	0.27
<i>lmo2552</i>	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	0.17	0.21	0.09	0.22	0.85	0.39
<i>lmo2553</i>	hypothetical protein	0.01	0.03	0.00	0.00	0.89	0.52
<i>lmo2554</i>	galactosyltransferase	0.05	0.40	0.01	0.25	0.90	0.54
<i>lmo2555</i>	N-acetylglucosaminyl-phosphatidylinositol biosynthesis protein	0.09	0.45	0.05	0.47	0.89	0.69
<i>lmo2556</i>	fructose-16-bisphosphate aldolase	0.08	0.33	0.01	0.10	0.87	0.26
<i>lmo2557</i>	lipid kinase	0.00	0.00	0.00	0.00	0.92	0.43
<i>lmo2559</i>	CTP synthetase	0.12	0.23	0.05	0.41	0.86	0.57
<i>lmo2560</i>	DNA-directed RNA polymerase subunit delta	0.39	0.00	0.13	0.21	0.63	0.20
<i>lmo2561</i>	arginyl-tRNA synthetase	0.18	0.05	0.06	0.38	0.65	0.20
<i>lmo2562</i>	hypothetical protein	0.19	0.12	0.03	0.52	0.76	0.32
<i>lmo2563</i>	hypothetical protein	0.10	0.11	0.07	0.17	0.70	0.24
<i>lmo2564</i>	4-oxalocrotonate isomerase	0.08	0.00	0.15	0.04	0.90	0.65
<i>lmo2565</i>	hypothetical protein	0.07	0.28	0.03	0.32	0.68	0.20
<i>lmo2566</i>	hypothetical protein	0.02	0.21	0.02	0.37	0.81	0.31
<i>lmo2567</i>	hypothetical protein	0.13	0.19	0.31	0.53	0.18	0.00
<i>lmo2568</i>	hypothetical protein	0.08	0.13	0.25	0.51	0.37	0.08
<i>lmo2569</i>	peptide ABC transporter substrate-binding protein	0.01	0.01	0.02	0.07	0.49	0.09
<i>lmo2570</i>	hypothetical protein	0.04	0.32	0.03	0.39	0.80	0.38
<i>lmo2571</i>	nicotinamidase	0.14	0.33	0.06	0.52	0.75	0.28
<i>lmo2572</i>	dihydrofolate reductase subunit A	0.18	0.19	0.07	0.44	0.75	0.26
<i>lmo2573</i>	zinc-binding dehydrogenase	0.17	0.22	0.07	0.43	0.75	0.30
<i>lmo2574</i>	hypothetical protein	0.08	0.36	0.06	0.15	0.88	0.63
<i>lmo2575</i>	cation transporter	0.31	0.31	0.31	0.44	0.65	0.24
<i>lmo2577</i>	hypothetical protein	0.00	0.01	0.00	0.04	0.75	0.33
<i>lmo2578</i>	hypothetical protein	0.15	0.40	0.04	0.44	0.92	0.70
<i>lmo2579</i>	hypothetical protein	0.38	0.22	0.04	0.34	0.70	0.27
<i>lmo2580</i>	ABC transporter ATP-binding protein	0.25	0.00	0.30	0.01	0.74	0.62
<i>lmo2581</i>	hypothetical protein	0.38	0.01	0.29	0.04	0.85	0.68
<i>lmo2582</i>	histidine kinase	0.00	0.00	0.01	0.07	0.74	0.21
<i>lmo2583</i>	DNA-binding response regulator	0.00	0.00	0.01	0.09	0.76	0.20
<i>lmo2584</i>	formate dehydrogenase accessory protein	0.01	0.03	0.01	0.12	0.85	0.19
<i>lmo2585</i>	hypothetical protein	0.01	0.03	0.01	0.10	0.90	0.18
<i>lmo2586</i>	formate dehydrogenase subunit alpha	0.04	0.32	0.01	0.19	0.92	0.21
<i>lmo2587</i>	hypothetical protein	0.00	0.00	0.01	0.02	0.82	0.52
<i>lmo2588</i>	multidrug transporter	0.35	0.48	0.25	0.53	0.85	0.58
<i>lmo2590</i>	ATP-binding protein	0.38	0.18	0.10	0.45	0.92	0.61
<i>lmo2591</i>	N-acetylmuramoyl-L-alanine amidase	0.04	0.38	0.02	0.45	0.74	0.50
<i>lmo2592</i>	aldo/keto reductase	0.01	0.02	0.12	0.53	0.75	0.33
<i>lmo2593</i>	MerR family transcriptional regulator	0.00	0.01	0.07	0.54	0.74	0.24
<i>lmo2596</i>	30S ribosomal protein S9	0.03	0.05	0.01	0.06	0.91	0.57
<i>lmo2597</i>	50S ribosomal protein L13	0.06	0.27	0.02	0.11	0.88	0.62
<i>lmo2598</i>	tRNA pseudouridine synthase A	0.14	0.42	0.09	0.43	0.69	0.41
<i>lmo2599</i>	hypothetical protein	0.14	0.48	0.18	0.30	0.73	0.48
<i>lmo2600</i>	cobalt ABC transporter ATP-binding subunit	0.09	0.11	0.04	0.09	0.74	0.41
<i>lmo2601</i>	cobalt ABC transporter ATP-binding protein	0.00	0.03	0.01	0.08	0.68	0.21
<i>lmo2602</i>	hypothetical protein	0.01	0.08	0.01	0.24	0.90	0.66
<i>lmo2603</i>	hypothetical protein	0.02	0.12	0.02	0.26	0.89	0.68
<i>lmo2605</i>	50S ribosomal protein L17	0.10	0.43	0.04	0.27	0.81	0.69

<i>lmo2606</i>	DNA-directed RNA polymerase subunit alpha	0.12	0.46	0.05	0.27	0.75	0.65
<i>lmo2607</i>	30S ribosomal protein S11	0.11	0.47	0.07	0.52	0.76	0.62
<i>lmo2608</i>	30S ribosomal protein S13	0.11	0.41	0.06	0.51	0.72	0.37
<i>lmo2609</i>	50S ribosomal protein L36	0.09	0.35	0.03	0.47	0.74	0.43
<i>lmo2610</i>	translation initiation factor IF-1	0.10	0.40	0.03	0.51	0.80	0.44
<i>lmo2611</i>	adenylate kinase	0.08	0.41	0.06	0.28	0.71	0.34
<i>lmo2612</i>	preprotein translocase subunit SecY	0.08	0.38	0.07	0.31	0.71	0.42
<i>lmo2613</i>	50S ribosomal protein L15	0.05	0.36	0.02	0.18	0.70	0.41
<i>lmo2614</i>	50S ribosomal protein L30	0.04	0.21	0.01	0.10	0.75	0.56
<i>lmo2615</i>	30S ribosomal protein S5	0.04	0.25	0.01	0.10	0.71	0.39
<i>lmo2616</i>	50S ribosomal protein L18	0.06	0.32	0.01	0.14	0.72	0.40
<i>lmo2617</i>	50S ribosomal protein L6	0.05	0.29	0.01	0.11	0.71	0.37
<i>lmo2618</i>	30S ribosomal protein S8	0.06	0.43	0.01	0.17	0.70	0.33
<i>lmo2619</i>	30S ribosomal protein S14	0.04	0.28	0.01	0.19	0.76	0.55
<i>lmo2620</i>	50S ribosomal protein L5	0.05	0.29	0.01	0.17	0.76	0.58
<i>lmo2621</i>	50S ribosomal protein L24	0.10	0.43	0.02	0.27	0.70	0.28
<i>lmo2622</i>	50S ribosomal protein L14	0.11	0.48	0.03	0.31	0.72	0.38
<i>lmo2623</i>	30S ribosomal protein S17	0.05	0.28	0.02	0.22	0.79	0.63
<i>lmo2624</i>	50S ribosomal protein L29	0.08	0.47	0.02	0.20	0.73	0.37
<i>lmo2625</i>	50S ribosomal protein L16	0.08	0.50	0.02	0.23	0.74	0.37
<i>lmo2626</i>	30S ribosomal protein S3	0.08	0.47	0.02	0.30	0.74	0.33
<i>lmo2627</i>	50S ribosomal protein L22	0.09	0.40	0.02	0.33	0.74	0.31
<i>lmo2628</i>	30S ribosomal protein S19	0.08	0.45	0.02	0.25	0.74	0.27
<i>lmo2629</i>	50S ribosomal protein L2	0.09	0.37	0.02	0.36	0.75	0.34
<i>lmo2630</i>	50S ribosomal protein L23	0.10	0.34	0.02	0.45	0.78	0.37
<i>lmo2631</i>	50S ribosomal protein L4	0.09	0.35	0.02	0.50	0.82	0.40
<i>lmo2632</i>	50S ribosomal protein L3	0.08	0.44	0.01	0.33	0.84	0.39
<i>lmo2633</i>	30S ribosomal protein S10	0.08	0.48	0.01	0.20	0.87	0.40
<i>lmo2634</i>	hypothetical protein	0.39	0.00	0.14	0.23	0.66	0.21
<i>lmo2635</i>	14-dihydroxy-2-naphthoate octaprenyltransferase	0.10	0.39	0.02	0.34	0.86	0.68
<i>lmo2636</i>	hypothetical protein	0.09	0.43	0.02	0.18	0.89	0.53
<i>lmo2637</i>	hypothetical protein	0.34	0.05	0.25	0.06	0.90	0.68
<i>lmo2638</i>	NADH dehydrogenase	0.13	0.15	0.19	0.41	0.89	0.66
<i>lmo2639</i>	hypothetical protein	0.35	0.16	0.25	0.16	0.85	0.52
<i>lmo2640</i>	hypothetical protein	0.29	0.03	0.21	0.07	0.83	0.50
<i>lmo2641</i>	heptaprenyl diphosphate synthase subunit II	0.26	0.00	0.25	0.03	0.71	0.33
<i>lmo2642</i>	hypothetical protein	0.20	0.23	0.10	0.40	0.74	0.59
<i>lmo2643</i>	hypothetical protein	0.12	0.29	0.09	0.44	0.92	0.47
<i>lmo2644a</i>	hypothetical protein	0.08	0.27	0.06	0.45	0.84	0.58
<i>lmo2646</i>	hypothetical protein	0.09	0.28	0.07	0.45	0.86	0.59
<i>lmo2647</i>	creatinine amidohydrolase	0.08	0.25	0.06	0.44	0.87	0.59
<i>lmo2648</i>	phosphotriesterase	0.09	0.25	0.07	0.48	0.89	0.62
<i>lmo2649</i>	PTS system ascorbate transporter subunit IIC	0.05	0.15	0.04	0.43	0.89	0.69
<i>lmo2650</i>	MFS transporter	0.11	0.34	0.06	0.53	0.91	0.67
<i>lmo2651</i>	PTS mannitol transporter subunit IIA	0.15	0.37	0.07	0.53	0.90	0.54
<i>lmo2652</i>	transcriptional antiterminator	0.08	0.20	0.06	0.35	0.89	0.59
<i>lmo2653</i>	elongation factor Tu	0.11	0.33	0.03	0.08	0.75	0.69
<i>lmo2654</i>	elongation factor G	0.05	0.24	0.01	0.08	0.86	0.60
<i>lmo2655</i>	30S ribosomal protein S7	0.05	0.27	0.01	0.21	0.87	0.64
<i>lmo2656</i>	30S ribosomal protein S12	0.05	0.28	0.01	0.25	0.90	0.54
<i>lmo2657</i>	deoxyguanosinetriphosphate triphosphohydrolase	0.00	0.01	0.01	0.12	0.88	0.48
<i>lmo2658</i>	acyltransferase	0.00	0.00	0.00	0.05	0.92	0.60
<i>lmo2659</i>	ribulose-phosphate 3-epimerase	0.06	0.35	0.05	0.30	0.90	0.31
<i>lmo2660</i>	transketolase	0.03	0.47	0.03	0.40	0.91	0.28
<i>lmo2661</i>	ribulose-5-phosphate 3-epimerase	0.02	0.48	0.02	0.36	0.91	0.32
<i>lmo2662</i>	ribose 5-phosphate epimerase	0.06	0.24	0.04	0.23	0.89	0.49
<i>lmo2663</i>	polyol dehydrogenase	0.04	0.37	0.02	0.39	0.89	0.37
<i>lmo2664</i>	sorbitol dehydrogenase	0.03	0.46	0.02	0.47	0.90	0.35
<i>lmo2665</i>	PTS galacticol transporter subunit IIC	0.03	0.46	0.02	0.45	0.90	0.32
<i>lmo2666</i>	PTS galacticol transporter subunit IIB	0.03	0.42	0.02	0.37	0.91	0.33
<i>lmo2667</i>	PTS galacticol transporter subunit IIA	0.03	0.42	0.02	0.38	0.91	0.28

<i>lmo2668</i>	transcriptional antiterminator BglG	0.05	0.32	0.03	0.33	0.88	0.34
<i>lmo2669</i>	hypothetical protein	0.30	0.32	0.12	0.41	0.92	0.65
<i>lmo2670</i>	hypothetical protein	0.34	0.00	0.17	0.10	0.69	0.20
<i>lmo2671</i>	hypothetical protein	0.35	0.00	0.18	0.12	0.71	0.25
<i>lmo2672</i>	AraC family transcriptional regulator	0.39	0.00	0.11	0.17	0.73	0.35
<i>lmo2673</i>	hypothetical protein	0.12	0.08	0.08	0.15	0.80	0.42
<i>lmo2674</i>	ribose-5-phosphate isomerase B	0.16	0.04	0.09	0.08	0.81	0.69
<i>lmo2675</i>	hypothetical protein	0.20	0.07	0.13	0.11	0.85	0.56
<i>lmo2676</i>	DNA polymerase IV	0.18	0.05	0.16	0.13	0.86	0.60
<i>lmo2677</i>	esterase	0.41	0.03	0.07	0.54	0.83	0.54
<i>lmo2678</i>	XRE family transcriptional regulator	0.22	0.08	0.04	0.47	0.83	0.65
<i>lmo2679</i>	histidine kinase	0.34	0.00	0.10	0.08	0.75	0.38
<i>lmo2680</i>	potassium-transporting ATPase subunit C	0.38	0.00	0.21	0.03	0.75	0.52
<i>lmo2681</i>	potassium-transporting ATPase subunit B	0.08	0.00	0.15	0.09	0.92	0.62
<i>lmo2682</i>	potassium-transporting ATPase subunit A	0.04	0.01	0.10	0.08	0.91	0.66
<i>lmo2683</i>	PTS cellbiose transporter subunit IIB	0.02	0.07	0.08	0.37	0.82	0.40
<i>lmo2687</i>	cell division protein FtsW	0.23	0.39	0.22	0.35	0.75	0.57
<i>lmo2688</i>	cell division protein FtsW	0.26	0.35	0.31	0.26	0.75	0.50
<i>lmo2689</i>	magnesium-translocating P-type ATPase	0.12	0.50	0.19	0.33	0.73	0.43
<i>lmo2690</i>	TetR family transcriptional regulator	0.38	0.08	0.20	0.16	0.92	0.68
<i>lmo2691</i>	autolysin	0.01	0.04	0.01	0.04	0.85	0.67
<i>lmo2692</i>	hypothetical protein	0.12	0.21	0.10	0.10	0.79	0.45
<i>lmo2693</i>	thymidylate kinase	0.05	0.24	0.10	0.53	0.91	0.63
<i>lmo2694</i>	lysine decarboxylase	0.05	0.34	0.02	0.43	0.91	0.52
<i>lmo2695</i>	dihydroxyacetone kinase subunit DhaK	0.08	0.16	0.03	0.33	0.76	0.31
<i>lmo2696</i>	dihydroxyacetone kinase	0.05	0.30	0.03	0.46	0.80	0.35
<i>lmo2697</i>	PTS mannose transporter subunit IIA	0.12	0.05	0.05	0.24	0.74	0.23
<i>lmo2698</i>	RpiR family transcriptional regulator	0.00	0.02	0.02	0.48	0.90	0.41
<i>lmo2699</i>	hypothetical protein	0.09	0.50	0.06	0.44	0.92	0.31
<i>lmo2700</i>	aldo/keto reductase	0.16	0.22	0.04	0.18	0.84	0.57
<i>lmo2701</i>	hypothetical protein	0.00	0.01	0.00	0.05	0.91	0.50
<i>lmo2702</i>	recombination protein RecR	0.15	0.42	0.04	0.36	0.92	0.60
<i>lmo2703</i>	hypothetical protein	0.00	0.01	0.01	0.08	0.60	0.21
<i>lmo2704</i>	DNA polymerase III subunit gamma/tau	0.01	0.03	0.01	0.04	0.83	0.45
<i>lmo2705</i>	hypothetical protein	0.01	0.01	0.01	0.14	0.88	0.48
<i>lmo2706</i>	hypothetical protein	0.00	0.00	0.01	0.16	0.90	0.46
<i>lmo2707</i>	hypothetical protein	0.00	0.01	0.01	0.29	0.90	0.47
<i>lmo2708</i>	PTS cellbiose transporter subunit IIC	0.04	0.18	0.05	0.23	0.86	0.53
<i>lmo2709</i>	hypothetical protein	0.07	0.00	0.26	0.03	0.62	0.25
<i>lmo2710</i>	hypothetical protein	0.38	0.10	0.08	0.51	0.90	0.59
<i>lmo2712</i>	gluconate kinase	0.01	0.00	0.06	0.08	0.88	0.48
<i>lmo2713</i>	internalin	0.03	0.30	0.05	0.44	0.75	0.65
<i>lmo2714</i>	pepididoglycan bound protein	0.01	0.12	0.03	0.51	0.86	0.57
<i>lmo2715</i>	ABC transporter ATP-binding protein	0.24	0.00	0.30	0.05	0.56	0.20
<i>lmo2716</i>	ABC transporter	0.31	0.00	0.32	0.04	0.59	0.21
<i>lmo2717</i>	cytochrome D ubiquinol oxidase subunit II	0.21	0.39	0.25	0.21	0.80	0.65
<i>lmo2718</i>	cytochrome D ubiquinol oxidase subunit I	0.34	0.20	0.24	0.03	0.75	0.51
<i>lmo2719</i>	hypothetical protein	0.42	0.13	0.11	0.00	0.92	0.66
<i>lmo2720</i>	acetate-CoA ligase	0.22	0.11	0.12	0.15	0.92	0.61
<i>lmo2721</i>	6-phosphogluconolactonase	0.38	0.17	0.26	0.05	0.92	0.60
<i>lmo2722</i>	MerR family transcripitonal regulator	0.08	0.06	0.07	0.16	0.46	0.15
<i>lmo2723</i>	hypothetical protein	0.07	0.05	0.07	0.11	0.40	0.12
<i>lmo2724</i>	hypothetical protein	0.05	0.21	0.03	0.24	0.87	0.59
<i>lmo2725</i>	hypothetical protein	0.10	0.29	0.07	0.35	0.74	0.43
<i>lmo2726</i>	MarR family transcriptional regulator	0.23	0.37	0.09	0.48	0.71	0.23
<i>lmo2727</i>	hypothetical protein	0.33	0.31	0.15	0.18	0.82	0.54
<i>lmo2728</i>	MerR family transcriptional regulator	0.00	0.00	0.00	0.02	0.73	0.18
<i>lmo2729</i>	hypothetical protein	0.00	0.00	0.00	0.02	0.75	0.18
<i>lmo2730</i>	phosphatase	0.14	0.43	0.13	0.31	0.89	0.67
<i>lmo2731</i>	RpiR family transcriptional regulator	0.28	0.23	0.26	0.13	0.92	0.69
<i>lmo2732</i>	hypothetical protein	0.25	0.44	0.16	0.55	0.89	0.37

<i>lmo2733</i>	PTS fructose transporter subunit IIABC	0.12	0.50	0.05	0.55	0.92	0.42
<i>lmo2734</i>	sugar hydrolase	0.12	0.47	0.04	0.47	0.91	0.65
<i>lmo2735</i>	sucrose phosphorylase	0.26	0.11	0.06	0.50	0.89	0.58
<i>lmo2736</i>	hypothetical protein	0.36	0.02	0.15	0.28	0.75	0.30
<i>lmo2737</i>	LacI family transcriptional regulator	0.06	0.00	0.12	0.08	0.83	0.44
<i>lmo2738</i>	hemolysin	0.15	0.44	0.02	0.17	0.57	0.19
<i>lmo2739</i>	NAD-dependent deacetylase	0.04	0.08	0.01	0.03	0.86	0.57
<i>lmo2740</i>	hypothetical protein	0.06	0.11	0.01	0.08	0.81	0.53
<i>lmo2741</i>	multidrug transporter	0.04	0.07	0.01	0.09	0.89	0.68
<i>lmo2742</i>	hypothetical protein	0.02	0.28	0.01	0.15	0.92	0.40
<i>lmo2744</i>	Crp/Fnr family transcriptional regulator	0.37	0.01	0.14	0.29	0.87	0.53
<i>lmo2745</i>	ABC transporter ATP-binding protein	0.11	0.33	0.05	0.28	0.74	0.54
<i>lmo2746</i>	hypothetical protein	0.27	0.40	0.23	0.43	0.92	0.70
<i>lmo2747</i>	seryl-tRNA synthetase	0.16	0.15	0.20	0.38	0.81	0.37
<i>lmo2748</i>	hypothetical protein	0.28	0.09	0.11	0.31	0.74	0.23
<i>lmo2749</i>	glutamine amidotransferase	0.31	0.10	0.16	0.20	0.91	0.66
<i>lmo2750</i>	para-aminobenzoate synthase subunit I	0.12	0.00	0.29	0.06	0.62	0.23
<i>lmo2752</i>	ABC transporter ATP-binding protein	0.27	0.08	0.19	0.51	0.89	0.67
<i>lmo2754</i>	D-alanyl-D-alanine carboxypeptidase	0.11	0.31	0.02	0.09	0.90	0.61
<i>lmo2755</i>	CoA-transferase	0.04	0.20	0.05	0.29	0.89	0.69
<i>lmo2756</i>	DNA topoisomerase III	0.25	0.06	0.16	0.52	0.61	0.32
<i>lmo2757</i>	ATP-dependent DNA helicase	0.14	0.19	0.04	0.09	0.88	0.59
<i>lmo2758</i>	inosine-monophosphate dehydrogenase	0.05	0.33	0.01	0.06	0.91	0.65
<i>lmo2759</i>	hypothetical protein	0.09	0.47	0.07	0.34	0.91	0.56
<i>lmo2760a</i>	hypothetical protein	0.13	0.35	0.02	0.42	0.90	0.65
<i>lmo2762</i>	PTS cellbiose transporter subunit IIB	0.20	0.39	0.16	0.26	0.91	0.54
<i>lmo2763</i>	PTS cellbiose transporter subunit IIC	0.25	0.33	0.20	0.23	0.89	0.58
<i>lmo2764</i>	ROK family transcriptional regulator	0.23	0.36	0.19	0.24	0.91	0.58
<i>lmo2766</i>	RpiR family transcriptional regulator	0.01	0.10	0.01	0.11	0.88	0.69
<i>lmo2767</i>	hypothetical protein	0.00	0.00	0.00	0.04	0.91	0.52
<i>lmo2769</i>	ABC transporter ATP-binding protein	0.01	0.00	0.02	0.04	0.63	0.27
<i>lmo2770</i>	bifunctional glutamate--cysteine ligase/glutathione synthetase	0.18	0.26	0.04	0.08	0.67	0.33
<i>lmo2771</i>	beta-glucosidase	0.04	0.02	0.01	0.03	0.86	0.53
<i>lmo2772</i>	PTS beta-glucoside transporter subunit IIABC	0.10	0.15	0.03	0.10	0.92	0.65
<i>lmo2773</i>	transcriptional antiterminator	0.17	0.42	0.03	0.25	0.90	0.63
<i>lmo2777</i>	multidrug transporter	0.08	0.47	0.06	0.48	0.84	0.59
<i>lmo2779</i>	GTP-binding protein EngD	0.15	0.38	0.04	0.34	0.92	0.67
<i>lmo2780</i>	PTS cellbiose transporter subunit IIA	0.00	0.00	0.02	0.23	0.87	0.52
<i>lmo2781</i>	beta-glucosidase	0.00	0.01	0.02	0.42	0.91	0.44
<i>lmo2782</i>	PTS cellbiose transporter subunit IIB	0.00	0.01	0.03	0.31	0.79	0.33
<i>lmo2783</i>	PTS cellbiose transporter subunit IIC	0.02	0.18	0.03	0.55	0.91	0.57
<i>lmo2784</i>	transcriptional antiterminator	0.02	0.18	0.05	0.45	0.92	0.18
<i>lmo2785</i>	catalase	0.16	0.17	0.14	0.26	0.85	0.55
<i>lmo2789</i>	hypothetical protein	0.03	0.14	0.05	0.35	0.92	0.64
<i>lmo2790</i>	partition protein ParB homolg	0.15	0.39	0.11	0.39	0.92	0.49
<i>lmo2791</i>	partition protein ParA-like protein	0.02	0.15	0.07	0.50	0.91	0.37
<i>lmo2792</i>	hypothetical protein	0.09	0.10	0.05	0.08	0.87	0.70
<i>lmo2793</i>	hypothetical protein	0.01	0.00	0.09	0.02	0.61	0.15
<i>lmo2794</i>	NA-binding protein Spo0J	0.01	0.04	0.01	0.05	0.91	0.70
<i>lmo2795</i>	RpiR family transcription regulator	0.01	0.09	0.01	0.26	0.90	0.54
<i>lmo2796</i>	transcriptional regulator	0.00	0.00	0.01	0.06	0.92	0.20
<i>lmo2797</i>	PTS mannitol transporter subunit IIA	0.00	0.02	0.01	0.10	0.93	0.31
<i>lmo2798</i>	phosphatase	0.00	0.00	0.00	0.06	0.93	0.36
<i>lmo2799</i>	PTS mannitol transporter subunit IIBC	0.01	0.02	0.01	0.11	0.90	0.69
<i>lmo2800</i>	dehydrogenase	0.01	0.07	0.01	0.12	0.82	0.54
<i>lmo2801</i>	N-acetylmannosamine-6-phosphate 2-epimerase	0.03	0.20	0.02	0.27	0.74	0.40
<i>lmo2802</i>	16S rRNA methyltransferase GidB	0.17	0.46	0.12	0.49	0.89	0.44
<i>lmo2810</i>	tRNA uridine 5-carboxymethylaminomethyl modification enzyme GidA	0.04	0.40	0.01	0.25	0.71	0.27
<i>lmo2811</i>	tRNA modification GTPase TrmE	0.21	0.40	0.03	0.50	0.74	0.30
<i>lmo2812</i>	D-alanyl-D-alanine carboxypeptidase	0.20	0.04	0.20	0.13	0.74	0.46
<i>lmo2814</i>	TetR family transcriptional regulator	0.01	0.02	0.01	0.03	0.71	0.30

<i>lmo2815</i>	3-ketoacyl-ACP reductase	0.02	0.02	0.04	0.10	0.74	0.33
<i>lmo2816</i>	MFS transporter	0.01	0.05	0.00	0.04	0.91	0.59
<i>lmo2817</i>	peptidase	0.02	0.22	0.01	0.30	0.90	0.47
<i>lmo2818</i>	MFS transporter	0.01	0.04	0.01	0.11	0.90	0.58
<i>lmo2819</i>	carboxypeptidase	0.01	0.08	0.01	0.21	0.88	0.65
<i>lmo2820</i>	amino-terminal domain-containing protein	0.01	0.01	0.15	0.33	0.90	0.52
<i>lmo2821</i>	internalin	0.01	0.02	0.02	0.09	0.86	0.54
<i>lmo2822</i>	hypothetical protein	0.35	0.35	0.11	0.31	0.84	0.58
<i>lmo2823</i>	sporulation protein SpoOJ	0.24	0.47	0.03	0.26	0.91	0.65
<i>lmo2824</i>	D-3-phosphoglycerate dehydrogenase	0.05	0.33	0.03	0.51	0.88	0.58
<i>lmo2825</i>	phosphoserine aminotransferase	0.12	0.40	0.05	0.52	0.76	0.67
<i>lmo2826</i>	MFS transporter	0.39	0.46	0.02	0.08	0.75	0.40
<i>lmo2827</i>	MarR family transcriptional regulator	0.22	0.25	0.05	0.15	0.75	0.42
<i>lmo2828</i>	hypothetical protein	0.20	0.28	0.31	0.04	0.92	0.48
<i>lmo2829</i>	nitroreductase	0.41	0.34	0.09	0.39	0.87	0.49
<i>lmo2830</i>	thioredoxin	0.06	0.48	0.03	0.47	0.87	0.57
<i>lmo2831</i>	phosphoglucomutase	0.00	0.01	0.02	0.17	0.68	0.19
<i>lmo2832</i>	hypothetical protein	0.00	0.00	0.01	0.10	0.60	0.14
<i>lmo2833</i>	maltose phosphorylase	0.00	0.00	0.01	0.08	0.76	0.28
<i>lmo2834</i>	oxidoreductase	0.01	0.01	0.02	0.18	0.75	0.29
<i>lmo2835</i>	xylose isomerase	0.02	0.00	0.01	0.08	0.87	0.34
<i>lmo2836</i>	alcohol dehydrogenase	0.00	0.00	0.00	0.04	0.78	0.07
<i>lmo2837</i>	sugar ABC transporter permease	0.01	0.01	0.01	0.24	0.75	0.10
<i>lmo2838</i>	sugar ABC transporter permease	0.14	0.44	0.16	0.31	0.72	0.09
<i>lmo2839</i>	sugar ABC transporter substrate-binding protein	0.12	0.38	0.10	0.45	0.81	0.11
<i>lmo2840</i>	sucrose phosphorylase	0.10	0.29	0.11	0.42	0.72	0.18
<i>lmo2841</i>	sucrose phosphorylase	0.31	0.43	0.23	0.50	0.74	0.37
<i>lmo2842</i>	LacI family transcriptional regulator	0.05	0.07	0.06	0.15	0.73	0.35
<i>lmo2843</i>	hypothetical protein	0.29	0.23	0.15	0.35	0.58	0.31
<i>lmo2844</i>	hypothetical protein	0.02	0.11	0.09	0.49	0.91	0.70
<i>lmo2845</i>	MFS transporter	0.00	0.00	0.00	0.00	0.89	0.25
<i>lmo2846</i>	hypothetical protein	0.04	0.04	0.03	0.20	0.92	0.46
<i>lmo2847</i>	rhamnulose-1-phosphate aldolase	0.07	0.29	0.03	0.47	0.91	0.25
<i>lmo2848</i>	L-rhamnose isomerase	0.14	0.44	0.06	0.52	0.90	0.55
<i>lmo2849</i>	rhamnulokinase	0.18	0.44	0.06	0.55	0.91	0.66
<i>lmo2850</i>	sugar transporter	0.25	0.30	0.12	0.30	0.89	0.67
<i>lmo2851</i>	AraC family transcriptional regulator	0.25	0.01	0.08	0.21	0.88	0.68
<i>lmo2852</i>	hypothetical protein	0.39	0.05	0.22	0.14	0.59	0.09
<i>lmo2853</i>	hypothetical protein	0.03	0.23	0.03	0.40	0.87	0.66
<i>lmo2854</i>	sporulation protein SpoJ	0.29	0.09	0.12	0.26	0.76	0.47
<i>lmo2855</i>	ribonuclease P	0.37	0.11	0.22	0.09	0.87	0.55
<i>lmo2856</i>	50S ribosomal protein L34	0.11	0.50	0.06	0.53	0.92	0.69
<i>lmo2857</i>	hypothetical protein	0.03	0.01	0.14	0.18	0.88	0.46

ABSTRACT

Listeria monocytogenes is a multifaceted foodborne pathogen characterized by its adaptability in adverse conditions and proliferation in a wide range of environments from soil to mammalian host cells. The genetic heterogeneity in *L. monocytogenes* is reflected on its diversified clonal structure which correlates, to some extent, with phenotypic traits such as virulence or stress resistance. The thesis investigated two most prominent phenotypes, biofilm formation and virulence potential, from various perspectives using state-of-the-art technologies. Throughout the studies, large panels of isolates were used to represent the intraspecific diversity. Unfavourable stimuli such as cold shock and nutrient deprivation induced bacterial adhesion step. Addition of NaCl to growth cultures stimulated biofilm production and, surprisingly, it significantly intensified biofilm maturation of nutrient-deprived cells. High degree of variation in relative biofilm productivity was observed among serotypes, genotypes, as well as isolates across culture conditions, however, certain genotype (clonal complex 26) revealed distinctively higher biofilm production under cold temperature (10°C) suggesting an association of genotype with biofilm phenotype. Pan-GWAS identified a number of genes among which those implicated in functions such as 'transformation/competence', 'phage-related genes', and 'metabolism of phosphate' will need further investigations for their roles in biofilm formation. RNA sequencing analysis revealed high intraspecific heterogeneity in basal transcriptome profiles that featured the role of regulatory network including certain transcriptional factors with key roles in virulence such as σB , PrfA, and CodY. The transcriptomic plasticity between lineage I and II as well as hyper- and hypovirulent genotypes supported the evolutionary and epidemiological characteristics of *L. monocytogenes*. Moreover, the central metabolic pathway was implicated in the infection in *Galleria mellonella* model system. Conclusively, the thesis explored intraspecific diversity in *L. monocytogenes* and resulted in ample phenotypic, genomic, and transcriptomic findings. With the integrative omics approach in listeriology, the present work will contribute to unveiling the physiology and pathogenesis of the bacterium.

Keywords: *Listeria monocytogenes*, biofilm, virulence, genomics, transcriptomics, intraspecific diversity

Étude à haut débit du biofilm et de la virulence de *Listeria monocytogenes* en utilisant des approches innovantes

RÉSUMÉ

Listeria monocytogenes est un pathogène d'origine alimentaire à multiples facettes caractérisé par sa capacité d'adaptation dans des conditions défavorables et par sa prolifération dans une vaste gamme d'environnements, du sol aux cellules hôtes des mammifères. L'hétérogénéité génétique de *L. monocytogenes* se reflète dans sa structure clonale diversifiée, ce qui corrèle, dans une certaine mesure, avec des traits phénotypiques tels que la virulence ou la résistance au stress. La thèse portait sur deux phénotypes les plus éminents, la formation d'un biofilm et le potentiel de virulence, sous différents angles et à l'aide des technologies les plus récentes. Tout au long des études, des grands panels d'isolats ont été utilisés pour représenter la diversité intraspécifique. Stimulants défavorables tels que le choc froid et la privation d'éléments nutritifs induits par l'étape d'adhésion bactérienne. L'ajout de NaCl aux cultures de croissance a stimulé la production de biofilm et, de manière surprenante, il a considérablement intensifié la maturation du biofilm de cellules privées de nutriments. Un degré élevé de variation de la productivité relative du biofilm a été observé parmi les sérotypes, les génotypes, de même que les isolats selon les conditions de culture. Cependant, un certain génotype (complexe clonal 26) a révélé de manière caractéristique une production de biofilm plus élevée à froid (10°C), suggérant une association du génotype avec le phénotype du biofilm. Pan-GWAS a identifié un certain nombre de gènes parmi lesquels ceux impliqués dans des fonctions telles que la 'transformation/compétence', les 'gènes liés aux phages' et le 'métabolisme du phosphate' devront faire l'objet d'études plus approfondies sur leur rôle dans la formation du biofilm. L'analyse du séquençage de l'ARN a révélé une grande hétérogénéité intraspécifique dans les profils de transcriptome basal qui mettaient en évidence le rôle du réseau de régulation, y compris certains facteurs transcriptionnels avec des rôles clés dans la virulence tels que σB , PrfA, et CodY. La plasticité transcriptomique entre les lignées I et II ainsi que les génotypes hyper et hypovirulents ont confirmé les caractéristiques évolutives et épidémiologiques de *L. monocytogenes*. De plus, la voie métabolique centrale a été impliquée dans l'infection dans le système modèle de *Galleria mellonella*. En conclusion, la thèse a exploré la diversité intraspécifique de *L. monocytogenes* et a donné lieu à de nombreux résultats phénotypiques, génomiques et transcriptomiques. Grâce à l'approche intégrative des omiques en listerologie, le présent travail contribuera à dévoiler la physiologie et la pathogénèse de la bactérie.

Mots-clés : *Listeria monocytogenes*, biofilm, virulence, génomique, transcriptomique, diversité intraspécifique.