박사학위논문

추자도 멸치액젓의 Microbiom 분석 및 신종 미생물 특성 규명

Study of Microbiome and Novel Strain in Fermented Anchovy sauce, Myeolchi-Aekjeot of Chuja island

제주대학교 대학원

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Study of Microbiome and Novel Strain in Fermented Anchovy sauce, Myeolchi-Aekjeot of Chuja island

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Abstract

Fermentation is one of the most economical and classical methods for producing and preserving foods by humans. Besides preserving, fermentation also changes the organoleptic characteristics of foods through developing a wide diversity of flavors, aromas and textures. These fermented foods have been separately developed according to various fermentation conditions such as raw materials, combination of various microorganisms including seed bacteria, temperature, and pH. In particular, various microorganisms in fermented foods are the main factors that determine the taste and flavor of fermented foods, and the degree of fermentation can be determined depending on interactions among microbial communities. Therefore, microbiome analysis of fermented foods has recently emerged as a very important study field from a microbiological point of view in conjunction with the scientification of fermented foods. Therefore, with NGS technique, we want to find out the various microorganisms that exist in the fermented anchovy sauce of Chuja Island.

Chuja Island became famous for anchovy, it is because when a spawning season of anchovy, many anchovies gather in Chuja island. In Chuja Island used anchovies to make salted anchovy sauce that can be used instead of soy sauce. The anchovy sauce for the Chuja Island is made by mixing salt and anchovies without adding any chemical seasoning and fermenting them for about three years. This MyeolchI-Aekjeot, traditional fermented anchovy sauce, has been consumed as an umami-tasting, seasoning ingredient. The umami of Myeolchi-Aekjeot is formed by exogenous enzymes of microorganisms, and despite the high concentration (20-30%) of salty environment, various microorganisms exist in fish sauces. Therefore, with NGS technique, we found out the various microorganisms that exist in the fermented anchovy sauce of Chuja Island.

The fermented anchovy sauce, Myeolchi-Aekjeot, of Chuja island, which was used for the analysis of bacterial communities, was made by Chujado Federation of Fisheries Cooperatives in Jeju. It showed pH 6.1, 27% salinity, and 37.9 brix. To identify bacterial community, total DNA was extracted from fermented anchovy sauce and analyzed by an Illumina MiSeq platform. So total valid reads of 36,376 were obtained. Among total valid reads, reads of the species level was 19,661 reads (54%) and found 132 species. In results of analysis the bacterial community of fermented anchovy sauces of Chuja island, bacteria of phylum *Firmicutes* (82.5%) dominated at sample. And the Class *Bacilli* (76.4%), Order *Bacillales* (64.6%), Family *Bacillaceae* (64.3%) were the dominant in taxon, respectively. At the Genus level, the sample were dominated *Lentibacillus* (46.4%), *Tetragenococcus* (11.7%), and *Pseudogracilibacillus* (10.6%). Although there is no study on analyzed the bacterial community of fermented anchovy sauce in Jeju region, the results of the analysis of the bacterial community in 9 types of fermented anchovy sauce of Korea showed that unlike the results of this study, the bacteria of genus *Tetragenococus* and *Halanaerobium* in phylum *Firmicutes* were dominant in all samples. And study of analyzed the bacterial community of fermented anchovy salted fish (Myeolchi-Jeotgal) in jeju region, genus *Tetragenococcus* (90%) in phylum *Firmicutes* were dominant. According to the results of these studies, including this study, it can be confirmed that all phylum *Firmicutes* dominate. This is thought to be because a large number of bacteria belonging to this taxon form endospores and have the ability to exist in extreme environments. In addition, it appears to be the result because it contains a large number of the fermentation-related bacteria in this taxon. The difference in the results of these studies is thought to be due to the fermentation period. The fermentation period of fermented anchovy sauce of Chuja island analyzed in this study is 3 to 5 years, but

the fermentation period of other fermented anchovy sauces and fermented anchovy salted fish is about 1 year, which is short. Through this, At the beginning of fermentation, bacteria that actively participate in fermentation, such as bacteria of genus *Tetragenococus*, appeared predominantly, and at the latter period of fermentation, genus *Lentibacillus*, which has a late-growth characteristic, appears to be predominant. For this reason, it could be seen that the difference in dominant bacteria occurs over the fermentation period. In the future, if you conduct a bacterial community analysis by fermentation period of fermented anchovy sauce of Chuja island, we will see more accurate results. As a result of this analysis, it can be seen that fermented anchovy sauce of Chuja island is a well-fermented fish sauce. It is known that fish sauce such as fermented anchovy sauce, is rich in essential nutrients and tastes better with a longer fermentation period. It is thought that the presence of genus *Lentibacillus* in fish sauce can be used as an indicator of fermentation period.

And in this study, strain JNUCC-1^T was characterized and classified and this study proposed that strain JNUCC-1^T isolated from fermented anchovy sauce in Chuja island is novel species via polyphasic taxonomy. Cells of strain JNUCC-1^T are Gram-positive, aerobic, motile by means of polar flagella, and spore-forming rods (0.3-0.8 ㎛ wide and 1.2-1.9 ㎛ length). Spherical endospores form at the cell-terminal position. Colonies are circular with opaque of beige and below 1.0 mm in diameter. Growth occurs in 0-20% (w/v) NaCl (optimal in 5%) and pH 4.0-10.0 (optimal at pH 7.0) at 20-45 ℃ (optimal at 30 ℃). Positive results in tests for oxidase, catalase, nitrate reduction and hydrolysis of Tween 20 and 60. The major fatty acid (>20%) is anteiso-$C_{15:0}$. The major polar lipids are diphosphatidylglycerol (DPG), phosphatidyl-glycerol (PG), and one unidentified phospholipid (PL). The predominant respiratory isoprenoid quinone is menaquinone-7 (MK-7). Comparative analysis of 16S rRNA gene sequences showed that strain

JNUCC-1^T is most closely related to *Lentibacillus alimentarius* M2024^T and *Virgibacillus kekensis* YIM-kkny16^T. However, phylogenetic analysis showed that strain JNUCC-1^T forms a phyletic lineage with members of the genus *Lentibacillus*. The topologies of phylogenetic trees built using the maximum-likelihood, maximum-parsimony, and neighbor-joining methods also supported these results, indicating that strain JNUCC-1^T formed a stable clade. The genome size is 3,687,469 bp, and GC content of the genomic DNA is 43.3 %. Protein-coding sequences were predicted by Prodigal version 2.6.2, which showed that the genome contained 3,833 genes. In addition, 66 tRNA genes were identified by tRNAscan-SE version 1.3.1, and 17 rRNA genes were identified by Rfam version 12.0. As a result of analyzing the genes classified according to the COG functional categories, the genome of strain JNUCC-1^T represented higher proportions in the categories of Replication, recombination and repair (7.7%), Amino acid transport and metabolism (7.7%), Inorganic ion transport and metabolism (5.6%), Carbohydrate transport and metabolism (5.3%), Energy production and conversion (5.2%), Transcription (5.1%), Cell wall/membrane/envelope biogenesis (4.81), Translation, ribosomal structure and biogenesis (4.6%). Analysis of phenotypic and genetic traits through COG functional categories gave the same results. The strain JNUCC-1^T found the presence of motility and flagella, and through genomic analysis, it was confirmed that it contained 43 predicted genes related to motility or flagella. And the genome of strain JNUCC-1^T contains 169 predicted genes associated with sporulation, such as spore germination protein GerD, GerM, and YaaH, and 33 predicted genes associated with antibiotic resistance such as pbp2A, ampC and multidrug resistance genes. The results of other biochemical tests, such as API system and hydrolysis of macromolecule test also related genes in COG functional categories of Amino acid transport and metabolism, Carbohydrate transport and metabolism, and Lipid transport and metabolism could confirm. This may be the basis for supporting the results of previous biochemical tests. Genes that could support the results of the chemotaxonomic test were identified. In genome of strain could confirm 9 predicted genes associated with phosphatidylglycerol and diphosphatidylglycerol such as umpA, lgt, and ltaS, and 14 predicted genes associated with menaquinone biosynthesis such as bioC, fadD, and ubiE, and 19 predicted genes associated with fatty acids biosynthesis such as fabG, fabH, and fabI. The genome of strain JNUCC-1T contains 19 predicted genes associated with osmotic stress regulation, such as choline glycine betaine transporter BetT2, osmoprotectant import permease protein OsmW. These genes could be key factors allowing strain JNUCC-1^T to adapt to high-salt environments via osmotic regulation and adjustment of cytoplasmic pH, respectively. Metabolites produced by extreme halophile bacteria such as the strain JNUCC-1^T have been utilized in various industries. Compatible solutes produced to overcome osmotic stress are utilized in the bio industry, enzymes that have activity at high concentrations of salinity are utilized in eco-friendly industries such as decomposition of pollutants and toxic substances, and enzymes such as esterase added in fermentation food used to improve the flavor of food. As a result of analyzing the genome of the strain, the strain is expected to have the potential ability to be used in various industries, and in the future, it will be able to derive the ability of the strain through additional studies such as metabolite regulation, efficacy evaluation, and genetic manipulation.

The genome sequence of strain JNUCC-1^T has been deposited in GenBank under accession no. WHOH00000000 (BioProject accession no. PRJNA577786 and BioSample accession no. SAMN13037569). The public version of the strain JNUCC-1^T genome sequence deposited in GenBank was annotated using the Prokaryotic Genome Annotation Pipeline (PGAP).

In this study, Phylogenetic tree showed that strain JNUCC-1^T forms a phyletic lineage with members of the genus *Lentibacillus*. The chemotaxonomic

and phenotypic characterizations of strain JNUCC-1^T showed typical features of members of the genus *Lentibacillus*, with MK-7 as the predominant respiratory isoprenoid quinone and major fatty acid including anteiso-$C_{15:0}$.

The strain JNUCC-1^T is considered as a novel species of the genus *Lentibacillus*, for which the name *Lentibacillus jejunsis* sp. nov., (Type strain JNUCC-1^T = KCTC 43912^T) is proposed.

This study analyzed the community of microorganisms present in fermented anchovy sauce of Chuja island using the Illumina Miseq platform to confirm that about species of 130 bacteria coexist. Among them, it was found that the bacteria in the genus *Lentibacillus* dominate, which means that fermentation is good for a long time, so that the essential nutrients are rich and the flavor is improved. In addition, the biodiversity was secured to respond to the implementation of the Nagoya Protocol by separating the new strains from the anchovy sauce and identifying their characteristics.

Chapter Ⅰ. General introduction

Fermentation is the most classical methods for producing and preserving foods by humans. Besides preserving, fermentation also changes the organoleptic characteristics of foods through improving a wide diversity of flavors, aromas and textures. Moreover, fermentation may enrichment of food substrates with vitamins, proteins, essential amino acids and essential fatty acids (Lee *et al.*, 1993; Lopetcharat *et al.*, 2001). So, fermented foods containing large amounts of nutrients have the advantage of preventing various adult diseases and preventing aging by increasing the amount of organic acids and beneficial bacteria, suppressing harmful bacteria, and increasing the concentration of dietary fiber and vitamins (Hayes *et al.*, 2007). These fermented foods have been separately developed according to various fermentation conditions such as raw materials, combination of various microorganisms including seed bacteria, temperature, and pH. In particular, various microorganisms in fermented foods are the main factors that determine the taste and flavor of fermented foods, and the degree of fermentation can be determined depending on interactions among microbial communities (Lee *et al.*, 2015). Therefore, microbiome analysis of fermented foods has recently emerged as a very important study field from a microbiological point of view in conjunction with the scientification of fermented foods. The term microbiome mean total of gene and microorganisms in a specific environment. It is known that only a fractionally microorganism in the environment can be cultured under general laboratory conditions, and this unclturability characteristic is the same as microbiome of human, animal, plant and food. In the analysis of microbiome, various molecular biological experimental methods were used to overcome the limitations of the existing culture method and to decipher genes in the entire microbiome. In particular, as the Next-generation sequencing (NGS) method developed after the 2000s became popular, metagenome research began very actively (Eckburg *et al.*, 2005). For metagenome research, DNA is extracted directly from the sample without isolating and culturing microorganisms. In the extracted metagenome has mixed total DNA of all microorganisms in the sample. The extracted metagenome contains a mixture of DNA of all microorganisms present in the sample, which is verified by NGS analysis, and the entire gene is analyzed directly at the gene level. This approach allows us to identify the entire microbial cluster present in the sample and to reveal what metabolic processes and functions individual microorganisms are involved in the cluster.

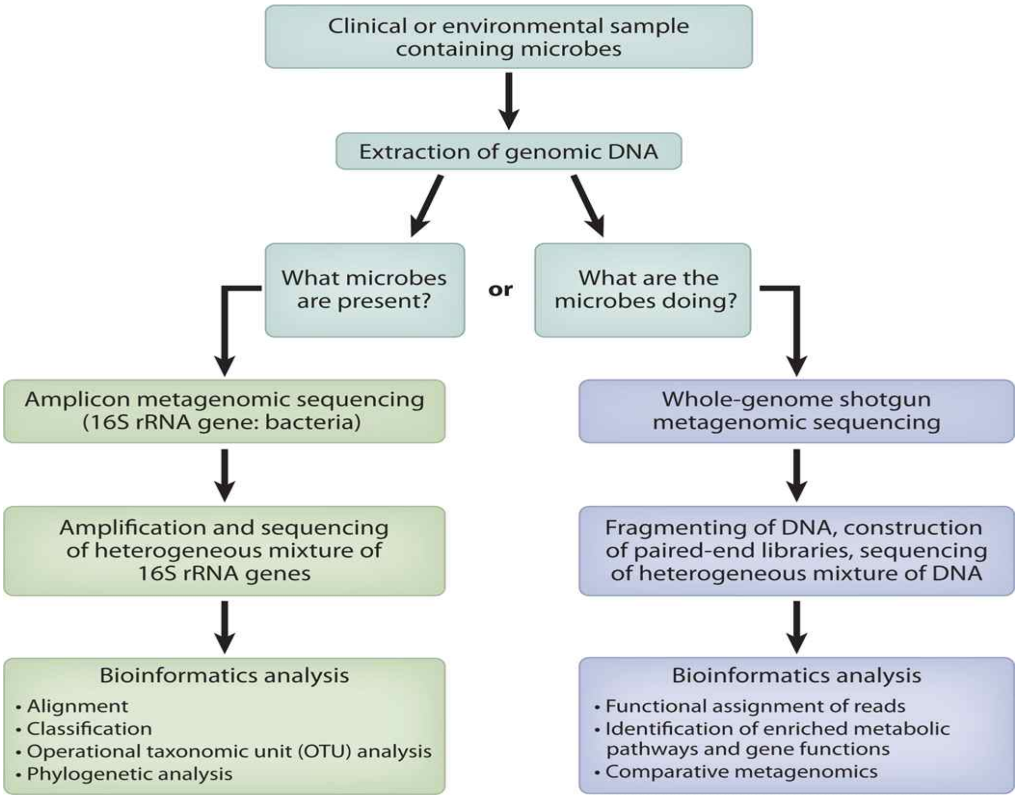


Fig. 1. 1. Workflow for metagenomic sequencing and analysis

For metagenome analysis, there are 16S rRNA amplicon sequencing that amplifies and analyzes 16S rRNA gene, and shotgun metagenome sequencing that sequencing all genes in environmental samples. In the case of 16S rRNA amplicon sequencing, only the composition of the strain in the environment can identify, and it is difficult to identify the functional aspects of the microbial community. However, the shotgun metagenome sequencing can analyze the functional aspects as well as the composition of strains of the cluster but has the disadvantage of high analytical amount and cost.

The basic principle of NGS platform is like each other, but it has different characteristics for each platform due to differences in the method of detecting the base sequence, and there are typically 454 Roche Pyrosequencing, Illumina sequencing, and PacBio SMRT. Among them, Illumina MiSeq is the most used platform for metagenome analysis. The analysis method of the Illumina MiSeq platform extracts total DNA from the sample and attaches the adapter using PCR according to the sequencing platform, which is called library preparation. Next, the library is expanded in the flow cell to make a complementary bond with the oligonucleotide attached to the flow cell. After that, the DNA is amplified to form a cluster and sequencing is performed. As described above, the Illumina MiSeq platform has the advantage of being able to rapidly analyze many DNA sequences, but has the disadvantage that the length of the readable gene is short, about 300 bp. Therefore, it is difficult to analyze the entire sequence of the entire 1,500 bp of 16S rRNA gene. However, within the 16S rRNA gene, there are 9 hypervariable regions that can have different sequences at the level of genus or species. Based on this, differences in specific hypervariable regions can be analyzed through bioinfromatics program (16S rRNA gene sequence DB such as SILVA, GreenGees, EzBioCloud) to analyze the composition of the microbial community.

As described above, the taste and function of fermented foods are determined not only by raw materials, but also by microbiome made in the manufacturing process, but research on the unique microbiome of each fermented food is currently insignificant. Therefore, in order to globalize traditional fermented foods in Korea, fermented foods should manufacture in a scientific and systematic way in connection with microbiome research, and a system is needed to build a standardized database.

Fermented anchovy sauce, Myeolchi-Akjeot, was made in Chuja island, a representative traditional fermented food of Jeju Island, which is listed as a World Natural Heritage, is a fermented food that many people enjoy. The purpose of this study is to identify the microbial community of fermented anchovy sauce, which is a traditional fermented food, by using the NGS platform and to isolate and characterize the bacteria present in the fermented anchovy sauce. Through this, we will be able to identify all the bacteria present in the fermented anchovy sauce and use it as a basic data for discovering fermented seed representing Jeju. In addition, we intend to isolate new strains and secure species diversity that can cope with the implementation of the Nagoya Protocol.

Chapter Ⅱ. Study of bacterial community in Fermented anchovy sauce, Myeolchi-Aekjeot of Chuja Island

2.1. Introduction

The words that *Jeotgal*, *Jeot*, and *Aekjeot*, mean fermented seafoods in Korea. They are made by a fermentation process for a long time using various marine organisms as anchovy, shellfish, squid, shrimp, fish eggs, fish intestines, and oyster (Hur, 1996). In Korea, these are individual dish, as well as additive for improving the taste of foods. It is made by adding 20-30% salt to various seafood and through fermentation. Salted-fermented seafoods produce distinctive flavors and tastes because of the fermentation products of diverse microorganisms during the fermentation (Lee *et al.*, 2014). According to the main raw materials and detailed manufacturing methods, there are about 150 types of fermented seafood in Korea (Hur, 1996).

Chuja Island became famous for anchovy, it is because when a spawning season of anchovy, many anchovies gather in Chuja island. At the time, the anchovy taste good because they are full of eggs and are caught via nets so anchovies get the highest rating and can stay fresh. Due to these conditions, in Chuja Island used anchovies to make salted anchovy sauce that can be used instead of soy sauce. The anchovy sauce for the Chuja Island is made by mixing salt and anchovies without adding any chemical seasoning and fermenting them for about three years. This MyeolchI- Aekjeot, traditional fermented anchovy sauce, has been consumed as an umami-tasting, seasoning ingredient (Moon *et al.*, 2013). The umami of Myeolchi-Aekjeot is formed by exogenous enzymes of microorganisms (Yongsawatdigul *et al.*, 2007), and despite the high concentration (20-30%) of salty environment, various microorganisms exist in fish sauces (Margesin *et al.*, 2001). Therefore, with NGS technique, we want to find out the various microorganisms that exist in the fermented anchovy sauce of Chuja Island.

2.2. Materials and methods

2.2.1. Collected sample and characteristic analysis

The fermented anchovy sauce (Myeolchi-Aekjeot) made by Chujado Federation of Fisheries Cooperatives in Jeju. The pH, percentage of salt, and sugar content were measured to find out the environment in the fermented anchovy sauce. The measuring equipment is as follows: pH meter (Orion Star A211, Thermo scientific, USA), Brix meter (PAL-1, ATAGO, Japan), Salt meter (PAL-03S, ATAGO, Japan).

Fig. 2. 1. Fermented anchovy sauce, Myeolchi-Aekjeot.

2.2.2. Bacterial community analysis

16S rRNA sequences of bacteria were amplified using universal primers of the Illumina protocol targeting the V3-V4 region (www.illumina.com, 16S Metagenomic Sequencing Library Preparation). The amplicons were sequenced using the Illumina Miseq platform with Miseq Reagent Kit v2 (500 cycles) and a 2 × 250 bp paired-end protocol.

For MiSeq sequencing analysis, total DNA of fermented anchovy sauce was extracted using FastDNA Spin Kit for soil (MP biomedicals, USA) by following the manufacturer′s protocol. Extracted DNA concentration and quality were determined by 1% agarose gel electrophoresis and spectrophotometry using Epoch Spectrometer (BioTek, USA).

Polymerase chain reaction (PCR) amplification was performed using primer targeting of the V3 to V4 hypervariable regions (468 bp) of the 16S rRNA gene of extracted DNA. For bacterial amplification, primers were V3-341F (5′-CCTACGGGNGGCWGCAG-3’) and V4-805R (5′-GAC TACHVGGGTATCT AATCC-3′) (Fadrosh *et al*., 2014). PCR reaction mixture included 10×Ex Taq Buffer (Takara, Japan), dNTP mixture (Takara, Japan), forward and reverse primer (10 pmole/μL), Ex Taq DNA polymerase (Takara, Japan) and extracted DNA, in a final volume of 25 μL. The amplifications of 16S rRNA gene were carried out using an initial denaturation at 95 ℃ for 3 minutes, followed by 25 cycles of denaturation at 95 ℃ for 30 seconds, primer annealing at 55 ℃ for 30 seconds, and extension at 72 ℃ for 30 seconds, with a final elongation at 72 ℃ for 5 minutes. PCR product was confirmed using 1% agarose gel electrophoresis with a 0.5×TAE buffer, and visualized using a Gel Doc system (BioRad, USA).

Table. 2. 1. Composition of first PCR reaction mixture.

Reagent	Volume	
10×buffer	2.5	㎕
dNTP	2.5	㎕
341F primer	1.0	㎕
805R primer	1.0	㎕
Taq polymerase	0.25	㎕
Extracted DNA	2.0	㎕
Distilled warer	15.75	㎕
Total	25.0	㎕

Table. 2. 2. Condition of first PCR reaction.

Step	℃	minute	cycle
Initial denaturation	95	3:00	
Denaturation	95	0:30	25
Annealing	55	0:30	
Extension	72	0:30	
Final extension	72	5:00	
Hold	4	∞	

The PCR product was used as a template in the secondary PCR (Index PCR). This step attaches duel indices and Illumina sequencing adapters using the Nextera XT Index Kit (DNA Library prep kit; Illumina, USA). Index forward primer i5 (5'-AATGATACGGCGACCACCGAGATCTACAC-XXXXXXXX-TCGTCGGCAGCGTC-3'; X indicates the barcode region) and index reverse primer i7 (5'-CAAGCAGAAGACGGCATACGAGAT-XXXXXXXX-GTCTCGTGGGCTCGG-3'; X indicates the barcode region) were used for secondary amplification conducted to attach the Illumina NexTera barcode. PCR reaction mixture included 10×Ex Taq Buffer (Takara, Japan), dNTP mixture (Takara, Japan), forward and reverse primer (10 pmole/μL), Ex Taq DNA polymerase (Takara, Japan) and first PCR product, in a final volume of 25 μL. The amplifications were carried out using an initial denaturation at 95 ℃ for 3 minutes, followed by 8 cycles of denaturation at 95 ℃ for 30 seconds, primer annealing at 55 ℃ for 30 seconds, and extension at 72 ℃ for 30 seconds, with a final elongation at 72℃ for 5 minutes. The PCR product was confirmed using 1% agarose gel electrophoresis. The amplified products were purified and short fragments (non-target products) were removed with the CleanPCR (CleanNA). Final DNA libraries were quantified by Quanti-iT PicoGreen dsDNA Assay kit (Invitrogen, USA). Quality and product size were assessed on a Bioanalyzer 2100 (Agilent, USA) using a DNA 7500 chip (Agilent, USA). Finally, identical quantities of PCR product were pooled and the pooled amplicons were sequenced using the Illumina MiSeq platform with MiSeq Reagent Kit v2 (500 cycles; Illumina, USA) and 2×250 bp paired-end protocol. The above preparation and sequencing processes were conducted at ChunLab Inc. (Korea) using an Illumina MiSeq sequencing system following the manufacturer's instructions.

For bacterial community analysis, the raw sequences were analyzed through the Microbiome Taxonomic Profiling Pipeline in EzBioCloud (https://www.ezbiocloud.net). Paired-end reads were filtered by quality (Q<25) (Bolger *et al.*, 2014), and merged using PANDAseq software (Masella *et al.*, 2012). Primers are then trimmed with Chunlab's in-house program at a similarity cut off of 0.8. A denoising step was conducted using Dude-seq software with 0.5% error-correction criteria (Lee *et al*, 2017), and non-redundant reads are extracted by UCLUST-clustering (Edgar 2010). After denoising and dereplication, the taxonomic assignment of sequences was performed using USEARCH (Edgar 2010) with a 97% similarity cut-off for species level identification against the EzBioCloud 16S database. Cutoff values are obtained from Yarza *et al.* (Yarza *et al.*, 2014). Chimera sequences were removed using the UCHIME algorithm. Sequence data were clustered using CD-HIT (Fu *et al.*, 2012) and UCLUST (Edgar 2010). The Chao 1 estimation and Shannon (Shannon *et al.*, 1949) and Simpson (Simpson, 1949) indices were used to determine the richness and diversity.

2.3. Results and discussion

2.3.1. Characteristics of sample

The fermented anchovy sauce, Myeolchi-Aekjeot, made by Chujado Federation of Fisheries Cooperatives in Jeju, the pH, percentage of salt, and sugar content were measured to find out the environment in the fermented anchovy sauce. The results showed that environment of the fermented anchovy sauce were pH 6.1, 27% of salinity and 37.9 brix (Table 2. 3.). According to Lee (Lee et al., 2016), the pH range of anchovy fish sauce prepared in nine regions of Korea, such as Jeon-nam, Chung-nam, Jeon-buk, and Gyeong-buk, was 5.4-6.5, and the salinity range was 20-26%. It was found that Chuja island's fermented anchovy sauce also has similar physical characteristics to other regions.

Table. 2. 3. Characteristic of fermented anchovy sauce.

Feature	value
pH	6.1
Salinity (%)	27.0
Sugar content (Brix)	37.9

2.3.2. Sequencing results and diversity indices

To identify bacterial community, bacterial DNA was extracted from the fermented anchovy sauce and analyzed by an Illumina MiSeq platform. The Table. 2. 4. shows the sequencing results of bacterial community, including the OTU numbers, Chao1 estimation, and alpha diversity tests, such as Good’s coverage, and the Shannon and Simpson indices. After filtering out low-quality and short sequence reads, the total reads of 39,880 were obtained from the total DNA of fermented anchovy sauce, Myeolchi-Aekjeot. The OTUs for bacteria obtained from the 97% sequence similarly cut-off values were 340. The observed OTUs were comparable to the Chao1-estimated values, suggesting that most of the phylotypes present in the samples were detected. This result suggests that it can fully represent the bacterial community of the sample. Chao1 is an indicator of species richness (total number of species in a sample) that is sensitive to rare OTUs. Higher values indicate higher diversity (Chao, 1987). The Good’s coverage of bacterial community was 99.9%, and the rarefaction curve reached the saturation phases (Fig. 2. 2). The Good’s coverage is an index of the extent to which the number of sequencing reads used for analysis represents the actual species population of the sample. The value can range from 0 to 100%, with 100% indicating a complete sampling of species, meaning that additional sequencing is unlikely to find anymore new species (Good, 1953). The rarefaction curve is a graph that expresses species diversity by plotting the correlation between the size of the sample data and the number of OTUs. The x-axis represents the number of sampled reads, and the y-axis represents the number of OTUs discovered. In general, as the number of reads increases, the number of OTUs converges to the maximum value.

The steeper the slope of the curve, the higher the species diversity (Heck *et al.*, 1975). The community diversity of the sample was estimated using the Shannon and Simpson indices based on the OTUs. The higher the Shannon index, the more diverse the microbial community, while the opposite is true for the Simpson index. Shannon is an indicator of species evenness (proportional distribution of the number of each species in a sample) that exhibits values greater than 0, and higher values indicate higher diversity, and the maximum value is achieved when all species are present in equal numbers (Magurran, 2013). Simpson is an indicator of species evenness that displays the probability that two randomly selected sequences are of the same species. Values range from 0 to 1, and lower values indicate higher diversity (Magurran, 2013). ACE is an indicator of species richness (total number of species in a sample) that is sensitive to rare OTUs. Higher values indicate higher diversity (Chao *et al.*, 1992).

Table. 2. 4. Numbers of sequences, OTUs (97%) and diversity indexes.

Diversity indicator	value
Reads	36,376
OTUs	340
ACE	351.0 (342.7-360.0)
Shannon (LCI-HCI)	2.871 (2.854-2.889)
Simpson (LCI-HCI)	0.114 (0.112-0.116)
Chao1 (LCI-HCI)	342.7 (340.7-350.0)
Coverage (%)	99.9

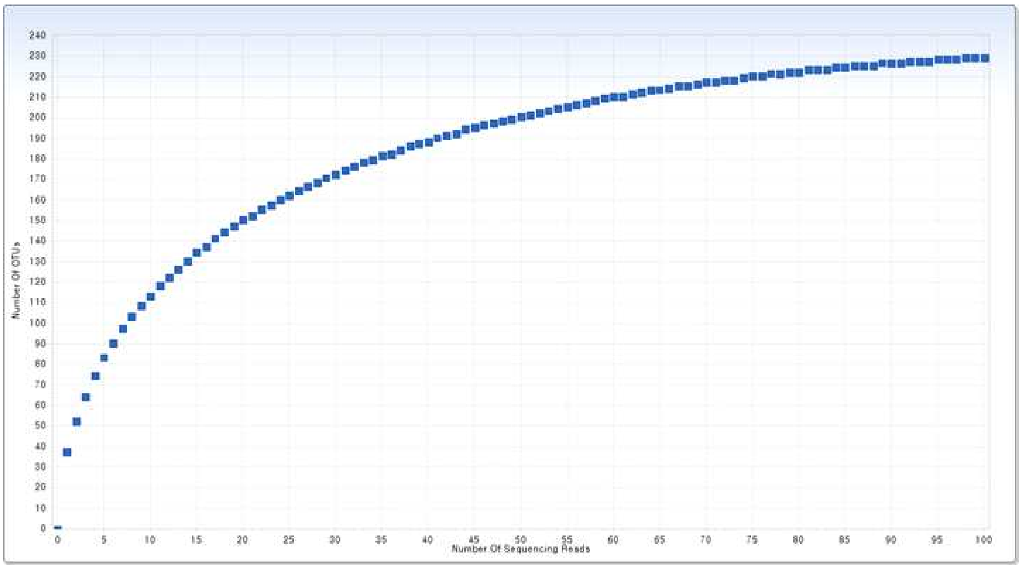


Fig. 2. 2. Rarefaction curve of diversity indicator.

2.3.3. Bacterial community in fermented anchovy sauce

To identify bacterial community, total DNA was extracted from fermented anchovy sauce of Chuja island and analyzed by an Illumina MiSeq platform. So total valid reads of 36,376 were obtained. Among total valid reads, reads of the species level was 19,661 reads (54%) and found 132 species.

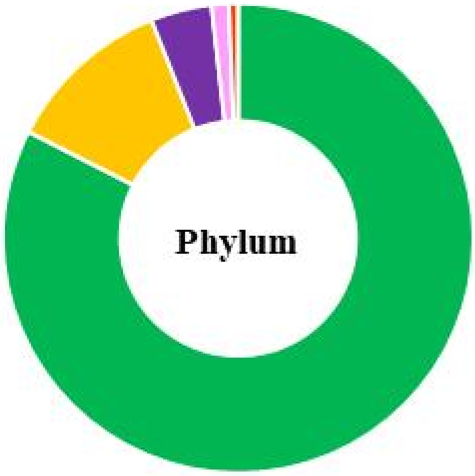
In results of analysis the bacterial community of fermented anchovy sauces of Chuja island, bacteria of phylum *Firmicutes* (82.5%) dominated at sample. And the Class *Bacilli* (76.4%), Order *Bacillales* (64.6%), Family *Bacillaceae* (64.3%) were the dominant in taxon, respectively. At the Genus level, the sample were dominated *Lentibacillus* (46.4%), *Tetragenococcus* (11.7%), and *Pseudogracilibacillus* (10.6%). The results of the analysis of the bacterial community of fermented anchovy sauce are shown below for each taxon.

Although there is no study on analyzed the bacterial community of fermented anchovy sauce in Jeju region, the results of the analysis of the bacterial community in 9 types of fermented anchovy sauce in Chung-nam, Jeon-nam, Jeon-buk, and Gyeong-buk regions of Korea showed that unlike the results of this study, the bacteria of genus *Tetragenococus* and *Halanaerobium* in phylum *Firmicutes* were dominant in all samples (Lee *et al.*, 2016). And study of analyzed the bacterial community of fermented anchovy salted fish (Myeolchi-Jeotgal) in jeju region, genus *Tetragenococcus* (90%) in phylum *Firmicutes* were dominant (Song *et al.*, 2018). According to the results of these studies, including this study, it can be confirmed that all phylum *Firmicutes* dominate. This is thought to be because a large number of bacteria belonging to this taxon form endospores and have the ability to exist in extreme environments. In addition, it appears to be the result because it contains a large number of the fermentation-related bacteria in this taxon. The difference in the results of these studies is thought to be due to the fermentation period. The fermentation period of fermented anchovy sauce of Chuja island analyzed in this study is 3 to 5 years, but the fermentation period of other fermented anchovy sauces and fermented anchovy salted fish is about 1 year, which is short. Through this, At the beginning of fermentation, bacteria that actively participate in fermentation, such as bacteria of genus *Tetragenococus*, appeared predominantly, and at the latter period of fermentation, genus *Lentibacillus*, which has a late-growth characteristic, appears to be predominant. For this reason, it could be seen that the difference in dominant bacteria occurs over the fermentation period. In the future, if you conduct a bacterial community analysis by fermentation period of fermented anchovy sauce of Chuja island, we will see more accurate results. As a result of this analysis, it can be seen that fermented anchovy sauce of Chuja island is a well-fermented fish sauce. It is known that fish sauce such as fermented anchovy sauce, is rich in essential nutrients and tastes better with a longer fermentation period. It is thought that the presence of genus *Lentibacillus* in fish sauce can be used as an indicator of fermentation period.

The genus *Lentibacillus* which appeared to dominate in fermented anchovy sauce of Chuja island, was first reported in 2002, and to date 19 species have been discovered. Bacteria of genus *Lentibacillus* has been reported to be present in salty conditions such as fermented food, and high salty sites in the natural environment (Yoon *et al.*, 2002; Namwong *et al.*, 2005; Tanasupawat *et al.*, 2006; Pakdeeto *et al.*, 2007; Jung *et al.*, 2010; Jung *et al.*, 2015; Oh *et al.*, 2016; Sundararaman *et al.*, 2018; Oh *et al.* 2020; Jeon *et al.*, 2005; Lim *et al.*, 2005; Yuan *et al.*, 2007; Lee *et al.*, 2008; Sanchez-Porro *et al.*, 2010; Lee *et al.*, 2008; Wang *et al.*, 2016; Guo *et al.*, 2017). But no research has been conducted on their efficacy yet. Bacteria of the genus *Lentibacillus* living in extreme conditions such as a high-salt environment seem to apparently have special properties that can be used in the bio-industry, and further studies such as genomic analysis and efficacy studies are needed to find these properties.

1) Community of Phylum level

In the fermented anchovy sauce, total 13 phyla were identified at the Phylum level. Among the bacterial phyla, the majority of sequences were assigned to *Firmicutes* (82.5%), and this followed by *Proteobacteria* (11.5%), *Cyanobacteria* (4.2%), *Actinobacteria* (1.2%), *Rhodothermaeota* (0.3%), *Bacteroidetes* (0.2%), *Acidobacteria* (0.07%), *Saccharibacteria* (0.04%), *Nitrospirae* (0.02%), *Chlamydiae* (0.01%), *Fusobacteria* (0.01%), *Planctomycetes* (0.01%), and *Tenericutes* (0.01%). The members of rare phyla, for which the abundance was less than 1.0% of all identified sequences were classified as Other, and accounted for 0.6% of the total bacterial community (Fig. 2. 3.).

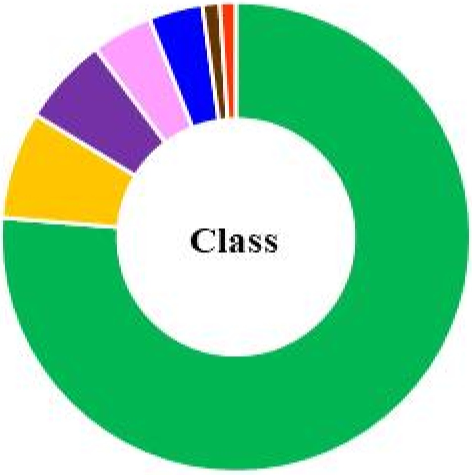


🟩	Phylum	*Firmicutes*	82.5%
🟨	Phylum	*Proteobacteria*	11.5%
🟪	Phylum	*Cyanobacteria*	4.2%
■	Phylum	*Actinobacteria*	1.2%
🟥		Others	0.6%

Fig. 2. 3. The diversity at Phylum level.

2) Community of Class level

Total 25 classes were identified at the Class level. Among the bacterial classes, the majority of sequences were assigned to *Bacilli* (76.4%), and this followed by *Betaproteobacteria* (7.4%), Clostridia (6.1%), PAC001562_c (4.2%), *Gammaproteobacteria* (3.7%), and *Actinobacteria* (1.2%). The members of rare classes, for which the abundance was less than 1.0% of all identified sequences were classified as Other, and accounted for 1.1% of the total bacterial community (Fig. 2. 4.). In result of analysis, the classes less than 1.0% appeared as *Alphaproteobacteria, Balneolia, Sphingobacteriia, Bacteroidia, Solibacteres, Saccharimonas, Rubrobacteria, Holophagae, Flavobacteria, Negativicutes, Tissierellia, Nitrospira, Erysipelotrichi, Chlamydiae, Fusobacteria, Epsilonproteobacteria, Mollicutes*, PAC001018_c, and *MarineActino*_c.

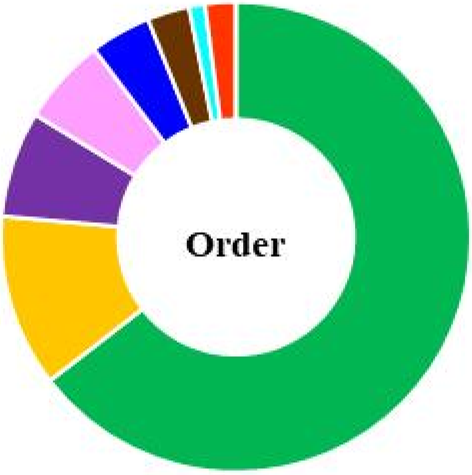


🟩	Class	*Bacilli*	76.4%
🟨	Class	*Betaproteobacteria*	7.4%
🟪	Class	*Clostridia*	6.1%
■	Class	PAC001562_c	4.2%
🟦	Class	*Gammaproteobacteria*	3.7%
🟫	Class	*Actinobacteria*	1.2%
🟥		Others	1.1%

Fig. 2. 4. The diversity at Class level.

3) Community of Order level

Total 42 orders were identified at the Order level. Among the bacterial orders, the majority of sequences were assigned to *Bacillales* (64.6%), and this followed by *Lactobacillales* (11.9%), *Burkholderiales* (7.3%), *Halanaerobiales* (6.0%), PAC001562_o (4.2%), *Oceanospirillales* (2.9%), and *Micrococcales* (1.1%). The members of rare orders, for which the abundance was less than 1.0% of all identified sequences were classified as Other, and accounted for 2.1% of the total bacterial community (Fig. 2. 5.). In result of analysis, the classes less than 1.0% appeared as *Alphaproteobacteria*, *Balneolia, Sphingobacteriia, Bacteroidia, Solibacteres, Saccharimonas, Rubrobacteria, Holophagae, Flavobacteria, Negativicutes, Tissierellia, Nitrospira, Erysipelotrichi, Chlamydiae, Fusobacteria, Epsilonproteobacteria, Mollicutes*, PAC001018_c, and *MarineActino*_c.

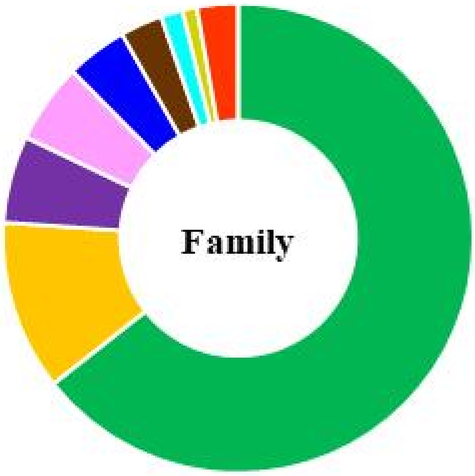


■	Order	Bacillales	64.6%
■	Order	Lactobacillales	11.9%
■	Order	Burkholderiales	7.3%
■	Order	Halanaerobiales	6.0%
■	Order	PAC001562_o	4.2%
■	Order	Oceanospirillales	2.9%
■	Order	Micrococcales	1.1%
■		Others	2.1%

Fig. 2. 5. The diversity at Order level.

4) Community of Family level

Total 65 families were identified at the Family level. Among the bacterial families, the majority of sequences were assigned to *Bacillaceae* (64.3%), and this followed by *Enterococcaceae* (11.7%), *Halanaerobiaceae* (6.0%), Ralstonia_f (5.5%), PAC001562_f (4.2%), *Halomonadaceae* (2.9%), *Burkholderiaceae* (1.5%), *Brevibacteriaceae* (1.0%) and others (2.8%) (Fig. 2. 6.). The members of rare families, for which the abundance was less than 1.0% of all identified sequences were classified as Others. In result of analysis, the families less than 1.0% appeared as *Staphylococcaceae, Balneolaceae, Moraxellaceae, Vibrionaceae, Comamonadaceae, Marinobacter, Bradyrhizobiaceae, Chitinophagaceae, Phyllobacteriaceae, Streptococcaceae, Corynebacteriaceae, Rhodospirillaceae, Neisseriaceae,* PAC000121_f, *Prevotellaceae, Alcanivoracaceae, Pseudomonadaceae, Sphingomonadaceae, Xanthomonadaceae, Saccharimonas, Carnobacteriaceae,* GU199451_f, *Porphyromonadaceae, Gaiellaceae, Salinisphaeraceae, Brucellaceae, Phreatobacter, Dermabacteraceae, Holophagaceae, Actinomycetaceae, Flavobacteriaceae, Nitrospiraceae, Selenomonadaceae, Tissierellaceae, Gottschalkiaceae, Caulobacteraceae, Erysipelotrichaceae, Lachnospiraceae, Micrococcaceae, Rhabdochlamydiaceae, Campylobacteraceae, Leptotrichiaceae, Mycoplasmataceae, Peptostreptococcaceae*, PAC001018_f, *Bosea, Mogibacterium,* PAC001921_f, *Actinomarinaceae, Alteromonadaceae, Fusobacteriaceae, Lactobacillaceae, Muribaculaceae, Rhodobacteraceae,* AHBI_f, *Lautropia,* and PAC002248_f.

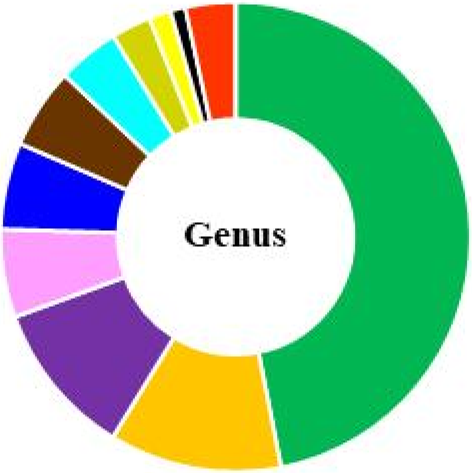


🟩	Family	*Bacillaceae*	64.3%
🟨	Family	*Enterococcaceae*	11.7%
🟪	Family	*Halanaerobiaceae*	6.0%
🟪	Family	*Ralstonia*	5.5%
🟦	Family	PAC001562_f	4.2%
🟫	Family	*Halomonadaceae*	2.9%
🟦	Family	*Burkholderiaceae*	1.5%
🟨	Family	*Brevibacteriaceae*	1.0%
🟥		Others	2.8%

Fig. 2. 6. The diversity at Family level.

5) Community of Genus level

Total 84 genera were identified at the Genus level. Among the bacterial genera, the majority of sequences were assigned to *Lentibacillus* (46.4%), and this followed by *Tetragenococcu*s (11.7%), *Pseudogracilibacillus* (10.6%), *Halanaerobium* (6.0%), *Jilinibacillus* (5.9%), *Ralstonia* (5.5%), PAC001562_g (4.2%), *Halomonas* (2.7%), *Paraburkholderia* (1.5%), *Brevibacterium* (1.0%) and others (3.4%) (Fig. 2. 7.). The members of rare genera, for which the abundance was less than 1.0% of all identified sequences were classified as Others. In result of analysis, the genera less than 1.0% appeared as *Virgibacillus, Staphylococcus, Fodinibius, Chromohalobacter, Marinobacter, Pelomonas, Acinetobacter, Vibrio, Bradyrhizobium, Enhydrobacter, Photobacterium, Mesorhizobium, Streptococcus, Corynebacterium, Sediminibacterium, Neisseria,* .PAC000121_g, *Prevotella, Alcanivorax, Pseudomonas, Rhodoplanes, Saccharimonas, Sphingomonas, Stenotrophomonas, Atopostipes, Curvibacter, Psychrobacter, Corticicoccus, Halovibrio, Porphyromonas,* EU801583_g, *Gaiella, Salinisphaera,* AF407727_g, *Brucellaceae,* PAC001999_g, *Phreatobacter, PAC001882_g, Brachybacterium. Holophaga, Actinomyces, Aquabacterium, Nitrospira, Selenomonas, Tissierella, Ornithinibacillus, Brevundimonas, Bulleidia, Flavobacterium, Campylobacter, Cerasibacillus, Lachnoanaerobaculum, Peptostreptococcus, Sneathia, Mycoplasma,* PAC001018_g, *Bosea, Kocuria, Rothia, Eubacterium,* PAC002583_g*, Actinomarina, Alteromonas, Bergeyella, Capnocytophaga, Cetobacterium, Dinoroseobacter, Lactobacillus, Lautropia, Oribacterium, Vagococcus, AHBI_g, PAC001286_g, PAC002248_g.*

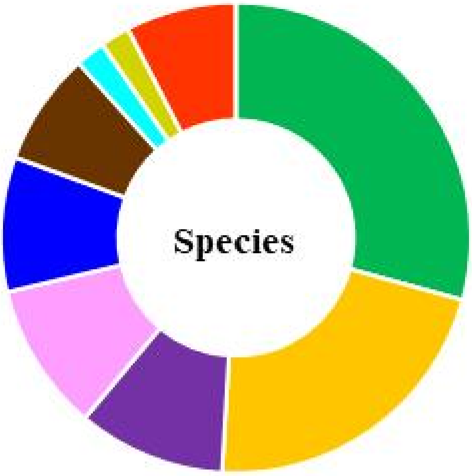


🟩	Genus	*Lentibacillus*	46.4%
🟧	Genus	*Tetragenococcus*	11.7%
🟪	Genus	*Pseudogracilibacillus*	10.6%
■	Genus	*Halanaerobium*	6.0%
🟦	Genus	*Jilinibacillus*	5.9%
🟫	Genus	*Ralstonia*	5.5%
■	Genus	PAC001562_g	4.2%
🟨	Genus	*Halomonas*	2.7%
🟨	Genus	*Paraburkholderia*	1.5%
⬛	Genus	*Brevibacterium*	1.0%
🟥		Others	3.4%

Fig. 2. 7. The diversity at Genus level.

5) Community of Species level

Total 132 species were identified at the Species level. Among the bacterial species, the majority of sequences were assigned to *Lentibacillus kimchii* (15.8%), and this followed by *Tetragenococcus muriaticus* (11.7%), *Ralstonia pickettii* (5.5%), *Halanaerobium fermentans* (5.5%), *Pseudogracilibacillus FJ380155_s* (5.0%), *PAC001562_g PAC001562_s* (4.2%), *Paraburkholderia caledonica* (1.1%), and *Halomonas garicola* (1.1%). The members of rare species, for which the abundance was less than 1.0% of all identified sequences were classified as Other, and accounted for 4.1% of the total bacterial community (Fig. 2. 8.). In result of analysis, the classes less than 1.0% appeared as *Paraburkholderia kururiensis, Halanaerobium saccharolyticum* group, *Staphylococcus aureus* group, *Virgibacillus* DQ842544_s, *Chromohalobacter beijerinckii* group, *Brevibacterium iodinum* group, *Marinobacter piscensis, Pelomonas saccharophila* group, *Halanaerobium praevalens, Bradyrhizobium japonicum* group, *Enhydrobacter aerosaccus* group, *Halomonas alimentaria, Lentibacillus salinarum, Paraburkholderia insulsa, Mesorhizobium loti* group, *Acinetobacter ursingii, Photobacterium leiognathi, Lentibacillus* FJ429315_s, *Halomonas venusta* group, *Sediminibacterium* FR853543_s, *Acinetobacter lwoffii* group, PAC000121_g PAC001780_s, *Paraburkholderia silvatlantica, Pseudomonas fulva* group, *Sphingomonas pruni* group, *Stenotrophomonas maltophilia* group, *Rhodoplanes* PAC002000_s, *Tetragenococcus halophilus* group, *Psychrobacter faecalis* group, *Saccharimonas* HQ697702_s, *Corticicoccus populi, Staphylococcus saprophyticus* group, *Vibrio alginolyticus* group, *Brevibacterium avium, Corynebacterium ammoniagenes, Corynebacterium glyciniphilum, Prevotella oris, Pseudomonas halophila,, Vibrio halioticoli* group, EU801583_g EU801583_s, *Gaiella occulta, Salinisphaera japonica, Brucellaceae* group, *Neisseria perflava, Pseudogracilibacillus* JX133320_s, PAC001999_g PAC001999_s group, *Halanaerobium congolense, Porphyromonas pasteri, Streptococcus pneumoniae* group, AF407727_g JF266208_s, PAC001882_g PAC001882_s, Phreatobacter PAC001949_s, *Brachybacterium faecium* group, *Vibrio sagamiensis, Curvibacter* CP015698_s, *Holophaga* EF562076_s, *Brevibacterium picturae* group, *Curvibacter lanceolatus, Neisseria subflava, Photobacterium angustum, Nitrospira* AY532586_s, *Aquabacterium* JRKM_s, *Paraburkholderia ferrariae, Streptococcus anginosus* group, *Brevundimonas vesicularis* group, *Bulleidia extructa, Flavobacterium antarcticum, Prevotella melaninogenica, Streptococcus salivarius* group, *Selenomonas* CP012071_s, *Campylobacter concisus* group, *Mycoplasma salivarium, Peptostreptococcus stomatis* group, *Porphyromonas endodontalis, Sneathia sanguinegens, Cerasibacillus BAXM_s* group, *Lachnoanaerobaculum* JH815185_s group, *Actinomyces* KE952139_s, *Acinetobacter proteolyticus* group, *Alcanivorax marinus, Bosea minatitlanensis* group, *Corynebacterium durum, Eubacterium brachy, Kocuria rhizophila* group, *Photobacterium phosphoreum* group, *Selenomonas sputigena, Streptococcus parasanguinis* group, *Streptococcus sanguinis* group, *Streptococcus sinensis* group, *PAC002583_g AM990454_s, Saccharimonas* CP007496_s, *Actinomyces* LT635457_s group, *Actinomyces odontolyticus, Alteromonas stellipolaris* group, *Brevibacterium linens, Capnocytophaga leadbetteri, Cetobacterium ceti, Dinoroseobacter shibae, Lactobacillus plantarum* group, *Lautropia mirabilis, Neisseria sicca* group, *Oribacterium sinus, Prevotella oulorum, Prevotella veroralis, Rothia aeria, Vagococcus teuberi* group, *Vibrio antiquarius, Virgibacillus siamensis,* AHBI_g AHBI_s group, PAC002248_g DQ395705_s, AF407727_g EU133389_s, PAC001286_g JF803519_s, *Pseudogracilibacillus* JX001242_s, *Rothia* KV831974_s group, *Bergeyella* PAC001338_s*, and Actinomarina* U70710_s.



■	*Lentibacillus kimchii*	15.8%
■	*Tetragenococcus muriaticus*	11.7%
■	*Ralstonia pickettii*	5.5%
■	*Halanaerobium fermentans*	5.5%
■	*Pseudogracilibacillus* FJ380155_s	5.0%
■	PAC001562_g PAC001562_s	4.2%
■	*Paraburkholderia caledonica*	1.1%
■	*Halomonas garicola*	1.1%
■	Others	4.1%

Fig. 2. 8. The diversity at Species level.

2.4. Conclusion

Chuja Island became famous for anchovy, it is because when a spawning season of anchovy, many anchovies gather in Chuja island. In Chuja Island used anchovies to make salted anchovy sauce that can be used instead of soy sauce. The anchovy sauce for the Chuja Island is made by mixing salt and anchovies without adding any chemical seasoning and fermenting them for about three years. This MyeolchI-Aekjeot, traditional fermented anchovy sauce, has been consumed as a umami-tasting, seasoning ingredient (Moon *et al.*, 2013). The umami of Myeolchi-Aekjeot is formed by exogenous enzymes of microorganisms (Yongsawatdigul *et al.*, 2007), and despite the high concentration (20-30%) of salty environment, various microorganisms exist in fish sauces (Margesin *et al.*, 2001). Therefore, with NGS technique, we found out the various microorganisms that exist in the fermented anchovy sauce of Chuja Island.

The fermented anchovy sauce, Myeolchi-Aekjeot, of Chuja island, which was used for the analysis of bacterial communities, was made by Chujado Federation of Fisheries Cooperatives in Jeju. It showed pH 6.1, 27% salinity, and 37.9 brix.

To identify bacterial community, total DNA was extracted from fermented anchovy sauce and analyzed by an Illumina MiSeq platform. So total valid reads of 36,376 were obtained. Among total valid reads, reads of the species level was 19,661 reads (54%) and found 132 species.

In results of analysis the bacterial community of fermented anchovy sauce of Chuja island, bacteria of phylum *Firmicutes* (82.5%) dominated at sample. And the Class *Bacilli* (76.4%), Order *Bacillales* (64.6%), Family *Bacillaceae* (64.3%) were the dominant in taxon, respectively. At the

Genus level, the sample were dominated *Lentibacillus* (46.4%), *Tetragenococcus* (11.7%), and *Pseudogracilibacillus* (10.6%).

When comparing the results of a study that analyzed the bacterial community between fermented anchovy sauce in other regions and anchovy salted fish (Myeolchi-Jeotgal) in Jeju, it was found that the dominant bacteria are different. In this study, the genus *Lentibacillus* was predominant, and the genus *Tetragenococus* was predominant in the fermented anchovy sauce in other regions and anchovy salted fish (Myeolchi-Jeotgal) in Jeju. This difference seems to have appeared depending on the fermentation period. The fermentation period of fermented anchovy sauce of Chuja island is about 3 to 5 years, and the fermentation period of fermented anchovy sauce in other regions and anchovy salted fish (Myeolchi-Jeotgal) in Jeju is less than one year. At the beginning of fermentation, bacteria that actively participate in fermentation, such as bacteria of genus *Tetragenococus*, appeared predominantly, and at the latter period of fermentation, genus *Lentibacillus*, which has a late-growth characteristic, appears to be predominant. For this reason, it could be seen that the difference in dominant bacteria occurs over the fermentation period.

In the future, if you conduct a bacterial community analysis by fermentation period of fermented anchovy sauce of Chuja island, we will see more accurate results. As a result of this analysis, it can be seen that fermented anchovy sauce of Chuja island is a well-fermented fish sauce. It is known that fish sauce such as fermented anchovy sauce, is rich in essential nutrients and tastes better with a longer fermentation period. It is thought that the presence of genus *Lentibacillus* in fish sauce can be used as an indicator of fermentation period.

Chapter Ⅲ. Polyphasic taxonomy of novel bacterium isolated from Fermented anchovy sauce, Myeolchi-Aekjeot of Chuja Island

3.1. Introduction

3.1.1. The Taxonomy of Bacteria

The classification of bacteria is called bacterial taxonomy. Bacterial taxonomy comprises the interrelated areas of classification, nomenclature, and identification and is supposed to reflect phylogeny and evolution. Classification refers to the arrangements of bacteria into groups or taxa on the basis of their mutual similarity or evolutionary relatedness. Nomenclature is the discipline concerned with the assignment of names to taxonomic groups as per published rules. Identification represents the practical side of taxonomy, which is the process of determining that a particular isolate belongs to a recognized taxon. Species is the basic taxonomic group in bacterial taxonomy. Groups of species are then collected into genus. Groups of genus are collected into family, family into order, order into class, class into phylum. Groups of bacteria at each rank or level have names with endings or suffixes characteristic to that rank or level. Polyphasic taxonomy refers to a consensus type of taxonomy and aims to utilize all the available data in delineating consensus groups, decisive for the final conclusions. Several phenotypic characteristics (morphological, physiological and metabolic, ecological) and genetic analysis have been used in bacterial taxonomy for many years. These characteristics are assessed, and the data are used to group bacteria up to the taxonomic ladder from species to domain. Classical characteristics are quite useful in routine identification of bacteria and provide clues for phylogenetic relationships among them as well as with other organisms. (Vandamme *et al.*, 1996; Monique *et al.*, 2015).

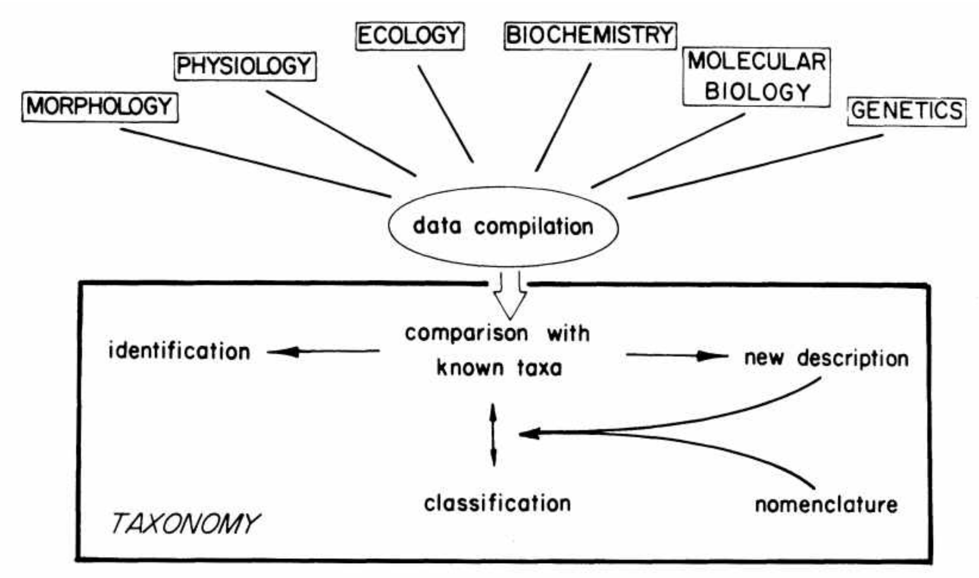


Fig. 3. 1. Flow of information in the characterization and classification of bacterial strain (Truper *et al.*, 1981).

3.1.2. Genus of *Lentibacillus*

The genus *Lentibacillus* was first proposed by Yoon *et al.* (2002) to accommodate an aerobic, Gram-variable, endospore-forming, rod-shaped and moderately halophilic bacterium isolated from a salt field of the Yellow Sea in Korea. Subsequently the description of the genus has been emended (Jeon *et al.*, 2005).

The genus *Lentibacillus* belongs to the family *Bacillaceae*, which currently contains 19 species (https://lpsn.dsmz.de/genus/lentibacillus; validly published, 17 species; not validly published 2 species, *Lentibacillus alimentarius*, *Lentibacillus cibarius*). The type species is *Lentibacillus salicampi*. The genus *Lentibacillus* includes Gram-variable rods that are catalase-positive, oxidase-variable and urease-negative. The cell-wall peptidoglycan contains meso-diaminopimelic acid, and the predominant menaquinone is MK-7. The major polar lipids are diphosphatidylglycerol and phosphatidylglycerol, and the major fatty acids are anteiso-$C_{15:0}$ and iso-$C_{16:0}$. The G+C content of the DNA of this genus is in the range 42-44 mol% (Jeon *et al.*, 2005).

Thus far, 18 species belonging to the genus *Lentibacillus* have been identified in a number of salty conditions such as fermented food (*Lentibacillus juripiscarius*, Namwong *et al.*, 2005; *Lentibacillus halophilus*, Tanasupawat *et al.*, 2006; *Lentibacillus kapialis*, Pakdeeto *et al.*, 2007; *Lentibacillus jeotgali*, Jung *et al.*, 2010; *Lentibacillus garicola*, Jung *et al.*, 2015; *Lentibacillus kimchii*, Oh *et al.*, 2016; *Lentibacillus alimentarius*, Sundararaman *et al.*, 2018; *Lentibacillus lipolyticus*, Booncharoen *et al.*, 2019; Lentibacillus cibarius, Oh *et al.* 2020), high salt sites in the natural environment (*Lentibacillus salarius*, Jeon *et al*., 2005; *Lentibacillus lacisals*, Lim *et al*., 2005; *Lentibacillus halodurans*, Yuan *et al*., 2007; *Lentibacillus salinarum*, Lee *et al*., 2008; *Lentibacillus persicus*, Sánchez-Porro *et al*., 2010), salt fileds (*Lentibacillus salicampi*, Yoon *et al*., 2002; *Lentibacillus salis*, Lee et al., 2008; *Lentibacillus amyloliquefaciens*, Wang *et al*., 2016; *Lentibacillus sediminis*, Guo et al., 2017), and 1 species belonging to the genus *Lentibacillus* have been identified in a poplar trees (*Lentibacillus populi*, Sun *et al*., 2016).

In genus *Lentibacillus*, genomic analysis among *Lentibacillus* species is currently lacking. But total of 9 genomes related to *Lentibacillus* species are published in NCBI, genome properties are indicated as following genome size (3,146,740-3,926,733 bp), CDSs (3,045-5,053), rRNA genes (10-30), and tRNA genes (50-86) (Oh *et al*., 2020).

In this study, strain JNUCC-1^T was characterized and classified and this study proposed that strain JNUCC-1^T isolated from fermented anchovy sauce in Chuja island is novel species via polyphasic taxonomy.

3.2. Materials and methods

3.2.1. Collected sample and isolation of bacteria

Bacteria was isolated from fermented anchovy sauce (Myeolchi-Aekjeot) made by Chujado Federation of Fisheries Cooperatives in Jeju. The anchovy sauce sample was diluted to 10^{-7}-fold with 0.85% NaCl through the serial dilution method. The sample was spread on Marine agar (MA; Difco 2216, USA) containing 5%, 10% and 15% NaCl and was incubated for 7 days at 30 ℃ under aerobic condition.

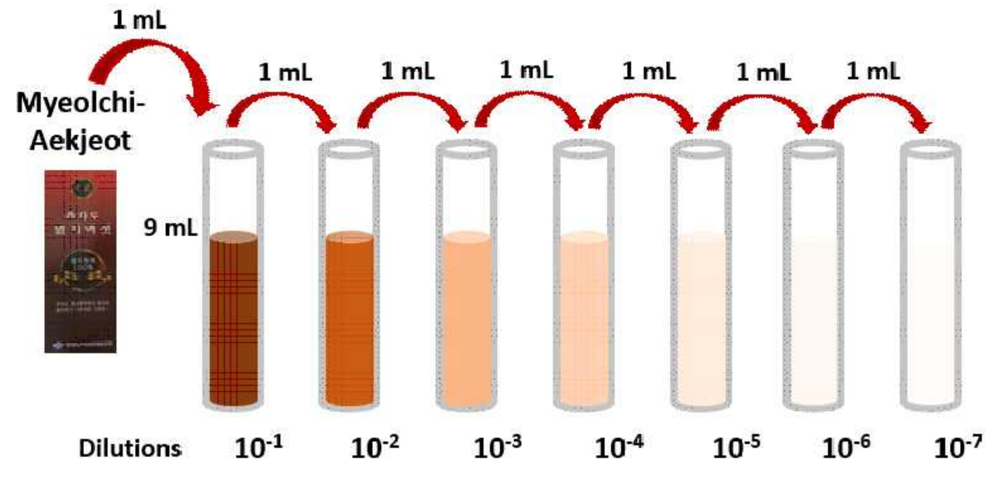


Fig. 3. 2. Serial dilution method.

Table. 3. 1. Composition of Marine agar (MA,; Difco 2216, USA).

Ingredient	Amounts	
Peptone	5.0	g
Yeast Extract	1.0	g
Ferric Citrate	0.1	g
Sodium Chloride	19.45	g
Magnesium Chloride	8.8	g
Magnesium Sulfate	3.24	g
Calcium Chloride	1.8	g
Potassium Chloride	0.55	g
Sodium Bicarbonate	0.16	g
Potassium Bromide	0.08	g
Strontium Chloride	34.0	mg
Boric Acid	22.0	mg
Sodium Silicate	4.0	mg
Sodium Fluoride	2.4	mg
Ammonium Nitrate	1.6	mg
Disodium Phosphate	8.0	mg
Agar	15.0	g
Distilled water	1.0	L
pH	7.6 ± 0.2	

3.2.2. Phylogenetic analysis

For the phylogenetic analysis, genomic DNA of strain was extracted using Chelex DNA Extraction Method. The 16S rDNA of strain was amplified and sequenced using the universal bacterial primer 27F and 1492R. Sequencing of purified 16S rDNA was performed by Solgent Inc. (Korea) using the BigDye Terminator v3.1 cycle sequencing kit (Applied Biosystems, USA) in an ABI 3730XL DNA analyzer (Applied Biosystems, USA).

The nearly complete 16S rRNA sequence was assembled using SeqMan program of DNAStar. Pairwise nucleotide similarity and identity of 16S rRNA gene sequences were calculated using EzBioCloud (https://www.ezbiocloud.net) and Basic Local Alignment Search Tool (https://blast.ncbi.nlm.nih.gov). Multiple alignments were performed by using the CLUSTAL *W* program (Thompson *et al*., 1994). Phylogenetic trees were generated using MEGA 7 with maximum-likelihood (ML), maximum-parsimony (MP), and neighbor-joining (NJ) algorithms (Kumar *et al*., 2016; Felsenstein, 1981; Saitou and Nei, 1987). The evolutionary distance matrices were calculated according to the algorithm of the Kimura's two-parameter model (Kimura, 1980) for the maximum-likelihood (ML) and neighbour-joining (NJ) method, and bootstrap analysis was performed with 1,000 random replicates (Felsenstein, 1985). The MP tree was obtained using the Subtree-Pruning-Regrafting (SPR) algorithm (Takahashi *et al*., 2000).

3.2.3. Whole genome sequencing and annotation

Genomic DNA was obtained from cells that had been cultivated for 5 days in Marine broth (MB; Difco 2216, USA) containing 5% NaCl using the FastDNA Spin kit for soil (MP Biomedicals, USA). The DNA quantity was analyzed with a Qubit 2.0 fluorometer using the Qubit double-stranded DNA (dsDNA) high-sensitivity (HS) assay kit (Invitrogen, USA) and the Quant-iT PicoGreen dsDNA assay kit (Invitrogen, USA). The size of the isolated DNA was measured with an Agilent 2100 Bioanalyzer using the DNA 12000 assay kit (Agilent, USA). A SMRTbell library was prepared according to the manufacturer's instructions (Pacific Biosciences, USA) with no size selection. The genome sequencing was performed on the Sequel platform (Pacific Biosciences, USA) with 2.0 sequencing chemistry and 600-min movies. *De novo* assembly of the sequencing reads was performed using the Hierarchical Genome Assembly Process version 2 (HGAP2) protocol (Pacific Biosciences, USA). The pipeline in single-molecule-real-time (SMRT) Analysis version 2.3.0 was used with default parameters. The resulting contigs were circularized using Circlator version 1.4.0 (Sanger Institute, UK). Potential contamination in the genome assemblies was evaluated by ContEst16S. The GC contents of strain was calculated from genome sequence.

The genome of strain was annotated using the NCBI Prokaryotic Genome Annotation Pipeline (PGAP) as previously described (Angiuoli *et al.*, 2008). Functional annotation of the predicted genes was conducted using the Clusters of Orthologous Groups of proteins (COGs) database (Galperin *et al.*, 2015).

3.2.4. Morphological, physiological, and biochemical analysis

1) Growth conditions

Cell growth at various range of temperature, salinity, pH and anaerobic condition was measured.

(1) The temperature range and optimum for growth was measured at 4, 10, 15, 20, 25, 30, 35, 40, 45 and 50 ℃ in Marine agar (MA; Difco 2216, USA) containing 5% NaCl.

(2) The pH range and optimum for growth was determined in Marine agar (M;, Difco 2216, USA) containing 5% NaCl adjusted to pH 4.0-11.0 (at 1.0 pH unit intervals).

(3) Growth at various concentration of NaCl (0, 5, 10, 15, 20, 25, and 30%) was investigated by supplementing with appropriate concentrations of NaCl in Marine agar (MA; Difco 2216, USA).

(4) Growth under anaerobic condition was determined after 1 week of incubation using the AnaeroPack system (OXOID, UK).

(5) Cell growth on Luria-Bertani (LB; Difco 244620, USA) agar, Tryptic Soy Agar (TSA; Difco 236950, USA), *Lactobacilli* MRS (MRS; Difco 288130, USA) agar, and Nutrient Agar (NA; Difco 213000, USA) with 5% NaCl (w/v) was evaluated at 30 ℃, for 5 days.

Table. 3. 2. Composition of media used cell growth test.

Medium	Ingredient	Amounts	
Luria-Bertani (LB; Difco 244620) agar	Tryptone	10.0	g
	Yeast Extract	5.0	g
	Sodium Chloride	10.0	g
	Agar	15.0	g
	Distilled water	1.0	L
	pH	7.0 ± 0.2	
Tryptic Soy Agar (TSA; Difco 236950)	Pancreatic Digest of Casein	15.0	g
	Papaic Digest of Soybean	5.0	g
	Sodium Chloride	5.0	g
	Agar	15.0	g
	Distilled water	1.0	L
	pH	7.3 ± 0.2	
Lactobacilli MRS (MRS; Difco 288130) agar	Proteose Peptone No. 3	10.0	g
	Beef Extract	10.0	g
	Yeast Extract	5.0	g
	Dextrose	25.0	g
	Polysorbate 80	1.0	g
	Ammonium Citrate	2.0	g
	Sodium Acetate	5.0	g
	Magnesium Sulfate	0.1	g
	Manganese Sulfate	0.05	g
	Dipotassium Phosphate	2.0	g
	Agar	15.0	g
	Distilled water	1.0	L
	pH	6.5 ± 0.2	
Nutrient Agar (NA; Difco 213000)	Beef Extract	3.0	g
	Peptone	5.0	g
	Agar	15.0	g
	Distilled water	1.0	L
	pH	6.8 ± 0.2	

2) Gram reaction

Gram reaction of strain was confirmed by staining using Gram stain kit (BBL, USA) according to the manufacturer's instructions.

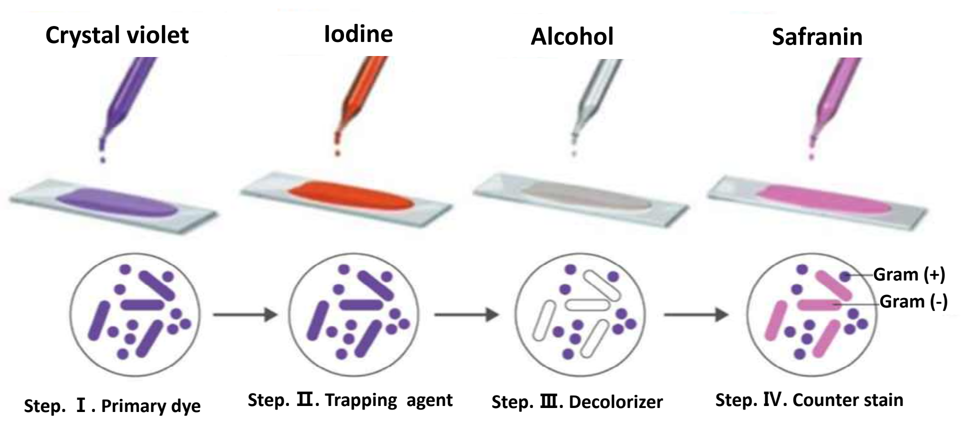


Fig. 3. 3. Gram staining protocol.

3) Cell morphology

Cell morphology and the presence of flagella were examined by Transmission Electronic Microscope (TEM). For TEM, cell of strain was left to settle on carbon-coated grid. The samples were stained using 2.0% uranyl acetate and air dried. Then, Grids were viewed under a Transmission Electron Microscopy (JEM-2100F, JEOL, Japan) at 200 kV. The presence of endosopores was observed by Transmission Electron Microscopy (JEM-2100F, JEOL, Japan) after the preprocessing course.

4) Motility

Flagellum-mediated motility was determined using semi-solid Marine agar (MA; Difco 2216, USA) contating 0.5% (w/v) agar (Wolf *et al.*, 1989).

5) Oxidase test

Oxidase activity was examined using the oxidase reagent (bioMérieux, France). A small amount of Oxidase reagent was added onto a slide glass coated with bacterial cells. Deep blue or purple color change within seconds is recorded as positive.

6) Catalase test

Catalase activity was tested by reaction with hydrogen peroxide. Few drop of 3% (v/v) hydrogen peroxide solution was added onto a slide glass coated with bacterial cells and determined by observing bubble production.

6) hydrolysis of macromolecule test

Hydrolysis of Casein (1.0% skimmed milk, w/v), Carboxymethyl cellulose (CM-cellulose; 1.0%, w/v), Chitin (1.0%, w/v), Starch (1.0%, w/v), Tween 20 (1.0%, v/v), Tween 60 (1.0%, v/v), Tween 80 (1.0%, v/v) and was tested on Marine agar (MA; Difco 2216, USA) (containing 5% NaCl) containing each compound. After incubation for 5 days, hydrolysis of Casein and Chitin was determined by observation of clear halo zones around the colonies. As for Tween 20, 60 and 80, presence of opaque halo zone around the colonies was considered to be positive. Congo red solution and iodine solution were used to determine the hydrolysis of CM-cellulose and starch, respectively.

7) API test system

Biochemical characteristics of strain were determined with API 20NE, ZYM, and 50CH strips; bioMerieux, France). API ZYM strips and API 20NE strips were used for detection of bacterial enzyme activities. Furthermore, API 20NE strips were utilized for identifying the strain's ability to assimilate carbohydrates. The bacterial abilities to ferment carbohydrates to produce acids were investigated by using API 50CH strips with API 50CHB/E media.

8) Antibiotic susceptibility test

Susceptibility to antibiotics was tested on Marine agar (containing 5% NaCl) plates by using antibiotic discs containing following:

Amoxycillin (30 μg, OXOID, UK), Ciprofloxacin (5 μg, BBL, USA), Doxycycline (30 μg, BBL, USA), Erythromycin (15 μg, BBL, USA), Florfenicol (30 μg, OXOID, UK), Flumequine (30 μg, OXOID, UK), Neomycin (30 μg, OXOID, UK), Oxolinic Acid (2 μg, OXOID, UK), Oxytetracycline (30 μg, BBL, USA), and Penicillin G (10 IU, OXOID, UK).

After incubation for 5 days, susceptibility to antibiotics was determined by observation of clear zone around the disc. Absence of clear zone around the disc was considered to be positive.

3.2.5. Chemotaxonomic analysis

1) Fatty acids

For determination of cellular fatty acid composition, strain was incubated for 5 days on Marine agar at 30 ℃. The cellular fatty acids were saponified, methylated and extracted according to the protocol of the Sherlock Microbial Identification System (MIDI), and then analysed via gas chromatography (GC 7890, Agilent, USA).

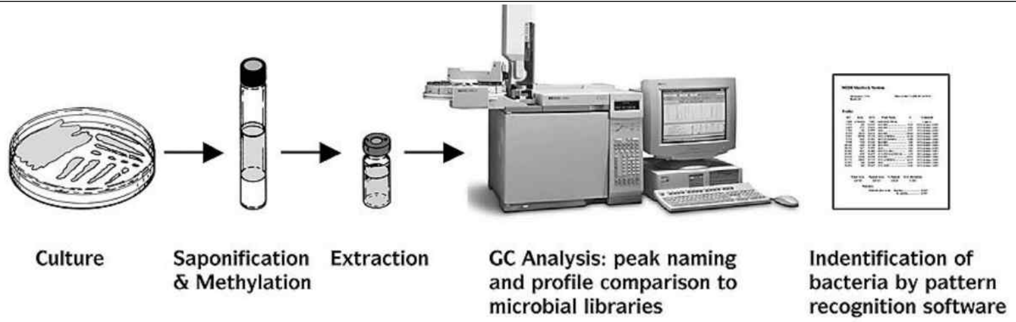


Fig. 3. 4. Fatty Acid-based Microbial Identification System (MIDI) workflow.

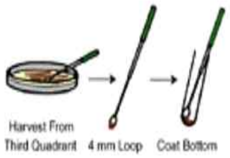
For the analysis of fatty acid methyl ester (FAME), the extraction of cellular fatty acids was conducted as follows. Cultured strain was harvested from colonies on the same sectors. The 40 mg of harvested cells were placed in the bottom of screw cap tubes. 1.0 mL of saponification reagent (Reagent. 1.) was added to each tube containing cells. After briefly vortexing, the tubes were heated in a boiling water bath for 5 minutes, at which time the tubes were vortexed for 5-10 seconds and returned to the water bath to complete the 25 minutes heating. Heated tubes were cooled in water bath on 37 ℃. 2.0 mL methylation reagent (Reagent. 2.) was added to the tubes. After vortexing, the tube was heated for 10±1 minutes at 80±1 °C. Addition of 1.25 mL of extraction reagent (Reagent. 3.) to the tubes was followed by gentle tumbling on a rotator for about 10 minutes. The aqueous lower phase was pipetted out and discarded. About 3.0 mL of base wash reagent (Reagent. 4.) was added to the organic phase remaining in the tubes and the tubes were tumbled for 5 minutes.

The fatty acids were separated using gas chromatography (GC 7890, Agilent, USA). The fatty acid methyl esters (FAME) were identified and quantified by using the TSBA6 database according to the instruction of the Microbial Identification System (MIDI) (Sasser, 1990).

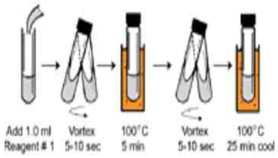
Table. 3. 3. Composition of reagents used fatty acid extraction.

-. Reagent. 1: Saponification reagent 45 g sodium hydroxide + 150 mL methanol + 150 mL distilled water
-. Reagent. 2: Methylation reagent 325 mL certified 6.0 N hydrochloric acid + 275 mL methanol
-. Reagent. 3: Extraction reagent 200 mL hexane + 200 mL methyl tert-butyl ether
-. Reagent. 4: Wash reagent 10.8 g sodium hydroxide dissolved in 900 mL distilled water

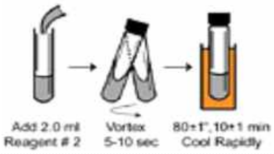
Step 1.
Harvesting



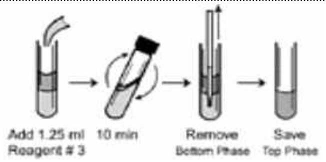
Step 2.
Saponification



Step 3.
Methylation



Step 4.
Extraction



Step 5.
Wash

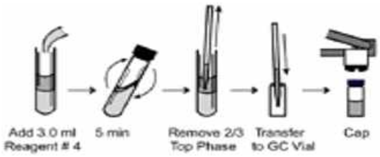


Fig. 3. 5. Process for extract of Fatty acids.

2) Isoprenoid quinone

For the analysis of quinone, strain was incubated for 7 days on Marine broth at 30 ℃. Cell of strain was collected by centrifuge. Collected cell was dried in Freeze dryer. The isoprenoid quinone of strain was extracted with chloroform/methanol solution (2:1, v/v) for 4 hours. The cells were filtered through filter paper and the extract was concentrated. Concentrated extract was dissolved chloroform/methanol (8.5:1.5, v/v) and centrifuged. Quinone was analyzed using high-performance lipid chromatography (HPLC; YL911, Young Lin, Korea) with a Spherisorb 5 μm ODS2 column (4.6 mm×150 mm; Waters) in an elution of methanol/isoprophylether (4:1, v/v). (Collins *et al.*, 1985; Hiraishi *et al.*, 1988)

3) Polar lipids

For the analysis of polar lipids, strain was incubated for 7 days on Marine broth at 30 ℃. Cell of strain was collected by centrifuging the cultured fluid. Collected cell was dried in Freeze dryer. Polar lipids were extracted by an integrated approach (Minnikin *et al.*, 1984) and determined using two-dimensional TLC on a silica gel 60 F254 plates (Merck, Germany).

The extraction of polar lipids was conducted as follows. Dried biomass of 50 mg were placed in test tube. 2.0 mL of aqueous methanol (10 mL of 0.3% aqueous NaCl added to 100 mL of methanol) and 2.0 mL of hexane was added to the tube and shake in a tube rotator for 15 minutes. The supernatant was removed by centrifugation at 13000 rpm for 10 minutes. After adding 1 mL of hexane to the lower layer, the mixture was mixed for 15 minutes and centrifuged to remove the upper layer again. The lower layer was boiled at 100 ℃ for 5 minutes, then cooled to 37 ℃ in water bath for 5 minutes, and adding 0.75 mL of chloroform/methanol/0.3% NaCl solution (w/v) (50:100:40, v/v) for 30 minutes to mix well for a while. After centrifugation, the supernatant was collected, 1.3 mL of chloroform and 0.3% NaCl solution were added, mixed well, and centrifuged. The lower layer solution was collected in a solution divided into two layers and dried at 37 ℃ for use in the analysis.

The extracted polar lipids were analyzed by a two-dimensional thin layer chromatography (TLC) method (Minnikin *et al.*, 1997). The extracted polar lipid was dissolved in 50 μL in a chloroform/methanol (2:1) solution, and then 5 μL in TLC plates were added dropwise to dryness, followed by drying of the primary developer chloroform/methanol/water (65:25:3.8, v/v), and secondary development solutions were developed for at least 30 minutes in chloroform/methanol/acetic acid/water (40:7.5:6:1.8, v/v), respectively.

Total polar lipids were detected by spraying with Molybdophosphoric acid spray solution followed by heating at 100 ℃ for 5 minutes (Gunstone *et al.*, 1972). Specific functional group-containing lipids were detected with the following spraying with Ninhydrin reagent for amino group lipids (Consden *et al.*, 1948), Zinzadze reagent for phosphorus-containing lipids (Dittmer *et al.*, 1964), and α-naphthol reagent for glycolipids (Jacin *et al.*, 1965).

Table. 3. 4. Spray solutions using polar lipids analysis.

-. Molybdophosphoric acid spray solution for all lipids

10% Molybdophosphoric acid (w/v) in 95% ethanol (v/v)

-. Ninhydrin spray solution for lipids containing free amino groups

0.2% Ninhydrin (w/v) in water saturated butan-1-ol

-. Zinzadze spray solution for phosphorus-containing lipids

Solution A: 40.11 g of molybdenum trioxide to l L of 25 N H_2SO_4
Solution B: 1.5 g of molybdenum to 500 mL of Solution A
Solution A/Solution B/Distilled water (1:1:2, v/v)

-. α-naphthol spray solution for glycolipid

Solution (15 g of α-Naphthol in 100 mL of 95 Ethanol) of 10.5 mL/ 6.5 mL of H_2SO_4/40.5 mL of 95% ethanol/4 mL of water

3.3. Results and discussion

3.3.1. Isolation of strain

Strain JNUCC-1^T was isolated from fermented anchovy sauce (Myeolchi-Aekjeot) made by Chujado Federation of Fisheries Cooperatives in Jeju. Strain JNUCC-1 was selected for cultured colonies on Marine agar plate containing 10% NaCl. The isolate was thereon routinely cultured on Marine agar (MA; Difco 2216, USA) at 30 ℃ and preserved as a suspension in Marine broth (MB; Difco 2216, USA) with 20% glycerol (w/v) at -80 ℃. The isolated strain JNUCC-1^T has been deposited in the Korean Collection for Type Cultures (KCTC) under accession no. KCTC 43912.

3.3.2. Morphological, physiological, and biochemical characteristics

Colonies of strain JNUCC-1^T formed beige, and circular colony. Cells of strain JNUCC-1^T was observed to be Gram-stain-positive, moderately halophilic, aerobic, motile, and rods of 0.3-0.8 μm width and 1.2-1.9 μm length. Flagella and endospore were observed by Transmission electron microscopy. Growth occurred at 20-45 ℃, 0-20% NaCl, and pH 4.0-10.0. Optimal growth of temperature, NaCl, and pH was observed at 30 ℃, 5% NaCl, and pH 7.0. Cell growth was observed on Luria-Bertani (LB; Difco 244620, USA) agar, and Tryptic Soy Agar (TSA; Difco 236950, USA), but growth was not observed on *Lactobacilli* MRS (MRS; Difco 288130, USA) agar and Nutrient Agar (NA; Difco 213000, USA). The strain JNUCC-1^T were positive for Oxidase test, Catalase test, and hydrolysis of Tween 60 and 80, but were negative for hydrolysis of Casein, CM-Cellulose, Chitin, and Starch.

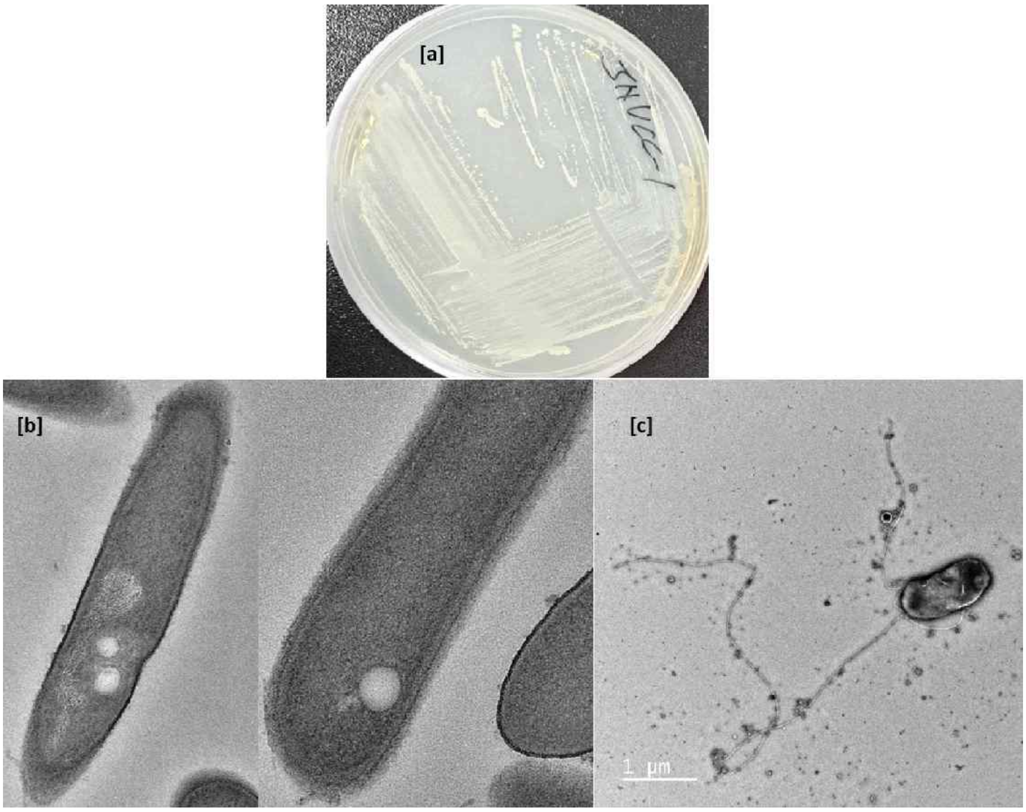


Fig. 3. 6. Image of morphological characteristic of strain JNUCC-1^T;
a, Cultured colony on Marine agar; b, Endospore of strain on TEM; c, Flagella of strain on TEM.

In the antibiotic sensitivity test, 10 types of antibiotics were used. The antibiotics used in the antibiotic sensitivity test were the types that inhibited cell wall synthesis, protein synthesis and nucleic acid synthesis. Cell wall synthetic inhibitory antibiotic were used Amoxicillin and Penicillin G of β-lactam antibiotics, protein synthesis inhibitory antibiotics were used Doxycycline and Oxytetracycline in Tetracycline class and, Erythromycin in Macrolide class and Florfenicol in Amphenicols class. In addition, Quinolones class Ciprofloxacin and Flumequine were used as antibiotics to inhibit nucleic acid synthesis. When it showed resistance to antibiotics, it showed positive results. And when growth was suppressed by antibiotics, the results were read as negative.

Table. 3. 5. Antibiotic susceptibility of strain JNUCC-1^{T}. +, Positive, absence of clear zone, resistant to antibiotic; −, Negative, presence of clear zone, susceptible to antibiotic.

Antibiotic disc	Result
Amoxicillin	+
Ciprofloxacin	−
Doxycycline	−
Erythromycin	+
Florfenicol	+
Flumequine	−
Neomycin	−
Oxolinic Acid	−
Oxytetracycline	+
Penicillin G	+

Cells of strain JNUCC-1^T were resistant to Amoxycillin (30 μg; OXOID, UK), Erythromycin (30 μg; BBL, USA), Florfenicol (30 μg; OXOID, UK), Oxytetracycline (30 μg; BBL, USA), Penicillin G (10 IU; OXOID, UK), but were susceptible to Flumequine (30 μg; OXOID, UK), Oxolinic acid (2 μg; OXOID, UK), Neomycin (30 μg; OXOID, UK), Ciprofloxacin (5 μg; BBL, USA), Doxycycline (30 μg; BBL, USA) (Table. 3. 5.).

The strain JNUCC-1^T was found to be resistant to Amoxicillin and Penicillin G of β-lactam antibiotics that inhibit cell wall synthesis inhibition and to be inhibited from growth of Ciprofloxacin and Flumequine of Quinolones class that inhibit nucleic acid synthesis. It showed resistance to Erythromycin of Macrolide class and Florfenicol of Amphenicols among protein synthesis inhibitory antibiotics, and it was found that growth was inhibited in Neomycin of Aminoglycosides. And among the Tetracycline class, which is a protein synthesis inhibitory antibiotic, growth was inhibited in Doxycycline, and resistance was shown in Oxytetracycline. Through these results, it was possible to know the characteristics of the strain JNUCC-1^T for antibiotic sensitivity, and additionally, it is necessary to investigate the sensitivity to more antibiotics that inhibit protein synthesis.

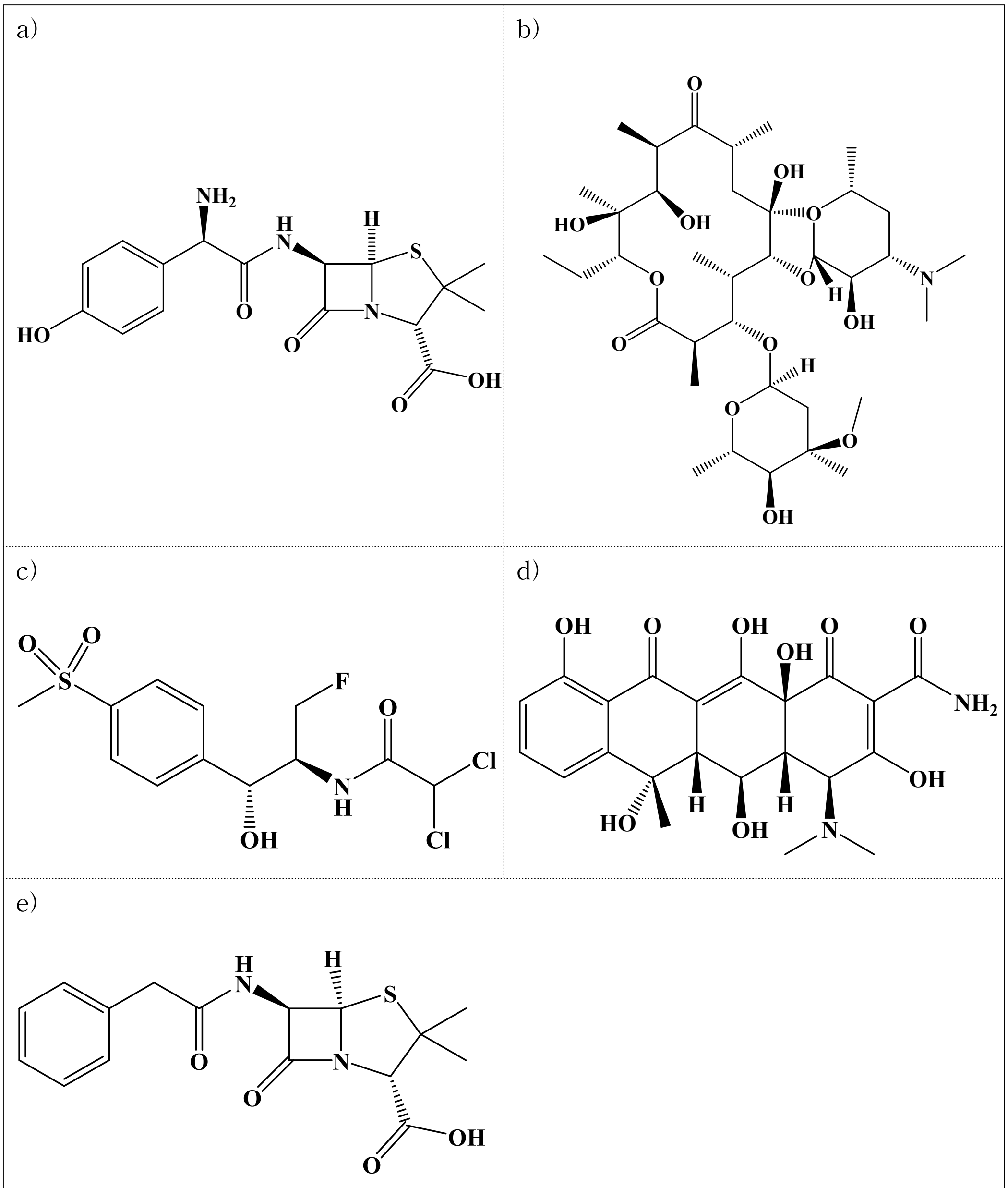


Fig. 3. 7. Structural formula of antibiotics for which strain JNUCC-1^T indicates resistance. a) Amoxicillin; b) Erythromycin; c) Florfenicol; d) Oxytetracycline; e) Penicillin G.

In API 20NE test system, the strain JNUCC-1^T was tested hydrolysis, fermentation, and assimilation reactions such as Nitrate reduction, L-tryptophane, D-glucose, L-arginine, Urea, Esculin ferric citrate, Gelatine, 4-nitrophenly-β-D-galactopyranoside, D-glucose, L-arabinose, D-mannose, D-mannitol, N-acetyl-glucosamine, D-maltose, Potassium gluconate, Capric acid, Adipic acid, Malic acid, Trisodium citrate, and Phenylacetic acid. The strain JNUCC-1^T was found to be positive for nitrate reduction, hydrolysis of gelatin and 4-nitrophenly-β-D-galactopyranoside.

In API ZYM test system, the strain JNUCC-1^T was tested enzyme activities such as Alkaline phosphatase, Esterase (C4), Esterase Lipase (C8), Lipase (C14), Leucine arylamidase, Valine arylamidase, Crystine arylamidase, Trypsin, α-chymotrysin, Acid phospatase, Naphtol-AS-BI-phosphohydrolase, α-galactosidase, β-glucuronidase, β-glucosidase, α-glucosidase, β-glucosidase, N-acetyl-β-glucosaminidase, α-mannosidase, and α-fucosidase. The strain JNUCC-1^T was found to be positive for enzyme activities of Esterase (C4), Esterase Lipase (C8), and Naphtol-AS-BI-phosphohydrolase, but negative for Alkaline phosphatase, Lipase(C14), Leucine arylamidase, Valine arylamidase, Crystine arylamidase, Trypsin, α-chymotrysin, Acid phospatase, α-galactosidase, β-glucuronidase, β-glucosidase, α-glucosidase, β-glucosidase, N-acetyl-β-glucosaminidase, α-mannosidase, and α-fucosidase.

In API 20E test system, the strain JNUCC-1^T was tested fermation-oxidation, production, and utilization reactions such as 2-nitrophenly-β-D-galactopyranoside, L-arginine, L-lysine, L-ornithine, Trisodium thiosulfate, Sodium thiosulfate, Urea, L-tryptophane, L-tryptophane, Sodium pyruvate, Gelatin, D-glucose, D-mannitol, Inositol, D-sorbitol, L-rhamnose, D-sucrose, D-melibiose, amygdalin, and L-arabinose. The strain JNUCC-1^T was found to be positive for gelatinase activity.

In API 50CH test system, the strain JNUCC-1^T was tested fermentation, oxidation, and assimilation via 49 kinds of substrate. Acid was found to be produced from N-acetylglucosamine, D-fructose, D-glucose, D-mannose, D-ribose, and D-trehalose. No acid was found to be produced from Glycerol, Erythritol, D-arabinose, L-arabinose, D-xylose, L-xylose, D-ADOnitol, Methyl-beta-D-xylopyranoside, D-galactose, L-sorbose, L-rhamnose, Dulcitol, Inositol, D-mannitol, D-sorbitol, Methyl-alpha-D-mannopyranoside, Methyl-alpha-D-glucopyranoside, Amygdalin, Arbutin, Esculin ferric citrate, Salicin, D-cellobiose, D-maltose, D-lactose, D-melibiose, D-saccharose, Inulin, D-melezitose, D-raffinose, Amidon, Glycogen, Xylitol, Gentiobiose, D-turanose, D-lyxose, D-tagatose, D-fucose, L-fucose, D-arabitol, L-arabitol, Potassium gluconate, Potassium 2-ketogluconate, and Potassium 5-ketogluconate.

Phenotypic and chemotaxonomic characteristics that strain JNUCC-1^T and related type strains are listed in Table. 3. 6.

Table. 3. 6. Differential characteristics of strain JNUCC-1^T and type strains of related species of the genera *Lentibacillus* and *Virgibacillus*. Strains: 1, JNUCC-1 (data from this study); 2, *Lentibacillus alimentarius* M2024^T (Sundararaman *et. al.*, 2018); 3, *Lentibacillus populi* WD4L-1^T (Sun *et. al.*, 2016); 4, *Lentibacillus garicola* SL-MJ1^T (Jung *et. al.*, 2015); 5, *Virgibacillus siamensis* MS3-4^T (Tanasupawat *et. al.*, 2010). +, positive; -, negative; ND, no data available; w, weakly; +* or -*, assessd by Leifson (1963). G, phosphatidyl-glycerol; DPG, diphosphatidylglycerol; PL, unidentified phospholipids; GL, unidentified glycolipid.

Characteristic	1	2	3	4	5
Morphology	Rod	Rod	Rod	Rod	Rod
Spore formation	+	+	+	-	+
Motility	+	+	+	-	+
Flagella	+	-	+	-	ND
Size					
Length (㎛)	1.2-1.9	0.6-1.0	1.5-2.9	1.5-2.1	2.0-5.0
Width (㎛)	0.3-0.8	0.3-0.5	0.4-0.6	1.0-1.3	0.5-0.7
Colony colour	Beige	Pale yellow	Opaque cream	Beige	Red
Gram stain	+	+	+	+	+
Growth for:					
range of Temperature (℃)	20-45	10-37	15-50	15-40	15-40
Optimal Temperature (℃)	30	25	30	30	37
range of NaCl (%)	0-20	0-5	0-15	0-20	1-20
Optimal NaCl (%)	5	2	7-8	6	5
range of pH	4.0-10.0	6.0-9.0	6.0-9.0	6.5-8.0	7.0-8.0
Optimal pH	7.0	7.0	7.0	7.0	7.0
Anaerobic condition	Aerobic	Aerobic	Aerobic	Aerobic	Aerobic & anaerobic

Table. 3. 6. Continue.

Characteristic	1	2	3	4	5
Growth at:					
Marine Agar	+	+	+	+	+
Luria-Bertani Agar	+	*w*	+	ND	ND
Tryptic Soy Agar	+	+	ND	+	ND
Lactobacilli MRS Agar	−	ND	ND	ND	ND
Nutrient Agar	−	+	+	*w*	ND
Hydrolysis of:					
Casein	−	ND	−	−	*w*
Cellulose	−	ND	ND	ND	ND
Chitin	−	ND	ND	ND	ND
Starch	−	ND	ND	−	−
Tween 20	+	ND	+	−	ND
Tween 60	+	ND	ND	ND	ND
Tween 80	−	ND	+	−	−
Oxidase activity	+	ND	+	−	+
Catalase activity	+	+	+	+	+
Nitrate reduction	+	+	+	+	−
Major fatty acid	anteiso-$C_{15:0}$	anteiso-$C_{15:0}$	anteiso-$C_{15:0}$	anteiso-$C_{15:0}$	anteiso-$C_{15:0}$
Isoprenoid quinone	MK-7	MK-7	MK-7	MK-7	MK-7
Polar lipids	PG, DPG, PL	PG, DPG, PE	PG, DPG, PL	PG, DPG, PL	PG, DPG, GL
DNA GC content (%)	43.3	36.2	36.9	42.8	38.0

Table. 3. 6. Continue.

Characteristic	1	2	3	4	5
Enzyme activities (API ZYM) of:					
Alkaline phosphatase	−	+	+	−	ND
Esterase (C4)	+	+	+	*W*	ND
Esterase Lipase (C8)	+	+	+	−	ND
Leucine arylamidase	−	+	+	−	ND
Valine arylamidase	−	−	+	−	ND
Crystine arylamidase	−	−	+	−	ND
α-chymotrysin	−	+	+	−	ND
Acid phospatase	−	+	+	+	ND
Naphtol-AS-BI-phosphohydrolase	+	−	+	+	ND
α-glucosidase	−	−	+	−	ND
N-acetyl-β-glucosaminidase	−	−	+	−	ND
Acid production (API 50CH)					
Glycerol	−	+	−	ND	−*
Erythritol	−	+	−	ND	ND
L-arabinose	−	+	−	ND	ND
D-ribose	+	+	−	ND	ND
D-galactose	−	+	−	+*	−*
D-glucose	+	−	+	+*	+*
D-fructose	+	+	−	+*	−*
D-mannose	+	−	+	+*	−*
Inositol	−	+	−	ND	ND

Table. 3. 6. Continue.

Characteristic	1	2	3	4	5
Acid production (API 50CH)					
D-mannitol	−	+	+	+*	ND
N-acetylglucosamine	+	−	−	ND	ND
Arbutin	−	+	−	ND	ND
Esculin ferric citrate	−	+	−	ND	ND
Salicin	−	+	−	ND	+*
D-cellobiose	−	+	−	ND	ND
D-maltose	−	+	−	ND	ND
D-saccharose (sucrose)	−	+	+	+*	ND
D-trehalose	−	+	−	ND	ND
Glycogen	−	+	−	ND	ND
Gentiobiose	−	+	−	ND	ND
D-lyxose	−	+	−	ND	ND
D-fucose	−	+	−	ND	ND
Potassium 5-ketogluconate	−	+	−	ND	ND
Assimilation (API 20NE)					
D-glucose	−	−	+	−	−
D-mannose	−	+	+	−	−
D-mannitol	−	+	+	−	−
N-acetyl-glucosamine	−	+	−	−	−
D-maltose	−	+	−	−	−
malic acid	−	−	+	−	−

3.3.3. Chemotaxonmic characteristics

The major cellular fatty acids of the strain JNUCC-1^T was anteiso-$C_{15:0}$ (68.3%), which are consistent with those of the *Lentibacillus* reference strains. The fatty acid composition of strain JNUCC-1^T was found to be in line with those of reference strains, and was dominated by large amounts of anteiso-branched fatty acids, although there were some qualitative and quantitative differences in the fatty acid contents of the strains (Table. 3. 7.).

Table. 3. 7. Cellular fatty acid composition (%) of strain $JNUCC^T$ and the closely related species. Strains: 1, JNUCC-1 (data from this study); 2, *Lentibacillus alimentarius* $M2024^T$ (Sundararaman *et. al.*, 2018); 3, *Lentibacillus populi* WD4L-1^T (Sun *et. al.*, 2016); 4, *Lentibacillus garicola* SL-$MJ1^T$ (Jung *et. al.*, 2015); 5, *Virgibacillus siamensis* MS3-4^T (Tanasupawat *et. al.*, 2010). The major fatty acids (> 20% of the total) are indicated in bold. Tr, trace (< 1.0%)

Characteristic	1	2	3	4	5
Saturated straight-chain					
$C_{16:0}$	1.0	2.8	2.9	1.7	1.5
Saturated branched-chain					
iso-$C_{14:0}$	11.0	5.2	5.6	5.1	3.9
iso-$C_{15:0}$	Tr	7.8	19.0	6.6	11.3
iso-$C_{16:0}$	9.6	9.6	9.8	16.7	6.6
iso-$C_{17:0}$	-	-	3.0	1.5	1.5
anteiso-$C_{15:0}$	**68.3**	**52.5**	**41.9**	**48.8**	**55.8**
anteiso-$C_{17:0}$	6.2	18.3	11.4	18.0	17.7
Unsaturated straight-chain					
$C_{16:1}$ *w7c* alcohol	1.3	-	2.2	Tr	-

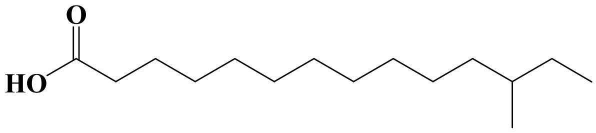


Fig. 3. 8. Structural formula of anteiso-$C_{15:0}$ that major fatty acid of strain JNUCC-1^T.

The sole respiratory quinone of strain JNUCC-1^T was found to contain menaquinone-7 (MK-7) which was consistent with the respiratory quinone of the genus *Lentibacillus* (Jung *et al.*, 2015).

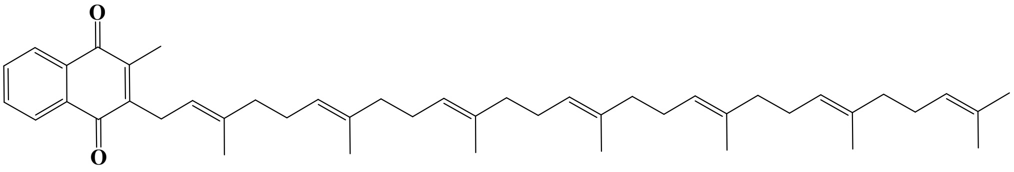


Fig. 3. 9. Structural formula of MK-7 that quinone of strain JNUCC-1^T.

The major polar lipids of strain JNUCC-1^T were diphosphatidylglycerol (DPG), phosphatidylglycerol (PG) and one unidentified phospholipid (Fig. 3. 10.), which was consistent with the profile of *Lentibacillus populi* WD4L-1^T (Sun *et al.*, 2016) and *Lentibacillus garicola* SL-MJ1^T (Jung *et al.*, 2015) among reference strains.

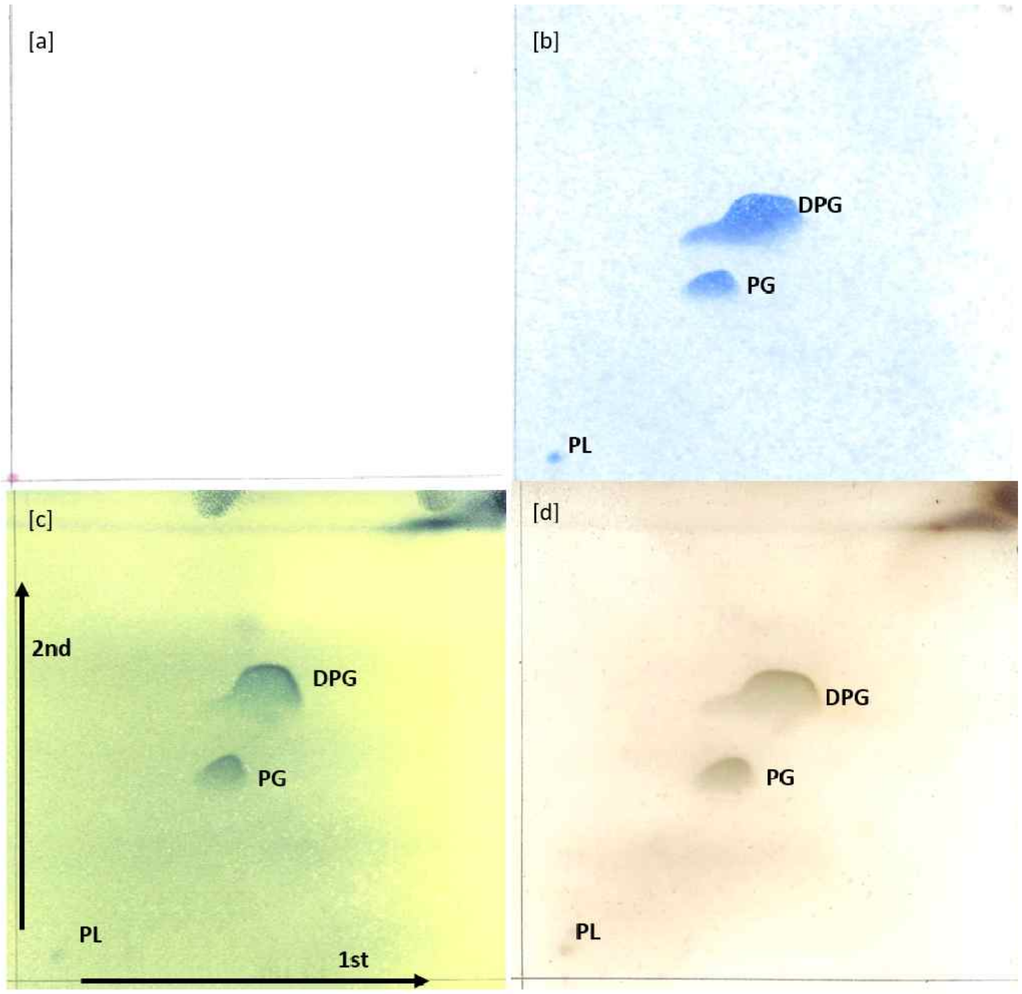


Fig. 3. 10. Polar lipid profiles of strain JNUCC-1^T were detected with (a), ninhydrin reagent; (b), zinzadze reagent; (c), molybdophosphoric acid reagent; d), α-naphthol reagent. PG, phosphatidylglycerol; DPG, diphosphatidylglycerol; PL, unidentified phospholipids.

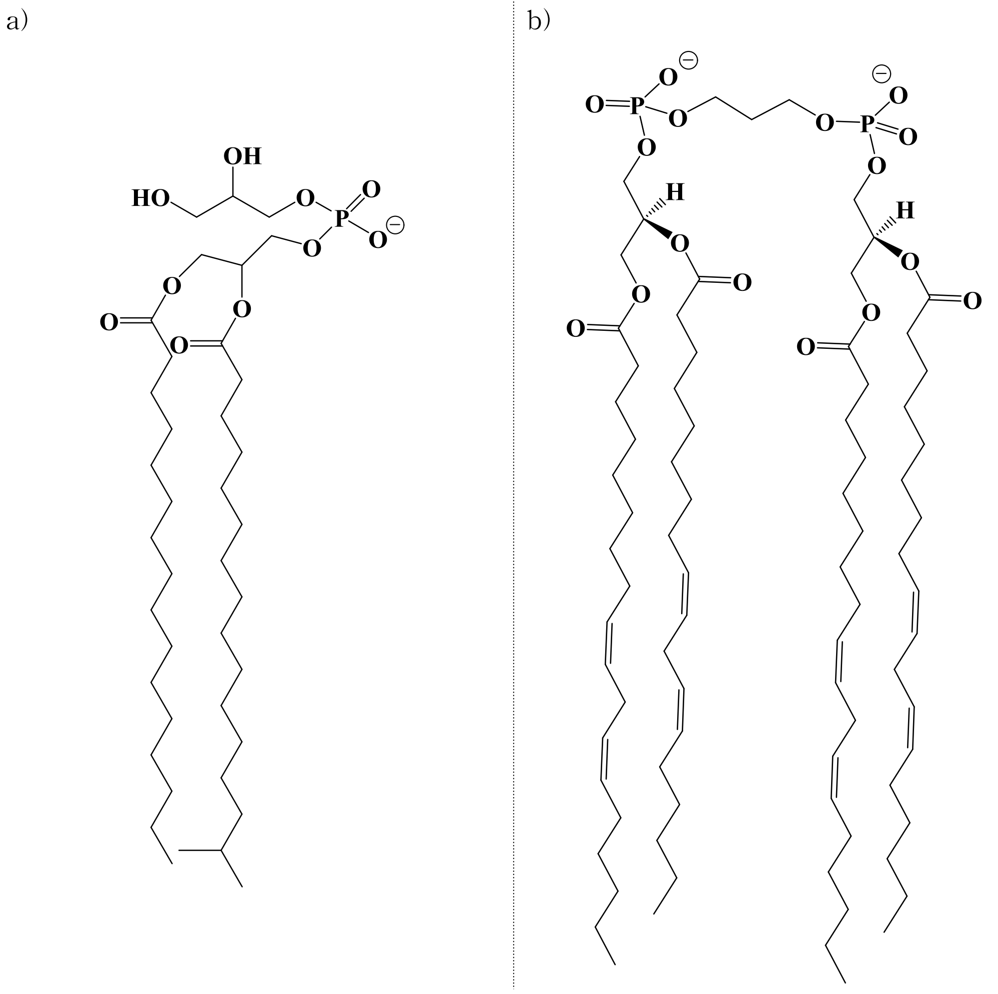


Fig. 3. 11. Structural formula of major Polar lipid of strain JNUCC-1^{T}. a), PG, phosphatidylglycerol; b), DPG, diphosphatidylglycerol.

3.3.4. Genomic characteristics

1) Phylogenetic analysis

The 16S rRNA gene sequence of strain JNUCC-1^T was 1,438 bp. The sequence has been deposited in GenBank under accession no. MT093730. The closet phylogenetic neighbours of strain JNUCC-1^T were identified using EzBioCloud (https://www.ezbiocloud.net) and Basic Local Alignment Search Tool (https://blast.ncbi.nlm.nih.gov) (Kim *et al.*, 2012). Preliminary comparisons with the 16S rRNA gene sequence revealed that strain JNUCC-1^T was most closely related to *Lentibacillus alimentarius* 2024^T (Percent identity: 98.5%, Query cover: 98%), *Virgibacillus kekensis* YIM-kkny16^T (95.6%, 100%), *Lentibacillus populi* WD4L-1^T (95.4%, 100%), *Lentibacillus juripiscarius* IS40-3^T (95.4%, 100%), *Virgibacillus phasianinus* LM2416^T (95.4%, 99%), *Lentibacillus massiliensis* Marseille-P3089^T (95.4%, 100%), and *Virgibacillus dakarensis* Marseille-P3469^T (95.4%, 100%). The accepted criterion for delineating a bacterial species states that strains with a 16S rRNA gene sequence similarity below 98.7% are considered to belong to separate species (Chun *et. al.*, 2018), so our data suggest that strain JNUCC-1^T represents a novel species of the genus *Lentibacillus*.

The maximum-likelihood phylogenetic tree reconstructed from 16S rRNA gene sequences of strain JNUCC-1^T and some related species of the genera *Lentibacillus* and *Virgibacillus* showed was located in a phylogenetic clade together with all recognized species of the genus *Lentibacillus*, and was most closely related to *Lentibacillus alimentarius* M2024^T (Fig. 3. 12.).

Comparative analysis of 16S rRNA gene sequences showed that strain JNUCC-1^T is most closely related to *Lentibacillus alimentarius* M2024^T and *Virgibacillus kekensis* YIM-kkny16^T. However, phylogenetic analysis showed that strain JNUCC-1^T forms a phyletic lineage with members of the genus *Lentibacillus*. The topologies of phylogenetic trees built using the maximum-likelihood, maximum-parsimony, and neighbor-joining methods also supported these results, indicating that strain JNUCC-1^T formed a stable clade.

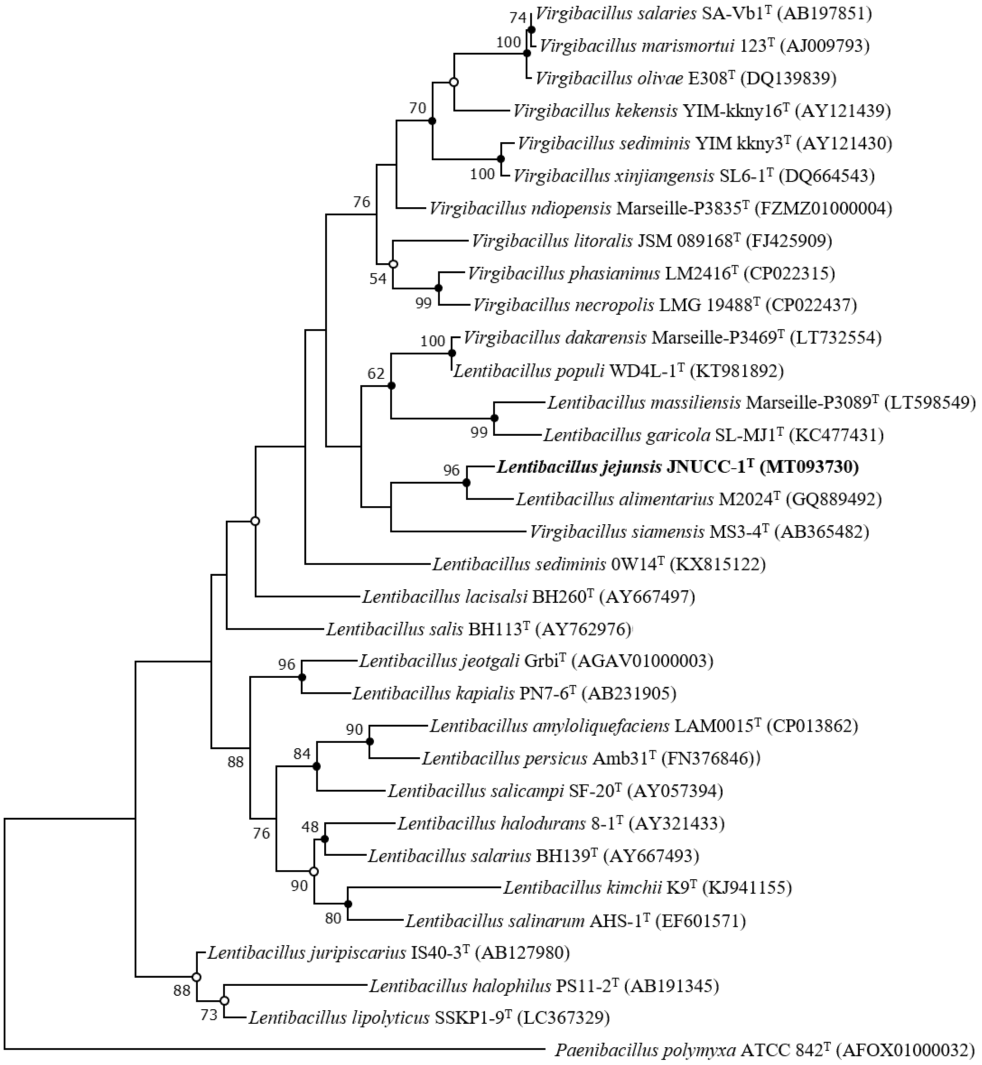


Fig. 3. 12. Phylogenetic tree generated with the maximum likelihood algorithm and based on 16S rRNA gene sequences shows the phylogenetic positions of strain JNUCC-1^T and related taxa. Branch points by bootstrap values (> 50%) calculated by the maximum-likelihood (ML), maximum-parsimony (MP), and neighbor-joining (NJ) methods. *Paenibacillus polymyxa* ATCC 842^T (AFOX01000032) was used as an outgroup. Filled circles indicate that the corresponding branch points were also rendered with the NJ and MP methods. Open circles indicate that the corresponding nodes were also rendered with either the MP or NJ methods. Scale bar represents 0.02 substitutions per nucleotide position.

2) Genomic characteristics

The genome sequence of strain Strain JNUCC-1^T contains 3,687,469 bp, with a GC contents of 43.3%, an N50 value of 2,174,790 bp, and 3 contigs with lengths of 2,174,790 bp, 25,650 bp, and 1,487,029 bp. The depth of coverage was 224.6-fold. The gene-finding and functional annotation pipelines in the EzBioCloud genome database were used. Protein-coding sequences were predicted by Prodigal version 2.6.2, which showed that the genome contained 3,833 genes. In addition, 66 tRNA genes were identified by tRNAscan-SE version 1.3.1, and 17 rRNA genes were identified by Rfam version 12.0. Eight genomes of type strains of genus *Lentibacillus* are published in EzBioCloud. They feature of genome size of 3,208,301-3,897,716 bp, CDSs of 3,045-5,053, GC content of 41.5-44.8%, rRNA genes of 10-30, and tRNA genes of 50-66. The JNUCC-1^T strain also has similar characteristics (Table. 3. 8.).

Table. 3. 8. Genome characteristics of each type strain of genus *Lentibacillus* published at EzBioCloud. Strains: 1, JNUCC-1^T; 2, *Lentibacillus salicampi* ATCC BAA-719^T; 3, *Lentibacillus sediminis* 0W14^T; 4, Lentibacillus amyloliquefaciens LAM0015^T; 5, *Lentibacillus halodurans* CGMCC 1.3702^T; 6, *Lentibacillus persicus* DSM 22530^T; 7, *Lentibacillus lipolyticus* SSKP1-9^T; 8, *Lentibacillus jeotgali* Grbi^T; 9, *Lentibacillus juripiscarius* JCM 12147^T.

	Genome size	GC content	CDSs	rRNA genes	tRNA genes
1	3,687,469 bp	43.3%	3,833	17	66
2	3,897,716 bp	43.0%	3,908	20	64
3	3,639,803 bp	44.8%	3,656	11	62
4	3,858,284 bp	42.1%	3,897	18	65
5	3,670,765 bp	41.5%	3,553	11	53
6	3,314,552 bp	42.7%	3,288	11	50
7	3,146,740 bp	44.1%	3,045	30	66
8	3,775,822 bp	42.5%	3,760	12	53
9	3,208,301 bp	44.1%	5,053	10	61

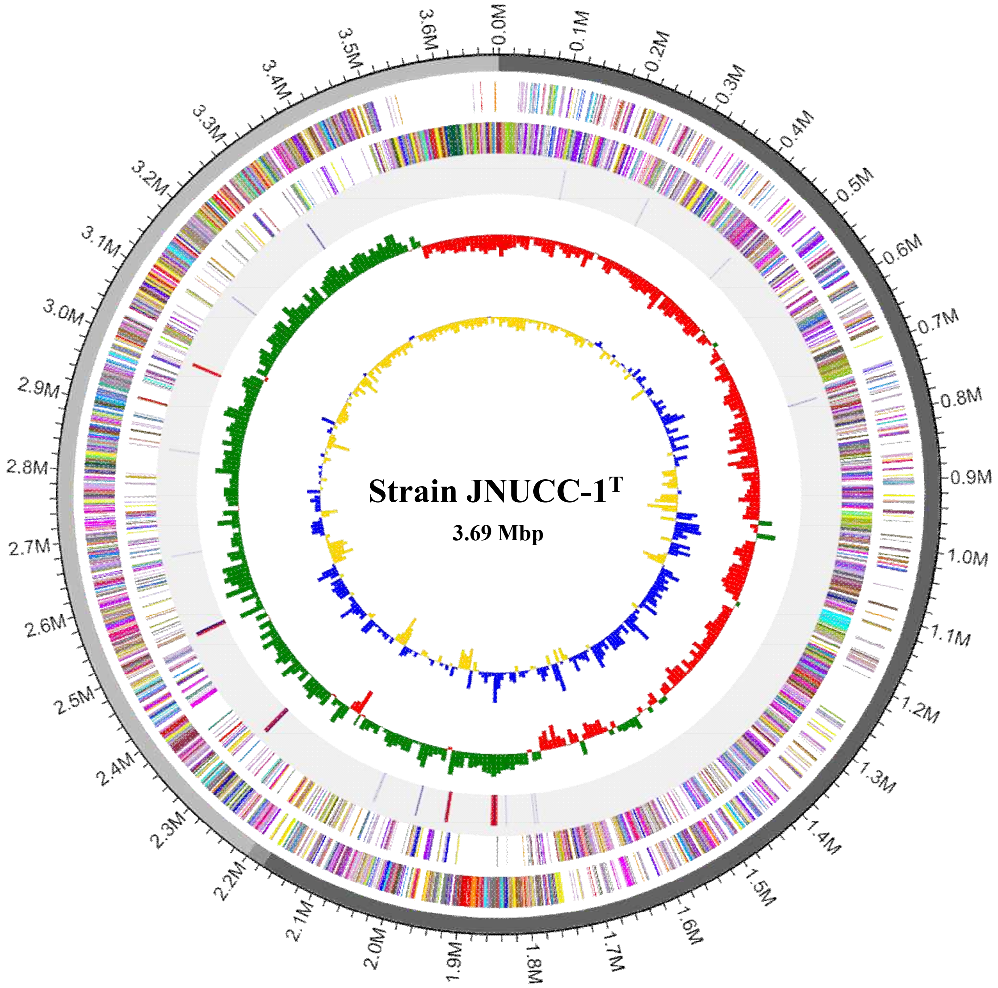
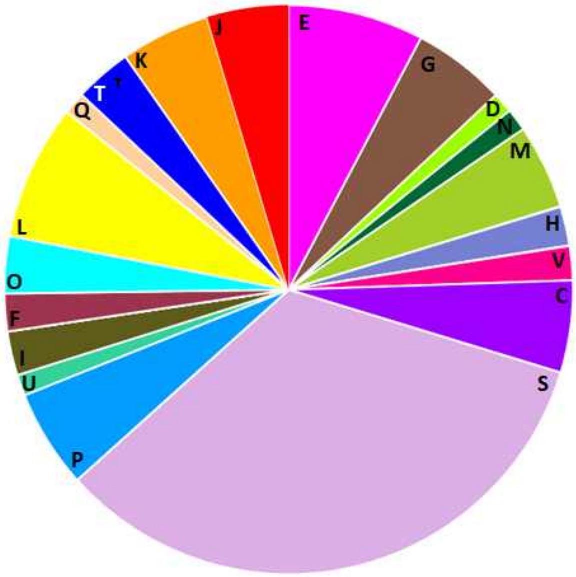


Fig. 3. 13. Graphical circular genome of strain JNUCC-1^T. From the outside to the inside; 1) contigs on pseudogenome (gray); 2) coding DNA sequences (CDS) on forward strand (colored following to COG categories); 3) coding DNA sequences (CDS) on reverse stand (colored following to COG categories); 4) RNA genes (red, rRNAs); 5) GC skew (green, higher-than-average values; red, lower than average values); 6) GC ratio (blue, higher than average values; yellow, lower than average values)



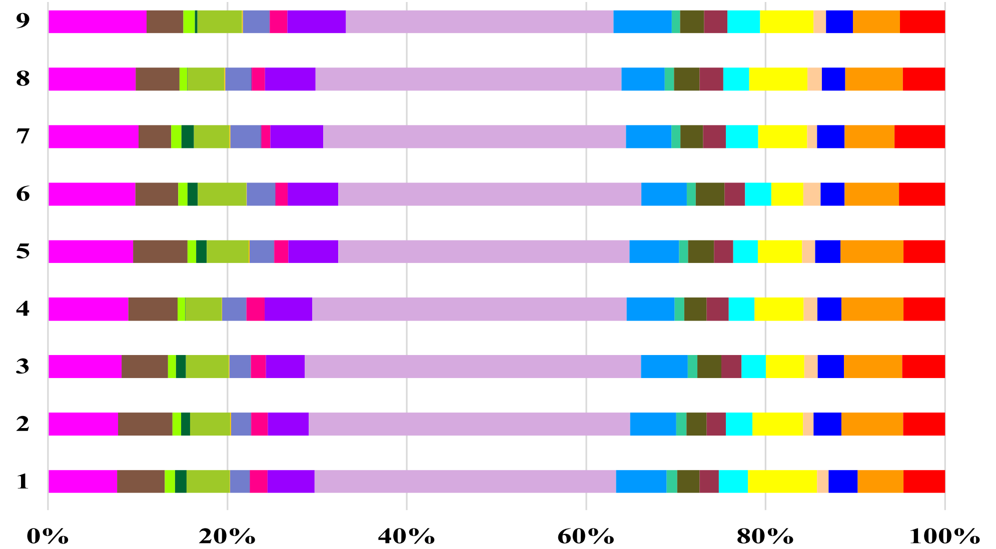
🟪	E, Amino acid transport and metabolism	7.71%
🟫	G, Carbohydrate transport and metabolism	5.29%
🟩	D, Cell cycle control, cell division, chromosome partitioning	1.17%
🟩	N, Cell Motility	1.28%
🟩	M, Cell wall/membrane/envelope biogenesis	4.81%
🟨	B, Chromatin structure and dynamics	0.03%
🟦	H, Coenzyme transport and metabolism	2.22%
🟪	Z, Cytoskeleton	0.03%
🟥	V, Defense mechanisms	1.94%
🟪	C, Energy production and conversion	5.24%
🟦	W, Extracellular structures	-
🟪	S, Function unknown	33.64%
🟥	R, General function prediction only	-
🟦	P, Inorganic ion transport and metabolism	5.61%
🟩	U, Intracellular trafficking, secretion, and vesicular transport	1.20%
🟫	I, Lipid transport and metabolism	2.50%
🟫	Y, Nuclear structure	-
🟥	F, Nucleotide transport and metabolism	2.13%
🟦	O, Posttranslational modification, protein turnover, chaperones	3.24%
🟨	A, RNA processing and modification	-
🟨	L, Replication, recombination and repair	7.71%
🟧	Q, Secondary metabolites biosynthesis, transport and catabolism	1.28%
🟦	T, Signal transduction mechanisms	3.24%
🟧	K, Transcription	5.09%
🟥	J, Translation, ribosomal structure and biogenesis	4.64%

Fig. 3. 14. The distribution of COG functional categories of strain JNUCC-1^T.

The distribution of COG functional categories is presented in Figure. 3. 12. The genome of strain JNUCC-1^T represented higher proportions in the categories of Replication, recombination and repair (L; 271 genes), Amino acid transport and metabolism (E; 271 genes), Inorganic ion transport and metabolism (P; 197 genes), Carbohydrate transport and metabolism (G; 186 genes), Energy production and conversion (C; 184 genes), Transcription (K; 179 genes), Cell wall/membrane/envelope biogenesis (M; 169 genes), Translation, ribosomal structure and biogenesis (J; 163 genes). As a result of analyzing the genes classified according to the COG functional categories, through the previous test, the strain JNUCC-1^T found the presence of motility and flagella, and through genomic analysis, it was confirmed that it contained 45 predicted genes related to motility or flagella. And the genome of strain JNUCC-1^T contains 169 predicted genes associated with sporulation, such as spore germination protein GerD, GerM, and YaaH, and 33 predicted genes associated with antibiotic resistance such as pbp2A, ampC and multidrug resistance genes. The results of other biochemical tests, such as API system and hydrolysis of macromolecule test also related genes in COG functional categories of Amino acid transport and metabolism, Carbohydrate transport and metabolism, and Lipid transport and metabolism could confirmed. This may be the basis for supporting the results of previous biochemical tests. Genes that could support the results of the chemotaxonomic test were identified. In genome of strain could confirm 9 predicted genes associated with phosphatidylglycerol and diphosphatidylglycerol such as umpA, lgt, and ltaS, and 14 predicted genes associated with menaquinone biosynthesis such as bioC, fadD, and ubiE, and 19 predicted genes associated with fatty acids biosynthesis such as fabG, fabH, and fabI.

The genome of strain JNUCC-1^T contains 19 predicted genes associated with osmotic stress regulation, such as choline glycine betaine transporter BetT2, osmoprotectant import permease protein OsmW. These genes could be key factors allowing strain JNUCC-1^T to adapt to high-salt environments via osmotic regulation and adjustment of cytoplasmic pH, respectively. Metabolites produced by extreme halophile bacteria such as the strain JNUCC-1^T have been utilized in various industries. Compatible solutes produced to overcome osmotic stress are utilized in the bio industry, enzymes that have activity at high concentrations of salinity are utilized in eco-friendly industries such as decomposition of pollutants and toxic substances, and enzymes such as esterase added in fermentation food used to improve the flavor of food. As a result of analyzing the genome of the strain, the strain is expected to have the potential ability to be used in various industries, and in the future, it will be able to derive the ability of the strain through additional studies such as metabolite regulation, efficacy evaluation, and genetic manipulation.

Additionally, the distribution of COG functional categories was examined based on genome of each type strain of the genus *Lentibacillus* published in EzBioCloud. Most of the contents of each category showed similar values. However, in the two strains without motility, there was no genes related to motility. In most strains's genome, similar to strain JNUCC-1^T, there were many genes associated with Amino acid transport and metabolism (Category E), Carbohydrate transport and metabolism (Category G), Cell wall/membrane/envelope biogenesis (Category M), Energy production and conversion (Category C), Inorganic ion transport and metabolism (Category P), Replication, recombination and repair (Category L), Transcription (Category K), and Translation, ribosomal structure and biogenesis (Category J). Through this, the strain JNUCC-1 could knew to have similar properties to other strains of the genus *Lentibacillus* (Fig. 3. 15.).



	COG functional categories	1	2	3	4	5	6	7	8	9
■	E, Amino acid transport and metabolism	7.7	7.8	8.2	9.0	9.5	9.7	10.1	9.8	11.0
■	G, Carbohydrate transport and metabolism	5.3	6.1	5.1	5.5	6.1	4.8	3.6	4.9	4.1
■	D, Cell cycle control, cell division, chromosome partitioning	1.2	1.0	0.9	0.8	1.0	1.0	1.1	0.9	1.3
■	N, Cell Motility	1.3	1.0	1.1	0.0	1.2	1.1	1.4	0.0	0.3
■	M, Cell wall/membrane/envelope biogenesis	4.8	4.4	4.8	4.0	4.7	5.4	4.0	4.1	5.0
■	B, Chromatin structure and dynamics	0.0	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1
■	H, Coenzyme transport and metabolism	2.2	2.2	2.4	2.7	2.7	3.2	3.4	2.9	3.0
■	Z, Cytoskeleton	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.1	0.0
■	V, Defense mechanisms	1.9	1.9	1.6	2.0	1.6	1.4	1.0	1.5	2.0
■	C, Energy production and conversion	5.2	4.6	4.3	5.3	5.6	5.6	5.9	5.6	6.5
■	W, Extracellular structures	-	-	-	-	-	-	-	-	-
■	S, Function unknown	33.6	35.8	37.5	35.1	32.5	33.8	33.7	34.1	29.8
■	R, General function prediction only	-	-	-	-	-	-	-	-	-
■	P, Inorganic ion transport and metabolism	5.6	5.2	5.2	5.3	5.5	5.1	5.1	4.8	6.5
■	U, Intracellular trafficking, secretion, and vesicular transport	1.2	1.1	1.1	1.1	1.0	1.0	1.0	1.0	0.9
■	I, Lipid transport and metabolism	2.5	2.3	2.7	2.5	2.9	3.2	2.6	2.9	2.6
■	Y, Nuclear structure	-	-	-	-	-	-	-	-	-
■	F, Nucleotide transport and metabolism	2.1	2.1	2.2	2.5	2.2	2.3	2.5	2.6	2.6
■	O, Posttranslational modification, protein turnover, chaperones	3.2	3.0	2.7	2.9	2.8	2.9	3.6	2.9	3.6
■	A, RNA processing and modification	-	-	0.0	0.0	-	-	-	-	-
■	L, Replication, recombination and repair	7.7	5.6	4.3	5.4	4.9	3.6	5.5	6.5	6.0
■	Q, Secondary metabolites biosynthesis, transport and catabolism	1.3	1.2	1.5	1.6	1.5	1.9	1.1	1.6	1.4
■	T, Signal transduction mechanisms	3.2	3.1	3.0	2.7	2.8	2.7	3.0	2.6	3.0
■	K, Transcription	5.1	6.9	6.5	6.9	7.1	6.1	5.6	6.4	5.3
■	J, Translation, ribosomal structure and biogenesis	4.6	4.7	4.8	4.6	4.6	5.1	5.6	4.7	5.0

Fig. 3. 15. The distribution of COG functional categories among strains of the genus *Lentibacillus* (%). Strains: 1, JNUCC-1^T; 2, *Lentibacillus salicampi* ATCC BAA-719^T; 3, *Lentibacillus sediminis* 0W14^T; 4, Lentibacillus amyloliquefaciens LAM0015^T; 5, *Lentibacillus halodurans* CGMCC 1.3702^T; 6, *Lentibacillus persicus* DSM 22530^T; 7, *Lentibacillus lipolyticus* SSKP1-9^T; 8, *Lentibacillus jeotgali* Grbi^T; 9, *Lentibacillus juripiscarius* JCM 12147^T.

The genome sequence of strain Strain JNUCC-1^T has been deposited in GenBank under accession no. WHOH00000000 (BioProject accession no. PRJNA577786 and BioSample accession no. SAMN13037569). The public version of the strain Strain JNUCC-1^T genome sequence deposited in GenBank was annotated using the Prokaryotic Genome Annotation Pipeline (PGAP).

Table. 3. 9. Genome features of strain JNUCC-1 annotated using the Prokaryotic Genome Annotation Pipeline (PGAP) (https://www.ncbi.nlm.nih.gov /nuccore /NZ_WHOH00000000.1).

Feature	Value
Genome size (bp)	3,687,469
GC content (%)	43.3
No. of contigs	3
Total genes	3,622
CDSs	3,170
tRNA genes	66
rRNA genes (5S, 16S, 23S)	17 (5, 6, 6)

3.3.5. Taxonomic conclusion

In this study, Phylogenetic tree showed that strain JNUCC-1^T forms a phyletic lineage with members of the genus *Lentibacillus*. The chemotaxonomic and phenotypic characterizations of strain JNUCC-1^T showed typical features of members of the genus *Lentibacillus*, with MK-7 as the predominant respiratory isoprenoid quinone and major fatty acid including anteiso-$C_{15:0}$.

The strain JNUCC-1^T is considered as a novel species of the genus *Lentibacillus*, for which the name *Lentibacillus jejunsis* sp. nov., (Type strain JNUCC-1^T = KCTC 43912^T) is proposed.

3.4. Conclusion

Description of *Lentibacillus jejunsis* sp. nov.

Lentibacillus jejuensis (je.ju.en′sis. N.L. fem. adj. *jejuensis* pertaining to Jeju, Republic of Korea, from where the type strain was isolated).

Cells are Gram-positive, aerobic, motile by means of polar flagella, and spore-forming rods (0.3-0.8 μm wide and 1.2-1.9 μm lengh). Spherical endospores form at the cell-terminal position. Colonies are circular with opaque of beige and below 1.0 mm in diameter. Growth occurs in 0 - 20% (w/v) NaCl (optimal in 5%) and pH 4.0-10.0 (optimal at pH 7.0) at 20-45 ℃ (optimal at 30 ℃). Positive results in tests for oxidase, catalase, nitrate reduction and hydrolysis of Tween 20 and 60, but negative results for hydrolysis of Casein, CM-Cellulose, Chitin, and Starch. In API ZYM test system, positive for Esterase (C4), Esterase Lipase (C8), and Naphtol-AS-BI-phosphohydrolase, but negative for Alkaline phosphatase, Lipase (C14), Leucine arylamidase, Valine arylamidase, Crystine arylamidase, Trypsin, α-chymotrysin, Acid phospatase, α-galactosidase, β-glucuronidase, β-glucosidase, α-glucosidase, β-glucosidase, N-acetyl-β-glucosaminidase, α-mannosidase, and α-fucosidase. In API 20NE test system, positive for nitrate reduction, hydrolysis of gelatine and 4-nitrophenly-βD-galacto-pyranoside, but negative for hydrolysis of L-tryptophane, urea, esculin ferric citrate and assimilation of all. In API 50CH test system, Cells produce acid from D-ribose, D-glucose, D-fructose, D-mannose, N-acetyl-glucosamine, and D-trehalose. The major fatty acid (>20%) is anteiso-

$C_{15:0}$. The major polar lipids are diphosphatidylglycerol (DPG), phosphatidyl -glycerol (PG), and one unidentified phospholipid (PL). The predominant respiratory isooprenoid quinone is menaquinone-7 (MK-7). The genome size is 3,687,469 bp, and GC content of the genomic DNA is 43.3 mol %.

The NCBI GenBank/EMBL/DDBJ accession numbers of the 16S rRNA gene sequence and the genome sequence are MT093730 and WHOH 00000000, respectively.

The Type strain is JNUCC-1^T (=KCTC 43912^T), isolated from fermented anchovy sauce (Myeolchi-Aekjeot) made by Chujado Federation of Fisheries Cooperatives in Chu-ja island, the Republic of Korea.

Chapter Ⅳ. References

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Chapter Ⅴ. Appendix

Table. 3. 10. Information of strain JNUCC-1 CDSs.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_00001		438	Uracil permease	F:COG2233
JNUCC-1_00002		996	Uracil permease	F:COG2233
JNUCC-1_00003	pyrR	543	Uracil phosphoribosyltransferase	F:COG2065
JNUCC-1_00004	rluD	912	23S rRNA pseudouridine(1911/1915/1917) synthase	J:COG0564
JNUCC-1_00005	lspA	471	Signal peptidase II	MU:COG0597
JNUCC-1_00006		504	Septum site-determining protein DivIVA	D:COG3599
JNUCC-1_00007		750	Putative RNA-binding protein YlmH	J:COG2302
JNUCC-1_00008		282	Uncharacterized membrane protein YlmG	S:COG0762
JNUCC-1_00009		432	Cell division protein SepF	S:COG1799
JNUCC-1_00010		696	UPF0001 protein	S:COG0325
JNUCC-1_00011	yfiH	810	Laccase domain protein YlmD	S:COG1496
JNUCC-1_00012		267	uncharacterized protein	S:COG1873
JNUCC-1_00013		780	RNA polymerase sigma-G factor	K:COG1191
JNUCC-1_00014		720	RNA polymerase sigma-35 factor	K:COG1191
JNUCC-1_00015	spoIIGA	921	Sporulation sigma-E factor-processing peptidase	S:ENOG4111PN7
JNUCC-1_00016		1146	Cell division protein FtsZ	D:COG0206
JNUCC-1_00017		936	Cell division protein FtsA	D:COG0849
JNUCC-1_00018		450	Cell division protein FtsA	D:COG0849
JNUCC-1_00019		786	Cell division protein DivIB	M:COG1589
JNUCC-1_00020		1110	Putative lipid II flippase FtsW	D:COG0772
JNUCC-1_00021	murD	1347	UDP-N-acetylmuramoyl-L-alanine-D-glutamate ligase	M:COG0771
JNUCC-1_00022	mraY	987	Phospho-N-acetylmuramoyl-pentapeptide-transferase	M:COG0472
JNUCC-1_00023	murF	1371	UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanine ligase	M:COG0770
JNUCC-1_00024	murE	297	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate--2,6-diaminopimelate ligase	M:COG0769
JNUCC-1_00025	murE	1173	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate--2,6-diaminopimelate ligase	M:COG0770

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_00026		735	Stage V sporulation protein D	M:COG0768
JNUCC-1_00027		1149	Stage V sporulation protein D	M:COG0768
JNUCC-1_00028		2202	Penicillin-binding protein 2B	M:COG0768
JNUCC-1_00029		378	Cell division protein FtsL	D:COG4839
JNUCC-1_00030	mraW|rsmH	792	16S rRNA (cytosine(1402)-N(4))-methyltransferase	M:COG0275
JNUCC-1_00031		432	Transcriptional regulator MraZ	S:COG2001
JNUCC-1_00032		1629	Putative cysteine ligase BshC	S:COG4365
JNUCC-1_00033		486	Uncharacterized N-acetyltransferase	S:ENOG4111MM0
JNUCC-1_00034		489	uncharacterized protein	K:ENOG4112D3N
JNUCC-1_00035	crt	582	Enoyl-CoA hydratase	I:COG1024
JNUCC-1_00036		174	50S ribosomal protein L32	J:COG0333
JNUCC-1_00037		525	uncharacterized protein	S:COG1399
JNUCC-1_00038		1218	UPF0348 protein	S:COG1323
JNUCC-1_00039		1029	uncharacterized protein	T:COG3480
JNUCC-1_00040		1206	Sporulation integral membrane protein YlbJ	S:COG3314
JNUCC-1_00041	coaD|kdtB	483	Pantetheine-phosphate adenylyltransferase	H:COG0669
JNUCC-1_00042	rsmD	579	16S rRNA (guanine(966)-N(2))-methyltransferase	L:COG0742
JNUCC-1_00043		273	UPF0298 protein	S:COG4471
JNUCC-1_00044		438	Regulatory protein YlbF	S:COG3679
JNUCC-1_00045		234	hypothetical protein	S:ENOG41126HU
JNUCC-1_00046		399	uncharacterized protein	S:ENOG4112AE1
JNUCC-1_00047		369	uncharacterized protein	S:ENOG4111TQW
JNUCC-1_00048		1059	UPF0118 membrane protein	S:COG0628
JNUCC-1_00049		906	Protein CtaG	S:COG3336
JNUCC-1_00050	coxD|ctaF	321	Cytochrome-c oxidase	C:COG3125

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_00051	coxC|ctaE	624	Cytochrome-c oxidase	C:COG1845
JNUCC-1_00052	coxA|ctaD	1854	Cytochrome-c oxidase	C:COG0843
JNUCC-1_00053	coxB|ctaC	1059	Cytochrome-c oxidase	C:COG1622|C:COG2857
JNUCC-1_00054		279	hypothetical protein	
JNUCC-1_00055		960	Heme A synthase	O:COG1612
JNUCC-1_00056		1188	Putative lipid II flippase FtsW	D:COG0772
JNUCC-1_00057		285	UPF0358 protein	S:COG4838
JNUCC-1_00058		489	uncharacterized protein	S:ENOG4111QGZ
JNUCC-1_00059		603	Uncharacterized lipoprotein YlaJ	S:ENOG4111U9D
JNUCC-1_00060		252	hypothetical protein	S:ENOG410ZGZW
JNUCC-1_00061		204	uncharacterized protein	S:COG4896
JNUCC-1_00062		312	Uncharacterized membrane protein YlaH	S:ENOG4111YNM
JNUCC-1_00063		177	hypothetical protein	
JNUCC-1_00064	IMPA|suhB	816	Inositol-phosphate phosphatase	G:COG0483
JNUCC-1_00065		192	hypothetical protein	S:ENOG410XZ2C
JNUCC-1_00066		621	UPF0637 protein	S:COG4493
JNUCC-1_00067		288	UPF0223 protein	S:COG4476
JNUCC-1_00068	fabK	714	Enoyl-[acyl-carrier-protein] reductase (NADH)	S:COG2070
JNUCC-1_00069	ncd2|npd	270	Nitronate monooxygenase	S:COG2070
JNUCC-1_00070		111	hypothetical protein	
JNUCC-1_00071		885	Peptidoglycan-N-acetylglucosamine deacetylase	S:COG3211
JNUCC-1_00072		1596	High-affinity choline transport protein	P:COG1292
JNUCC-1_00073	DLD|lpd|pdhD	1410	Dihydrolipoyl dehydrogenase	C:COG1249
JNUCC-1_00074	DLAT|aceF|pdhC	1302	Dihydrolipoyllysine-residue acetyltransferase	C:COG0508
JNUCC-1_00075	PDHB|pdhB	978	Pyruvate dehydrogenase (acetyl-transferring)	C:COG0022

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_00076	PDHA|pdhA	1083	Pyruvate dehydrogenase (acetyl-transferring)	C:COG1071
JNUCC-1_00077		669	Uncharacterized lipoprotein YkyA	S:ENOG4112BHZ
JNUCC-1_00078	PDF|def	552	Peptide deformylase	J:COG0242
JNUCC-1_00079		210	UPF0356 protein	S:COG5503
JNUCC-1_00080	rnj	1668	Ribonuclease J1	S:COG0595
JNUCC-1_00081		663	Ktr system potassium uptake protein	P:COG0569
JNUCC-1_00082		1842	Uncharacterized ABC transporter ATP-binding protein YknV	V:COG1132
JNUCC-1_00083		1749	Uncharacterized ABC transporter ATP-binding protein YknU	V:COG1132
JNUCC-1_00084		453	Thiol-disulfide oxidoreductase YkuV	O:COG0526
JNUCC-1_00085	PRDX2_4|ahpC	543	Peroxiredoxin	O:COG0450
JNUCC-1_00086		843	Uncharacterized MscS family protein YkuT	M:COG0668
JNUCC-1_00087		441	CBS domain-containing protein YkuL	S:COG0517
JNUCC-1_00088		300	Transcriptional repressor SdpR	K:COG0640
JNUCC-1_00089		903	Cadmium, cobalt and zinc/H(+)-K(+) antiporter	P:COG1230
JNUCC-1_00090		852	Uncharacterized metallophosphoesterase YkuE	S:COG1408
JNUCC-1_00091		477	uncharacterized protein	S:ENOG4111WDJ
JNUCC-1_00092		453	hypothetical protein	
JNUCC-1_00093		1284	hypothetical protein	L:COG3547
JNUCC-1_00094		693	Iron-sulfur cluster repair protein YtfE	D:COG2846
JNUCC-1_00095		135	hypothetical protein	
JNUCC-1_00096		183	hypothetical protein	
JNUCC-1_00097	lepB	531	Signal peptidase I	U:COG0681
JNUCC-1_00098		1158	hypothetical protein	S:ENOG4111GGI
JNUCC-1_00099	degP|htrA	1137	Peptidase Do	O:COG0265
JNUCC-1_00100	yegE	1977	Diguanylate cyclase	T:ENOG410XNMH

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_00101		1362	Ktr system potassium uptake protein	P:COG0168
JNUCC-1_00102		411	uncharacterized protein	S:ENOG41125JA
JNUCC-1_00103	moaA|CNX2	1023	GTP 3′,8-cyclase	H:COG2896
JNUCC-1_00104	moeA	1281	Molybdopterin molybdotransferase	H:COG0303
JNUCC-1_00105		207	hypothetical protein	S:ENOG41125GP
JNUCC-1_00106		459	hypothetical protein	S:ENOG410Y74D
JNUCC-1_00107		324	Stage V sporulation protein AC	S:ENOG4111PFY
JNUCC-1_00108		879	Stage V sporulation protein AD	S:ENOG410XNPK
JNUCC-1_00109		138	hypothetical protein	S:ENOG410XNPK
JNUCC-1_00110		309	Stage V sporulation protein AEB	S:ENOG4111UXX
JNUCC-1_00111		204	hypothetical protein	S:ENOG41125GP
JNUCC-1_00112		858	UPF0702 transmembrane protein YrbG	S:COG2323
JNUCC-1_00113		531	uncharacterized protein	S:COG2427
JNUCC-1_00114	fdoG|fdhF|fdwA	2937	Formate dehydrogenase	C:COG3383
JNUCC-1_00115		1422	Uncharacterized membrane protein YhfA	S:ENOG410XQ4W
JNUCC-1_00116		573	Thiamine transporter ThiT	S:COG3859
JNUCC-1_00117	pepF|pepB	1779	Oligoendopeptidase F, plasmid	E:COG1164
JNUCC-1_00118	ACO|acnA	1944	Aconitate hydratase	C:COG1048
JNUCC-1_00119		861	uncharacterized protein	V:COG2720
JNUCC-1_00120		252	hypothetical protein	
JNUCC-1_00121		102	hypothetical protein	
JNUCC-1_00122	ndh	1215	NADH dehydrogenase	C:COG1252
JNUCC-1_00123	alkA	651	DNA-3-methyladenine glycosylase II	L:COG0122
JNUCC-1_00124	idnO	696	Gluconate 5-dehydrogenase	S:ENOG410XNW1
JNUCC-1_00125		1389	uncharacterized protein	S:COG2304

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_00126	dacB	414	D-alanyl-D-alanine carboxypeptidase DacC	M:COG2027
JNUCC-1_00127	dacB	1149	D-alanyl-D-alanine carboxypeptidase	M:COG2027
JNUCC-1_00128		1125	Putative transposase	L:COG3385
JNUCC-1_00129		255	hypothetical protein	
JNUCC-1_00130	ltrA	1260	RNA-directed DNA polymerase	L:COG3344
JNUCC-1_00131		1146	Multidrug resistance protein	G:COG0477
JNUCC-1_00132		1410	Multidrug resistance protein	P:ENOG410XNN3
JNUCC-1_00134		780	hypothetical protein	P:COG0614
JNUCC-1_00135		690	hypothetical protein	M:COG2885
JNUCC-1_00136		1821	hypothetical protein	S:ENOG410XQKS
JNUCC-1_00137		690	Anaerobic regulatory protein	T:COG0664
JNUCC-1_00138		195	Sec-independent protein translocase protein TatAd	U:ENOG410XUF0
JNUCC-1_00139		591	hypothetical protein	
JNUCC-1_00140	phsA|psrA	3099	Thiosulfate reductase (quinone)	C:COG0243
JNUCC-1_00141		687	hypothetical protein	C:COG5557
JNUCC-1_00142		585	Putative dimethyl sulfoxide reductase membrane subunit	C:COG5557
JNUCC-1_00143		885	Tetrathionate reductase subunit B	C:COG0437
JNUCC-1_00144	qoxC	573	Menaquinol oxidase (H(+)-transporting)	C:COG1845
JNUCC-1_00145	qoxB	1923	Menaquinol oxidase (H(+)-transporting)	C:COG0843
JNUCC-1_00146	qoxA	717	Menaquinol oxidase (H(+)-transporting)	C:COG1622
JNUCC-1_00147	tsdA	228	Thiosulfate dehydrogenase	
JNUCC-1_00148	tsdA	705	Thiosulfate dehydrogenase	C:COG3258
JNUCC-1_00149	PPIB|ppiB	684	Peptidylprolyl isomerase	O:COG0652
JNUCC-1_00150		90	hypothetical protein	
JNUCC-1_00151		570	hypothetical protein	S:ENOG4111GYN

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_00152		456	hypothetical protein	O:COG0071
JNUCC-1_00153		603	Chemotaxis response regulator protein-glutamate methylesterase	T:COG2197
JNUCC-1_00154	desK	1128	Histidine kinase	T:COG4585
JNUCC-1_00155	FAD6|desA	1053	Acyl-lipid (n+3)-(Z)-desaturase (ferredoxin)	I:COG3239
JNUCC-1_00156		375	hypothetical protein	
JNUCC-1_00157		780	uncharacterized protein	O:COG5504
JNUCC-1_00158		294	hypothetical protein	
JNUCC-1_00159		108	hypothetical protein	
JNUCC-1_00160		141	hypothetical protein	
JNUCC-1_00161	lepB	540	Signal peptidase I	U:COG0681
JNUCC-1_00162		588	hypothetical protein	
JNUCC-1_00163		774	hypothetical protein	S:ENOG410YRFR
JNUCC-1_00164		435	hypothetical protein	
JNUCC-1_00165		912	uncharacterized protein	S:ENOG410XTDQ
JNUCC-1_00166		207	hypothetical protein	S:ENOG410ZC2K
JNUCC-1_00167		162	hypothetical protein	
JNUCC-1_00168		915	Uncharacterized membrane protein YndG	S:ENOG410YXTH
JNUCC-1_00169	thiO	1176	Glycine oxidase	E:COG0665
JNUCC-1_00170	soxB	273	Sarcosine oxidase	S:COG0446
JNUCC-1_00171	soxA	402	Sarcosine oxidase	S:COG0446
JNUCC-1_00172	soxA	1215	Sarcosine oxidase	S:COG0446
JNUCC-1_00173		1587	Peptide chain release factor	J:COG4108
JNUCC-1_00174		420	hypothetical protein	S:COG3296
JNUCC-1_00175		870	Glycine betaine-binding protein OpuAC	E:COG2113
JNUCC-1_00176		159	hypothetical protein	

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_00178		1188	Nuclease SbcCD subunit	L:COG0420
JNUCC-1_00179	pcaC	381	4-carboxymuconolactone decarboxylase	S:COG0599
JNUCC-1_00180		423	Protein	O:COG1765
JNUCC-1_00181		1257	Uncharacterized MFS-type transporter	G:ENOG41106BF
JNUCC-1_00182		153	hypothetical protein	S:ENOG410Z43B
JNUCC-1_00183		909	hypothetical protein	S:ENOG4111I5M
JNUCC-1_00184		1191	ATP-binding/permease protein CydD	V:COG4987
JNUCC-1_00185		594	ATP-binding/permease protein CydD	V:COG4987
JNUCC-1_00186		1731	ATP-binding/permease protein CydC	V:COG4988
JNUCC-1_00187	cydB	1014	Ubiquinol oxidase (electrogenic, non H(+)-transporting)	C:COG1294
JNUCC-1_00188	cydA	1407	Ubiquinol oxidase (electrogenic, non H(+)-transporting)	C:COG1271
JNUCC-1_00189		1605	Glycine betaine transporter BetP	P:COG1292
JNUCC-1_00190		399	hypothetical protein	
JNUCC-1_00191		924	hypothetical protein	S:ENOG4111GRW
JNUCC-1_00192		606	hypothetical protein	S:COG4990
JNUCC-1_00193		2184	Putative membrane protein	S:COG2409
JNUCC-1_00194		408	uncharacterized protein	J:COG1098
JNUCC-1_00195		825	hypothetical protein	S:COG1408
JNUCC-1_00196	PTS-Glc-EIIA|crr	495	Lactose permease	G:COG1263
JNUCC-1_00197		819	Levansucrase and sucrase synthesis operon antiterminator	K:COG3711
JNUCC-1_00198	PTS-Glc1-EIIA|ptsG|glcA|glcB	1485	Protein-N(pi)-phosphohistidine-D-glucose phosphotransferase	G:COG1263
JNUCC-1_00199		564	uncharacterized protein	S:ENOG4111GPK
JNUCC-1_00200		330	Putative DNA-binding protein YwzG	K:COG1695
JNUCC-1_00201		678	hypothetical protein	S:ENOG41127MF
JNUCC-1_00202		183	hypothetical protein	S:ENOG410ZR1M

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_00203		690	Uncharacterized NAD(P)H oxidoreductase YrkL	S:COG2249
JNUCC-1_00204	glpQ|ugpQ	1809	Glycerophosphodiester phosphodiesterase	C:COG0584
JNUCC-1_00205		558	Macro domain-containing protein	S:COG2110
JNUCC-1_00206		297	hypothetical protein	V:COG0534
JNUCC-1_00207		1056	Multidrug export protein MepA	V:COG0534
JNUCC-1_00208		615	hypothetical protein	S:ENOG410ZYS9
JNUCC-1_00209		363	hypothetical protein	S:ENOG411255S
JNUCC-1_00210		198	uncharacterized protein	S:ENOG410ZBY0
JNUCC-1_00211		132	hypothetical protein	
JNUCC-1_00212		342	hypothetical protein	S:ENOG411299W
JNUCC-1_00213	pphA	690	Protein-serine/threonine phosphatase	T:COG0639
JNUCC-1_00214	tehB	564	Tellurite methyltransferase	Q:COG0500
JNUCC-1_00215	fabG	726	3-oxoacyl-[acyl-carrier-protein] reductase	S:ENOG410XNW1
JNUCC-1_00216		117	hypothetical protein	S:ENOG41125W6
JNUCC-1_00217	ALDO	885	Fructose-bisphosphate aldolase	G:COG3588
JNUCC-1_00218	ftnA|ftn	624	Bacterial non-heme ferritin	P:COG1528
JNUCC-1_00219		1341	Uncharacterized amino acid permease YvbW	E:COG0531
JNUCC-1_00220		957	Formamidase	C:COG2421
JNUCC-1_00221	cobU|cobT	1071	Nicotinate-nucleotide-dimethylbenzimidazole phosphoribosyltransferase	L:COG0675
JNUCC-1_00222		900	Uncharacterized transposase-like protein	L:COG2801
JNUCC-1_00223		690	hypothetical protein	L:COG2963
JNUCC-1_00224	codA	1269	Cytosine deaminase	F:COG0402
JNUCC-1_00225		1269	Cytosine permease	F:COG1457
JNUCC-1_00226		201	uncharacterized protein	S:ENOG410XUTA
JNUCC-1_00227		579	Ribonuclease	L:COG0328

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_00228		882	Uncharacterized transporter YxxF	S:ENOG410XQC3
JNUCC-1_00229		1971	Bacitracin export permease protein BceB	V:COG0577
JNUCC-1_00230		762	Bacitracin export ATP-binding protein BceA	E:COG4175
JNUCC-1_00231	bceS	987	Histidine kinase	T:COG0642
JNUCC-1_00232		693	Response regulator ArlR	T:COG0745
JNUCC-1_00233		750	Uncharacterized HTH-type transcriptional regulator FruR	K:COG1349
JNUCC-1_00234	pfkB	924	6-phosphofructokinase	G:COG1105
JNUCC-1_00235	PTS-Fru-EIIA|fruB	1884	Protein-N(pi)-phosphohistidine-D-fructose phosphotransferase	G:COG1299
JNUCC-1_00236		1458	Uncharacterized transporter YflA	E:COG1115
JNUCC-1_00237		483	hypothetical protein	
JNUCC-1_00238	qor|CRYZ	609	NADPH:quinone reductase	C:COG0604
JNUCC-1_00239		1521	Transposase	L:COG4584
JNUCC-1_00240		765	Putative ATP-binding protein in insertion sequence	L:COG1484
JNUCC-1_00241	qor|CRYZ	333	NADPH:quinone reductase	C:COG0604
JNUCC-1_00242		153	hypothetical protein	
JNUCC-1_00243		192	hypothetical protein	S:ENOG4111N6K
JNUCC-1_00244		969	Glycine betaine-binding protein OpuAC	E:COG2113
JNUCC-1_00245		1284	hypothetical protein	L:COG3547
JNUCC-1_00246		465	hypothetical protein	
JNUCC-1_00247	catB	1110	Muconate cycloisomerase	M:COG4948
JNUCC-1_00248		726	hypothetical protein	S:ENOG41123Q6
JNUCC-1_00249	menA	927	hypothetical protein	H:ENOG410ZXH3
JNUCC-1_00250		390	Sodium-dependent dicarboxylate transporter SdcS	P:COG0471
JNUCC-1_00251		927	Sodium-dependent low-affinity dicarboxylate transporter	P:COG0471
JNUCC-1_00252	cobU|cobT	1071	Nicotinate-nucleotide-dimethylbenzimidazole phosphoribosyltransferase	L:COG0675

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_00253		426	Sodium-dependent dicarboxylate transporter SdcS	P:COG0471
JNUCC-1_00254	amhX	1122	Amidohydrolase AmhX	E:COG1473
JNUCC-1_00255	mutT|NUDT15|MTH2	912	8-oxo-dGTP diphosphatase	S:ENOG41122J1
JNUCC-1_00256		1044	hypothetical protein	S:ENOG410ZU16
JNUCC-1_00257		261	hypothetical protein	S:ENOG4111QPN
JNUCC-1_00258		219	hypothetical protein	S:ENOG4111QPN
JNUCC-1_00259		1248	hypothetical protein	S:ENOG410ZKMU
JNUCC-1_00260	cysE	300	Serine O-acetyltransferase	S:COG2151
JNUCC-1_00261	hemQ	747	Putative heme-dependent peroxidase	S:COG3253
JNUCC-1_00262	allC	1230	Allantoate deiminase	E:COG0624
JNUCC-1_00263		213	hypothetical protein	
JNUCC-1_00264		639	Gluconate 2-dehydrogenase (acceptor)	G:ENOG410ZF7P
JNUCC-1_00265		1755	Gluconate 2-dehydrogenase (acceptor)	E:COG2303
JNUCC-1_00266		264	Transcriptional regulator SplA	S:ENOG41128IQ
JNUCC-1_00267	splB	1029	Spore photoproduct lyase	L:COG1533
JNUCC-1_00268		576	hypothetical protein	S:ENOG4111H48
JNUCC-1_00269		270	hypothetical protein	S:COG2110
JNUCC-1_00270		897	Putative transposase in snaA-snaB intergenic region	L:COG0675
JNUCC-1_00271	mutT|NUDT15|MTH2	558	8-oxo-dGTP diphosphatase	J:COG1670
JNUCC-1_00272	pepT	1230	Tripeptide aminopeptidase	E:COG2195
JNUCC-1_00273		2238	Phage infection protein	S:COG1511
JNUCC-1_00274		555	Putative metallophosphoesterase	S:COG0622
JNUCC-1_00275		1581	Uncharacterized transporter YebQ	P:ENOG410XNNX
JNUCC-1_00276		1227	ATP-dependent protease	L:COG3464
JNUCC-1_00277		1494	Uncharacterized transporter YclF	E:COG3104

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_00278	panC	900	Pantoate--beta-alanine ligase (AMP-forming)	S:ENOG410YMGN
JNUCC-1_00279		1704	Uncharacterized membrane protein YkoS	S:ENOG410XSIV
JNUCC-1_00280	wecE|rffA	1122	dTDP-4-amino-4,6-dideoxygalactose transaminase	E:COG0399
JNUCC-1_00281		357	Probable 4-amino-4-deoxy-L-arabinose-phosphoundecaprenol flippase subunit ArnE	EG:COG0697
JNUCC-1_00282		684	hypothetical protein	S:ENOG41125W0
JNUCC-1_00283	gtrB|csbB	945	Uncharacterized glycosyltransferase	M:COG0463
JNUCC-1_00284	rfbB|rffG	1032	dTDP-glucose 4,6-dehydratase	M:COG1088
JNUCC-1_00285	rfbA|rffH	927	Glucose-1-phosphate thymidylyltransferase	M:COG1209
JNUCC-1_00286	rlmI	1191	23S rRNA (cytosine(1962)-C(5))-methyltransferase	S:COG1092
JNUCC-1_00287		180	hypothetical protein	
JNUCC-1_00288		654	hypothetical protein	S:ENOG411249K
JNUCC-1_00289		276	hypothetical protein	
JNUCC-1_00290		294	hypothetical protein	S:COG4841
JNUCC-1_00291		1551	Glycine betaine transporter BetL	P:COG1292
JNUCC-1_00292		1227	ATP-dependent protease	L:COG3464
JNUCC-1_00293	surA	783	Peptidylprolyl isomerase	S:ENOG4111XMR
JNUCC-1_00294	dhaA	903	Haloalkane dehalogenase	S:ENOG410ZVHB
JNUCC-1_00295		531	hypothetical protein	S:ENOG410Z7P3
JNUCC-1_00297	msbA	1731	Uncharacterized ABC transporter ATP-binding protein YfiC	V:COG1132
JNUCC-1_00298		1818	Uncharacterized ABC transporter ATP-binding protein YfiC	V:COG1132
JNUCC-1_00299		753	uncharacterized protein	P:COG2382
JNUCC-1_00300	thpR	519	RNA 2′,3′-cyclic 3′-phosphodiesterase	J:COG1514
JNUCC-1_00301		423	Uncharacterized N-acetyltransferase YjcF	S:ENOG41121PI
JNUCC-1_00302		708	UPF0702 transmembrane protein YetF	S:COG2323
JNUCC-1_00303		336	hypothetical protein	

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_00304		456	hypothetical protein	S:ENOG4112BG2
JNUCC-1_00305		525	hypothetical protein	M:ENOG410Z73J
JNUCC-1_00306		1359	Magnesium transporter MgtE	P:COG2239
JNUCC-1_00307		1170	Rod shape-determining protein RodA	D:COG0772
JNUCC-1_00308		741	Protein-serine/threonine phosphatase	T:COG0639
JNUCC-1_00309	rluD	891	23S rRNA pseudouridine synthase	J:COG0564
JNUCC-1_00310	ppnK|NADK	816	NAD(+) kinase	G:COG0061
JNUCC-1_00311		609	GTP diphosphokinase	S:COG2357
JNUCC-1_00312	GST|gst	573	Glutathione transferase	S:COG4116
JNUCC-1_00313		381	Group 2 truncated hemoglobin YjbI	S:COG2346
JNUCC-1_00314		909	UPF0413 protein	Q:COG2761
JNUCC-1_00315		180	Uncharacterized membrane protein YizD	
JNUCC-1_00316	pepF|pepB	1818	Group B oligopeptidase PepB	E:COG1164
JNUCC-1_00317		1179	Putative competence protein CoiA	S:COG4469
JNUCC-1_00318		684	Adapter protein MecA	O:COG4862
JNUCC-1_00319		396	Regulatory protein Spx	P:COG1393
JNUCC-1_00320		594	Putative acetyltransferase YjbC	S:ENOG4111G6J
JNUCC-1_00321		1227	hypothetical protein	S:COG1306
JNUCC-1_00322	WARS|trpS	990	Tryptophan-tRNA ligase	J:COG0180
JNUCC-1_00323		759	UPF0736 protein	S:ENOG4110YGV
JNUCC-1_00324	ltrA	1260	RNA-directed DNA polymerase	L:COG3344
JNUCC-1_00325	fabF	1239	Beta-ketoacyl-[acyl-carrier-protein] synthase II	I:COG0304
JNUCC-1_00326	fabH	939	Beta-ketoacyl-[acyl-carrier-protein] synthase III	I:COG0332
JNUCC-1_00327		981	Transcriptional activator protein med	S:COG1744
JNUCC-1_00328		615	hypothetical protein	S:ENOG410YWHX

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_00329		180	hypothetical protein	S:ENOG410Z4HK
JNUCC-1_00330		366	hypothetical protein	S:ENOG410Y06K
JNUCC-1_00331	bacA	819	Undecaprenyl-diphosphate phosphatase	V:COG1968
JNUCC-1_00332		1146	Coenzyme PQQ synthesis protein	S:COG0535
JNUCC-1_00333		453	hypothetical protein	T:COG0664
JNUCC-1_00334		234	Molybdopterin synthase sulfur carrier subunit	H:COG1977
JNUCC-1_00335	MOCS2B|moaE	474	Molybdopterin synthase	H:COG0314
JNUCC-1_00336		615	Probable molybdopterin-guanine dinucleotide biosynthesis adapter protein	H:COG1763
JNUCC-1_00337		312	MIP18 family protein YitW	S:COG2151
JNUCC-1_00338		762	Esterase	S:COG1073
JNUCC-1_00339	ycsE|yitU|ywtE	840	5-amino-6-(5-phospho-D-ribitylamino)uracil phosphatase	S:COG0561
JNUCC-1_00340		150	hypothetical protein	S:ENOG410XYB3
JNUCC-1_00341		186	hypothetical protein	
JNUCC-1_00342		393	hypothetical protein	
JNUCC-1_00343		264	hypothetical protein	S:ENOG410ZMZS
JNUCC-1_00344		471	hypothetical protein	S:ENOG410Z6RC
JNUCC-1_00345		468	UPF0750 membrane protein YitT	S:COG1284
JNUCC-1_00346		381	UPF0750 membrane protein YitT	S:COG1284
JNUCC-1_00347		867	DegV domain-containing protein	S:COG1307
JNUCC-1_00348	fabG	2178	3-oxoacyl-[acyl-carrier-protein] reductase	S:ENOG410XTIV
JNUCC-1_00349		906	hypothetical protein	L:COG3666
JNUCC-1_00350		744	hypothetical protein	L:COG3666
JNUCC-1_00351		1308	hypothetical protein	L:COG3666
JNUCC-1_00352		168	hypothetical protein	
JNUCC-1_00353	ltaS	1842	Phosphatidylglycerol-membrane-oligosaccharide glycerophosphotransferase	M:COG1368

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_00354	phnW	1611	2-aminoethylphosphonate--pyruvate transaminase	E:COG0075
JNUCC-1_00355	plsY	420	Glycerol-3-phosphate 1-O-acyltransferase	S:COG0344
JNUCC-1_00356	AMY|amyA|malS	1473	Alpha-amylase	G:COG0366
JNUCC-1_00357		363	UPF0344 protein	S:ENOG411295K
JNUCC-1_00358	rocD|OAT	1194	Ornithine aminotransferase	E:COG4992
JNUCC-1_00359		558	hypothetical protein	S:ENOG4111X7P
JNUCC-1_00360		636	hypothetical protein	S:COG1999
JNUCC-1_00361	coxA|ctaD	1686	Cytochrome-c oxidase	C:COG0843
JNUCC-1_00362	coxB|ctaC	462	Cytochrome-c oxidase	C:COG1622
JNUCC-1_00363		147	hypothetical protein	
JNUCC-1_00364	addA	1419	ATP-dependent helicase/nuclease subunit	L:COG1074
JNUCC-1_00365	addA	2307	ATP-dependent helicase/nuclease subunit	L:COG1074
JNUCC-1_00366	addB	3231	ATP-dependent helicase/deoxyribonuclease subunit B	L:COG3857
JNUCC-1_00367	addB	282	ATP-dependent helicase/deoxyribonuclease subunit	L:COG3857
JNUCC-1_00368		279	Uncharacterized membrane protein YhjE	S:COG0398
JNUCC-1_00369		372	Uncharacterized membrane protein YhjE	S:COG0398
JNUCC-1_00370		390	uncharacterized protein	S:ENOG41129Y8
JNUCC-1_00371		528	hypothetical protein	K:COG4903
JNUCC-1_00372		192	Putative NAD(P)H nitroreductase	C:COG0778
JNUCC-1_00373	nfnB|nfsB	483	Putative NAD(P)H nitroreductase YfkO	C:COG0778
JNUCC-1_00374	lplA|lplJ	996	Lipoate-protein ligase	H:COG0095
JNUCC-1_00375	rnz	726	Ribonuclease Z	S:COG1234
JNUCC-1_00376	pepF|pepB	1815	Oligoendopeptidase F like protein	E:COG1164
JNUCC-1_00377		2238	Diguanylate cyclase DosC	T:ENOG410XNMH
JNUCC-1_00378	PPOX|hemY	1404	Protoporphyrinogen oxidase	H:COG1232

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_00379	hemH|FECH	939	Protoporphyrin ferrochelatase	H:COG0276
JNUCC-1_00380	hemE|UROD	1071	Uroporphyrinogen decarboxylase	H:COG0407
JNUCC-1_00381		741	Penicillin-binding protein 1F	M:COG0744
JNUCC-1_00382	pbp2A	1458	Peptidoglycan glycosyltransferase	M:COG0744
JNUCC-1_00383	mhuD|hmoB	507	Heme oxygenase (mycobilin-producing)	S:COG2329
JNUCC-1_00384		468	hypothetical protein	O:COG0526
JNUCC-1_00385		435	Probable disulfide formation protein	O:COG1495
JNUCC-1_00386		630	Chemotaxis response regulator protein-glutamate methylesterase of group 1 operon	T:COG3279
JNUCC-1_00387	liaS	1068	Histidine kinase	T:COG4585
JNUCC-1_00388		768	Protein LiaF	S:COG4758
JNUCC-1_00389	bcrC	636	Undecaprenyl-diphosphate phosphatase	I:COG0671
JNUCC-1_00390	bfr	426	Ferroxidase	P:ENOG4111QFN
JNUCC-1_00391	K01436	1170	Uncharacterized hydrolase	E:COG1473
JNUCC-1_00392		1218	Protein EcsB	U:COG4473
JNUCC-1_00393		732	sn-glycerol-3-phosphate import ATP-binding protein UgpC	E:COG0410
JNUCC-1_00394		426	Protein HitA	S:ENOG4111MVJ
JNUCC-1_00395		519	Probable tryptophan transport protein	S:ENOG4111UPK
JNUCC-1_00396		369	Uncharacterized membrane protein YhaH	S:COG4980
JNUCC-1_00397		969	Glycine betaine-binding protein OpuAC	E:COG2113
JNUCC-1_00398		843	Bicarbonate transport system permease protein CmpB	E:COG4176
JNUCC-1_00399	proV	1212	Quaternary-amine-transporting ATPase	E:COG4175
JNUCC-1_00400		345	Putative HTH-type transcriptional regulator	K:COG1510
JNUCC-1_00401		546	Uncharacterized membrane protein YhaJ	S:ENOG41121QX
JNUCC-1_00402		186	hypothetical protein	S:ENOG410ZC2Y
JNUCC-1_00403	prsA	939	Peptidylprolyl isomerase	O:COG0760

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_00404		306	Sporulation protein YhaL	S:ENOG410XX7D
JNUCC-1_00405	cbf|cbf1	945	3′-5′ exoribonuclease YhaM	S:COG3481
JNUCC-1_00406		543	Putative HTH-type transcriptional regulator YvaV	K:COG1510
JNUCC-1_00407		2988	uncharacterized protein	S:COG4717
JNUCC-1_00408		1233	Uncharacterized metallophosphoesterase YhaO	L:COG0420
JNUCC-1_00409		186	hypothetical protein	S:ENOG410XWXD
JNUCC-1_00410	ltrA	1260	RNA-directed DNA polymerase	L:COG3344
JNUCC-1_00411	ECI2|PECI	777	Delta(3)-Delta(2)-enoyl-CoA isomerase	I:COG1024
JNUCC-1_00412		783	Chaperone protein HtpG	O:COG0326
JNUCC-1_00413		1104	Chaperone protein HtpG	O:COG0326
JNUCC-1_00414		363	Putative fluoride ion transporter CrcB	D:COG0239
JNUCC-1_00415		381	Putative fluoride ion transporter CrcB	D:COG0239
JNUCC-1_00416	dapdh	987	Diaminopimelate dehydrogenase	E:ENOG410XPX2
JNUCC-1_00417	dge1	1110	Diguanylate cyclase	T:ENOG410XNMH
JNUCC-1_00418		858	hypothetical protein	S:COG3342
JNUCC-1_00419	fabG	366	3-oxoacyl-[acyl-carrier-protein] reductase	S:COG1028
JNUCC-1_00420	fabG	396	3-oxoacyl-[acyl-carrier-protein] reductase	S:COG1028
JNUCC-1_00421		600	Putative gamma-glutamylcyclotransferase YkqA	S:ENOG41126S6
JNUCC-1_00422		531	Uncharacterized membrane protein YozB	S:COG2322
JNUCC-1_00423	ltrA	1260	RNA-directed DNA polymerase	L:COG3344
JNUCC-1_00424		1800	K(+)/H(+) antiporter NhaP2	P:COG0025
JNUCC-1_00425	TMEM86B	654	Lysoplasmalogenase	S:COG3714
JNUCC-1_00426		2220	Putative membrane protein	S:COG2409
JNUCC-1_00427		1698	hypothetical protein	D:COG5279
JNUCC-1_00428		330	hypothetical protein	K:COG1396

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_00429	HMGCL|hmgL	906	Hydroxymethylglutaryl-CoA lyase	E:COG0119
JNUCC-1_00430		1644	hypothetical protein	S:ENOG410XP5I
JNUCC-1_00431	lptB	801	Zinc import ATP-binding protein ZnuC	P:COG1121
JNUCC-1_00432		363	UPF0342 protein	S:COG3679
JNUCC-1_00433		897	uncharacterized protein	K:COG2508
JNUCC-1_00434	malK|mtlK|thuK	1098	Phosphonates import ATP-binding protein PhnC	G:COG3839
JNUCC-1_00435		198	Small, acid-soluble spore protein	S:ENOG411226C
JNUCC-1_00436	fumC|FH	1386	Fumarate hydratase	C:COG0114
JNUCC-1_00437		915	hypothetical protein	S:ENOG4111JFU
JNUCC-1_00438		861	Uncharacterized MFS-type transporter YxiO	G:COG2270
JNUCC-1_00439		489	Autophagy-related protein 22-1	G:COG2270
JNUCC-1_00440		1458	Heme-based aerotactic transducer HemAT	S:COG0840
JNUCC-1_00441		234	hypothetical protein	S:ENOG410ZCCH
JNUCC-1_00442		1221	Bacillibactin exporter	P:ENOG410XNN3
JNUCC-1_00443		882	Uncharacterized transporter YdbO	P:COG1230
JNUCC-1_00444		540	Uncharacterized N-acetyltransferase YuaI	S:ENOG4111NHW
JNUCC-1_00445		294	hypothetical protein	E:ENOG411249J
JNUCC-1_00446		726	Uncharacterized membrane protein	E:COG1296
JNUCC-1_00447	map	753	Methionyl aminopeptidase	J:COG0024
JNUCC-1_00448	yueD	762	Benzil reductase ((S)-benzoin forming)	S:ENOG4111N99
JNUCC-1_00449	DUG2	1371	Succinyl-diaminopimelate desuccinylase	E:COG0624
JNUCC-1_00450		642	Lipoprotein YhcN	K:ENOG41124IJ
JNUCC-1_00451		237	uncharacterized protein	S:ENOG4112ABM
JNUCC-1_00452	degP|htrA	828	Peptidase Do	O:COG0265
JNUCC-1_00453		2028	Probable multidrug resistance ABC transporter ATP-binding/permease protein YheH	V:COG1132

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_00454		1629	Probable multidrug resistance ABC transporter ATP-binding/permease protein YheI	V:COG1132
JNUCC-1_00455		240	hypothetical protein	
JNUCC-1_00456	proV	1233	Quaternary-amine-transporting ATPase	E:COG4175
JNUCC-1_00457		861	Glycine betaine transport system permease protein OpuAB	E:COG4176
JNUCC-1_00458		999	hypothetical protein	E:COG2113
JNUCC-1_00459	murG	1071	Undecaprenyldiphospho-muramoylpentapeptide beta-N-acetylglucosaminyltransferase	M:COG0707
JNUCC-1_00460	DLST|sucB	1308	Dihydrolipoyllysine-residue succinyltransferase	C:COG0508
JNUCC-1_00461	OGDH|sucA	2925	Oxoglutarate dehydrogenase (succinyl-transferring)	C:COG0567
JNUCC-1_00462		102	hypothetical protein	
JNUCC-1_00463	trmL|cspR	474	tRNA (cytidine(34)-2′-O)-methyltransferase	J:COG0219
JNUCC-1_00464		843	Uncharacterized 35.5 kDa protein in gldA 3′region	S:ENOG4111IEN
JNUCC-1_00465	ogt|MGMT	540	Methylated-DNA--[protein]-cysteine S-methyltransferase	L:COG0350
JNUCC-1_00466	queG	1161	Epoxyqueuosine reductase	C:COG1600
JNUCC-1_00467		1704	hypothetical protein	S:COG3044
JNUCC-1_00469	dat	882	D-amino-acid transaminase	E:COG0115
JNUCC-1_00470	APEH	2007	Acylaminoacyl-peptidase	E:COG1506
JNUCC-1_00471		960	uncharacterized protein	S:COG1073
JNUCC-1_00472		1101	Putative transport permease YfiN	V:COG0842
JNUCC-1_00473		1272	hypothetical protein	V:COG0842
JNUCC-1_00474		933	Putative ribose/galactose/methyl galactoside import ATP-binding protein	P:COG1120
JNUCC-1_00475		1194	Transposase for insertion sequence element IS905	L:COG3328
JNUCC-1_00476		723	Putative transposase InsK for insertion sequence element IS150	L:COG2801
JNUCC-1_00477		510	hypothetical protein	L:ENOG4111X46
JNUCC-1_00478		660	Chemotaxis response regulator protein-glutamate methylesterase	T:COG3279
JNUCC-1_00479	uhpB	1080	Histidine kinase	T:COG4585

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_00480	FAR	1098	Alcohol-forming fatty acyl-CoA reductase	Q:COG3320
JNUCC-1_00481		435	hypothetical protein	S:ENOG41122RI
JNUCC-1_00482	ampC	1119	Beta-lactamase	V:COG1680
JNUCC-1_00483	yvaK	759	Carboxylesterase	S:COG1647
JNUCC-1_00484		318	hypothetical protein	
JNUCC-1_00485		1413	Multidrug resistance protein Stp	G:COG2814
JNUCC-1_00486	glxK|garK	1143	Glycerate 2-kinase	G:COG1929
JNUCC-1_00487		1290	hypothetical protein	S:ENOG410ZWGT
JNUCC-1_00488		537	ECF RNA polymerase sigma-E factor	K:COG1595
JNUCC-1_00489	narB	2352	Ferredoxin--nitrate reductase	C:COG0243
JNUCC-1_00490		276	hypothetical protein	
JNUCC-1_00491		810	Protein FdhD like protein	C:COG1526
JNUCC-1_00492	uppS	537	Ditrans,polycis-undecaprenyl-diphosphate synthase ((2E,6E)-farnesyl-diphosphate specific)	I:COG0020
JNUCC-1_00493		1467	hypothetical protein	S:ENOG41100W0
JNUCC-1_00494		636	uncharacterized protein	S:ENOG410YK21
JNUCC-1_00495		333	Putative DNA-binding protein YwzG	K:COG1695
JNUCC-1_00496	PRODH	978	Proline dehydrogenase	E:COG0506
JNUCC-1_00497	pfpI	516	Protein deglycase	S:COG0693
JNUCC-1_00498		144	hypothetical protein	
JNUCC-1_00499		306	hypothetical protein	
JNUCC-1_00500		192	hypothetical protein	S:ENOG410Y0GA
JNUCC-1_00501		219	hypothetical protein	S:ENOG410XVJW
JNUCC-1_00502		225	hypothetical protein	S:ENOG410ZIZC
JNUCC-1_00503	NUDT7	618	Peroxisomal coenzyme A diphosphatase NUDT7	L:COG0494
JNUCC-1_00504		111	hypothetical protein	

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_00505		1890	Uncharacterized ABC transporter ATP-binding protein YfmR	S:COG0488
JNUCC-1_00506	moeZR|moeBR	309	UPF0033 protein YrkF	P:COG0607
JNUCC-1_00507		1515	p-aminobenzoyl-glutamate transport protein	H:COG2978
JNUCC-1_00508		1341	hypothetical protein	S:ENOG41121Y4
JNUCC-1_00509	pydC	1257	Beta-ureidopropionase	E:COG0624
JNUCC-1_00510		1320	Indole-3-acetyl-aspartic acid hydrolase	E:COG1473
JNUCC-1_00511	hipO	1185	Hippurate hydrolase	E:COG1473
JNUCC-1_00512		726	Manganese transport system ATP-binding protein MntB	E:COG0411
JNUCC-1_00513		756	Arginine transport system permease protein ArtQ	E:COG0765
JNUCC-1_00514		834	Probable ABC transporter arginine-binding protein ArtJ	E:COG0834
JNUCC-1_00515	CYP152A	1260	Fatty-acid peroxygenase	Q:COG2124
JNUCC-1_00516		1314	hypothetical protein	S:ENOG4111TS1
JNUCC-1_00517		675	hypothetical protein	S:ENOG4111ZJB
JNUCC-1_00518		180	hypothetical protein	S:ENOG410XWAP
JNUCC-1_00519		156	hypothetical protein	S:ENOG410ZRTA
JNUCC-1_00520		159	hypothetical protein	
JNUCC-1_00521		603	Fatty acid metabolism regulator protein	K:ENOG410XUF9
JNUCC-1_00522	dagK	906	Diacylglycerol kinase (ATP)	I:COG1597
JNUCC-1_00523		1188	hypothetical protein	E:COG3616
JNUCC-1_00524	GULO	1320	L-gulonolactone oxidase	C:COG0277
JNUCC-1_00525	ABC.PA.A	1485	Polar-amino-acid-transporting ATPase	P:COG1129
JNUCC-1_00526		654	Uncharacterized ABC transporter permease protein YvrB	P:COG0609
JNUCC-1_00527		996	Uncharacterized ABC transporter substrate-binding lipoprotein YvrC	P:COG0614
JNUCC-1_00528		1596	Periplasmic oligopeptide-binding protein	E:COG0747
JNUCC-1_00529		879	uncharacterized protein	S:COG0714

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_00530		1920	uncharacterized protein	P:COG4548
JNUCC-1_00531		1239	Uncharacterized transporter YycB	G:ENOG4111JNW
JNUCC-1_00532		645	Lipid A export ATP-binding/permease protein MsbA	V:COG4988
JNUCC-1_00533		831	Probable iron export permease protein FetB	S:COG0390
JNUCC-1_00534		417	hypothetical protein	S:ENOG411298E
JNUCC-1_00535		315	hypothetical protein	
JNUCC-1_00536		273	hypothetical protein	S:ENOG410Z5XV
JNUCC-1_00537	narG|narZ|nxrA	936	Chlorate reductase subunit alpha	C:COG5013
JNUCC-1_00538	narG|narZ|nxrA	2751	Respiratory nitrate reductase 1 alpha chain	C:COG5013
JNUCC-1_00539	narH|narY|nxrB	1509	Nitrate reductase beta chain	C:COG1140
JNUCC-1_00540		636	Probable nitrate reductase molybdenum cofactor assembly chaperone NarJ	C:COG2180
JNUCC-1_00541	narI|narV	714	Respiratory nitrate reductase 1 gamma chain	C:COG2181
JNUCC-1_00542		708	Anaerobic regulatory protein	T:COG0664
JNUCC-1_00543		426	hypothetical protein	
JNUCC-1_00544		1038	uncharacterized protein	C:COG2141
JNUCC-1_00545		453	hypothetical protein	
JNUCC-1_00546		1278	Serpin A12	O:COG4826
JNUCC-1_00547		1077	Putative transposase	L:COG0675
JNUCC-1_00548		399	hypothetical protein	L:COG1943
JNUCC-1_00549	thiE	639	Thiamine phosphate synthase	H:COG0352
JNUCC-1_00550	thiM	333	Hydroxyethylthiazole kinase	H:COG2145
JNUCC-1_00551	thiM	468	Hydroxyethylthiazole kinase	H:COG2145
JNUCC-1_00552	thiD	801	Hydroxymethylpyrimidine kinase	H:COG0351
JNUCC-1_00553	ecfA1	330	hypothetical protein	S:COG4732
JNUCC-1_00554		183	hypothetical protein	S:COG4732

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_00555		498	UPF0699 transmembrane protein YdbS	S:COG3402
JNUCC-1_00556		1500	UPF0699 transmembrane protein YdbT	S:COG3428
JNUCC-1_00557		765	UPF0271 protein	S:COG1540
JNUCC-1_00558		510	KipI antagonist	E:COG1984
JNUCC-1_00559	atzF	399	Allophanate hydrolase	E:COG1984
JNUCC-1_00560		714	uncharacterized protein	E:COG2049
JNUCC-1_00561	prkC|stkP	1146	Non-specific serine/threonine protein kinase	C:COG1413
JNUCC-1_00562		1071	Beta-(1->2)glucan export ATP-binding/permease protein NdvA	V:COG5265
JNUCC-1_00563		1521	Choline transport system permease protein OpuBB	E:COG1174
JNUCC-1_00564		570	hypothetical protein	S:ENOG410XW7F
JNUCC-1_00565	ldcA	936	Muramoyltetrapeptide carboxypeptidase	V:COG1619
JNUCC-1_00566		720	Sucrose operon repressor	K:COG1609
JNUCC-1_00567		264	Ribose operon repressor	K:COG1609
JNUCC-1_00568	rbsK|RBKS	885	Ribokinase	G:COG0524
JNUCC-1_00569		1245	Uncharacterized transporter YutK	F:COG1972
JNUCC-1_00570	URH1	948	Uridine nucleosidase	F:COG1957
JNUCC-1_00571		1344	hypothetical protein	S:ENOG410ZYHH
JNUCC-1_00572	nhoA	813	N-hydroxyarylamine O-acetyltransferase	Q:COG2162
JNUCC-1_00573		1485	hypothetical protein	L:COG3666
JNUCC-1_00574	benD-xylL	750	17-beta-hydroxysteroid dehydrogenase 14	Q:ENOG410XR6K
JNUCC-1_00575		333	General stress protein 17M	S:ENOG410Y25X
JNUCC-1_00576		450	uncharacterized protein	S:COG4876
JNUCC-1_00577		786	Regulatory protein PocR	T:COG4753
JNUCC-1_00578		1296	Trehalose/maltose-binding protein MalE	G:COG1653
JNUCC-1_00579		1194	Transposase for insertion sequence element IS905	L:COG3328

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_00580		1095	sn-glycerol-3-phosphate transport system permease protein UgpA	P:COG1175
JNUCC-1_00581		123	hypothetical protein	P:COG1175
JNUCC-1_00582		834	Maltose transport system permease protein	G:COG0395
JNUCC-1_00583		2304	Alpha,alpha-trehalose phosphorylase	G:COG1554
JNUCC-1_00584	pgmB	672	Beta-phosphoglucomutase	S:COG0637
JNUCC-1_00585		1596	Uncharacterized transporter	P:COG2985
JNUCC-1_00586		204	hypothetical protein	S:ENOG41122AV
JNUCC-1_00587		1668	Probable protein kinase UbiB	S:COG0661
JNUCC-1_00588		1008	Putative oligopeptide transport ATP-binding protein YkfD	S:ENOG4111FMH
JNUCC-1_00589		1035	Oligopeptide transport ATP-binding protein AppF	S:COG1123
JNUCC-1_00590		1824	Oligopeptide-binding protein AppA	E:COG0747
JNUCC-1_00591		969	Putative peptide permease protein	P:COG0601
JNUCC-1_00592		930	Putative peptide transport permease protein	P:COG1173
JNUCC-1_00593		1224	N-acyl-D-amino-acid deacylase	F:COG0402
JNUCC-1_00594	codA	1209	Cytosine deaminase	F:COG0044
JNUCC-1_00595		1578	Periplasmic murein peptide-binding protein	E:COG0747
JNUCC-1_00596		900	Dipeptide transport system permease protein DppC	P:COG1173
JNUCC-1_00597		921	Probable peptide ABC transporter permease protein	P:COG0601
JNUCC-1_00598		1023	Oligopeptide transport ATP-binding protein OppF	EP:COG0444
JNUCC-1_00599		990	Glutathione import ATP-binding protein GsiA	S:COG1123
JNUCC-1_00600	yesM	777	Histidine kinase	T:COG2972
JNUCC-1_00601		687	Sensory transduction protein LytT	T:COG2197
JNUCC-1_00602		1308	hypothetical protein	E:COG0591
JNUCC-1_00603		1596	Periplasmic oligopeptide-binding protein	E:COG4166
JNUCC-1_00604		561	uncharacterized protein	S:COG2322

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_00605	srtA	606	Sortase A	M:COG3764
JNUCC-1_00606		1248	C4-dicarboxylate transport protein	C:COG1301
JNUCC-1_00607		438	Uncharacterized Na(+)/H(+) antiporter	C:COG1757
JNUCC-1_00608		957	Arginine/ornithine antiporter ArcD	C:COG1757
JNUCC-1_00609	UNG|UDG	675	Uracil-DNA glycosylase	L:COG0692
JNUCC-1_00610		927	Transcriptional regulator LytR	K:COG1316
JNUCC-1_00611	manA|MPI	960	Mannose-6-phosphate isomerase	G:COG1482
JNUCC-1_00612		1173	Transposase for insertion sequence element IS256 in transposon Tn4001	L:COG3328
JNUCC-1_00613		1284	Putative branched-chain amino acid carrier protein	E:COG1114
JNUCC-1_00614	msrAB	747	Peptide-methionine (S)-S-oxide reductase	O:COG0229
JNUCC-1_00615	PTS-Glc-EIIA|crr	498	PTS system beta-glucoside-specific EIIBCA component	G:COG2190
JNUCC-1_00616	fabG	663	3-oxoacyl-[acyl-carrier-protein] reductase	S:COG1028
JNUCC-1_00617	fabG	105	3-oxoacyl-[acyl-carrier-protein] reductase	
JNUCC-1_00618	K08884	1089	Non-specific serine/threonine protein kinase	S:COG2340
JNUCC-1_00619	nagK	543	3-fumarylpyruvate hydrolase	Q:COG0179
JNUCC-1_00620	dhaK	768	Phosphoenolpyruvate-glycerone phosphotransferase	G:COG2376
JNUCC-1_00621	dhaK	225	Phosphoenolpyruvate-glycerone phosphotransferase	G:COG2376
JNUCC-1_00622	dhaL	591	Phosphoenolpyruvate-glycerone phosphotransferase	G:COG2376
JNUCC-1_00623	dhaM	384	Phosphoenolpyruvate-glycerone phosphotransferase	G:COG3412
JNUCC-1_00624		1221	Ferric-chelate reductase (NADH)	S:COG5505
JNUCC-1_00625		903	Probable nitrate transporter NarT	P:COG2223
JNUCC-1_00626		621	Nitrate transporter	P:COG2223
JNUCC-1_00627		288	hypothetical protein	
JNUCC-1_00628		510	hypothetical protein	
JNUCC-1_00629		546	hypothetical protein	

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_00630		876	hypothetical protein	S:ENOG4111SQT
JNUCC-1_00631		420	hypothetical protein	U:COG4969
JNUCC-1_00632		1200	Type II secretion system protein	U:COG1459
JNUCC-1_00633		1035	Twitching mobility protein	NU:COG5008
JNUCC-1_00634		1626	Bacteriophage N4 adsorption protein	U:COG2804
JNUCC-1_00635		417	hypothetical protein	
JNUCC-1_00636		432	hypothetical protein	
JNUCC-1_00637		1179	hypothetical protein	S:ENOG4111KY4
JNUCC-1_00638	adhP	1020	Alcohol dehydrogenase	C:COG1064
JNUCC-1_00639		450	hypothetical protein	O:ENOG410XSSM
JNUCC-1_00640	copA|ATP7	207	Cu(+) exporting ATPase	P:COG2217
JNUCC-1_00641	copB	2016	Cu(2+)-exporting ATPase	P:COG2217
JNUCC-1_00642	uvsE|UVE1	378	hypothetical protein	S:ENOG4111M1E
JNUCC-1_00643		633	Response regulator protein VraR	T:COG2197
JNUCC-1_00644	vraS	819	Histidine kinase	T:COG4585
JNUCC-1_00645	liaS	171	Histidine kinase	
JNUCC-1_00646		732	Protein LiaF	S:COG4758
JNUCC-1_00647		636	Protein LiaH	KT:COG1842
JNUCC-1_00648		354	hypothetical protein	S:ENOG411236G
JNUCC-1_00649		276	hypothetical protein	
JNUCC-1_00650		357	hypothetical protein	
JNUCC-1_00651		354	hypothetical protein	
JNUCC-1_00652		2250	hypothetical protein	S:ENOG410ZV05
JNUCC-1_00653		318	hypothetical protein	S:ENOG410Z5I0
JNUCC-1_00654		576	RNA polymerase sigma factor SigV	K:COG1595

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_00655		978	Uncharacterized zinc-type alcohol dehydrogenase-like protein YogA	C:COG0604
JNUCC-1_00656	iolS	930	Protein IolS	C:COG0667
JNUCC-1_00657	lytE|cwlF	1107	Probable peptidoglycan endopeptidase LytE	NU:COG1705
JNUCC-1_00658		1374	Uncharacterized transporter	E:COG1115
JNUCC-1_00659		852	hypothetical protein	S:ENOG410Z15C
JNUCC-1_00660		1464	hypothetical protein	S:ENOG410XPWT
JNUCC-1_00661	mucR	1032	Diguanylate cyclase	T:ENOG410XNMH
JNUCC-1_00662	glcD	1389	(S)-2-hydroxy-acid oxidase	C:COG0277
JNUCC-1_00663		1065	hypothetical protein	S:COG3180
JNUCC-1_00664	qor|CRYZ	975	NADPH:quinone reductase	C:COG0604
JNUCC-1_00665		2010	hypothetical protein	S:COG1033
JNUCC-1_00666		1845	hypothetical protein	S:COG1511
JNUCC-1_00667	GalDH	918	L-galactose 1-dehydrogenase	C:COG0667
JNUCC-1_00668		1038	Transcriptional regulator ManR	K:COG3711
JNUCC-1_00669		858	Transcriptional regulator ManR	K:COG3711
JNUCC-1_00670	PTS-Fru2-EIIB	1953	PTS system fructose-specific EIIBBC component	G:COG1299
JNUCC-1_00671		228	hypothetical protein	S:ENOG410XYNU
JNUCC-1_00672		1191	Serine/threonine transporter SstT	C:COG1301
JNUCC-1_00673		1404	hypothetical protein	T:ENOG410XNMH
JNUCC-1_00674		1173	hypothetical protein	S:ENOG410ZSZ2
JNUCC-1_00675	URA4|pyrC	1266	Dihydroorotase	Q:COG1228
JNUCC-1_00676	ampC	1389	Beta-lactamase	V:COG1680
JNUCC-1_00677		1281	hypothetical protein	L:ENOG4111KQP
JNUCC-1_00678	panD	393	Aspartate 1-decarboxylase	H:COG0853
JNUCC-1_00679	nadX|ASPDH	780	Aspartate dehydrogenase	H:COG1712

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_00680	hyi|gip	750	Hydroxypyruvate isomerase	G:COG3622
JNUCC-1_00681	BLVRA|bvdR	1260	Biliverdin reductase	S:COG0673
JNUCC-1_00682	galK	1188	Galactokinase	G:COG0153
JNUCC-1_00683	galE|GALE	993	UDP-glucose 4-epimerase	M:COG0451
JNUCC-1_00684	galT|GALT	1482	UDP-glucose--hexose-1-phosphate uridylyltransferase	G:COG4468
JNUCC-1_00685	galM|GALM	1098	Aldose 1-epimerase	G:COG2017
JNUCC-1_00686	glk	1179	Glucokinase	G:COG1940
JNUCC-1_00687		1380	Putative 2,3-dihydroxypropane-1-sulfonate exporter	G:COG2211
JNUCC-1_00688	bglB	753	Beta-glucosidase	G:COG2723
JNUCC-1_00689	bglB	570	Beta-glucosidase	G:COG2723
JNUCC-1_00690		264	hypothetical protein	G:COG2211
JNUCC-1_00691		213	hypothetical protein	G:COG2211
JNUCC-1_00692		900	Putative xylose-proton symporter	G:COG2211
JNUCC-1_00693	K01138	1491	Arylsulfatase	P:COG3119
JNUCC-1_00694		306	hypothetical protein	
JNUCC-1_00695		1728	Acyl-CoA dehydrogenase family member 11	I:COG1960
JNUCC-1_00696	fadD3	1512	3-((3aS,4S,7aS)-7a-methyl-1,5-dioxo-octahydro-1H-inden-4-yl)propanoate-CoA ligase	IQ:COG0318
JNUCC-1_00697		1689	hypothetical protein	L:COG3666
JNUCC-1_00698		984	hypothetical protein	S:COG1408
JNUCC-1_00699		1155	hypothetical protein	E:COG4091
JNUCC-1_00700	rfbC|rmlC	585	dTDP-4-dehydrorhamnose 3,5-epimerase	M:COG1898
JNUCC-1_00701	rfbA|rffH	903	Glucose-1-phosphate thymidylyltransferase	M:COG1209
JNUCC-1_00702	pgaC|icaA	978	Uncharacterized glycosyltransferase YibD	M:ENOG410ZVME
JNUCC-1_00703		1770	Energy-coupling factor transporter ATP-binding protein EcfA1	V:COG1132
JNUCC-1_00704	wcaL|amsK	1203	Uncharacterized glycosyltransferase	M:COG0438

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_00705		843	Putative membrane-bound acyltransferase YfiQ	G:COG3936
JNUCC-1_00706		249	hypothetical protein	
JNUCC-1_00707	wcaL|amsK	903	Uncharacterized glycosyltransferase	M:COG0438
JNUCC-1_00708		240	hypothetical protein	M:COG0438
JNUCC-1_00709	wcaL|amsK	1197	Amylovoran biosynthesis glycosyltransferase AmsK	M:COG0438
JNUCC-1_00710	wapR	915	Uncharacterized glycosyltransferase EpsJ	M:COG0463
JNUCC-1_00711	gmhC|hldE|waaE|rfaE	417	D-glycero-beta-D-manno-heptose-7-phosphate kinase	M:COG2870
JNUCC-1_00712	tagF	1182	Teichoic acid poly(glycerol phosphate) polymerase	M:COG1887
JNUCC-1_00713	waaH	690	Uncharacterized glycosyltransferase EpsJ	M:COG0463
JNUCC-1_00714	epsD	1236	hypothetical protein	M:COG0438
JNUCC-1_00715	epsF	1155	Putative glycosyltransferase EpsF	M:COG0438
JNUCC-1_00716		372	HTH-type transcriptional regulator SinR	K:COG1396
JNUCC-1_00717	kdnA	756	8-amino-3,8-dideoxy-alpha-D-manno-octulosonate transaminase	E:COG0399
JNUCC-1_00718	epsN	444	Putative pyridoxal phosphate-dependent aminotransferase EpsN	E:COG0399
JNUCC-1_00719	epsM	630	Putative acetyltransferase EpsM	M:COG2148
JNUCC-1_00720		597	UDP-glucose:undecaprenyl-phosphate glucose-1-phosphate transferase	M:COG2148
JNUCC-1_00721	galE|GALE	1086	UDP-glucose 4-epimerase	M:COG1087
JNUCC-1_00722		453	hypothetical protein	
JNUCC-1_00723		1284	hypothetical protein	L:COG3547
JNUCC-1_00724		1074	Transmembrane protein EpsG	M:ENOG41121S3
JNUCC-1_00725		885	Uncharacterized glycosyltransferase	M:COG0463
JNUCC-1_00726	epsF	1146	Putative glycosyltransferase EpsF	M:COG0438
JNUCC-1_00727	epsD	1164	Putative glycosyltransferase EpsD	M:COG0438
JNUCC-1_00728		1827	Capsular polysaccharide biosynthesis protein CapD	M:COG1086
JNUCC-1_00729		1389	Capsular polysaccharide biosynthesis protein CapA	M:COG3944

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_00730	rfbB|rffG	1062	dTDP-glucose 4,6-dehydratase	M:COG1088
JNUCC-1_00731	UGP2|galU|galF	432	UTP-glucose-1-phosphate uridylyltransferase	M:COG1210
JNUCC-1_00732	UGP2|galU|galF	423	UTP-glucose-1-phosphate uridylyltransferase	M:COG1210
JNUCC-1_00733		1305	hypothetical protein	S:COG4325
JNUCC-1_00734	ahcY	1227	Adenosylhomocysteinase	S:COG5441
JNUCC-1_00735		825	uncharacterized protein	S:COG5564
JNUCC-1_00736		1197	uncharacterized protein	T:COG4753
JNUCC-1_00737		1080	hypothetical protein	S:ENOG410XRGW
JNUCC-1_00738		1140	hypothetical protein	S:ENOG410XRGW
JNUCC-1_00739		780	Uncharacterized membrane protein YlbC	S:ENOG410XWH5
JNUCC-1_00740		285	hypothetical protein	S:ENOG410ZZD3
JNUCC-1_00741		1005	Probable low-affinity inorganic phosphate transporter	P:COG0306
JNUCC-1_00742		624	UPF0111 protein YkaA	P:COG1392
JNUCC-1_00743		213	hypothetical protein	
JNUCC-1_00744		1794	Lipid A export ATP-binding/permease protein MsbA	V:COG1132
JNUCC-1_00745	msbA	1734	Uncharacterized ABC transporter ATP-binding protein	V:COG1132
JNUCC-1_00746		465	hypothetical protein	K:ENOG410ZYS6
JNUCC-1_00747		1485	Uncharacterized MFS-type transporter	G:COG2814
JNUCC-1_00748		1380	Uncharacterized MFS-type transporter YcnB	G:COG0477
JNUCC-1_00749	butA|budC	666	Diacetyl reductase ((S)-acetoin forming)	S:COG1028
JNUCC-1_00750		102	hypothetical protein	
JNUCC-1_00753	pncB|NAPRT1	1455	Nicotinate phosphoribosyltransferase	H:COG1488
JNUCC-1_00754		570	hypothetical protein	S:ENOG411272C
JNUCC-1_00755		750	Creatininase	S:ENOG4111WB4
JNUCC-1_00756		456	hypothetical protein	S:ENOG4111N76

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_00757		798	hypothetical protein	S:ENOG410XQ7F
JNUCC-1_00758	mmsB|HIBADH	897	3-hydroxyisobutyrate dehydrogenase	I:COG2084
JNUCC-1_00759	xylA	1452	Aldehyde dehydrogenase, thermostable	C:COG1012
JNUCC-1_00760		1563	Adenylate cyclase	K:COG3835
JNUCC-1_00761	pcm	582	Protein-L-isoaspartate(D-aspartate) O-methyltransferase	O:COG2518
JNUCC-1_00762		1575	Glycine betaine transporter BetP	P:COG1292
JNUCC-1_00763	cobU|cobT	1071	Nicotinate-nucleotide-dimethylbenzimidazole phosphoribosyltransferase	L:COG0675
JNUCC-1_00764		177	hypothetical protein	
JNUCC-1_00765	pntA	1116	NAD(P)(+) transhydrogenase (Re/Si-specific)	E:COG0686
JNUCC-1_00766		1464	hypothetical protein	S:COG1524
JNUCC-1_00767		888	Protein LicA	M:COG0510
JNUCC-1_00768		462	hypothetical protein	S:ENOG410Y0PA
JNUCC-1_00769		918	WAT1-related protein chloroplastic	EG:COG0697
JNUCC-1_00770		1143	hypothetical protein	S:ENOG410Y3NI
JNUCC-1_00771		216	uncharacterized protein	S:COG4895
JNUCC-1_00772		249	hypothetical protein	
JNUCC-1_00773	fucA	627	L-fuculose-phosphate aldolase	G:COG0235
JNUCC-1_00774	mtaD	1299	S-methyl-5′-thioadenosine deaminase	F:COG0402
JNUCC-1_00775		729	Exu regulon transcriptional regulator	K:COG2186
JNUCC-1_00776	mtnA	1044	S-methyl-5-thioribose-1-phosphate isomerase	J:COG0182
JNUCC-1_00777		732	Sodium/nucleoside cotransporter	F:COG1972
JNUCC-1_00778		498	Pyrimidine nucleoside transport protein	F:COG1972
JNUCC-1_00779	udp|UPP	735	Uridine phosphorylase	F:COG2820
JNUCC-1_00780		762	hypothetical protein	S:ENOG410XPGN
JNUCC-1_00781		771	hypothetical protein	S:ENOG410XPGN

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_00782		723	hypothetical protein	S:ENOG4111PAT
JNUCC-1_00783		705	Lactate utilization protein	S:COG1556
JNUCC-1_00784		309	Lactate utilization protein B	C:COG1139
JNUCC-1_00785		1134	Lactate utilization protein B	C:COG1139
JNUCC-1_00786		717	Lactate utilization protein A	C:COG0247
JNUCC-1_00787		501	hypothetical protein	S:COG4333
JNUCC-1_00788		1578	hypothetical protein	S:ENOG410XQG1
JNUCC-1_00789		1530	hypothetical protein	S:ENOG410YAIS
JNUCC-1_00790		915	Uncharacterized HTH-type transcriptional regulator	K:COG1737
JNUCC-1_00791	glk	771	Glucokinase	G:COG1940
JNUCC-1_00792		825	L-arabinose transport system permease protein AraQ	G:COG0395
JNUCC-1_00793		909	sn-glycerol-3-phosphate transport system permease protein UgpA	P:COG1175
JNUCC-1_00794		1347	Putative binding protein	G:COG1653
JNUCC-1_00795	cpdA	864	3′,5′-cyclic-AMP phosphodiesterase	
JNUCC-1_00796		774	hypothetical protein	
JNUCC-1_00797		1020	Transcriptional regulator ICP22 like protein	S:ENOG410YPKC
JNUCC-1_00798		345	uncharacterized protein	S:COG3361
JNUCC-1_00799		375	hypothetical protein	S:COG3361
JNUCC-1_00800		339	hypothetical protein	
JNUCC-1_00801		189	hypothetical protein	S:COG4309
JNUCC-1_00802		459	hypothetical protein	
JNUCC-1_00803	URA4|pyrC	1122	Dihydroorotase	Q:COG1228
JNUCC-1_00804		1263	GTPase Der	S:COG1160
JNUCC-1_00805		498	hypothetical protein	K:ENOG4111VI2
JNUCC-1_00806		498	hypothetical protein	K:ENOG4111TV7

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_00807	iacA	1092	Indole-3-acetate monooxygenase	I:ENOG410XT0V
JNUCC-1_00808		399	hypothetical protein	
JNUCC-1_00809		486	hypothetical protein	
JNUCC-1_00810	arlS	1323	Histidine kinase	T:COG0642
JNUCC-1_00811		672	Virulence sensor protein BvgS	T:COG0745
JNUCC-1_00812		648	uncharacterized protein	S:ENOG410YNGS
JNUCC-1_00813	cwlO	930	Probable peptidoglycan endopeptidase LytE	M:COG3409
JNUCC-1_00814		1164	Peptidase M20 domain-containing protein	E:COG1473
JNUCC-1_00815		1419	uncharacterized protein	S:COG1288
JNUCC-1_00816		390	hypothetical protein	S:COG0673
JNUCC-1_00817	DHDH	633	Trans-1,2-dihydrobenzene-1,2-diol dehydrogenase	S:COG0673
JNUCC-1_00818		1044	hypothetical protein	S:COG2110
JNUCC-1_00819		813	hypothetical protein	S:ENOG4111RVZ
JNUCC-1_00820		339	hypothetical protein	
JNUCC-1_00821		1227	Thermitase	O:COG1404
JNUCC-1_00822		666	hypothetical protein	K:COG1309
JNUCC-1_00823	PPOX|hemY	1344	Protoporphyrinogen oxidase	S:ENOG410XRVV
JNUCC-1_00824		687	hypothetical protein	S:ENOG41124R2
JNUCC-1_00825		423	hypothetical protein	S:ENOG41124R2
JNUCC-1_00826		573	hypothetical protein	S:ENOG4111XM6
JNUCC-1_00827		267	hypothetical protein	
JNUCC-1_00828		1446	uncharacterized protein	S:COG1288
JNUCC-1_00829	cpg	1149	Glutamate carboxypeptidase	E:COG0624
JNUCC-1_00830		1173	Transposase for insertion sequence element IS256 in transposon Tn4001	L:COG3328
JNUCC-1_00831		162	hypothetical protein	

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_00832	ACSS|acs	1968	Acetate-CoA ligase	I:COG0365
JNUCC-1_00833		222	hypothetical protein	
JNUCC-1_00834	soxB	648	Sarcosine oxidase	S:ENOG410XNXW
JNUCC-1_00835		492	FAD-dependent oxidoreductase domain-containing protein	S:ENOG410XNXW
JNUCC-1_00836	ala	963	Alanine dehydrogenase	E:COG2423
JNUCC-1_00837		216	hypothetical protein	
JNUCC-1_00838		228	hypothetical protein	
JNUCC-1_00839		1242	Uncharacterized symporter YwcA	E:COG0591
JNUCC-1_00840		597	hypothetical protein	
JNUCC-1_00841		252	hypothetical protein	
JNUCC-1_00842	argH|ASL	666	Argininosuccinate lyase	E:COG0165
JNUCC-1_00843	argH|ASL	348	Argininosuccinate lyase	E:COG0165
JNUCC-1_00844	argH|ASL	375	Argininosuccinate lyase	E:COG0165
JNUCC-1_00845	GNS	489	N-acetylglucosamine-6-sulfatase	P:COG3119
JNUCC-1_00846	GNS	384	N-acetylglucosamine-6-sulfatase	P:COG3119
JNUCC-1_00847	betC	390	Choline-sulfatase	P:COG3119
JNUCC-1_00848		828	L-arabinose transport system permease protein AraQ	G:COG0395
JNUCC-1_00849		909	Probable ABC transporter permease protein	P:ENOG410YZTA
JNUCC-1_00850		1293	sn-glycerol-3-phosphate-binding periplasmic protein UgpB	G:ENOG4111ISI
JNUCC-1_00851	bshB2	678	Probable N-acetyl-alpha-D-glucosaminyl L-malate deacetylase	S:COG2120
JNUCC-1_00852		360	uncharacterized protein	S:ENOG4111UV1
JNUCC-1_00853	glk	1206	Glucokinase	G:COG1940
JNUCC-1_00854	lepB	549	Signal peptidase I	U:COG0681
JNUCC-1_00855		576	hypothetical protein	
JNUCC-1_00856		780	hypothetical protein	S:ENOG410YRFR

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_00857		576	hypothetical protein	
JNUCC-1_00858		150	hypothetical protein	
JNUCC-1_00859	dgoD	1149	Galactonate dehydratase	M:COG4948
JNUCC-1_00860	xylB|XYLB	1503	Xylulokinase	G:COG1070
JNUCC-1_00861	ghrB	969	Glyoxylate reductase (NADP(+))	C:COG1052
JNUCC-1_00862		1485	Uncharacterized 52.8 kDa protein in TAR-I ttuC′ 3′region	S:COG3333
JNUCC-1_00863		444	hypothetical protein	S:ENOG410XVM8
JNUCC-1_00864		1020	Protein BugT	S:COG3181
JNUCC-1_00865	dgoK	1017	2-dehydro-3-deoxygalactonokinase	G:COG3734
JNUCC-1_00866	eda	636	2-dehydro-3-deoxy-phosphogluconate aldolase	G:COG0800
JNUCC-1_00867		771	Uncharacterized HTH-type transcriptional regulator YagI	K:COG1414
JNUCC-1_00868		903	hypothetical protein	G:ENOG410XNP4
JNUCC-1_00869	iolE	804	Myo-inosose-2 dehydratase	G:ENOG41100PA
JNUCC-1_00870	ltrA	1260	RNA-directed DNA polymerase	L:COG3344
JNUCC-1_00871		858	Flagellin	N:COG1344
JNUCC-1_00872		228	Flagellar filament 33 kDa core protein	N:COG1344
JNUCC-1_00873	murF	2451	UDP-N-acetylmuramoyl-tripeptide-D-alanyl-D-alanine ligase	S:ENOG4111H85
JNUCC-1_00874		1116	hypothetical protein	S:ENOG4111SES
JNUCC-1_00875		414	hypothetical protein	
JNUCC-1_00876		672	hypothetical protein	
JNUCC-1_00877		1275	hypothetical protein	S:ENOG4111QGS
JNUCC-1_00878		1362	hypothetical protein	L:ENOG410XQ88
JNUCC-1_00879		615	hypothetical protein	
JNUCC-1_00880		540	hypothetical protein	
JNUCC-1_00881	mcrB	1479	5-methylcytosine-specific restriction enzyme	V:COG1401

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_00882		1269	hypothetical protein	V:COG4268
JNUCC-1_00883		1287	uncharacterized protein	S:ENOG410XRS1
JNUCC-1_00884		360	uncharacterized protein	S:ENOG4111VTB
JNUCC-1_00885		348	hypothetical protein	S:ENOG410XWMC
JNUCC-1_00886		1044	hypothetical protein	S:ENOG4111T2W
JNUCC-1_00887		1161	uncharacterized protein	E:COG3457
JNUCC-1_00888	deoB	1215	Phosphopentomutase	G:COG1015
JNUCC-1_00889	iscS|NFS1	1113	Cysteine desulfurase	E:ENOG410Z1QN
JNUCC-1_00890		762	Phosphotriesterase like proteiny protein	S:COG1735
JNUCC-1_00891		780	uncharacterized protein	S:ENOG410YBQW
JNUCC-1_00892		150	hypothetical protein	S:ENOG410YBQW
JNUCC-1_00893	glpA|glpD	1578	Glycerol-3-phosphate dehydrogenase	C:COG0578
JNUCC-1_00894		567	uncharacterized protein	K:COG1954
JNUCC-1_00895		576	4-nitrophenylphosphatase	G:COG0647
JNUCC-1_00896		1707	Molybdate/tungstate transport system permease protein WtpB	P:COG1178
JNUCC-1_00897	lptB	1122	ABC transporter F family member	G:COG3839
JNUCC-1_00898		1038	hypothetical protein	P:COG1840
JNUCC-1_00899	glpQ|ugpQ	2298	Glycerophosphodiester phosphodiesterase	C:COG0584
JNUCC-1_00900		1233	Transposase for insertion sequence element IS1557	L:COG3464
JNUCC-1_00901		903	Glycine betaine-binding protein OpuAC	E:COG2113
JNUCC-1_00902	pepQ	1215	Xaa-Pro dipeptidase	E:COG0006
JNUCC-1_00903		711	Transcriptional regulator NanR	K:COG2188
JNUCC-1_00904		138	hypothetical protein	
JNUCC-1_00905		288	hypothetical protein	S:ENOG410ZX42
JNUCC-1_00906	doxD	519	Thiosulfate dehydrogenase (quinone)	S:COG2259

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_00907		1047	hypothetical protein	S:COG4927
JNUCC-1_00908		564	hypothetical protein	
JNUCC-1_00909		1821	Heat shock protein SSC1, mitochondrial	O:COG0443
JNUCC-1_00910		1245	hypothetical protein	S:ENOG410XV60
JNUCC-1_00911		105	hypothetical protein	
JNUCC-1_00912		519	DNA-directed RNA polymerase	S:ENOG410XW7V
JNUCC-1_00913		288	hypothetical protein	S:ENOG410ZX42
JNUCC-1_00914		306	hypothetical protein	S:ENOG41123KX
JNUCC-1_00915	xthA	681	Exodeoxyribonuclease III	S:ENOG4111MA6
JNUCC-1_00916		444	hypothetical protein	
JNUCC-1_00917		258	hypothetical protein	S:ENOG410ZXAB
JNUCC-1_00918		1890	ABC transporter permease protein YxdM	V:COG0577
JNUCC-1_00919		765	Energy-coupling factor transporter ATP-binding protein EcfA1	P:COG1122
JNUCC-1_00920	yxdK	1002	Histidine kinase	T:COG0642
JNUCC-1_00921		705	Response regulator ArlR	T:COG0745
JNUCC-1_00922		180	hypothetical protein	
JNUCC-1_00923		765	hypothetical protein	
JNUCC-1_00924		915	Putative oxidoreductase YceM	S:COG0673
JNUCC-1_00925	gatA|QRSL1	1389	Asparaginyl-tRNA synthase (glutamine-hydrolyzing)	J:COG0154
JNUCC-1_00926		279	hypothetical protein	
JNUCC-1_00927	SORD|gutB	1086	L-iditol 2-dehydrogenase	E:COG1063
JNUCC-1_00928	aldB	570	Aldehyde dehydrogenase	C:COG1012
JNUCC-1_00929		1560	Transposase	L:COG4584
JNUCC-1_00930		765	Putative ATP-binding protein in insertion sequence	L:COG1484
JNUCC-1_00931	ALDH	1035	Aldehyde dehydrogenase (NAD(+))	C:COG1012

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_00932		690	hypothetical protein	
JNUCC-1_00933		1536	hypothetical protein	
JNUCC-1_00934		852	hypothetical protein	S:ENOG410XQHH
JNUCC-1_00935		234	hypothetical protein	S:ENOG4111WH3
JNUCC-1_00936		360	hypothetical protein	S:ENOG4111WH3
JNUCC-1_00937		381	HTH-type transcriptional regulator Xre	K:ENOG410XUC3
JNUCC-1_00938		543	DNA-directed RNA polymerase	S:ENOG410XW7V
JNUCC-1_00939		297	hypothetical protein	S:ENOG41126P2
JNUCC-1_00940		690	hypothetical protein	S:ENOG4111R20
JNUCC-1_00941		687	hypothetical protein	
JNUCC-1_00942		792	hypothetical protein	S:ENOG4111I5K
JNUCC-1_00943		1050	Oligopeptide transport ATP-binding protein AppF	E:COG4608
JNUCC-1_00944		963	Glutathione import ATP-binding protein GsiA	EP:COG0444
JNUCC-1_00945		903	Dipeptide transport system permease protein	P:COG1173
JNUCC-1_00946		915	Oligopeptide transport system permease protein AppB	P:COG0601
JNUCC-1_00947		1557	uncharacterized protein	E:COG0747
JNUCC-1_00948	hipO	504	Hippurate hydrolase	E:COG1473
JNUCC-1_00949	hipO	660	Hippurate hydrolase	E:COG1473
JNUCC-1_00950	dapE	1398	Succinyl-diaminopimelate desuccinylase	E:COG0624
JNUCC-1_00951		717	Uxu operon regulator	K:COG2186
JNUCC-1_00952		1005	uncharacterized protein	G:COG1638
JNUCC-1_00953		465	hypothetical protein	G:COG3090
JNUCC-1_00954		1263	Sialic acid TRAP transporter permease protein SiaT	G:COG1593
JNUCC-1_00955	ttuC|dmlA	1068	Tartrate dehydrogenase	E:COG0473
JNUCC-1_00956		258	hypothetical protein	

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_00957		777	hypothetical protein	L:COG1943
JNUCC-1_00958		1551	uncharacterized protein	O:COG0606
JNUCC-1_00959		897	Transposase for insertion sequence element IS21-like	L:COG4584
JNUCC-1_00960		642	Insertion sequence IS21-like putative ATP-binding protein	L:COG1484
JNUCC-1_00961		495	uncharacterized protein	O:COG0606
JNUCC-1_00962		1140	Competence protein ComM	O:COG0606
JNUCC-1_00963		468	Insertion sequence IS408 putative ATP-binding protein	L:COG1484
JNUCC-1_00964		258	hypothetical protein	L:COG4584
JNUCC-1_00965		765	Putative ATP-binding protein in insertion sequence	L:COG1484
JNUCC-1_00966		1560	Transposase	L:COG4584
JNUCC-1_00967		1398	Putative transposase y4bL/y4kJ/y4tB	L:COG4584
JNUCC-1_00968		258	hypothetical protein	
JNUCC-1_00969		723	HTH-type transcriptional regulator FrlR	K:COG2188
JNUCC-1_00970	UGDH|ugd	204	UDP-glucose 6-dehydrogenase	M:COG1004
JNUCC-1_00971	UGDH|ugd	966	UDP-glucose 6-dehydrogenase	M:COG1004
JNUCC-1_00972		1032	UDP-glucuronate 4-epimerase	M:COG0451
JNUCC-1_00973		1404	hypothetical protein	M:COG2244
JNUCC-1_00974		498	hypothetical protein	M:COG3774
JNUCC-1_00975		336	hypothetical protein	
JNUCC-1_00976	epsF	1122	Putative glycosyltransferase EpsF	M:COG0438
JNUCC-1_00977		1233	Transposase for insertion sequence element IS1557	L:COG3464
JNUCC-1_00978		1239	hypothetical protein	S:ENOG410XUBN
JNUCC-1_00979	paaK	1176	Phenylacetate--CoA ligase	M:COG0438
JNUCC-1_00980		897	hypothetical protein	S:ENOG410Y8FN
JNUCC-1_00981	wbtD	1101	N,N'-diacetylbacillosaminyl-diphospho-undecaprenol alpha-1,3-N-acetylgalactosaminyltransferase	M:ENOG410XNZB

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_00982	galE|GALE	864	UDP-glucose 4-epimerase	M:COG0451
JNUCC-1_00983		636	Putative undecaprenyl-phosphate N-acetylgalactosaminyl 1-phosphate transferase	M:COG2148
JNUCC-1_00984	UGP2|galU|galF	882	UTP-glucose-1-phosphate uridylyltransferase	M:COG1210
JNUCC-1_00985		1839	Capsular polysaccharide biosynthesis protein CapD	M:COG1086
JNUCC-1_00986		657	Chemotaxis response regulator protein-glutamate methylesterase	T:COG2197
JNUCC-1_00987		600	Protein-tyrosine-phosphatase	GM:COG4464
JNUCC-1_00988		162	Protein-tyrosine-phosphatase	GM:COG4464
JNUCC-1_00989		315	hypothetical protein	
JNUCC-1_00990		474	Protein-tyrosine-phosphatase	GM:COG4464
JNUCC-1_00991		258	Protein-tyrosine-phosphatase	GM:COG4464
JNUCC-1_00992		570	D-ribose-binding protein	G:COG1879
JNUCC-1_00993		201	hypothetical protein	
JNUCC-1_00994		531	hypothetical protein	K:ENOG41126TB
JNUCC-1_00995		144	hypothetical protein	
JNUCC-1_00996		423	hypothetical protein	
JNUCC-1_00997	PRPS|prsA	2190	Ribose-phosphate diphosphokinase	S:COG4666
JNUCC-1_00998		549	hypothetical protein	
JNUCC-1_00999		1038	31 kDa immunogenic protein	P:COG2358
JNUCC-1_01000		417	hypothetical protein	
JNUCC-1_01001		948	Glycine betaine-binding protein OpuAC	E:COG2113
JNUCC-1_01002	iolE	558	Myo-inosose-2 dehydratase	G:COG1082
JNUCC-1_01003	nfo	417	Deoxyribonuclease IV	G:COG1082
JNUCC-1_01004	spnN|oleW	1035	dTDP-3,4-didehydro-2,6-dideoxy-alpha-D-glucose 3-reductase	S:COG0673
JNUCC-1_01005		993	Catabolite control protein	K:COG1609
JNUCC-1_01006		1056	Ribose transport system permease protein RbsC	G:COG1172

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_01007	cysA	1482	Sulfate-transporting ATPase	S:COG4152
JNUCC-1_01008		189	hypothetical protein	G:COG1879
JNUCC-1_01009		807	hypothetical protein	G:COG1879
JNUCC-1_01010	pht4	1053	Phthalate 4,5-cis-dihydrodiol dehydrogenase	S:COG0673
JNUCC-1_01011		258	hypothetical protein	
JNUCC-1_01012		675	Probable 4-methylmuconolactone transporter	G:ENOG410Y09Q
JNUCC-1_01013		588	hypothetical protein	G:ENOG41129SF
JNUCC-1_01014		651	uncharacterized protein	S:COG0637
JNUCC-1_01015		1173	hypothetical protein	S:COG4552
JNUCC-1_01016		747	Histidine utilization repressor	K:COG2188
JNUCC-1_01017		780	Putative gamma-glutamylcyclotransferase YkqA	S:ENOG41126S6
JNUCC-1_01018	frlD	660	Fructoselysine 6-kinase	G:COG0524
JNUCC-1_01019		855	Probable ABC transporter permease protein YurM	G:COG0395
JNUCC-1_01020		696	Probable ABC transporter permease protein YurN	P:COG1175
JNUCC-1_01021		1275	Uncharacterized ABC transporter extracellular-binding protein YurO	G:ENOG410XPV5
JNUCC-1_01022	frlB	975	Fructoselysine 6-phosphate deglycase	M:COG2222
JNUCC-1_01023		957	Short-chain fatty acids transporter	I:COG2031
JNUCC-1_01024		369	Short-chain fatty acids transporter	I:COG2031
JNUCC-1_01025		969	Probable cystine transporter YijE	S:ENOG410Y0KE
JNUCC-1_01026		306	hypothetical protein	
JNUCC-1_01027		1512	Sodium-coupled monocarboxylate transporter	E:COG0591
JNUCC-1_01028	nanA|NPL	870	N-acetylneuraminate lyase	E:COG0329
JNUCC-1_01029		498	hypothetical protein	
JNUCC-1_01030		708	Uxu operon transcriptional regulator	K:COG2186
JNUCC-1_01031		672	Uxu operon transcriptional regulator	K:COG2186

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_01032	glk	864	Glucokinase	G:COG1940
JNUCC-1_01033	nanE	669	N-acylglucosamine-6-phosphate 2-epimerase	G:COG3010
JNUCC-1_01034		1359	Uncharacterized sodium-dependent transporter YhdH	P:COG0733
JNUCC-1_01035	soxB	1164	Sarcosine oxidase	S:ENOG410XNXW
JNUCC-1_01036		1176	uncharacterized protein	K:COG3835
JNUCC-1_01037		1422	hypothetical protein	E:COG0786
JNUCC-1_01038		231	hypothetical protein	
JNUCC-1_01039		1032	hypothetical protein	S:ENOG410Y5TV
JNUCC-1_01040		246	hypothetical protein	
JNUCC-1_01041		702	hypothetical protein	
JNUCC-1_01042		1362	Magnesium transporter MgtE	P:COG2239
JNUCC-1_01043	gabD	1404	Succinate-semialdehyde dehydrogenase (NAD(P)(+))	C:COG1012
JNUCC-1_01044		537	hypothetical protein	
JNUCC-1_01045		2055	Putative serine esterase	S:COG2936
JNUCC-1_01046	pepX	1731	Xaa-Pro dipeptidyl-peptidase	E:ENOG410XPUZ
JNUCC-1_01047		708	hypothetical protein	K:COG1309
JNUCC-1_01048		912	Putative peptide permease protein	P:COG1173
JNUCC-1_01049		960	Glutathione transport system permease protein GsiC	P:COG0601
JNUCC-1_01050		1752	Dipeptide-binding protein DppE	E:COG4166
JNUCC-1_01051		1053	Glutathione import ATP-binding protein GsiA	E:COG4608
JNUCC-1_01052		999	Oligopeptide transport ATP-binding protein	P:COG1122
JNUCC-1_01053		825	hypothetical protein	S:ENOG410XSWV
JNUCC-1_01054		4848	Endonuclease YhcR	S:COG4085
JNUCC-1_01055	malZ	2337	Alpha-glucosidase	G:COG1501
JNUCC-1_01056	K01138	399	hypothetical protein	P:COG3119

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_01057	GNS	597	N-acetylglucosamine-6-sulfatase	P:COG3119
JNUCC-1_01058	ARSD_F_H	438	Arylsulfatase	P:COG3119
JNUCC-1_01059		708	hypothetical protein	G:COG4813
JNUCC-1_01060	FUCA	1638	Alpha-L-fucosidase	S:COG5263
JNUCC-1_01061	pht4	1032	Phthalate 4,5-cis-dihydrodiol dehydrogenase	S:COG0673
JNUCC-1_01062	ebgA	3078	Beta-galactosidase	G:COG3250
JNUCC-1_01063		540	hypothetical protein	S:COG0673
JNUCC-1_01064	iolG	528	Inositol 2-dehydrogenase	S:COG0673
JNUCC-1_01065		867	hypothetical protein	G:ENOG4111FQJ
JNUCC-1_01066	iolG	984	Inositol 2-dehydrogenase	S:COG0673
JNUCC-1_01067	iolG	945	Inositol 2-dehydrogenase	S:ENOG410XSS6
JNUCC-1_01068		756	hypothetical protein	G:ENOG4111FQJ
JNUCC-1_01069		1032	hypothetical protein	G:COG3525
JNUCC-1_01070	ansA|ansB	690	Asparaginase	E:COG4448
JNUCC-1_01071	ansA|ansB	363	Asparaginase	E:COG4448
JNUCC-1_01072	MAN2C1	3123	Alpha-mannosidase	G:COG0383
JNUCC-1_01073		1608	hypothetical protein	G:COG1653
JNUCC-1_01074		912	Probable ABC transporter permease protein YtcP	G:COG0395
JNUCC-1_01075		972	Protein LplB	G:COG4209
JNUCC-1_01076	yesM	2250	Histidine kinase	K:COG2207
JNUCC-1_01077		621	uncharacterized protein	S:COG5578
JNUCC-1_01078		1302	Meiotically up-regulated 157 protein	S:COG3538
JNUCC-1_01079	MAN2C1	2709	Alpha-mannosidase	G:COG0383
JNUCC-1_01080	glk	915	Glucokinase	G:COG1940
JNUCC-1_01081	nanK	555	N-acylmannosamine kinase	G:COG1940

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_01082	glk	435	Glucokinase	G:COG1940
JNUCC-1_01083		234	hypothetical protein	G:COG1940
JNUCC-1_01084		3075	hypothetical protein	G:ENOG410XQQZ
JNUCC-1_01085	SUMF1|FGE	816	Formylglycine-generating enzyme	S:COG1262
JNUCC-1_01086		162	hypothetical protein	
JNUCC-1_01087		822	Probable ABC transporter permease protein	G:COG0395
JNUCC-1_01088		942	Trehalose/maltose transport system permease protein MalF	P:ENOG410Y2SR
JNUCC-1_01089		1305	Uncharacterized ABC transporter extracellular-binding protein	G:ENOG410XQ0Q
JNUCC-1_01090		1434	Uncharacterized transcriptional regulatory protein YesN	T:COG2197
JNUCC-1_01091		1446	Sensor protein LytS	T:COG2972
JNUCC-1_01092		990	hypothetical protein	G:COG1879
JNUCC-1_01093		699	Putative tyrosine-protein kinase CapB	D:COG0489
JNUCC-1_01094		762	Probable capsular polysaccharide biosynthesis protein YwqC	M:COG3944
JNUCC-1_01095	glpK|GK	1284	Glycerol kinase	C:COG0554
JNUCC-1_01096		1434	uncharacterized protein	K:COG1316
JNUCC-1_01097		1590	Periplasmic oligopeptide-binding protein	S:ENOG410XPRS
JNUCC-1_01098		1263	hypothetical protein	E:COG2195
JNUCC-1_01099	PREP	1788	Prolyl oligopeptidase	E:COG1506
JNUCC-1_01100	pip	858	Prolyl aminopeptidase	S:COG0596
JNUCC-1_01101	tagA|tarA	732	N-acetylglucosaminyldiphosphoundecaprenol N-acetyl-beta-D-mannosaminyltransferase	M:COG1922
JNUCC-1_01102		1323	Teichoic acids export ATP-binding protein TagH	GM:COG1134
JNUCC-1_01103		825	Teichoic acid translocation permease protein TagG	V:COG1682
JNUCC-1_01104	tagF	2118	Teichoic acid poly(glycerol phosphate) polymerase	M:COG1887
JNUCC-1_01105		543	UPF0398 protein	S:ENOG410YBQA
JNUCC-1_01106		288	hypothetical protein	

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_01107	tagD	399	Glycerol-3-phosphate cytidylyltransferase	IM:COG0615
JNUCC-1_01108	tagB|tarB	1176	Teichoic acid glycerol-phosphate primase	M:COG1887
JNUCC-1_01109		987	Transcriptional regulator LytR	K:COG1316
JNUCC-1_01110	bpr	5130	Bacillopeptidase	O:COG1404
JNUCC-1_01111		2151	Lactocepin	O:COG1404
JNUCC-1_01112		2406	Lactocepin	O:COG1404
JNUCC-1_01113		390	hypothetical protein	S:ENOG410Y59U
JNUCC-1_01114		126	hypothetical protein	
JNUCC-1_01115	bpr	3945	Bacillopeptidase	O:COG1404
JNUCC-1_01116	vpr	3306	Minor extracellular protease vpr	O:COG1404
JNUCC-1_01117	vpr	963	Subtilisin-like serine protease	O:COG1404
JNUCC-1_01118		1707	Bifunctional autolysin	M:COG5632
JNUCC-1_01119		105	hypothetical protein	
JNUCC-1_01120	mshA	1092	D-inositol-3-phosphate glycosyltransferase	M:COG0438
JNUCC-1_01121		1419	hypothetical protein	S:ENOG410YUYC
JNUCC-1_01122		1995	Putative peptidoglycan O-acetyltransferase YrhL	I:COG1835
JNUCC-1_01123		2373	Lactocepin	M:COG2247
JNUCC-1_01124	tagA|tarA	783	N-acetylglucosaminyldiphosphoundecaprenol N-acetyl-beta-D-mannosaminyltransferase	M:COG1922
JNUCC-1_01125	wecC	1269	UDP-N-acetyl-D-mannosamine dehydrogenase	M:COG0677
JNUCC-1_01126	wecA|tagO|rfe	879	UDP-N-acetylglucosamine-undecaprenyl-phosphateN-acetylglucosaminephosphotransferase	M:COG0472
JNUCC-1_01127	wecA|tagO|rfe	180	UDP-N-acetylglucosamine-undecaprenyl-phosphateN-acetylglucosaminephosphotransferase	M:COG0472
JNUCC-1_01128		1047	hypothetical protein	S:ENOG410ZSNG
JNUCC-1_01129	bshB1	894	hypothetical protein	S:COG2120
JNUCC-1_01130		1506	Putative lipid II flippase MurJ	S:COG0728
JNUCC-1_01131	ltaS	651	Phosphatidylglycerol-membrane-oligosaccharide glycerophosphotransferase	M:COG1368

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_01132	K01138	699	Lipoteichoic acid synthase-like YqgS	M: COG1368
JNUCC-1_01133		111	hypothetical protein	
JNUCC-1_01134		174	hypothetical protein	
JNUCC-1_01135	assT	1677	Aryl-sulfate sulfotransferase	S: ENOG410ZB20
JNUCC-1_01136	G6PD|zwf	1488	Glucose-6-phosphate dehydrogenase (NADP(+))	G: COG0364
JNUCC-1_01137	kynB	624	Arylformamidase	S: COG1878
JNUCC-1_01138		1020	hypothetical protein	S: ENOG410ZM9N
JNUCC-1_01139		594	hypothetical protein	S: ENOG410ZN9B
JNUCC-1_01140		795	hypothetical protein	
JNUCC-1_01141	PGD|gnd|gntZ	1455	Phosphogluconate dehydrogenase (NADP(+)-dependent, decarboxylating)	G: COG0362
JNUCC-1_01142	wecA|tagO|rfe	1092	UDP-N-acetylglucosamine-undecaprenyl-phosphateN-acetylglucosaminephosphotransferase	M: COG0472
JNUCC-1_01143		459	Uncharacterized HTH-type transcriptional regulator YmfC	K: COG2188
JNUCC-1_01144		261	Uncharacterized HTH-type transcriptional regulator YmfC	K: COG2188
JNUCC-1_01145		1140	CD4+ T-cell-stimulating antigen	S: COG1744
JNUCC-1_01146		1530	Uncharacterized ABC transporter ATP-binding protein YufO	S: COG3845
JNUCC-1_01147		1050	Uncharacterized ABC transporter permease protein YufP	S: COG4603
JNUCC-1_01148		951	Uncharacterized ABC transporter permease protein YufQ	S: COG1079
JNUCC-1_01149		219	Putative transposase InsK for insertion sequence element IS150	L: COG2801
JNUCC-1_01150		633	Putative transposase InsK for insertion sequence element IS150	L: COG2801
JNUCC-1_01151		510	hypothetical protein	L: ENOG4111X46
JNUCC-1_01152		255	hypothetical protein	
JNUCC-1_01153		402	hypothetical protein	S: ENOG410Z0A9
JNUCC-1_01154	SOD2	429	Superoxide dismutase	S: ENOG4111QY6
JNUCC-1_01155		744	hypothetical protein	S: COG2966
JNUCC-1_01156		513	UPF0442 protein	S: COG3610

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_01157		1512	Amino-acid permease RocC	E:COG0531
JNUCC-1_01158		954	2-nitroimidazole transporter	G:COG2807
JNUCC-1_01159		288	Uncharacterized transporter YycB	G:COG2807
JNUCC-1_01160		3078	Multidrug resistance protein MexB	P:COG0841
JNUCC-1_01161	pycB	873	Pyruvate carboxylase	M:COG0845
JNUCC-1_01162		885	Uncharacterized HTH-type transcriptional regulator YuxN	K:COG1309
JNUCC-1_01163		486	Competence transcription factor	K:COG4903
JNUCC-1_01164		189	hypothetical protein	
JNUCC-1_01165		294	Glycosyltransferase-like protein gnt13	S:ENOG4110FEQ
JNUCC-1_01166	fabZ	420	3-hydroxyacyl-[acyl-carrier-protein] dehydratase	I:COG0764
JNUCC-1_01167		180	hypothetical protein	S:ENOG411271C
JNUCC-1_01168		210	hypothetical protein	
JNUCC-1_01169		831	Flagellar hook protein FlgE	N:COG4786
JNUCC-1_01170		807	Flagellar hook-basal body complex protein FlhO	N:COG4786
JNUCC-1_01171		144	MreB-like protein	D:COG1077
JNUCC-1_01172		861	MreB-like protein	D:COG1077
JNUCC-1_01173		264	Stage III sporulation protein	K:ENOG4111VHI
JNUCC-1_01174		1026	hypothetical protein	S:ENOG4112CUQ
JNUCC-1_01175		807	Stage II sporulation protein	M:COG0739
JNUCC-1_01176		1158	Stage II sporulation protein D	D:COG2385
JNUCC-1_01177		960	Putative oligopeptide transport ATP-binding protein YkfD	E:COG4608
JNUCC-1_01178		1677	Dipeptide-binding protein DppE	E:COG4166
JNUCC-1_01179		1005	Dipeptide transport ATP-binding protein DppD	V:COG4170
JNUCC-1_01180		957	Dipeptide transport system permease protein DppC	P:COG1173
JNUCC-1_01181		942	Dipeptide transport system permease protein DppB	P:COG0601

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_01182	murA	834	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	M:COG0766
JNUCC-1_01183	murA	435	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	M:COG0766
JNUCC-1_01184		714	hypothetical protein	S:ENOG410YZWN
JNUCC-1_01185		231	Uncharacterized membrane protein YwzB	S:COG4836
JNUCC-1_01186		396	ATP synthase epsilon chain	C:COG0355
JNUCC-1_01187	ATPF1B|atpD	300	H(+)-transporting two-sector ATPase	C:COG0055
JNUCC-1_01188	ATPF1B|atpD	1074	H(+)-transporting two-sector ATPase	C:COG0055
JNUCC-1_01189		858	ATP synthase gamma chain	C:COG0224
JNUCC-1_01190	ATPF1A|atpA	1512	H(+)-transporting two-sector ATPase	C:COG0056
JNUCC-1_01191		546	ATP synthase subunit delta	C:COG0712
JNUCC-1_01192		525	ATP synthase subunit	M:ENOG4111RTE
JNUCC-1_01193		216	ATP synthase subunit	C:COG0636
JNUCC-1_01194		723	ATP synthase subunit a	C:COG0356
JNUCC-1_01195		369	ATP synthase protein	C:ENOG410Z3R1
JNUCC-1_01196	vpr	2244	Minor extracellular protease vpr	O:COG1404
JNUCC-1_01197	wecB	279	UDP-N-acetylglucosamine 2-epimerase (non-hydrolyzing)	M:COG0381
JNUCC-1_01198	wecB	849	UDP-N-acetylglucosamine 2-epimerase (non-hydrolyzing)	M:COG0381
JNUCC-1_01199	upp|UPRT	630	Uracil phosphoribosyltransferase	F:COG0035
JNUCC-1_01200	glyA|SHMT	534	Glycine hydroxymethyltransferase	E:COG0112
JNUCC-1_01201	glyA|SHMT	279	Glycine hydroxymethyltransferase	E:COG0112
JNUCC-1_01202	glyA|SHMT	369	Glycine hydroxymethyltransferase	E:COG0112
JNUCC-1_01203		561	UPF0340 protein	S:COG4475
JNUCC-1_01204	rpiB	447	Ribose-5-phosphate isomerase	G:COG0698
JNUCC-1_01205		1293	Methyl-accepting chemotaxis protein	S:ENOG410YD9G
JNUCC-1_01206	ARSC2|arsC	618	Arsenate reductase (glutaredoxin)	T:COG0394

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_01207		225	Putative manganese efflux pump MntP	S:COG1971
JNUCC-1_01208		312	Putative manganese efflux pump MntP	S:COG1971
JNUCC-1_01209	tsaC|rimN|SUA5	1050	L-threonylcarbamoyladenylate synthase	J:COG0009
JNUCC-1_01210		402	hypothetical protein	S:ENOG410Z0HZ
JNUCC-1_01211		627	Stage II sporulation protein	S:ENOG4111PGF
JNUCC-1_01212	hemK|prmC|HEMK	894	Peptide chain release factor N(5)-glutamine methyltransferase	J:COG2890
JNUCC-1_01213		1071	Peptide chain release factor	J:COG0216
JNUCC-1_01214	tdk|TK	621	Thymidine kinase	F:COG1435
JNUCC-1_01215		246	50S ribosomal protein L31 type	J:COG0254
JNUCC-1_01216		1278	Transcription termination factor Rho	K:COG1158
JNUCC-1_01217	glpX	972	Fructose-bisphosphatase	G:COG1494
JNUCC-1_01218	murA	1287	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	M:COG0766
JNUCC-1_01219	talA|talB	642	Transaldolase	G:COG0176
JNUCC-1_01220	gatY-kbaY	864	Tagatose-bisphosphate aldolase	G:COG0191
JNUCC-1_01221		321	Probable transcriptional regulatory protein TcrX	T:COG0745
JNUCC-1_01222	pyrG|CTPS	294	CTP synthase (glutamine hydrolyzing)	F:COG0504
JNUCC-1_01223	pyrG|CTPS	1320	CTP synthase (glutamine hydrolyzing)	F:COG0504
JNUCC-1_01224		543	Probable DNA-directed RNA polymerase subunit delta	K:COG3343
JNUCC-1_01225	icmF	3240	Isobutyryl-CoA mutase	E:COG1703
JNUCC-1_01226		642	Fatty acid metabolism regulator protein	K:ENOG410ZWAV
JNUCC-1_01227	argK	957	Putative GTPase	E:COG1703
JNUCC-1_01228	mmgC	1140	Probable acyl-CoA dehydrogenase YngJ	I:COG1960
JNUCC-1_01229	ACADM|acd	1140	Medium-chain acyl-CoA dehydrogenase	I:COG1960
JNUCC-1_01230	paaH|hbd|fadB|mmgB	852	3-hydroxybutyryl-CoA dehydrogenase	I:COG1250
JNUCC-1_01231	atoB	1188	Acetyl-CoA C-acetyltransferase	I:COG0183

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_01232		813	Putative transposase InsK for insertion sequence element IS150	L:COG2801
JNUCC-1_01233		162	hypothetical protein	L:ENOG4111X46
JNUCC-1_01234		351	hypothetical protein	L:ENOG4111X46
JNUCC-1_01235		2112	uncharacterized protein	C:COG0247
JNUCC-1_01236	RARS|argS	1671	Arginine-tRNA ligase	J:COG0018
JNUCC-1_01237		423	Uncharacterized beta-barrel protein YwiB	S:COG4506
JNUCC-1_01238	mrcA	2052	Peptidoglycan glycosyltransferase	M:COG0744
JNUCC-1_01239		900	hypothetical protein	S:ENOG410Y00A
JNUCC-1_01240		519	uncharacterized protein	S:ENOG4111716
JNUCC-1_01241		495	uncharacterized protein	S:COG3465
JNUCC-1_01242		1323	uncharacterized protein	S:COG1078
JNUCC-1_01243	lipL	933	Octanoyl-[GcvH]:protein N-octanoyltransferase	H:COG0095
JNUCC-1_01244	pta	972	Phosphate acetyltransferase	C:COG0280
JNUCC-1_01245	hemQ	750	Putative heme-dependent peroxidase	S:COG3253
JNUCC-1_01246		471	Spore coat protein GerQ	S:ENOG4111U21
JNUCC-1_01247		267	hypothetical protein	
JNUCC-1_01248		369	UPF0382 membrane protein	S:COG2363
JNUCC-1_01249		279	hypothetical protein	
JNUCC-1_01250		123	hypothetical protein	
JNUCC-1_01251		303	hypothetical protein	S:ENOG410ZIB2
JNUCC-1_01252		1356	uncharacterized protein	S:COG3314
JNUCC-1_01253	spuC	1314	Putrescine-pyruvate transaminase	E:COG0161
JNUCC-1_01254	gapN	1440	Glyceraldehyde-3-phosphate dehydrogenase (NADP(+))	C:COG1012
JNUCC-1_01255	doeA	1206	Ectoine hydrolase	E:COG0006
JNUCC-1_01256		1665	Transcriptional activator AdeR	K:COG2508

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_01257	rfbD|rmlD	828	dTDP-4-dehydrorhamnose reductase	M:COG1091
JNUCC-1_01258		1026	Putative membrane-bound acyltransferase YkrP	G:COG3594
JNUCC-1_01259		858	Non-like proteinous end joining protein Ku	L:COG1273
JNUCC-1_01260	ligD	1779	DNA ligase (ATP)	L:COG3285
JNUCC-1_01261		585	Putative uncharacterized transporter	P:COG2059
JNUCC-1_01262		600	Probable chromate transport protein	P:COG2059
JNUCC-1_01263	MPG	369	DNA-3-methyladenine glycosylase II	S:COG3189
JNUCC-1_01264		489	Uncharacterized membrane protein YkoY	P:COG0861
JNUCC-1_01265		336	Uncharacterized membrane protein YkoY	P:COG0861
JNUCC-1_01266	pgm	1737	Phosphoglucomutase (alpha-D-glucose-1,6-bisphosphate-dependent)	G:COG1109
JNUCC-1_01267		1056	UPF0118 membrane protein YubA	S:COG0628
JNUCC-1_01268		183	hypothetical protein	S:ENOG410Y2PH
JNUCC-1_01269		318	hypothetical protein	P:COG0025
JNUCC-1_01270		1533	K(+)/H(+) antiporter NhaP2	P:COG0025
JNUCC-1_01271	recQ	2157	DNA helicase	L:COG0514
JNUCC-1_01272	ampS|pepS|ampT	1245	Aminopeptidase	E:COG2309
JNUCC-1_01273		168	hypothetical protein	
JNUCC-1_01274	hutG	171	Formimidoylglutamase	E:COG0010
JNUCC-1_01275	hutG	804	Formimidoylglutamase	E:COG0010
JNUCC-1_01276	hutI|AMDHD1	1254	Imidazolonepropionase	Q:COG1228
JNUCC-1_01277	hutU|UROC1	1653	Urocanate hydratase	E:COG2987
JNUCC-1_01278	hutH|HAL	1527	Histidine ammonia-lyase	E:COG2986
JNUCC-1_01279	yciA	519	Uncharacterized acyl-CoA thioester hydrolase YkhA	I:COG1607
JNUCC-1_01280	clsA_B	807	Cardiolipin synthase	I:COG1502
JNUCC-1_01281	clsA_B	648	Cardiolipin synthase	I:COG1502

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_01282		1122	Methionine gamma-lyase	E:COG0626
JNUCC-1_01283		450	hypothetical protein	S:ENOG410XPJ1
JNUCC-1_01284		909	Protein RarD	S:COG2962
JNUCC-1_01285		936	uncharacterized protein	E:COG2755
JNUCC-1_01286		621	hypothetical protein	S:COG4698
JNUCC-1_01287		987	hypothetical protein	S:ENOG410XNQB
JNUCC-1_01288		453	hypothetical protein	S:ENOG4111VD1
JNUCC-1_01289		180	hypothetical protein	S:ENOG4111VD1
JNUCC-1_01290		1623	Uncharacterized ABC transporter ATP-binding protein YkpA	S:COG0488
JNUCC-1_01291	TDH	936	L-threonine 3-dehydrogenase	M:COG0451
JNUCC-1_01292	kbl|GCAT	1191	Glycine C-acetyltransferase	H:COG0156
JNUCC-1_01293		90	hypothetical protein	
JNUCC-1_01294	cobU|cobT	1068	Nicotinate-nucleotide-dimethylbenzimidazole phosphoribosyltransferase	L:COG0675
JNUCC-1_01295	lytE|cwlF	798	Muramidase-2	M:COG3773
JNUCC-1_01296		897	Oligopeptide transport system permease protein OppC	P:COG1173
JNUCC-1_01297		966	Oligopeptide transport system permease protein OppB	P:COG0601
JNUCC-1_01298		1746	Oligopeptide-binding protein AppA	E:COG0747
JNUCC-1_01299		1023	Oligopeptide transport ATP-binding protein AppF	V:COG1136
JNUCC-1_01300		1029	Glutathione import ATP-binding protein GsiA	S:COG1123
JNUCC-1_01301		594	uncharacterized protein	S:COG4086
JNUCC-1_01302		327	hypothetical protein	S:COG4086
JNUCC-1_01303		1425	Uncharacterized MFS-type transporter YuxJ	G:ENOG410XSE0
JNUCC-1_01304	ridA|tdcF|RIDA	378	2-iminobutanoate/2-iminopropanoate deaminase	J:COG0251
JNUCC-1_01305	ycjG|ykfB	1263	L-Ala-D/L-Glu epimerase	K:ENOG4111T28
JNUCC-1_01306		333	hypothetical protein	

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_01307		3168	Non-specific serine/threonine protein kinase	L:COG0553
JNUCC-1_01308		1197	Quinolone resistance protein NorA	G:ENOG410XPHU
JNUCC-1_01309		435	Oligopeptide transport ATP-binding protein AppF	E:COG4608
JNUCC-1_01310	cobU|cobT	1071	Nicotinate-nucleotide-dimethylbenzimidazole phosphoribosyltransferase	L:COG0675
JNUCC-1_01311	SOD1	603	Superoxide dismutase	P:COG2032
JNUCC-1_01312		378	uncharacterized protein	S:ENOG4111UJ8
JNUCC-1_01313		1224	hypothetical protein	L:COG3547
JNUCC-1_01314	prkC|stkP	213	Non-specific serine/threonine protein kinase	S:ENOG4112B2B
JNUCC-1_01315		786	hypothetical protein	S:COG1714
JNUCC-1_01316		714	hypothetical protein	S:COG1300
JNUCC-1_01317		267	hypothetical protein	S:COG1300
JNUCC-1_01318		315	hypothetical protein	S:COG1721
JNUCC-1_01319		1044	hypothetical protein	S:COG1721
JNUCC-1_01320	moxR	930	uncharacterized protein	S:COG0714
JNUCC-1_01321		150	hypothetical protein	
JNUCC-1_01322		993	hypothetical protein	S:ENOG410Y47Z
JNUCC-1_01323		648	hypothetical protein	S:ENOG410XUHP
JNUCC-1_01324		930	hypothetical protein	S:ENOG410ZZ7N
JNUCC-1_01325		1266	hypothetical protein	S:ENOG410YFBG
JNUCC-1_01326	nrdB|nrdF	1044	Ribonucleoside-diphosphate reductase	F:COG0208
JNUCC-1_01327		435	Probable flavodoxin-1	C:COG0716
JNUCC-1_01328	nrdA|nrdE	534	Ribonucleoside-diphosphate reductase	F:COG0209
JNUCC-1_01329	nrdA|nrdE	1689	Ribonucleoside-diphosphate reductase	F:COG0209
JNUCC-1_01330		906	HTH-type transcriptional regulator BsdA	K:ENOG410XSIF
JNUCC-1_01331		1440	hypothetical protein	L:COG3316

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_01332	gdhA	1386	Glutamate dehydrogenase (NADP(+))	E:COG0334
JNUCC-1_01333	sat|met3	1311	Sulfate adenylyltransferase	P:COG2046
JNUCC-1_01334	sat|met3	399	Sulfate adenylyltransferase	P:COG2046
JNUCC-1_01335	npdA	729	NAD-dependent protein deacetylase	K:COG0846
JNUCC-1_01336		795	Methionine import ATP-binding protein MetN	E:COG1125
JNUCC-1_01337		987	uncharacterized protein	S:COG4120
JNUCC-1_01338		996	uncharacterized protein	S:COG2984
JNUCC-1_01339	DLD|lpd|pdhD	1446	Dihydrolipoyl dehydrogenase	C:COG1249
JNUCC-1_01340	DLAT|aceF|pdhC	1242	Dihydrolipoyllysine-residue acetyltransferase	C:COG0508
JNUCC-1_01341	BCKDHB|bkdA2	1011	3-methyl-2-oxobutanoate dehydrogenase (2-methylpropanoyl-transferring)	C:COG0022
JNUCC-1_01342	acoA	627	Pyruvate dehydrogenase E1 component subunit alpha	C:COG1071
JNUCC-1_01343	PDHA|pdhA	423	Pyruvate dehydrogenase (acetyl-transferring)	C:COG1071
JNUCC-1_01344	pdh	1152	Phenylalanine dehydrogenase	E:COG0334
JNUCC-1_01345	fabK	984	Enoyl-[acyl-carrier-protein] reductase (NADH)	S:COG2070
JNUCC-1_01346	fadA|fadI	1206	Acetyl-CoA C-acyltransferase	I:COG0183
JNUCC-1_01347	paaH|hbd|fadB|mmgB	876	3-hydroxybutyryl-CoA dehydrogenase	I:COG1250
JNUCC-1_01348	feaB	1524	Phenylacetaldehyde dehydrogenase	C:COG1012
JNUCC-1_01349	paaG	786	2-(1,2-epoxy-1,2-dihydrophenyl)acetyl-CoA isomerase	I:COG1024
JNUCC-1_01350	paaF|echA	771	Enoyl-CoA hydratase	I:COG1024
JNUCC-1_01351		306	Uncharacterized 11.0 kDa protein in thcB-thcC intergenic region	S:ENOG4111YC7
JNUCC-1_01352		567	Putative 1,2-phenylacetyl-CoA epoxidase, subunit D	S:COG2151
JNUCC-1_01353	paaC	819	Phenylacetyl-CoA 1,2-epoxidase	Q:COG3396
JNUCC-1_01354		354	hypothetical protein	Q:COG3460
JNUCC-1_01355	paaA	987	Phenylacetyl-CoA 1,2-epoxidase	Q:COG3396
JNUCC-1_01356		858	Transcriptional repressor PaaX	K:COG3327

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_01357	GAMMA CA	528	Uncharacterized transferase YtoA	S:COG0663
JNUCC-1_01358		426	hypothetical protein	Q:COG2050
JNUCC-1_01359		735	3(or 17)-beta-hydroxysteroid dehydrogenase	S:COG1028
JNUCC-1_01360		645	UPF0702 transmembrane protein YdfR	S:COG2323
JNUCC-1_01361		624	uncharacterized protein	S:ENOG4111XDS
JNUCC-1_01362		417	hypothetical protein	S:ENOG410Z83I
JNUCC-1_01363		363	uncharacterized protein	S:COG3815
JNUCC-1_01364		399	hypothetical protein	S:ENOG4111XDS
JNUCC-1_01365		1023	uncharacterized protein	C:COG2141
JNUCC-1_01366	purC	684	Phosphoribosylaminoimidazolesuccinocarboxamide synthase	F:COG0152
JNUCC-1_01367	ltrA	1317	RNA-directed DNA polymerase	L:COG3344
JNUCC-1_01368		717	hypothetical protein	S:ENOG4112BM1
JNUCC-1_01369	xylG	870	Monosaccharide-transporting ATPase	S:COG4152
JNUCC-1_01370		210	Uncharacterized HTH-type transcriptional regulator	K:COG1476
JNUCC-1_01371		543	hypothetical protein	
JNUCC-1_01372		783	Sodium channel protein type 11 subunit alpha	P:COG1226
JNUCC-1_01373		423	hypothetical protein	S:ENOG410YJIT
JNUCC-1_01374		690	hypothetical protein	S:ENOG4111G3C
JNUCC-1_01375	ecfA1	1677	Energy-coupling factor transporter ATP-binding protein EcfA	P:COG1122
JNUCC-1_01376		879	Energy-coupling factor transporter transmembrane protein EcfT	P:ENOG410Y3V4
JNUCC-1_01377		933	uncharacterized protein	S:COG0724
JNUCC-1_01378		1989	Lactocepin	S:ENOG410Y2PX
JNUCC-1_01379		480	hypothetical protein	S:ENOG4111IYE
JNUCC-1_01380	ndh	1017	NADH dehydrogenase	C:COG1252
JNUCC-1_01381	gmhB	546	D-glycero-beta-D-manno-heptose 1,7-bisphosphate 7-phosphatase	E:COG0241

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_01382		144	hypothetical protein	
JNUCC-1_01383		1131	Uncharacterized MscS family protein YhdY	M:COG0668
JNUCC-1_01384		756	hypothetical protein	S:ENOG410ZG0I
JNUCC-1_01385		405	hypothetical protein	S:ENOG4111UYM
JNUCC-1_01386		318	hypothetical protein	S:ENOG411226W
JNUCC-1_01387	ABC.FEV.A	828	Iron-chelate-transporting ATPase	P:COG1120
JNUCC-1_01388	poxB	1716	Pyruvate dehydrogenase (quinone)	E:COG0028
JNUCC-1_01389	mgsC	1566	Methylamine--glutamate N-methyltransferase	E:COG0069
JNUCC-1_01390	JHAMT	621	Juvenile hormone-III synthase	Q:COG0500
JNUCC-1_01391	lgt|umpA	1167	Phosphatidylglycerol--prolipoprotein diacylglyceryl transferase	S:COG1916
JNUCC-1_01392		615	uncharacterized protein	S:ENOG4111X1S
JNUCC-1_01393		609	hypothetical protein	
JNUCC-1_01394		1248	C4-dicarboxylate transport protein	C:COG1301
JNUCC-1_01395	zntA	2445	Cadmium-exporting ATPase	P:COG2217
JNUCC-1_01396		327	hypothetical protein	K:COG0640
JNUCC-1_01397		810	hypothetical protein	S:ENOG410XV6C
JNUCC-1_01398		243	hypothetical protein	S:COG4709
JNUCC-1_01399		324	hypothetical protein	S:COG4709
JNUCC-1_01400		327	Putative DNA-binding protein YizB	K:COG1695
JNUCC-1_01401		390	hypothetical protein	S:ENOG4111XTX
JNUCC-1_01402		693	uncharacterized protein	S:COG2340
JNUCC-1_01403	modC	636	Molybdate-transporting ATPase	E:COG3842
JNUCC-1_01404	modC	684	Molybdate-transporting ATPase	P:COG4149
JNUCC-1_01405		822	Molybdate-binding periplasmic protein	P:COG0725
JNUCC-1_01406		921	uncharacterized protein	P:COG1910

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_01407	bdh	777	3-hydroxybutyrate dehydrogenase	C:ENOG410XPTP
JNUCC-1_01408	BLVRA|bvdR	1068	Biliverdin reductase	S:COG0673
JNUCC-1_01409		1197	Uncharacterized membrane protein YjcL	S:COG5505
JNUCC-1_01410		282	hypothetical protein	S:ENOG411242F
JNUCC-1_01411		843	hypothetical protein	S:ENOG4111FBQ
JNUCC-1_01412		1656	KsdD-like steroid dehydrogenase	C:COG3573
JNUCC-1_01413		1167	Lactate 2-monooxygenase	C:COG1304
JNUCC-1_01414		519	hypothetical protein	
JNUCC-1_01415		360	hypothetical protein	S:ENOG4111UGG
JNUCC-1_01416		849	Methionine import ATP-binding protein MetN	V:COG1136
JNUCC-1_01417		180	Methionine import ATP-binding protein MetN	P:COG1135
JNUCC-1_01418		663	Methionine import system permease protein MetP	P:COG2011
JNUCC-1_01419		888	D-methionine-binding lipoprotein MetQ	P:COG1464
JNUCC-1_01420	K01436	735	p-aminobenzoyl-glutamate hydrolase subunit A like protein	E:COG1473
JNUCC-1_01421		225	hypothetical protein	
JNUCC-1_01422		567	hypothetical protein	S:ENOG410ZWWS
JNUCC-1_01423		279	hypothetical protein	S:ENOG410XZUR
JNUCC-1_01424		744	Uncharacterized membrane protein YkoY	P:COG0861
JNUCC-1_01425	frdA	1275	Fumarate reductase (quinol)	S:COG2081
JNUCC-1_01426		216	hypothetical protein	
JNUCC-1_01427		1224	hypothetical protein	L:COG3547
JNUCC-1_01428	ppc	2751	Phosphoenolpyruvate carboxylase	C:COG2352
JNUCC-1_01429		237	hypothetical protein	
JNUCC-1_01430		762	hypothetical protein	S:ENOG4111IRS
JNUCC-1_01431		669	hypothetical protein	S:ENOG410ZW6I

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_01432		423	General stress protein	S:COG3871
JNUCC-1_01433	fabG	705	3-oxoacyl-[acyl-carrier-protein] reductase	S:ENOG410XS73
JNUCC-1_01434	ssuE	537	FMN reductase (NADPH)	S:COG0431
JNUCC-1_01435		1131	Salicylate 1-monooxygenase	CH:COG0654
JNUCC-1_01436		1281	hypothetical protein	L:ENOG410ZPEB
JNUCC-1_01437		870	UPF0750 membrane protein YdeO	S:COG1284
JNUCC-1_01438		1152	hypothetical protein	G:COG2814
JNUCC-1_01439		801	Meiotically up-regulated 14 protein	G:COG0235
JNUCC-1_01440		1608	Sodium/pantothenate symporter	H:COG4145
JNUCC-1_01441		1659	Multidrug resistance protein fnx1	G:COG0477
JNUCC-1_01442		465	Uncharacterized HTH-type transcriptional regulator YhbI	K:ENOG410XUB6
JNUCC-1_01443	thiE	1344	Thiamine phosphate synthase	O:COG1397
JNUCC-1_01444	katE|CAT|catB|srpA	2052	Catalase	P:COG0753
JNUCC-1_01445		363	hypothetical protein	
JNUCC-1_01446	BDH|butB	1053	(R,R)-butanediol dehydrogenase	E:COG1063
JNUCC-1_01447	mutT|NUDT15|MTH2	393	8-oxo-dGTP diphosphatase	L:COG0494
JNUCC-1_01448	hsdR	2865	Type I site-specific deoxyribonuclease	L:COG1061
JNUCC-1_01449		300	hypothetical protein	
JNUCC-1_01450	IRC3	1560	DEAD-box ATP-dependent RNA helicase 13	L:COG1061
JNUCC-1_01451		885	hypothetical protein	L:COG1061
JNUCC-1_01452		306	uncharacterized protein	S:COG4997
JNUCC-1_01453		954	uncharacterized protein	S:COG1073
JNUCC-1_01454		357	hypothetical protein	S:ENOG410Y1YU
JNUCC-1_01455		357	hypothetical protein	
JNUCC-1_01456		786	Gluconate 2-dehydrogenase (acceptor)	G:ENOG410ZF7P

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_01457		1755	Gluconate 2-dehydrogenase (acceptor)	E:COG2303
JNUCC-1_01458		195	Sec-independent protein translocase protein TatA	U:ENOG410XUF0
JNUCC-1_01459		576	Putative copper-binding protein	S:COG1999
JNUCC-1_01460		129	hypothetical protein	
JNUCC-1_01461		873	Uncharacterized transporter	P:COG2116
JNUCC-1_01462		396	hypothetical protein	S:ENOG410XRQD
JNUCC-1_01463		804	hypothetical protein	S:ENOG410XRQD
JNUCC-1_01464		387	hypothetical protein	
JNUCC-1_01465		714	Potassium channel protein	P:COG1226
JNUCC-1_01466		483	hypothetical protein	S:ENOG410Y00A
JNUCC-1_01467		420	hypothetical protein	S:ENOG410Y00A
JNUCC-1_01468		210	hypothetical protein	
JNUCC-1_01469	menA	927	1,4-dihydroxy-2-naphthoate octaprenyltransferase	H:COG1575
JNUCC-1_01470		507	hypothetical protein	S:ENOG410YKMK
JNUCC-1_01471	ldhA	996	D-lactate dehydrogenase	C:COG1052
JNUCC-1_01472		1071	hypothetical protein	S:COG3641
JNUCC-1_01473		1461	UPF0061 protein	S:COG0397
JNUCC-1_01474		465	hypothetical protein	S:COG2318
JNUCC-1_01475		1293	Formamidase	C:COG2421
JNUCC-1_01476		390	hypothetical protein	
JNUCC-1_01477	fdhA	1218	Formaldehyde dehydrogenase	E:COG1063
JNUCC-1_01478	MMAB|pduO	414	Cob(I)yrinic acid a,c-diamide adenosyltransferase	S:COG3193
JNUCC-1_01479		498	RNA polymerase sigma factor SigM	K:ENOG410ZXCP
JNUCC-1_01480		312	hypothetical protein	S:ENOG4111SX1
JNUCC-1_01481		183	hypothetical protein	

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_01482		312	hypothetical protein	
JNUCC-1_01483	iscS|NFS1	1302	Cysteine desulfurase	E:COG0520
JNUCC-1_01484		324	hypothetical protein	S:ENOG410YTG4
JNUCC-1_01485		699	hypothetical protein	S:ENOG410YZIG
JNUCC-1_01486		1578	Na(+)/H(+) antiporter NhaG	P:COG0025
JNUCC-1_01487		1044	Uncharacterized membrane protein	P:COG1275
JNUCC-1_01488	rutE	606	hypothetical protein	C:COG0778
JNUCC-1_01489		255	hypothetical protein	
JNUCC-1_01490	hmp|YHB1	1230	Nitric oxide dioxygenase	C:COG1017
JNUCC-1_01491		435	HTH-type transcriptional regulator NsrR	K:COG1959
JNUCC-1_01492		3252	hypothetical protein	K:COG2909
JNUCC-1_01493		450	hypothetical protein	S:ENOG410YTWV
JNUCC-1_01494		1011	hypothetical protein	S:ENOG410ZAZJ
JNUCC-1_01495		1329	hypothetical protein	E:COG0683
JNUCC-1_01496		768	Ribose import ATP-binding protein RbsA	E:COG0410
JNUCC-1_01497	znuC	708	Zinc import ATP-binding protein ZnuC	V:COG1131
JNUCC-1_01498		861	High-affinity branched-chain amino acid transport system permease protein	E:COG0559
JNUCC-1_01499		1008	Probable branched-chain amino acid transport permease protein LivM	E:COG4177
JNUCC-1_01500	fabH	1017	Beta-ketoacyl-[acyl-carrier-protein] synthase III	I:COG0332
JNUCC-1_01501	pcaD	525	3-oxoadipate enol-lactonase	S:COG0596
JNUCC-1_01502		411	hypothetical protein	S:COG0596
JNUCC-1_01503	fabG	747	3-oxoacyl-[acyl-carrier-protein] reductase	S:ENOG410XQPQ
JNUCC-1_01504	ACSF2	1506	Surfactin synthase subunit	IQ:COG0318
JNUCC-1_01505		240	Sporulation-specific transcription factor SpoVIF	S:ENOG4112CKD
JNUCC-1_01506		114	hypothetical protein	

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_01507	mqo	1503	Malate dehydrogenase (quinone)	C:COG0579
JNUCC-1_01508		120	hypothetical protein	
JNUCC-1_01509		465	hypothetical protein	S:ENOG41124G8
JNUCC-1_01510		1434	NADH:ubiquinone reductase (H(+)-translocating)	GM:COG0702
JNUCC-1_01511		189	hypothetical protein	
JNUCC-1_01512		285	hypothetical protein	S:ENOG410Y00A
JNUCC-1_01513		648	hypothetical protein	S:ENOG410Y00A
JNUCC-1_01514	PCBD|phhB	324	4a-hydroxytetrahydrobiopterin dehydratase	H:COG2154
JNUCC-1_01515		492	uncharacterized protein	G:COG0662
JNUCC-1_01516		537	hypothetical protein	
JNUCC-1_01517		594	hypothetical protein	S:ENOG410Z0CQ
JNUCC-1_01518		243	hypothetical protein	
JNUCC-1_01519		711	hypothetical protein	L:ENOG410XQ88
JNUCC-1_01520		684	hypothetical protein	L:ENOG410XQ88
JNUCC-1_01521		954	Glycine betaine-binding protein OpuAC	E:COG2113
JNUCC-1_01522	nicF	684	Maleamate amidohydrolase	Q:COG1335
JNUCC-1_01523		438	HTH-type transcriptional repressor OpcR	K:COG1510
JNUCC-1_01524	bdh	804	3-hydroxybutyrate dehydrogenase	S:COG1028
JNUCC-1_01525	ict-Y	1284	4-hydroxybutyrate coenzyme A transferase	C:COG0427
JNUCC-1_01526	bdh	756	3-hydroxybutyrate dehydrogenase	S:COG1028
JNUCC-1_01527		1257	Uncharacterized MFS-type transporter YbfB	G:ENOG410ZWA1
JNUCC-1_01528		336	Na(+)/H(+) antiporter NhaC	C:COG1757
JNUCC-1_01529		1077	Malate-2H(+)/Na(+)-lactate antiporter	C:COG1757
JNUCC-1_01530	wrbA	609	NAD(P)H dehydrogenase (quinone)	S:COG0655
JNUCC-1_01531		462	HTH-type transcriptional regulator MhqR	K:ENOG4111UT8

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_01532		261	hypothetical protein	
JNUCC-1_01533	PTS-Cel-EIIB|celA|chbB	321	Protein-N(pi)-phosphohistidine-N,N′-diacetylchitobiosephosphotransferase	G:COG1440
JNUCC-1_01534		897	Cellobiose permease IIC component	G:COG1455
JNUCC-1_01535		393	Cellobiose permease IIC component	G:COG1455
JNUCC-1_01536	PTS-Cel-EIIA|celC|chbA	339	Protein-N(pi)-phosphohistidine-N,N′-diacetylchitobiosephosphotransferase	G:COG1447
JNUCC-1_01537	iolU	984	Uncharacterized oxidoreductase	S:COG0673
JNUCC-1_01538		162	hypothetical protein	S:ENOG4112223
JNUCC-1_01539		759	3-alpha(or 20-beta)-hydroxysteroid dehydrogenase	S:COG1028
JNUCC-1_01540		522	Queuosine precursor transporter QueT	S:COG4708
JNUCC-1_01541		336	hypothetical protein	
JNUCC-1_01542		408	hypothetical protein	
JNUCC-1_01543		1017	Probable siderophore-binding lipoprotein YfiY	P:COG0614
JNUCC-1_01544		1980	Vitamin B12 import system permease protein BtuC	P:COG0609
JNUCC-1_01545	fnr	768	Ferredoxin--NADP(+) reductase	O:COG0492
JNUCC-1_01546	fnr	339	Ferredoxin--NADP(+) reductase	O:COG0492
JNUCC-1_01547		759	RsbT co-antagonist protein RsbRD	T:COG1366
JNUCC-1_01548	metH|MTR	660	Methionine synthase	S:COG5012
JNUCC-1_01549		354	hypothetical protein	S:ENOG410ZCY3
JNUCC-1_01550		834	UPF0750 membrane protein YxkD	S:COG1284
JNUCC-1_01551	ldcA	1032	Muramoyltetrapeptide carboxypeptidase	V:COG1619
JNUCC-1_01552		747	Mercuric resistance operon regulatory protein	K:COG0789
JNUCC-1_01553		1224	hypothetical protein	L:COG3547
JNUCC-1_01554		942	hypothetical protein	S:ENOG4111MYZ
JNUCC-1_01555		126	hypothetical protein	
JNUCC-1_01556		609	Putative hydrolase	S:COG0400

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_01557		987	Putative ring-cleaving dioxygenase MhqA	E:COG0346
JNUCC-1_01558		132	hypothetical protein	
JNUCC-1_01559		531	hypothetical protein	S:ENOG410Z7G6
JNUCC-1_01560	GLO1|gloA	372	Lactoylglutathione lyase	E:COG0346
JNUCC-1_01561	gli	762	D-galactarolactone isomerase	S:COG3618
JNUCC-1_01562		585	hypothetical protein	S:COG3575
JNUCC-1_01563	MTHFS	456	5-formyltetrahydrofolate cyclo-ligase	S:COG4405
JNUCC-1_01564		219	hypothetical protein	
JNUCC-1_01565	cwlJ|sleB	441	N-acetylmuramoyl-L-alanine amidase	M:COG3773
JNUCC-1_01566		882	hypothetical protein	S:ENOG410ZGBP
JNUCC-1_01567		594	hypothetical protein	S:ENOG410Y3VT
JNUCC-1_01568		432	hypothetical protein	S:ENOG4111WT4
JNUCC-1_01569		615	Uncharacterized HTH-type transcriptional regulator YvkB	K:COG1309
JNUCC-1_01570		1017	Inner membrane transport permease	V:COG0842
JNUCC-1_01571		741	Sulfate/thiosulfate import ATP-binding protein CysA	P:COG1116
JNUCC-1_01572		390	hypothetical protein	S:COG4270
JNUCC-1_01573	cobU|cobT	1071	Nicotinate-nucleotide-dimethylbenzimidazole phosphoribosyltransferase	L:COG0675
JNUCC-1_01574		366	hypothetical protein	S:ENOG4111JAS
JNUCC-1_01575		690	uncharacterized protein	S:ENOG410XSNF
JNUCC-1_01576		186	hypothetical protein	
JNUCC-1_01577		189	uncharacterized protein	S:ENOG410Y6YS
JNUCC-1_01578		507	hypothetical protein	
JNUCC-1_01579		411	hypothetical protein	
JNUCC-1_01580		156	hypothetical protein	
JNUCC-1_01581		480	hypothetical protein	S:ENOG4111NWG

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_01582		603	hypothetical protein	
JNUCC-1_01583	ABC.FEV.A	348	Iron-chelate-transporting ATPase	S:COG4898
JNUCC-1_01584		540	Cell wall-binding protein YocH	S:COG3584
JNUCC-1_01585	gloB|gloC|HAGH	939	Hydroxyacylglutathione hydrolase	S:COG0491
JNUCC-1_01586		1218	Protein translocase subunit SecA	S:ENOG4111VGM
JNUCC-1_01587		312	hypothetical protein	S:ENOG410Y103
JNUCC-1_01588		1158	Uncharacterized MFS-type transporter YfkF	G:ENOG410XR1I
JNUCC-1_01589	pdxS|pdx1	867	Pyridoxal 5′-phosphate synthase (glutamine hydrolyzing)	H:COG0214
JNUCC-1_01590		1404	Uncharacterized HTH-type transcriptional regulator YhdI	K:COG1167
JNUCC-1_01591		429	hypothetical protein	
JNUCC-1_01592		726	HTH-type transcriptional activator mta	K:COG0789
JNUCC-1_01593		567	Uncharacterized membrane protein YmcC	S:ENOG4111PNY
JNUCC-1_01594		951	Glycine betaine-binding protein OpuAC	E:COG2113
JNUCC-1_01595	lysC	1215	Aspartate kinase	E:COG0527
JNUCC-1_01596	asd	1047	Aspartate-semialdehyde dehydrogenase	E:COG0136
JNUCC-1_01597	ectC	390	Ectoine synthase	H:ENOG4111NEJ
JNUCC-1_01598	ectB|dat	1311	Diaminobutyrate-2-oxoglutarate transaminase	E:COG0160
JNUCC-1_01599	ectA	480	Diaminobutyrate acetyltransferase	K:COG0454
JNUCC-1_01600		1020	hypothetical protein	S:ENOG410ZAZJ
JNUCC-1_01601	cheBR	1062	Protein-glutamate O-methyltransferase	T:ENOG410XNMH
JNUCC-1_01602	kinA	1296	Histidine kinase	T:ENOG410XNMH
JNUCC-1_01603		969	Glycine betaine-binding protein OpuAC	E:COG2113
JNUCC-1_01604	kinA	732	Histidine kinase	T:ENOG410XQ4K
JNUCC-1_01605	atoS	648	Histidine kinase	T:COG0642
JNUCC-1_01606		291	hypothetical protein	

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_01607	moeZR|moeBR	1125	uncharacterized protein	S:COG0491
JNUCC-1_01608		237	hypothetical protein	
JNUCC-1_01609		849	hypothetical protein	S:ENOG41126P2
JNUCC-1_01610		183	hypothetical protein	L:ENOG410Y1QP
JNUCC-1_01611		381	hypothetical protein	S:ENOG41127R5
JNUCC-1_01612	hsdR	1470	Type I site-specific deoxyribonuclease	V:COG0610
JNUCC-1_01613	hsdR	1383	Type I site-specific deoxyribonuclease	V:COG0610
JNUCC-1_01614	hsdS	1281	Type I site-specific deoxyribonuclease	V:COG0732
JNUCC-1_01615	hsdM	2007	Site-specific DNA-methyltransferase (adenine-specific)	V:COG0286
JNUCC-1_01616		351	hypothetical protein	S:COG4043
JNUCC-1_01617		627	hypothetical protein	S:ENOG41120MI
JNUCC-1_01618		123	hypothetical protein	S:ENOG41123R4
JNUCC-1_01619		915	hypothetical protein	S:ENOG410XXBD
JNUCC-1_01620		1020	hypothetical protein	S:ENOG410ZAZJ
JNUCC-1_01621		843	hypothetical protein	
JNUCC-1_01622		297	hypothetical protein	
JNUCC-1_01623	K01436	1179	Putative amidohydrolase YhaA	E:COG1473
JNUCC-1_01624		642	Osmoprotectant import permease protein OsmW	P:ENOG4111NED
JNUCC-1_01625		915	Choline-binding protein	E:COG1732
JNUCC-1_01626		651	Carnitine transport permease protein OpuCD	E:COG1174
JNUCC-1_01627		1128	Methionine import ATP-binding protein MetN	P:COG1135
JNUCC-1_01628		537	HTH-type transcriptional repressor OpcR	K:COG1510
JNUCC-1_01629		321	hypothetical protein	
JNUCC-1_01630		258	Copper-sensing transcriptional repressor CsoR	S:COG1937
JNUCC-1_01631		807	UPF0721 transmembrane protein YrkJ	S:COG0730

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_01632	tusA|sirA	228	UPF0033 protein YrkI	O:COG0425
JNUCC-1_01633	gloB|gloC|HAGH	1128	Hydroxyacylglutathione hydrolase	S:COG0491
JNUCC-1_01634		237	hypothetical protein	O:COG0695
JNUCC-1_01635	tusA|sirA	570	UPF0033 protein YrkI	P:COG0607
JNUCC-1_01636	tusA|sirA	480	uncharacterized protein	S:COG2210
JNUCC-1_01637		1452	Multidrug resistance protein	G:ENOG41113NI
JNUCC-1_01638		321	hypothetical protein	S:ENOG410XV04
JNUCC-1_01639		1614	hypothetical protein	L:COG0249
JNUCC-1_01640		798	Mercuric resistance operon regulatory protein	K:COG0789
JNUCC-1_01641		423	hypothetical protein	S:ENOG410Z2MQ
JNUCC-1_01642		216	Uncharacterized HTH-type transcriptional regulator	K:COG1476
JNUCC-1_01643		426	hypothetical protein	
JNUCC-1_01644	cobU|cobT	1071	Nicotinate-nucleotide-dimethylbenzimidazole phosphoribosyltransferase	L:COG0675
JNUCC-1_01645		207	hypothetical protein	
JNUCC-1_01646		465	hypothetical protein	
JNUCC-1_01647		546	hypothetical protein	S:ENOG411227H
JNUCC-1_01648	pheA2	876	Prephenate dehydratase	E:COG0077
JNUCC-1_01649		237	hypothetical protein	S:ENOG4112485
JNUCC-1_01650	pheA1	1098	Chorismate mutase	E:COG1605
JNUCC-1_01651	aroC	1173	Chorismate synthase	E:COG0082
JNUCC-1_01652	hisC	1110	Histidinol-phosphate transaminase	E:COG0079
JNUCC-1_01653	tyrA2	1104	Prephenate dehydrogenase	E:COG0287
JNUCC-1_01654	aroA	1287	3-phosphoshikimate 1-carboxyvinyltransferase	E:COG0128
JNUCC-1_01655		399	hypothetical protein	E:COG0346
JNUCC-1_01656		1113	hypothetical protein	S:ENOG410XRP6

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_01657		3228	Autophagy-related protein 23	S:ENOG410YCDF
JNUCC-1_01658		714	hypothetical protein	S:ENOG410YFWX
JNUCC-1_01659		1419	hypothetical protein	S:ENOG410YBDV
JNUCC-1_01660		1311	hypothetical protein	S:ENOG410YH0T
JNUCC-1_01661	metC	1194	Cystathionine beta-lyase	E:COG0626
JNUCC-1_01662		969	hypothetical protein	S:ENOG410ZPED
JNUCC-1_01663	ykfC	1158	Gamma-D-glutamyl-L-lysine dipeptidyl-peptidase	M:COG0791
JNUCC-1_01664		462	hypothetical protein	S:COG1988
JNUCC-1_01665	metE	1119	5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase	E:COG0620
JNUCC-1_01666		222	hypothetical protein	S:ENOG41123GI
JNUCC-1_01667		438	hypothetical protein	S:ENOG4111WT4
JNUCC-1_01668	ltrA	1794	RNA-directed DNA polymerase	L:COG3344
JNUCC-1_01669	BDH|butB	1050	(R,R)-butanediol dehydrogenase	E:COG1063
JNUCC-1_01670		147	hypothetical protein	
JNUCC-1_01671		1194	Transposase for insertion sequence element IS905	L:COG3328
JNUCC-1_01672		204	hypothetical protein	
JNUCC-1_01673		843	Probable tyrosine recombinase XerC-like	L:COG0582
JNUCC-1_01674		201	hypothetical protein	S:ENOG410XZA3
JNUCC-1_01675	rlmH	480	23S rRNA (pseudouridine(1915)-N(3))-methyltransferase	S:COG1576
JNUCC-1_01676		261	hypothetical protein	
JNUCC-1_01677		477	hypothetical protein	S:COG2403
JNUCC-1_01678		891	hypothetical protein	S:COG2403
JNUCC-1_01679		390	hypothetical protein	S:ENOG411239Y
JNUCC-1_01680		234	hypothetical protein	
JNUCC-1_01681		552	hypothetical protein	S:ENOG410ZH9B

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_01682		126	hypothetical protein	
JNUCC-1_01683	coxD|ctaF	318	Cytochrome-c oxidase	S:ENOG41120NW
JNUCC-1_01684		135	hypothetical protein	
JNUCC-1_01685		726	hypothetical protein	S:ENOG4111XTT
JNUCC-1_01686	assT	1056	Aryl-sulfate sulfotransferase	S:ENOG410ZB20
JNUCC-1_01687	assT	417	Aryl-sulfate sulfotransferase	S:ENOG410ZB20
JNUCC-1_01688		414	hypothetical protein	S:ENOG41121X3
JNUCC-1_01689		663	Glutamic acid-rich protein	S:ENOG411081U
JNUCC-1_01690		336	Gas vesicle protein GvpJ	S:ENOG41121P7
JNUCC-1_01691		285	Protein GvpK	S:ENOG41100E0
JNUCC-1_01692		279	Gas vesicle protein GvpS	S:ENOG410ZYJ4
JNUCC-1_01693		804	hypothetical protein	S:ENOG4111RFK
JNUCC-1_01694		270	hypothetical protein	S:ENOG410XX3V
JNUCC-1_01695		765	Protein GvpF	S:ENOG4111RFK
JNUCC-1_01696		921	Gas vesicle protein GvpN	S:COG0714
JNUCC-1_01697		261	hypothetical protein	S:ENOG410Y7YF
JNUCC-1_01698		261	Gas vesicle structural protein	S:ENOG411257U
JNUCC-1_01699		465	Beta-mannosyltransferase	S:ENOG410XQKR
JNUCC-1_01700		525	hypothetical protein	
JNUCC-1_01701	bcrC	702	Undecaprenyl-diphosphate phosphatase	I:COG0671
JNUCC-1_01702		1347	Uncharacterized MFS-type transporter YwoD	G:ENOG410XSSD
JNUCC-1_01703		309	hypothetical protein	
JNUCC-1_01704		1347	Spore germination protein YaaH	G:COG3858
JNUCC-1_01705		537	hypothetical protein	S:ENOG4111NNA
JNUCC-1_01706		1767	hypothetical protein	S:ENOG410ZK1N

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_01707		333	hypothetical protein	S:ENOG410ZK1N
JNUCC-1_01708	psuG	915	Pseudouridylate synthase	Q:COG2313
JNUCC-1_01709	psuK	1119	Pseudouridine kinase	K:ENOG410ZKAN
JNUCC-1_01710	rimL	543	Putative ribosomal N-acetyltransferase YdaF	J:COG1670
JNUCC-1_01711		462	hypothetical protein	S:ENOG410Y2S8
JNUCC-1_01712	msbA	1452	Lipid A export ATP-binding/permease protein MsbA	V:COG1132
JNUCC-1_01713		240	Uncharacterized ABC transporter ATP-binding protein YwjA	V:COG1132
JNUCC-1_01714		387	hypothetical protein	S:ENOG410ZF2I
JNUCC-1_01715		831	Nodulation protein J	V:COG0842
JNUCC-1_01716	rbsA	945	Monosaccharide-transporting ATPase	E:COG0411
JNUCC-1_01717	degP|htrA	888	Peptidase Do	O:COG0265
JNUCC-1_01718		291	hypothetical protein	
JNUCC-1_01719	gloB|gloC|HAGH	807	Hydroxyacylglutathione hydrolase	S:COG1235
JNUCC-1_01720		927	hypothetical protein	S:COG4853
JNUCC-1_01721		1317	hypothetical protein	S:ENOG410ZZTG
JNUCC-1_01722	vicK	1833	Histidine kinase	T:ENOG410XNMH
JNUCC-1_01723		696	Nisin biosynthesis regulatory protein NisR	T:COG0745
JNUCC-1_01724		1473	uncharacterized protein	M:COG0739
JNUCC-1_01725	purA|ADSS	1293	Adenylosuccinate synthase	F:COG0104
JNUCC-1_01726		1464	hypothetical protein	S:ENOG410XPWT
JNUCC-1_01727		1485	hypothetical protein	L:COG3666
JNUCC-1_01728	dnaB	1371	DNA helicase	L:COG0305
JNUCC-1_01729		447	50S ribosomal protein L9	J:COG0359
JNUCC-1_01730	gdpP	1971	uncharacterized protein	T:COG3887
JNUCC-1_01731		948	uncharacterized protein	S:COG4241

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_01732		507	hypothetical protein	S:ENOG410Z28J
JNUCC-1_01733		231	30S ribosomal protein S18	J:COG0238
JNUCC-1_01734		483	Single-stranded DNA-binding protein	L:COG0629
JNUCC-1_01735		291	30S ribosomal protein S6, chloroplastic	J:COG0360
JNUCC-1_01736		1101	Ribosome-binding ATPase YchF	J:COG0012
JNUCC-1_01737		198	uncharacterized protein	S:COG4481
JNUCC-1_01738		1020	uncharacterized protein	S:COG3949
JNUCC-1_01739		612	uncharacterized protein	S:ENOG4111N5J
JNUCC-1_01740		363	Uncharacterized membrane protein YdfK	S:COG1811
JNUCC-1_01741		405	hypothetical protein	S:COG1811
JNUCC-1_01742	sufS	1155	Cysteine desulfurase	E:COG0520
JNUCC-1_01743		1227	ATP-dependent protease	L:COG3464
JNUCC-1_01744		837	Nucleoid occlusion protein	K:COG1475
JNUCC-1_01745		774	Chromosome partitioning protein ParA	D:COG1192
JNUCC-1_01746		843	Nucleoid occlusion protein	K:COG1475
JNUCC-1_01747	gidB|rsmG	717	16S rRNA (guanine(527)-N(7))-methyltransferase	M:COG0357
JNUCC-1_01748		1887	tRNA uridine 5-carboxymethylaminomethyl modification enzyme MnmG	D:COG0445
JNUCC-1_01749	mnmE|trmE|MSS1	1377	tRNA modification GTPase MnmE	S:COG0486
JNUCC-1_01750		711	Protein jag	S:COG1847
JNUCC-1_01751		768	Membrane protein insertase MisCA	U:COG0706
JNUCC-1_01752	rnpA	345	Ribonuclease P	J:COG0594
JNUCC-1_01753		135	50S ribosomal protein L34	J:COG0230
JNUCC-1_01754		1356	Chromosomal replication initiator protein DnaA	L:COG0593
JNUCC-1_01755	dnaN	1134	DNA-directed DNA polymerase	L:COG0592
JNUCC-1_01756		222	uncharacterized protein	S:COG2501

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_01757		1116	DNA replication and repair protein RecF	L:COG1195
JNUCC-1_01758		291	hypothetical protein	S:ENOG411235W
JNUCC-1_01759	gyrB	1374	DNA topoisomerase (ATP-hydrolyzing)	L:COG0187
JNUCC-1_01760	gyrB	576	DNA topoisomerase (ATP-hydrolyzing)	L:COG0187
JNUCC-1_01761	gyrA	2532	DNA topoisomerase (ATP-hydrolyzing)	L:COG0188
JNUCC-1_01762		1110	Cyclic di-GMP phosphodiesterase response regulator RpfG	T:COG2206
JNUCC-1_01763		966	uncharacterized protein	S:ENOG4111I87
JNUCC-1_01764	IMPDH|guaB	1470	IMP dehydrogenase	F:COG0516
JNUCC-1_01765	dacC|dacA|dacD	1326	Serine-type D-Ala-D-Ala carboxypeptidase	M:COG1686
JNUCC-1_01766		903	Dipeptide transport system permease protein DppC	P:COG1173
JNUCC-1_01767		921	Dipeptide transport system permease protein	P:COG0601
JNUCC-1_01768		1023	Oligopeptide transport ATP-binding protein OppD	EP:COG0444
JNUCC-1_01769		531	Oligopeptide transport ATP-binding protein OppF	E:COG4608
JNUCC-1_01770		456	Oligopeptide transport ATP-binding protein AmiE	EP:COG0444
JNUCC-1_01771		165	hypothetical protein	
JNUCC-1_01772		1635	Glutathione-binding protein GsiB	E:COG0747
JNUCC-1_01773	SARS|serS	1275	Serine-tRNA ligase	J:COG0172
JNUCC-1_01775		225	TRAP-T-associated universal stress protein TeaD	T:COG0589
JNUCC-1_01776		180	hypothetical protein	T:COG0589
JNUCC-1_01777		906	Putative sulfate transporter YbaR	P:COG0659
JNUCC-1_01778		603	Putative sulfate transporter YbaR	P:COG0659
JNUCC-1_01779	proC	810	Pyrroline-5-carboxylate reductase	E:COG0345
JNUCC-1_01780	dck	681	Deoxyadenosine kinase	F:COG1428
JNUCC-1_01781	dgk	642	Deoxyguanosine kinase	F:COG1428
JNUCC-1_01783		717	hypothetical protein	S:ENOG410XQDK

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_01784	ACSS|acs	1716	Acetate--CoA ligase	I:COG0365
JNUCC-1_01785		708	hypothetical protein	S:ENOG410Z6T7
JNUCC-1_01786		204	hypothetical protein	
JNUCC-1_01787		573	hypothetical protein	
JNUCC-1_01788		273	hypothetical protein	
JNUCC-1_01789		393	hypothetical protein	
JNUCC-1_01790		402	hypothetical protein	
JNUCC-1_01791		171	hypothetical protein	
JNUCC-1_01792		1242	Bile acid transporter	G:COG0477
JNUCC-1_01793		237	hypothetical protein	S:ENOG4111Q3E
JNUCC-1_01794		315	hypothetical protein	
JNUCC-1_01795		345	uncharacterized protein	S:ENOG41121QV
JNUCC-1_01796		1287	Spore germination protein YaaH	G:COG3858
JNUCC-1_01797		864	Protein CtaG	S:COG3336
JNUCC-1_01798	tadA	483	tRNA(adenine(34)) deaminase	FJ:COG0590
JNUCC-1_01799		381	hypothetical protein	
JNUCC-1_01800	dnaX	1707	DNA-directed DNA polymerase	L:COG2812
JNUCC-1_01801		318	Nucleoid-associated protein	S:COG0718
JNUCC-1_01802		597	Recombination protein RecR	L:COG0353
JNUCC-1_01803		219	uncharacterized protein	S:ENOG410Z9RY
JNUCC-1_01804		363	hypothetical protein	
JNUCC-1_01805		222	Sigma-K factor-processing regulatory protein BofA	S:ENOG41128H6
JNUCC-1_01806		195	Protein CsfB	S:ENOG410ZSYW
JNUCC-1_01807	tmk|DTYMK	648	dTMP kinase	F:COG0125
JNUCC-1_01808		330	uncharacterized protein	S:COG3870

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_01809		441	uncharacterized protein	S:COG1728
JNUCC-1_01810	holB	990	DNA-directed DNA polymerase	L:COG0470
JNUCC-1_01811		831	Stage 0 sporulation protein YaaT	S:COG1774
JNUCC-1_01812		345	Initiation-control protein YabA	S:COG4467
JNUCC-1_01813	prmA	741	uncharacterized protein	S:COG4123
JNUCC-1_01814		288	UPF0213 protein	L:COG2827
JNUCC-1_01815	rsmI	879	16S rRNA (cytidine(1402)-2'-O)-methyltransferase	S:COG0313
JNUCC-1_01816		285	Transition state regulatory protein AbrB	K:COG2002
JNUCC-1_01817	MARS|metG	1959	Methionine-tRNA ligase	J:COG0143
JNUCC-1_01818	tatD	780	Uncharacterized metal-dependent hydrolase YabD	L:COG0084
JNUCC-1_01819		1254	uncharacterized protein	S:COG3583
JNUCC-1_01820	rnmV	573	Ribonuclease M5	L:COG1658
JNUCC-1_01821	ksgA	885	16S rRNA (adenine(1518)-N(6)/adenine(1519)-N(6))-dimethyltransferase	J:COG0030
JNUCC-1_01822		912	Sporulation-specific protease YabG	S:ENOG410XQ69
JNUCC-1_01823		267	Protein Veg	S:COG4466
JNUCC-1_01824	SCP2|SCPX	351	Propanoyl-CoA C-acyltransferase	I:COG3255
JNUCC-1_01825		153	Protein SspF	S:ENOG41124V1
JNUCC-1_01826	ispE	855	4-(cytidine 5'-diphospho)-2-C-methyl-D-erythritol kinase	I:COG1947
JNUCC-1_01827		822	Pur operon repressor	F:COG0503
JNUCC-1_01828		297	Putative septation protein SpoVG	M:COG2088
JNUCC-1_01829	glmU	1380	UDP-N-acetylglucosamine diphosphorylase	M:COG1207
JNUCC-1_01830	PRPS|prsA	954	Ribose-phosphate diphosphokinase	F:COG0462
JNUCC-1_01831		636	50S ribosomal protein L25	J:COG1825
JNUCC-1_01832	PTH1|pth|spoVC	603	Aminoacyl-tRNA hydrolase	J:COG0193
JNUCC-1_01833		234	uncharacterized protein	S:ENOG41125K9

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_01834	mfd	3531	UvrABC system protein	L:COG1197
JNUCC-1_01835		534	Stage V sporulation protein	K:COG2002
JNUCC-1_01836		1569	Uncharacterized membrane protein YabM	M:COG2244
JNUCC-1_01837		1455	uncharacterized protein	S:COG3956
JNUCC-1_01838		261	uncharacterized protein	J:COG1188
JNUCC-1_01839		306	Spore protein YabP	S:ENOG41122J9
JNUCC-1_01840		603	Spore protein YabQ	S:ENOG410XV6S
JNUCC-1_01841		378	Cell division protein DivIC	D:COG2919
JNUCC-1_01842		384	uncharacterized protein	J:COG1098
JNUCC-1_01843		1227	ATP-dependent protease	L:COG3464
JNUCC-1_01845	spoIIE	2445	Protein-serine/threonine phosphatase	T:COG2208
JNUCC-1_01846		732	uncharacterized protein	S:COG2304
JNUCC-1_01847	K08884	933	Non-specific serine/threonine protein kinase	T:COG0515
JNUCC-1_01848	hprT|hpt|HPRT1	1395	Hypoxanthine phosphoribosyltransferase	F:COG0634
JNUCC-1_01849	hprT|hpt|HPRT1	549	Hypoxanthine phosphoribosyltransferase	F:COG0634
JNUCC-1_01850	ftsH|hflB	648	ATP-dependent zinc metalloprotease FtsH	O:COG0465
JNUCC-1_01851	ftsH|hflB	1470	ATP-dependent zinc metalloprotease FTSH 1, chloroplastic	O:COG0465
JNUCC-1_01852	coaX	801	Pantothenate kinase	K:COG1521
JNUCC-1_01853		885	33 kDa chaperonin	O:COG1281
JNUCC-1_01854	prsA	906	Peptidylprolyl isomerase	O:COG0760
JNUCC-1_01855	cysK	927	Cysteine synthase	E:COG0031
JNUCC-1_01856	folP	939	Dihydropteroate synthase	H:COG0294
JNUCC-1_01857	folB	366	Dihydroneopterin aldolase	H:COG1539
JNUCC-1_01858	folK	513	2-amino-4-hydroxy-6-hydroxymethyldihydropteridine diphosphokinase	H:COG0801
JNUCC-1_01859		219	Uncharacterized HTH-type transcriptional regulator YazB	K:COG1396

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_01860	KARS|lysS	1482	Lysine-tRNA ligase	J:COG1190
JNUCC-1_01861		171	hypothetical protein	
JNUCC-1_01877		690	uncharacterized protein	S:COG1285
JNUCC-1_01878		468	Transcriptional regulator CtsR	K:COG4463
JNUCC-1_01879		555	Protein-arginine kinase activator protein	S:COG3880
JNUCC-1_01880	mcsB	1065	Protein arginine kinase	E:COG3869
JNUCC-1_01881		2433	Chaperone protein ClpB	O:COG0542
JNUCC-1_01882		1374	DNA repair protein RadA like protein	O:COG1066
JNUCC-1_01883		1098	Uncharacterized PIN and TRAM-domain containing protein	S:COG4956
JNUCC-1_01884	EARS|gltX	1470	Glutamate-tRNA ligase	J:COG0008
JNUCC-1_01885	cysE	660	Serine O-acetyltransferase	E:COG1045
JNUCC-1_01886	CARS|cysS	1413	Cysteine-tRNA ligase	J:COG0215
JNUCC-1_01887	K11145	420	Mini-ribonuclease	S:COG1939
JNUCC-1_01888	rlmB	753	23S rRNA (guanosine(2251)-2′-O)-methyltransferase	J:COG0566
JNUCC-1_01889		516	uncharacterized protein	S:COG3688
JNUCC-1_01890		663	RNA polymerase sigma-H factor	K:COG1595
JNUCC-1_01891		180	Protein translocase subunit SecE	U:ENOG410XUXP
JNUCC-1_01892		534	Transcription termination/antitermination protein NusG	K:COG0250
JNUCC-1_01893		426	50S ribosomal protein L11-1	J:COG0080
JNUCC-1_01894		696	50S ribosomal protein L1, chloroplastic	J:COG0081
JNUCC-1_01895		501	50S ribosomal protein L10	J:COG0244
JNUCC-1_01896		366	50S ribosomal protein L7/L12	J:COG0222
JNUCC-1_01897	rsmC	603	16S rRNA (guanine(1207)-N(2))-methyltransferase	J:COG2813
JNUCC-1_01898	rpoB	3447	DNA-directed RNA polymerase	K:COG0085
JNUCC-1_01899	rpoC	3624	DNA-directed RNA polymerase	K:COG0086

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_01900		252	Putative ribosomal protein L7Ae-like	J:COG1358
JNUCC-1_01901		420	30S ribosomal protein S12	J:COG0048
JNUCC-1_01902		471	30S ribosomal protein S7-1	J:COG0049
JNUCC-1_01903		2079	Elongation factor G	J:COG0480
JNUCC-1_01904		1191	Elongation factor Tu-A	J:COG0050
JNUCC-1_01905		309	30S ribosomal protein S10, chloroplastic	J:COG0051
JNUCC-1_01906		633	50S ribosomal protein L3	J:COG0087
JNUCC-1_01907		624	50S ribosomal protein L4	J:COG0088
JNUCC-1_01908		291	50S ribosomal protein L23	J:COG0089
JNUCC-1_01909		831	50S ribosomal protein L2	J:COG0090
JNUCC-1_01910		279	30S ribosomal protein S19, chloroplastic	J:COG0185
JNUCC-1_01911		342	50S ribosomal protein L22, chloroplastic	J:COG0091
JNUCC-1_01912		642	30S ribosomal protein S3	J:COG0092
JNUCC-1_01913		435	50S ribosomal protein L16, plastid	J:COG0197
JNUCC-1_01914		201	50S ribosomal protein L29	J:COG0255
JNUCC-1_01915		264	30S ribosomal protein S17	J:COG0186
JNUCC-1_01916		336	50S ribosomal protein L14	J:COG0093
JNUCC-1_01917		312	50S ribosomal protein L24	J:COG0198
JNUCC-1_01918		540	50S ribosomal protein L5	J:COG0094
JNUCC-1_01919		186	30S ribosomal protein S14 type Z	J:COG0199
JNUCC-1_01920		399	30S ribosomal protein S8	J:COG0096
JNUCC-1_01921		537	50S ribosomal protein L6	J:COG0097
JNUCC-1_01922		363	50S ribosomal protein L18	J:COG0256
JNUCC-1_01923		216	30S ribosomal protein	J:COG0098
JNUCC-1_01924		291	30S ribosomal protein	J:COG0098

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_01925		183	50S ribosomal protein L30	J:COG1841
JNUCC-1_01926		441	50S ribosomal protein L15	J:COG0200
JNUCC-1_01927		1293	Protein translocase subunit SecY	U:COG0201
JNUCC-1_01928	adk|AK	639	Adenylate kinase	F:COG0563
JNUCC-1_01929		309	Putative ribosome-binding protein YbzG	S:ENOG410XUZY
JNUCC-1_01930		219	Translation initiation factor IF-1	J:COG0361
JNUCC-1_01931		114	50S ribosomal protein L36, chloroplastic	J:COG0257
JNUCC-1_01932		366	Cyanelle 30S ribosomal protein S13	J:COG0099
JNUCC-1_01933		396	30S ribosomal protein S11	J:COG0100
JNUCC-1_01934	rpoA	945	DNA-directed RNA polymerase	K:COG0202
JNUCC-1_01935		354	50S ribosomal protein L17	J:COG0203
JNUCC-1_01936	ecfA1	840	Energy-coupling factor transporter ATP-binding protein EcfA1	P:COG1122
JNUCC-1_01937	ecfA2	873	Energy-coupling factor transporter ATP-binding protein EcfA2	P:COG1122
JNUCC-1_01938		804	Energy-coupling factor transporter transmembrane protein EcfT	P:COG0619
JNUCC-1_01939	truA|PUS1	744	tRNA pseudouridine(38-40) synthase	J:COG0101
JNUCC-1_01940		591	hypothetical protein	S:ENOG410Z9NZ
JNUCC-1_01941		438	50S ribosomal protein L13	J:COG0102
JNUCC-1_01942		393	30S ribosomal protein S9	J:COG0103
JNUCC-1_01943		1578	uncharacterized protein	L:COG3436
JNUCC-1_01944		327	hypothetical protein	S:ENOG4112839
JNUCC-1_01945		414	hypothetical protein	S:ENOG410ZH0A
JNUCC-1_01946		579	Sensory transduction protein LytT	T:COG3279
JNUCC-1_01947	cbiD	849	Cobalt-precorrin-5B (C(1))-methyltransferase	H:COG1903
JNUCC-1_01948		708	hypothetical protein	V:COG0842
JNUCC-1_01949		1173	hypothetical protein	S:COG4552

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_01950	amiABC	714	N-acetylmuramoyl-L-alanine amidase	M:COG0860
JNUCC-1_01951		1122	Sensory transduction protein LytR	T:COG3947
JNUCC-1_01952		7095	Pheromone-processing carboxypeptidase KEX1	DZ:COG5184
JNUCC-1_01953		3048	Sensor histidine kinase ResE	T:COG0784
JNUCC-1_01954		1071	Iron-sulfur cluster carrier protein	D:COG0489
JNUCC-1_01955		645	Spore germination protein GerD	S:ENOG4111QQN
JNUCC-1_01956		645	KinB-signaling pathway activation protein	S:ENOG4111SF0
JNUCC-1_01957	pdaA	765	Probable polysaccharide deacetylase PdaB	S:ENOG41112BD
JNUCC-1_01958		207	hypothetical protein	S:ENOG41124HY
JNUCC-1_01966		1152	Integrase	L:COG0582
JNUCC-1_01967		219	hypothetical protein	
JNUCC-1_01968	lexA	360	Repressor LexA	S:ENOG4111HJM
JNUCC-1_01969		228	Uncharacterized HTH-type transcriptional regulator YqaF	K:ENOG410XUC3
JNUCC-1_01970		225	hypothetical protein	
JNUCC-1_01971		804	hypothetical protein	S:ENOG4111V35
JNUCC-1_01972		795	DNA replication protein DnaC	L:COG1484
JNUCC-1_01973		147	hypothetical protein	
JNUCC-1_01974		234	hypothetical protein	
JNUCC-1_01975		264	hypothetical protein	
JNUCC-1_01976		480	hypothetical protein	
JNUCC-1_01977		228	hypothetical protein	
JNUCC-1_01978		186	hypothetical protein	S:ENOG41120NW
JNUCC-1_01979	mutT|NUDT15|MTH2	486	8-oxo-dGTP diphosphatase	L:COG0494
JNUCC-1_01980	BDH|butB	1050	(R,R)-butanediol dehydrogenase	E:COG1063
JNUCC-1_01981		558	hypothetical protein	L:ENOG4111UUE

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_01982		459	hypothetical protein	L:ENOG410XPK3
JNUCC-1_01983		615	hypothetical protein	L:ENOG410XPK3
JNUCC-1_01984	ltrA	1794	RNA-directed DNA polymerase	L:COG3344
JNUCC-1_01985		234	HTH-type transcriptional regulator ClcR	K:ENOG410XR9S
JNUCC-1_01986		597	hypothetical protein	K:ENOG410XNYY
JNUCC-1_01987	panE|apbA	936	2-dehydropantoate 2-reductase	H:COG1893
JNUCC-1_01988	buk	1098	Butyrate kinase	C:COG3426
JNUCC-1_01989	ptb	918	Phosphate butyryltransferase	C:COG0280
JNUCC-1_01990		1056	hypothetical protein	S:COG3641
JNUCC-1_01991	DLD|lpd|pdhD	1413	Dihydrolipoyl dehydrogenase	C:COG1249
JNUCC-1_01992	DLAT|aceF|pdhC	1353	Dihydrolipoyllysine-residue acetyltransferase	C:COG0508
JNUCC-1_01993	PDHB|pdhB	975	Pyruvate dehydrogenase (acetyl-transferring)	C:COG0022
JNUCC-1_01994	PDHA|pdhA	1119	Pyruvate dehydrogenase (acetyl-transferring)	C:COG1071
JNUCC-1_01995		255	hypothetical protein	E:COG0747
JNUCC-1_01996		558	hypothetical protein	L:ENOG4111UUE
JNUCC-1_01997		1056	hypothetical protein	L:ENOG410XPK3
JNUCC-1_01998	hsdS	915	Type I site-specific deoxyribonuclease	V:COG0732
JNUCC-1_01999	hsdR	312	Type I site-specific deoxyribonuclease	V:COG0610
JNUCC-1_02000	hsdR	2760	Type I site-specific deoxyribonuclease	V:COG0610
JNUCC-1_02001		1665	hypothetical protein	S:ENOG410ZT94
JNUCC-1_02002	uvrD|pcrA	1773	DNA helicase	L:COG0210
JNUCC-1_02003		1059	hypothetical protein	L:ENOG410XPK3
JNUCC-1_02004		504	hypothetical protein	L:ENOG4111UUE
JNUCC-1_02005		585	hypothetical protein	
JNUCC-1_02006		990	hypothetical protein	

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_02007		168	hypothetical protein	
JNUCC-1_02008		429	UPF0132 membrane protein	S:COG4818
JNUCC-1_02009		696	CAI-1 autoinducer sensor kinase/phosphatase CqsS	T:COG0745
JNUCC-1_02010		1920	Histidine protein kinase DivJ	T:COG0784
JNUCC-1_02011		882	hypothetical protein	T:ENOG410XNMH
JNUCC-1_02012		465	hypothetical protein	T:COG0642
JNUCC-1_02013	SOD1	633	Superoxide dismutase	P:COG2032
JNUCC-1_02014		255	hypothetical protein	
JNUCC-1_02015		126	hypothetical protein	
JNUCC-1_02016		789	hypothetical protein	S:COG5438
JNUCC-1_02017		1137	hypothetical protein	S:COG5438
JNUCC-1_02018	qor|CRYZ	933	NADPH:quinone reductase	C:COG0604
JNUCC-1_02019		894	HTH-type transcriptional regulator CfxR	K:COG0583
JNUCC-1_02020		627	UPF0324 membrane protein	S:COG2855
JNUCC-1_02021		429	UPF0324 membrane protein	S:COG2855
JNUCC-1_02022		420	Universal stress protein	T:COG2206
JNUCC-1_02023		714	hypothetical protein	S:COG5522
JNUCC-1_02024	fabI	777	Enoyl-[acyl-carrier-protein] reductase (NADH)	I:COG0623
JNUCC-1_02030	mvaA	1290	Hydroxymethylglutaryl-CoA reductase	I:COG1257
JNUCC-1_02031	MVK|mvaK1	990	Mevalonate kinase	I:COG1577
JNUCC-1_02032	MVD|mvaD	981	Diphosphomevalonate decarboxylase	I:COG3407
JNUCC-1_02033	mvaK2	1068	Phosphomevalonate kinase	I:COG1577
JNUCC-1_02034	rocF|arg	903	Arginase	E:COG0010
JNUCC-1_02035		204	hypothetical protein	
JNUCC-1_02036		564	ECF RNA polymerase sigma factor SigW	K:COG1595

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_02037		696	Anti-sigma-W factor RsiW	K:COG5662
JNUCC-1_02038	dacA	816	Diadenylate cyclase	S:COG1624
JNUCC-1_02039	dacA	1236	Diadenylate cyclase	S:COG4856
JNUCC-1_02040	glmM	1350	Phosphoglucosamine mutase	G:COG1109
JNUCC-1_02041		342	Thioredoxin	O:COG0526
JNUCC-1_02042		270	hypothetical protein	
JNUCC-1_02043	msbA	1476	Multidrug resistance ABC transporter ATP-binding/permease protein BmrA	V:COG1132
JNUCC-1_02044	abcA|bmrA	1767	Xenobiotic-transporting ATPase	V:COG1132
JNUCC-1_02045		543	hypothetical protein	
JNUCC-1_02046		1296	Probable inactive metalloprotease YmfF	O:COG0612
JNUCC-1_02047	IDE|ide	1290	Insulysin	O:COG0612
JNUCC-1_02048	agrC|blpH|fsrC	1317	Histidine kinase	T:COG3290
JNUCC-1_02049		744	Chemotaxis response regulator protein-glutamate methylesterase of group 1 operon	T:COG3279
JNUCC-1_02050		681	Transcriptional regulatory protein AfsQ1	T:COG0745
JNUCC-1_02051	K02484	1383	Histidine kinase	T:ENOG410XNMH
JNUCC-1_02052	APEH	1791	Acylaminoacyl-peptidase	E:COG1506
JNUCC-1_02053		249	hypothetical protein	S:ENOG41125W6
JNUCC-1_02054	glmS|GFPT	1803	Glutamine--fructose-6-phosphate transaminase (isomerizing)	M:COG0449
JNUCC-1_02055		378	Uncharacterized membrane protein YdeH	S:ENOG410Z0H8
JNUCC-1_02056		618	hypothetical protein	S:ENOG410XX5W
JNUCC-1_02057		1083	hypothetical protein	S:ENOG4111Q2H
JNUCC-1_02058		525	RNA polymerase sigma factor SigX	K:ENOG4111UY6
JNUCC-1_02059		522	uncharacterized protein	S:ENOG4111JP1
JNUCC-1_02060		1743	Gluconate 2-dehydrogenase (acceptor)	E:COG2303
JNUCC-1_02061		729	Gluconate 2-dehydrogenase (acceptor)	G:ENOG410ZF7P

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_02062		129	hypothetical protein	
JNUCC-1_02063		564	hypothetical protein	S:COG5483
JNUCC-1_02064		564	hypothetical protein	S:ENOG411227Y
JNUCC-1_02065		462	hypothetical protein	S:ENOG410XW98
JNUCC-1_02066	aac6-I	456	Aminoglycoside 6′-N-acetyltransferase	S:ENOG4111P9X
JNUCC-1_02067		579	hypothetical protein	S:COG2320
JNUCC-1_02068		690	cAMP-dependent protein kinase regulatory subunit	T:COG0664
JNUCC-1_02069		357	hypothetical protein	S:COG3564
JNUCC-1_02070	aldB	1521	EPTC-inducible aldehyde dehydrogenase	C:COG1012
JNUCC-1_02071		1440	Lincomycin resistance protein LmrB	P:ENOG410XNN3
JNUCC-1_02072		489	Large-conductance mechanosensitive channel	M:COG1970
JNUCC-1_02073		2256	UvrABC system protein	L:COG0178
JNUCC-1_02074		405	hypothetical protein	S:ENOG41122N1
JNUCC-1_02075		408	hypothetical protein	S:COG2445
JNUCC-1_02076		474	hypothetical protein	S:ENOG4111FRS
JNUCC-1_02077		324	hypothetical protein	S:ENOG4111FRS
JNUCC-1_02078		504	hypothetical protein	S:COG3542
JNUCC-1_02079	fabG	774	3-oxoacyl-[acyl-carrier-protein] reductase	S:COG1028
JNUCC-1_02080		756	hypothetical protein	S:COG0730
JNUCC-1_02081		1266	hypothetical protein	S:ENOG410Y2S8
JNUCC-1_02082		1464	hypothetical protein	S:ENOG410XPWT
JNUCC-1_02083		1233	Transposase for insertion sequence element IS1557	L:COG3464
JNUCC-1_02084	codA	651	Cytosine deaminase	GM:COG0702
JNUCC-1_02085		1014	NADPH-dependent curcumin reductase	S:COG2130
JNUCC-1_02086		549	hypothetical protein	K:COG1595

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_02087		327	hypothetical protein	
JNUCC-1_02088		885	hypothetical protein	
JNUCC-1_02089		810	hypothetical protein	S:ENOG4111H5W
JNUCC-1_02090		888	Energy-coupling factor transporter ATP-binding protein EcfA1	S:COG0488
JNUCC-1_02091		597	hypothetical protein	K:COG1309
JNUCC-1_02092		810	SPBc2 prophage-derived uncharacterized HTH-type transcriptional regulator YonR	S:ENOG410ZJRR
JNUCC-1_02093		426	hypothetical protein	
JNUCC-1_02094		429	hypothetical protein	S:ENOG4112AIM
JNUCC-1_02095		2769	UPF0182 protein	S:COG1615
JNUCC-1_02096	dehH	771	Haloacetate dehalogenase	S:COG0596
JNUCC-1_02097	thiD	810	Hydroxymethylpyrimidine kinase	H:COG0351
JNUCC-1_02098	coaE	531	Dephospho-CoA kinase	S:COG2320
JNUCC-1_02099	ncd2|npd	408	Nitronate monooxygenase	S:COG0432
JNUCC-1_02100	ncd2|npd	1068	Nitronate monooxygenase	S:COG2070
JNUCC-1_02101		552	hypothetical protein	S:ENOG410YV3G
JNUCC-1_02102	rluD	672	23S rRNA pseudouridine synthase	J:COG0564
JNUCC-1_02103	CARP|pepA	1383	Leucyl aminopeptidase	E:COG0260
JNUCC-1_02104		966	hypothetical protein	S:ENOG410YMU0
JNUCC-1_02105		204	hypothetical protein	S:ENOG41127PI
JNUCC-1_02107	katE|CAT|catB|srpA	1338	Catalase	P:COG0753
JNUCC-1_02108	katE|CAT|catB|srpA	714	Catalase	P:COG0753
JNUCC-1_02110	aes	753	hypothetical protein	I:COG0657
JNUCC-1_02111	allC	1248	Allantoate deiminase	E:COG0624
JNUCC-1_02112	ylbA|UGHY	765	(S)-ureidoglycine aminohydrolase	S:COG3257
JNUCC-1_02113	allD	1050	Ureidoglycolate dehydrogenase (NAD(+))	C:COG2055

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_02114	allD	1053	Ureidoglycolate dehydrogenase (NAD(+))	C:COG2055
JNUCC-1_02115		1386	Purine-uracil permease NCS1	FH:COG1953
JNUCC-1_02116	allB	1359	Allantoinase	F:COG0044
JNUCC-1_02117	DPYS|dht|hydA	1320	Dihydropyrimidinase	F:COG0044
JNUCC-1_02118	ridA|tdcF|RIDA	387	2-iminobutanoate/2-iminopropanoate deaminase	J:COG0251
JNUCC-1_02119		219	uncharacterized protein	S:COG1288
JNUCC-1_02120		1128	uncharacterized protein	S:COG1288
JNUCC-1_02121		1665	Purine catabolism regulatory protein	K:COG2508
JNUCC-1_02122		1329	Putative purine permease YbbY	F:COG2233
JNUCC-1_02123		1749	uncharacterized protein	C:COG0074
JNUCC-1_02124		1263	uncharacterized protein	S:ENOG410XPNV
JNUCC-1_02125	arcC	918	Carbamate kinase	S:ENOG4111STC
JNUCC-1_02126	arcC	939	Carbamate kinase	E:COG0549
JNUCC-1_02127		2625	Drug sensory protein	S:COG0840
JNUCC-1_02128		702	DNA-binding response regulator MtrA	T:COG0745
JNUCC-1_02129		561	Probable sulfoacetate transporter SauU	G:ENOG410XPWC
JNUCC-1_02130		744	Putative metabolite transport protein NicT	G:ENOG410XPWC
JNUCC-1_02131		762	hypothetical protein	S:ENOG4111PA4
JNUCC-1_02132		549	Protein LemA	S:COG1704
JNUCC-1_02133	htpX	888	Protease HtpX like protein	O:COG0501
JNUCC-1_02134		468	hypothetical protein	S:ENOG410ZDZD
JNUCC-1_02135	moxR	936	Protein MoxR	S:COG0714
JNUCC-1_02136		1212	hypothetical protein	S:ENOG410Z8N5
JNUCC-1_02137		1203	hypothetical protein	S:ENOG41100N5
JNUCC-1_02138		813	Putative transposase InsK for insertion sequence element IS150	L:COG2801

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_02139		510	hypothetical protein	L:ENOG4111X46
JNUCC-1_02140		231	Uncharacterized HTH-type transcriptional regulator	K:COG1476
JNUCC-1_02141		309	hypothetical protein	S:ENOG410ZCSR
JNUCC-1_02142		900	hypothetical protein	M:COG0739
JNUCC-1_02143		651	hypothetical protein	S:ENOG4111PVR
JNUCC-1_02144		381	HTH-type transcriptional repressor YtrA	K:COG1725
JNUCC-1_02145		894	Ribose import ATP-binding protein RbsA	E:COG0411
JNUCC-1_02146		753	hypothetical protein	S:ENOG41128JE
JNUCC-1_02147		810	hypothetical protein	
JNUCC-1_02148		180	hypothetical protein	
JNUCC-1_02149	MPG	597	DNA-3-methyladenine glycosylase II	L:COG2094
JNUCC-1_02150		495	UPF0178 protein	S:COG1671
JNUCC-1_02151		447	uncharacterized protein	S:ENOG410ZRDN
JNUCC-1_02152	cobU|cobT	1071	Nicotinate-nucleotide-dimethylbenzimidazole phosphoribosyltransferase	L:COG0675
JNUCC-1_02153		900	Uncharacterized transporter	EG:COG0697
JNUCC-1_02154		276	hypothetical protein	S:ENOG410ZC68
JNUCC-1_02155	purC	1170	Phosphoribosylaminoimidazolesuccinocarboxamide synthase	S:COG0628
JNUCC-1_02156		690	hypothetical protein	T:ENOG410XNMH
JNUCC-1_02157	sadC	783	Diguanylate cyclase	T:ENOG410XNMH
JNUCC-1_02158		261	Purine efflux pump PbuE	G:COG2814
JNUCC-1_02159		384	Purine efflux pump PbuE	G:COG2814
JNUCC-1_02160		525	Purine efflux pump PbuE	G:COG2814
JNUCC-1_02161		333	Protein CsaA	J:COG0073
JNUCC-1_02162	FDFT1	834	Squalene synthase	I:COG1562
JNUCC-1_02163		195	hypothetical protein	

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_02164	aprX	363	hypothetical protein	
JNUCC-1_02165		426	hypothetical protein	S:ENOG41129P7
JNUCC-1_02166		285	hypothetical protein	S:ENOG41126EN
JNUCC-1_02167		1443	Sodium/pantothenate symporter	H:COG4145
JNUCC-1_02168		186	hypothetical protein	
JNUCC-1_02169		156	hypothetical protein	
JNUCC-1_02170	NAGA	390	Alpha-N-acetylgalactosaminidase	S:COG3011
JNUCC-1_02171		1023	hypothetical protein	S:ENOG410XV6C
JNUCC-1_02172	AACS|acsA	441	Acetoacetate--CoA ligase	I:COG0365
JNUCC-1_02173	AACS|acsA	1563	Acetoacetate--CoA ligase	I:COG0365
JNUCC-1_02174		486	hypothetical protein	
JNUCC-1_02175		1284	hypothetical protein	L:COG3547
JNUCC-1_02176		510	hypothetical protein	L:ENOG4111UUE
JNUCC-1_02177		1056	hypothetical protein	L:ENOG410XPK3
JNUCC-1_02178		153	Small, acid-soluble spore protein	M:ENOG410Z56S
JNUCC-1_02179		249	hypothetical protein	S:ENOG4112A8Z
JNUCC-1_02180		870	UPF0750 membrane protein YvjA	S:ENOG410ZKXS
JNUCC-1_02181		453	uncharacterized protein	S:COG5506
JNUCC-1_02182		177	hypothetical protein	S:ENOG410ZQCJ
JNUCC-1_02183	ltaS	1926	Phosphatidylglycerol-membrane-oligosaccharide glycerophosphotransferase	M:COG1368
JNUCC-1_02184		615	Spore coat protein F-like protein YhcQ	M:COG5577
JNUCC-1_02185		252	hypothetical protein	S:ENOG410ZCVP
JNUCC-1_02186		1353	hypothetical protein	S:ENOG410Y9PX
JNUCC-1_02187		912	hypothetical protein	
JNUCC-1_02188		393	hypothetical protein	S:ENOG411214K

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_02189	selU	1038	uncharacterized protein	S:COG2603
JNUCC-1_02190	selD|SEPHS	1041	Selenide, water dikinase	E:COG0709
JNUCC-1_02191	xthA	765	Exodeoxyribonuclease III	L:COG0708
JNUCC-1_02192		1077	Uncharacterized HTH-type transcriptional regulator YhcF	K:COG1725
JNUCC-1_02193		834	hypothetical protein	S:ENOG4111MGN
JNUCC-1_02194		1221	hypothetical protein	S:ENOG4112659
JNUCC-1_02195		402	hypothetical protein	S:ENOG41129M6
JNUCC-1_02196		438	hypothetical protein	
JNUCC-1_02197		333	Thioredoxin-like protein YdfQ	O:COG0526
JNUCC-1_02198		213	hypothetical protein	
JNUCC-1_02199		552	hypothetical protein	
JNUCC-1_02200	copA|ATP7	210	Cu(+) exporting ATPase	P:COG2217
JNUCC-1_02201	zntA	1893	Cadmium-exporting ATPase	P:COG2217
JNUCC-1_02202		375	hypothetical protein	S:ENOG410Y63F
JNUCC-1_02203	ddl	1104	D-alanine--D-alanine ligase	M:COG1181
JNUCC-1_02204		291	hypothetical protein	
JNUCC-1_02205		561	Putative NAD(P)H nitroreductase YfhC	C:COG0778
JNUCC-1_02206		1038	hypothetical protein	S:COG3641
JNUCC-1_02207	FCY1	339	Cytosine deaminase	FJ:COG0590
JNUCC-1_02208	psd|PISD	864	Phosphatidylserine decarboxylase	G:COG3001
JNUCC-1_02209		453	hypothetical protein	S:ENOG4112D7N
JNUCC-1_02210		525	Putative phosphohydrolase YueE	S:COG1418
JNUCC-1_02211		885	hypothetical protein	GM:COG0702
JNUCC-1_02212	vanY	1071	Zinc D-Ala-D-Ala carboxypeptidase	M:COG1876
JNUCC-1_02213		1209	Multidrug resistance protein	P:ENOG410XNN3

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_02214	TST|MPST|sseA	837	Thiosulfate sulfurtransferase	P:COG2897
JNUCC-1_02215	tag	579	DNA-3-methyladenine glycosylase I	L:COG2818
JNUCC-1_02216		321	UPF0145 protein	S:COG0393
JNUCC-1_02217		1761	Methyl-accepting chemotaxis protein	S:COG0840
JNUCC-1_02218	csn1|cas9	2829	CRISPR-associated endonuclease Cas9	L:COG3513
JNUCC-1_02219		123	hypothetical protein	
JNUCC-1_02220	csn1|cas9	501	CRISPR-associated endonuclease Cas9	L:COG3513
JNUCC-1_02221		903	CRISPR-associated endonuclease Cas1	L:COG1518
JNUCC-1_02222		309	CRISPR-associated endoribonuclease Cas2	L:COG3512
JNUCC-1_02223		195	hypothetical protein	L:COG3344
JNUCC-1_02224		207	hypothetical protein	L:ENOG410XPK3
JNUCC-1_02225		459	hypothetical protein	L:ENOG410XPK3
JNUCC-1_02226		294	hypothetical protein	L:ENOG4111UUE
JNUCC-1_02227		219	hypothetical protein	L:ENOG4111UUE
JNUCC-1_02228	BDH|butB	1050	(R,R)-butanediol dehydrogenase	E:COG1063
JNUCC-1_02229	mutT|NUDT15|MTH2	486	8-oxo-dGTP diphosphatase	L:COG0494
JNUCC-1_02230	coxD|ctaF	318	Cytochrome-c oxidase	S:ENOG41120NW
JNUCC-1_02231		228	hypothetical protein	
JNUCC-1_02232		480	hypothetical protein	
JNUCC-1_02233		264	hypothetical protein	
JNUCC-1_02234		234	hypothetical protein	
JNUCC-1_02235		183	hypothetical protein	
JNUCC-1_02236		795	DNA replication protein DnaC	L:COG1484
JNUCC-1_02237		804	hypothetical protein	S:ENOG4111V35
JNUCC-1_02238		225	hypothetical protein	

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_02239		228	Uncharacterized HTH-type transcriptional regulator YqaF	K:ENOG410XUC3
JNUCC-1_02240	lexA	360	Repressor LexA	S:ENOG4111HJM
JNUCC-1_02241		219	hypothetical protein	
JNUCC-1_02242		1152	Integrase	L:COG0582
JNUCC-1_02243		504	hypothetical protein	L:ENOG4111UUE
JNUCC-1_02244		1059	hypothetical protein	L:ENOG410XPK3
JNUCC-1_02245	uvrD|pcrA	1740	DNA helicase	L:COG0210
JNUCC-1_02246		1665	hypothetical protein	S:ENOG410ZT94
JNUCC-1_02247	hsdR	3036	Type I site-specific deoxyribonuclease	V:COG0610
JNUCC-1_02248		99	hypothetical protein	
JNUCC-1_02249		450	hypothetical protein	L:ENOG410XPK3
JNUCC-1_02250		219	hypothetical protein	L:ENOG410XPK3
JNUCC-1_02251		243	hypothetical protein	L:ENOG4111UUE
JNUCC-1_02252		255	hypothetical protein	E:COG0747
JNUCC-1_02253	PDHA|pdhA	552	Pyruvate dehydrogenase (acetyl-transferring)	C:COG1071
JNUCC-1_02254	BCKDHA|bkdA1	309	3-methyl-2-oxobutanoate dehydrogenase (2-methylpropanoyl-transferring)	C:COG1071
JNUCC-1_02255	PDHB|pdhB	657	Pyruvate dehydrogenase (acetyl-transferring)	C:COG0022
JNUCC-1_02256		855	hypothetical protein	S:ENOG4111HY7
JNUCC-1_02257		756	hypothetical protein	S:ENOG4111PJJ
JNUCC-1_02258		168	hypothetical protein	
JNUCC-1_02259		612	hypothetical protein	S:ENOG410Y422
JNUCC-1_02260		585	hypothetical protein	S:ENOG4111KAX
JNUCC-1_02261		3558	hypothetical protein	S:ENOG410XPJ6
JNUCC-1_02262		3558	hypothetical protein	V:COG1002
JNUCC-1_02263		2544	hypothetical protein	S:ENOG410XQ4Q

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_02264	dkgA	825	2,5-didehydrogluconate reductase (2-dehydro-L-gulonate-forming)	S:COG0656
JNUCC-1_02265	relA	543	GTP diphosphokinase	KT:COG0317
JNUCC-1_02266	fabG	759	3-oxoacyl-[acyl-carrier-protein] reductase	S:COG1028
JNUCC-1_02267	idi|IDI	1056	Isopentenyl-diphosphate Delta-isomerase	C:COG1304
JNUCC-1_02268	gloB|gloC|HAGH	576	Hydroxyacylglutathione hydrolase	S:COG0491
JNUCC-1_02269		321	Probable metallo-hydrolase YflN	S:COG0491
JNUCC-1_02270		651	Protein disulfide-isomerase	Q:COG2761
JNUCC-1_02271		954	Uncharacterized ABC transporter permease protein YclN	P:COG4606
JNUCC-1_02272		951	Ferric anguibactin transport system permease protein FatC	P:COG4605
JNUCC-1_02273	tauB	756	Taurine-transporting ATPase	E:COG0411
JNUCC-1_02274		1014	Ferric anguibactin-binding protein	P:COG4607
JNUCC-1_02275		711	hypothetical protein	S:ENOG410Y0P5
JNUCC-1_02276	murB	948	UDP-N-acetylmuramate dehydrogenase	M:COG0812
JNUCC-1_02277		1704	hypothetical protein	L:COG3666
JNUCC-1_02278		819	Spermidine/putrescine import ATP-binding protein PotA	V:COG1132
JNUCC-1_02279		729	General L-amino acid transport system permease protein AapM	E:ENOG4111FRH
JNUCC-1_02280		660	Arginine transport system permease protein ArtQ	E:ENOG4111IRP
JNUCC-1_02281		891	Probable amino-acid ABC transporter periplasmic-binding protein	E:ENOG4111IMY
JNUCC-1_02282		159	hypothetical protein	
JNUCC-1_02283	plsY	624	Glycerol-3-phosphate 1-O-acyltransferase	S:COG0344
JNUCC-1_02284		486	uncharacterized protein	S:COG2839
JNUCC-1_02285	thiD	834	Hydroxymethylpyrimidine kinase	H:COG0351
JNUCC-1_02286		552	Uncharacterized isochorismatase family protein PncA	Q:COG1335
JNUCC-1_02287	PARS|proS	1440	Proline--tRNA ligase	J:COG0442
JNUCC-1_02288	gpx	474	Glutathione peroxidase	O:COG0386

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_02289		972	UPF0176 protein	S:COG1054
JNUCC-1_02290		2388	Penicillin amidase	S:COG2366
JNUCC-1_02291		1620	hypothetical protein	S:ENOG4111IJ6
JNUCC-1_02292		342	hypothetical protein	
JNUCC-1_02293		198	Cold shock-like protein CspB	K:COG1278
JNUCC-1_02294	bioC	693	Malonyl-[acyl-carrier protein] O-methyltransferase	S:ENOG4111M0S
JNUCC-1_02295		321	uncharacterized protein	S:ENOG41123PV
JNUCC-1_02296	ltnD	705	L-threonate 2-dehydrogenase	I:COG2084
JNUCC-1_02297	mmsB|HIBADH	201	3-hydroxyisobutyrate dehydrogenase	I:COG2084
JNUCC-1_02298		447	UPF0039 protein	S:COG2153
JNUCC-1_02299		672	uncharacterized protein	T:COG1734
JNUCC-1_02300		210	uncharacterized protein	S:COG3478
JNUCC-1_02301	degP|htrA	1365	Peptidase Do	O:COG0265
JNUCC-1_02302		687	Transcriptional regulatory protein BaeR	T:COG0745
JNUCC-1_02303	glrK|qseE	1359	Histidine kinase	T:ENOG4111IQG
JNUCC-1_02304		1836	GTP-binding protein TypA/BipA like protein	T:COG1217
JNUCC-1_02305		1347	Transposase for insertion sequence element IS231E	L:ENOG411247V
JNUCC-1_02306		279	hypothetical protein	S:COG3339
JNUCC-1_02307		357	Transcriptional repressor SmtB like protein	K:ENOG41101ZW
JNUCC-1_02308		1299	Arsenical pump membrane protein	P:COG1055
JNUCC-1_02309	ARSC2|arsC	417	Arsenate reductase (glutaredoxin)	T:COG0394
JNUCC-1_02310	ltrA	1347	RNA-directed DNA polymerase	L:COG3344
JNUCC-1_02311		996	uncharacterized protein	S:COG1277
JNUCC-1_02312	ABC.FEV.A	918	Iron-chelate-transporting ATPase	V:COG1131
JNUCC-1_02313	fadA|fadI	1116	Acetyl-CoA C-acyltransferase	I:COG0183

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_02314		1182	Capsule biosynthesis protein CapA	M:COG2843
JNUCC-1_02315		108	hypothetical protein	S:COG2035
JNUCC-1_02316		609	hypothetical protein	S:COG2035
JNUCC-1_02317		321	Thioredoxin-like protein YdbP	O:COG0526
JNUCC-1_02318		645	hypothetical protein	S:ENOG4112CUH
JNUCC-1_02319		693	Transcriptional regulatory protein ZraR	T:COG2204
JNUCC-1_02320	arlS	1353	Histidine kinase	T:COG0642
JNUCC-1_02321		717	hypothetical protein	S:COG3212
JNUCC-1_02322		696	Hemin import ATP-binding protein HmuV	G:COG3839
JNUCC-1_02323		1389	hypothetical protein	
JNUCC-1_02324		237	hypothetical protein	O:COG0695
JNUCC-1_02325		246	hypothetical protein	S:COG1647
JNUCC-1_02326	yvaK	444	Carboxylesterase	S:COG1647
JNUCC-1_02327		615	DegV domain-containing protein YitS	S:COG1307
JNUCC-1_02328		249	DegV domain-containing protein	S:COG1307
JNUCC-1_02329		912	Uncharacterized transporter	S:ENOG410XPK1
JNUCC-1_02330	srmB	1470	RNA helicase	L:COG0513
JNUCC-1_02331		480	UPF0699 transmembrane protein YdbS	S:COG3402
JNUCC-1_02332		951	UPF0699 transmembrane protein YdbT	S:COG3428
JNUCC-1_02333		513	hypothetical protein	S:COG3428
JNUCC-1_02334	gluP	774	Rhomboid protease	S:COG0705
JNUCC-1_02335	acpS	366	Holo-[acyl-carrier-protein] synthase	I:COG0736
JNUCC-1_02336	nnr	1515	ADP-dependent NAD(P)H-hydrate dehydratase	G:COG0062
JNUCC-1_02337		1023	Sporulation protein YdcC	M:COG2834
JNUCC-1_02338	alr	1125	Alanine racemase	M:COG0787

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_02339		291	hypothetical protein	K:COG0864
JNUCC-1_02340	mazF|ndoA|chpA	348	Endoribonuclease EndoA	T:COG2337
JNUCC-1_02341		870	RsbT co-antagonist protein RsbRA	T:COG1366
JNUCC-1_02342		366	RsbT antagonist protein RsbS	T:COG1366
JNUCC-1_02343	rsbT	399	Non-specific serine/threonine protein kinase	T:COG2172
JNUCC-1_02344	rsbU_P	1011	Phosphoserine phosphatase	T:COG2208
JNUCC-1_02345		330	Anti-sigma-B factor antagonist	T:COG1366
JNUCC-1_02346	rsbW	477	Non-specific serine/threonine protein kinase	T:COG2172
JNUCC-1_02347		792	RNA polymerase sigma-B factor	K:COG1191
JNUCC-1_02348	rsbX	588	Phosphoserine phosphatase	T:ENOG41125MR
JNUCC-1_02349		2178	uncharacterized protein	K:COG2183
JNUCC-1_02350	katE|CAT|catB|srpA	1491	Catalase	P:COG0753
JNUCC-1_02351		456	Protein SprT-like	S:COG3091
JNUCC-1_02368	thiL	963	Thiamine-phosphate kinase	H:COG0611
JNUCC-1_02369		456	tRNA threonylcarbamoyladenosine biosynthesis protein TsaE	S:COG3178
JNUCC-1_02370		711	tRNA threonylcarbamoyladenosine biosynthesis protein TsaB	O:COG1214
JNUCC-1_02371	rimI	456	[Ribosomal protein S18]-alanine N-acetyltransferase	S:COG0456
JNUCC-1_02372	KAE1|tsaD|QRI7	1014	N(6)-L-threonylcarbamoyladenine synthase	O:COG0533
JNUCC-1_02373		1431	ABC transporter F family member	S:COG0488
JNUCC-1_02374	nikE	456	Nickel-transporting ATPase	E:COG0410
JNUCC-1_02375	moaC|CNX3	504	Cyclic pyranopterin monophosphate synthase	H:COG0315
JNUCC-1_02376		630	Redox-sensing transcriptional repressor Rex	K:COG2344
JNUCC-1_02377		1413	Uncharacterized MFS-type transporter	G:COG0477
JNUCC-1_02378		198	hypothetical protein	
JNUCC-1_02379		714	Putative membrane peptidase YdiL	S:COG1266

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_02380		285	10 kDa chaperonin	O:COG0234
JNUCC-1_02381		1632	60 kDa chaperonin	O:COG0459
JNUCC-1_02382		1200	ICEBs1 integrase	L:COG0582
JNUCC-1_02383		1125	Putative transposase	L:COG3385
JNUCC-1_02384		1284	hypothetical protein	L:COG3547
JNUCC-1_02385		468	Phage-like element PBSX protein XkdA	S:ENOG4112AJI
JNUCC-1_02386		378	Uncharacterized HTH-type transcriptional regulator YqaE	K:ENOG410XUC3
JNUCC-1_02387		201	Uncharacterized HTH-type transcriptional regulator YqaF	K:ENOG410ZT4W
JNUCC-1_02388		357	hypothetical protein	S:ENOG410Z7YW
JNUCC-1_02389		393	hypothetical protein	S:ENOG4111V35
JNUCC-1_02390		510	hypothetical protein	L:ENOG4111UUE
JNUCC-1_02391		1056	hypothetical protein	L:ENOG410XPK3
JNUCC-1_02392	ltrA	552	RNA-directed DNA polymerase	L:COG3344
JNUCC-1_02393	ltrA	165	RNA-directed DNA polymerase	L:COG3344
JNUCC-1_02394		606	Ca(2+)/H(+) antiporter ChaA	P:COG0387
JNUCC-1_02395	hpxO	1125	FAD-dependent urate hydroxylase	CH:COG0654
JNUCC-1_02396		1356	Uncharacterized sodium-dependent transporter YocR	P:COG0733
JNUCC-1_02397	clsA_B	1431	Major cardiolipin synthase ClsA	I:COG1502
JNUCC-1_02398		246	hypothetical protein	
JNUCC-1_02399		999	hypothetical protein	E:COG2113
JNUCC-1_02400	codA	648	Cytosine deaminase	F:COG0402
JNUCC-1_02401	codA	585	Cytosine deaminase	F:COG0402
JNUCC-1_02402		1167	Hydroxymethylglutaryl-CoA synthase	I:COG3425
JNUCC-1_02403		249	hypothetical protein	
JNUCC-1_02404	coxB|ctaC	522	Cytochrome-c oxidase	C:COG1622

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_02405	coxA|ctaD	1482	Cytochrome-c oxidase	C:ENOG410XQ2G
JNUCC-1_02406		564	hypothetical protein	S:ENOG4111X7P
JNUCC-1_02407	IARS|ileS	3099	Isoleucine--tRNA ligase	J:COG0060
JNUCC-1_02408		642	hypothetical protein	S:ENOG410XSC0
JNUCC-1_02409		252	hypothetical protein	
JNUCC-1_02410	GCH1|folE	570	GTP cyclohydrolase I	H:COG0302
JNUCC-1_02411		1179	hypothetical protein	S:ENOG4111H1X
JNUCC-1_02412		1158	hypothetical protein	S:ENOG4111H1X
JNUCC-1_02413		1698	hypothetical protein	S:ENOG410ZZXC
JNUCC-1_02414		435	hypothetical protein	
JNUCC-1_02415		480	hypothetical protein	S:ENOG4111RB7
JNUCC-1_02416		1551	Spore germination protein KA	S:ENOG410XNMP
JNUCC-1_02417		1098	Spore germination protein A2	S:ENOG4110XW1
JNUCC-1_02418		1194	Spore germination protein GerLC	S:ENOG4110N81
JNUCC-1_02419		162	hypothetical protein	
JNUCC-1_02420	amiE	1293	Amidase	J:COG0154
JNUCC-1_02421	amiE	204	Amidase	J:COG0154
JNUCC-1_02422		159	hypothetical protein	
JNUCC-1_02423		960	hypothetical protein	S:ENOG410Y5TV
JNUCC-1_02424	moxR	960	uncharacterized protein	S:COG0714
JNUCC-1_02425		1266	uncharacterized protein	S:COG1721
JNUCC-1_02426	tgpA	2292	Protein-glutamine gamma-glutamyltransferase	E:COG1305
JNUCC-1_02427	guaA|GMPS	1536	GMP synthase (glutamine-hydrolyzing)	F:COG0518
JNUCC-1_02428		1335	Putative permease	S:COG2252
JNUCC-1_02429		729	Maltose permease	G:ENOG410XQVS

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_02430		438	Uncharacterized transporter YwbF	G:ENOG410XQVS
JNUCC-1_02431	msrA	528	Peptide-methionine (S)-S-oxide reductase	O:COG0225
JNUCC-1_02432		714	Protein YiiM	S:COG2258
JNUCC-1_02433		732	UPF0316 protein	S:COG4843
JNUCC-1_02434	purE	492	5-(carboxyamino)imidazole ribonucleotide mutase	F:COG0041
JNUCC-1_02435	purK	1131	5-(carboxyamino)imidazole ribonucleotide synthase	F:COG0026
JNUCC-1_02436	purB|ADSL	1302	Adenylosuccinate lyase	F:COG0015
JNUCC-1_02437	purL|PFAS	2220	Phosphoribosylformylglycinamidine synthase	F:COG0046
JNUCC-1_02438	purF|PPAT	1173	Amidophosphoribosyltransferase	F:COG0034
JNUCC-1_02439	purF|PPAT	228	Amidophosphoribosyltransferase	F:COG0034
JNUCC-1_02440	purM	1023	Phosphoribosylformylglycinamidine cyclo-ligase	F:COG0150
JNUCC-1_02441	purN	585	Phosphoribosylglycinamide formyltransferase	F:COG0299
JNUCC-1_02442	purH	1533	Phosphoribosylaminoimidazolecarboxamide formyltransferase	F:COG0138
JNUCC-1_02443	purD	1236	Phosphoribosylamine-glycine ligase	F:COG0151
JNUCC-1_02444	ade	1740	Adenine deaminase	F:COG1001
JNUCC-1_02445		1071	Putative lipoprotein YerB	S:ENOG4111FHM
JNUCC-1_02446		291	uncharacterized protein	S:COG4496
JNUCC-1_02447		615	Spore coat-associated protein	S:ENOG4111M2C
JNUCC-1_02448		870	Protein ORF73	U:COG0681
JNUCC-1_02449	SEC11|sipW	567	Signal peptidase I	U:COG0681
JNUCC-1_02450		642	hypothetical protein	S:ENOG410Y0XY
JNUCC-1_02451	pcrB	693	Heptaprenylglyceryl phosphate synthase	S:COG1646
JNUCC-1_02452	uvrD|pcrA	453	DNA helicase	L:COG0210
JNUCC-1_02453	uvrD|pcrA	1800	DNA helicase	L:COG0210
JNUCC-1_02454	ligA|ligB	2004	DNA ligase (NAD(+))	L:COG0272

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_02455		1128	Uncharacterized lipoprotein YerH	S:COG4851
JNUCC-1_02456		1551	L-glutamate gamma-semialdehyde dehydrogenase	C:COG1012
JNUCC-1_02457		1266	Transcriptional activator NprA	S:COG0457
JNUCC-1_02458		141	hypothetical protein	
JNUCC-1_02459	gatC|GATC	291	Asparaginyl-tRNA synthase (glutamine-hydrolyzing)	J:COG0721
JNUCC-1_02460	gatA|QRSL1	1470	Asparaginyl-tRNA synthase (glutamine-hydrolyzing)	J:COG0154
JNUCC-1_02461	gatB|PET112	1431	Asparaginyl-tRNA synthase (glutamine-hydrolyzing)	J:COG0064
JNUCC-1_02462	dagK	909	Diacylglycerol kinase (ATP)	I:COG1597
JNUCC-1_02463	rumA	1377	23S rRNA (uracil(1939)-C(5))-methyltransferase	J:COG2265
JNUCC-1_02464	dusA	957	Probable tRNA-dihydrouridine synthase	J:COG0042
JNUCC-1_02465		735	hypothetical protein	S:ENOG410Y19C
JNUCC-1_02466		243	hypothetical protein	S:ENOG410XYUU
JNUCC-1_02467		396	Toxin Doc	S:COG3654
JNUCC-1_02468	bdh	735	3-hydroxybutyrate dehydrogenase	S:COG1028
JNUCC-1_02469	hisC	1065	Histidinol-phosphate transaminase	E:COG0079
JNUCC-1_02470	hisI	636	Phosphoribosyl-AMP cyclohydrolase	E:COG0139
JNUCC-1_02471	hisF	768	Imidazole glycerol phosphate synthase subunit HisF	E:COG0107
JNUCC-1_02472	hisA	708	1-(5-phosphoribosyl)-5-((5-phosphoribosylamino)methylideneamino)imidazole-4-carboxamideisomerase	E:COG0139
JNUCC-1_02473	hisB	585	Imidazoleglycerol-phosphate dehydratase	E:COG0131
JNUCC-1_02474	hisD	1302	Histidinol dehydrogenase	E:COG0141
JNUCC-1_02475	hisG	627	ATP phosphoribosyltransferase	E:COG0040
JNUCC-1_02476		1245	Histidine--tRNA ligase	E:COG3705
JNUCC-1_02477		804	Histidinol-phosphatase	E:COG1387
JNUCC-1_02478		441	uncharacterized protein	O:COG1764
JNUCC-1_02479		492	Queuosine precursor transporter QueT	S:COG4708

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_02480		342	hypothetical protein	S:ENOG411231V
JNUCC-1_02481	katE|CAT|catB|srpA	2061	Catalase	P:COG0753
JNUCC-1_02482		168	hypothetical protein	S:ENOG410XXNX
JNUCC-1_02483		486	Chemotaxis protein CheW	NT:COG0835
JNUCC-1_02484		1692	Sensory rhodopsin II transducer	S:COG0840
JNUCC-1_02485		819	Membrane protein insertase YidC	U:COG0706
JNUCC-1_02486		366	hypothetical protein	
JNUCC-1_02487	COX10|ctaB|cyoE	939	Heme o synthase	O:COG0109
JNUCC-1_02488		693	Copper homeostasis protein cutC like protein	P:COG3142
JNUCC-1_02489	dmpA|dap	651	D-stereospecific aminopeptidase	EQ:COG3191
JNUCC-1_02490	dmpA|dap	354	D-stereospecific aminopeptidase	EQ:COG3191
JNUCC-1_02491		447	Large-conductance mechanosensitive channel	M:COG1970
JNUCC-1_02492		459	hypothetical protein	S:ENOG410YVVW
JNUCC-1_02493		744	Cytochrome c-type bioproteinis protein CcdA	O:COG0785
JNUCC-1_02494		225	hypothetical protein	
JNUCC-1_02495		273	Sporulation thiol-disulfide oxidoreductase	O:COG0526
JNUCC-1_02496	rsbU_P	684	Phosphoserine phosphatase	T:COG0745
JNUCC-1_02497	baeS|smeS	1095	Histidine kinase	T:COG0642
JNUCC-1_02498		198	hypothetical protein	
JNUCC-1_02499		1053	hypothetical protein	S:COG4927
JNUCC-1_02500		921	hypothetical protein	EG:COG0697
JNUCC-1_02501		672	hypothetical protein	S:ENOG4111KPR
JNUCC-1_02502	cdr	1344	CoA-disulfide reductase	S:COG0446
JNUCC-1_02503	TDO2|kynA	840	Tryptophan 2,3-dioxygenase	E:COG3483
JNUCC-1_02504	kynB	648	Arylformamidase	S:COG1878

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_02505	KYNU|kynU	1266	Kynureninase	E:COG3844
JNUCC-1_02506		1689	hypothetical protein	L:COG3666
JNUCC-1_02507	mtnE|mtnV	1182	LL-diaminopimelate aminotransferase	E:COG0436
JNUCC-1_02508	ilvB|ilvG|ilvI	1314	Acetolactate synthase	E:COG0028
JNUCC-1_02509	ilvB|ilvG|ilvI	330	Acetolactate synthase	E:COG0028
JNUCC-1_02510	xylC	1497	Benzaldehyde dehydrogenase (NAD(+))	C:COG1012
JNUCC-1_02511	lysDH	1173	Lysine 6-dehydrogenase	E:COG1748
JNUCC-1_02512		744	Uncharacterized HTH-type transcriptional regulator YagI	K:COG1414
JNUCC-1_02513		312	hypothetical protein	S:ENOG4111V5Y
JNUCC-1_02514		327	hypothetical protein	
JNUCC-1_02515		453	hypothetical protein	
JNUCC-1_02516	gabD	1446	Succinate-semialdehyde dehydrogenase (NAD(P)(+))	C:COG1012
JNUCC-1_02517	ACADS|bcd	1191	Short-chain acyl-CoA dehydrogenase	I:COG1960
JNUCC-1_02518	AMACR|mcr	1149	Alpha-methylacyl-CoA racemase	C:COG1804
JNUCC-1_02519		375	MreB-like protein	D:COG1077
JNUCC-1_02520		600	MreB-like protein	D:COG1077
JNUCC-1_02521	plsC	546	1-acylglycerol-3-phosphate O-acyltransferase	I:COG0204
JNUCC-1_02522	plsC	225	1-acylglycerol-3-phosphate O-acyltransferase	I:COG0204
JNUCC-1_02523	glsA|GLS	996	Glutaminase	E:COG2066
JNUCC-1_02524		672	Putative SOS response-associated peptidase YoaM	S:COG2135
JNUCC-1_02525		474	Protein-tyrosine-phosphatase	T:COG0394
JNUCC-1_02526		279	hypothetical protein	S:ENOG410ZGXE
JNUCC-1_02527		657	Putative ribonuclease-like protein YfkH	S:COG1295
JNUCC-1_02528		1488	Glycine betaine transporter BetL	P:COG1292
JNUCC-1_02529	zntA	1941	Cadmium-exporting ATPase	P:COG2217

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_02530		408	hypothetical protein	O:COG1765
JNUCC-1_02531		810	uncharacterized protein	S:ENOG410ZTIF
JNUCC-1_02532		1308	Uncharacterized membrane protein	S:COG2056
JNUCC-1_02533	pdaA	804	Chitooligosaccharide deacetylase	G:COG0726
JNUCC-1_02534	ACSS|acs	1569	Acetate-CoA ligase	I:COG0365
JNUCC-1_02535		2139	Chaperone protein ClpB	O:COG0542
JNUCC-1_02536		1020	hypothetical protein	
JNUCC-1_02537		876	ComE operon protein	S:COG2333
JNUCC-1_02538		558	hypothetical protein	S:ENOG410YYTS
JNUCC-1_02539		561	hypothetical protein	S:ENOG410YYTS
JNUCC-1_02540		909	sn-glycerol-3-phosphate import ATP-binding protein UgpC	V:COG1131
JNUCC-1_02541		585	hypothetical protein	L:ENOG4111UUE
JNUCC-1_02542		936	hypothetical protein	L:COG2801
JNUCC-1_02543		1263	hypothetical protein	S:ENOG410ZQAG
JNUCC-1_02544		315	hypothetical protein	
JNUCC-1_02545		666	hypothetical protein	
JNUCC-1_02546		1284	hypothetical protein	L:COG3547
JNUCC-1_02547		669	hypothetical protein	
JNUCC-1_02548		378	Uncharacterized HTH-type transcriptional regulator YhcF	K:COG1725
JNUCC-1_02549		864	Sulfate/thiosulfate import ATP-binding protein CysA	S:COG4152
JNUCC-1_02550		702	hypothetical protein	S:ENOG410YZCM
JNUCC-1_02551		255	hypothetical protein	S:ENOG41124RA
JNUCC-1_02552	coxD|ctaF	318	Cytochrome-c oxidase	S:ENOG41120NW
JNUCC-1_02553		777	Uncharacterized transmembrane protein YxlG	S:ENOG4111KEE
JNUCC-1_02554		909	ABC transporter ATP-binding protein uup-1	S:COG0488

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_02555		204	Negative regulatory protein YxlE	S:ENOG410ZPJM
JNUCC-1_02556		1494	Glycine betaine transporter BetL	P:COG1292
JNUCC-1_02557	tehB	423	Tellurite methyltransferase	K:ENOG410ZS81
JNUCC-1_02558		294	hypothetical protein	
JNUCC-1_02559		558	hypothetical protein	S:ENOG4111J2U
JNUCC-1_02560		903	Epimerase family protein	S:COG1090
JNUCC-1_02561		819	Regulatory protein RecX	S:COG2137
JNUCC-1_02562	bdh	660	3-hydroxybutyrate dehydrogenase	S:ENOG410XQPQ
JNUCC-1_02563		327	uncharacterized protein	S:ENOG4111X8E
JNUCC-1_02564		987	uncharacterized protein	S:COG1988
JNUCC-1_02565	mutY	1068	Adenine glycosylase	L:COG1194
JNUCC-1_02566		165	Small, acid-soluble spore protein gamma-type	S:ENOG410Y5QD
JNUCC-1_02567		594	UPF0374 protein	J:COG3557
JNUCC-1_02568	msbA	1767	Putative multidrug export ATP-binding/permease protein	V:COG1132
JNUCC-1_02569		426	Protein LctB	P:COG1226
JNUCC-1_02570	pdxB	951	4-phosphoerythronate dehydrogenase	E:COG0111
JNUCC-1_02571	MMAB|pduO	558	Cob(I)yrinic acid a,c-diamide adenosyltransferase	S:COG2096
JNUCC-1_02572		444	Peroxide operon regulator	K:COG0735
JNUCC-1_02590	rlmN	1074	23S rRNA (adenine(2503)-C(2))-methyltransferase	J:COG0820
JNUCC-1_02591		681	uncharacterized protein	S:COG2364
JNUCC-1_02592		570	hypothetical protein	S:COG4636
JNUCC-1_02593		834	uncharacterized protein	CP:COG1668
JNUCC-1_02594		228	uncharacterized protein	CP:COG1668
JNUCC-1_02595	ABC.SS.A	900	Monosaccharide-transporting ATPase	S:COG4152
JNUCC-1_02596		486	hypothetical protein	S:ENOG410Y582

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_02597		201	Uncharacterized HTH-type transcriptional regulator YgzD	K:COG1476
JNUCC-1_02598		543	hypothetical protein	S:ENOG41125GJ
JNUCC-1_02599		339	hypothetical protein	K:COG1695
JNUCC-1_02600		486	hypothetical protein	S:COG0840
JNUCC-1_02601		465	Sodium/proline symporter	E:COG0591
JNUCC-1_02602		336	hypothetical protein	E:COG0591
JNUCC-1_02603		624	High-affinity choline transporter	E:COG0591
JNUCC-1_02604		1203	uncharacterized protein	S:COG2311
JNUCC-1_02605		732	Adenosine monophosphate-protein transferase FICD	S:COG3177
JNUCC-1_02606		1005	hypothetical protein	
JNUCC-1_02607		309	hypothetical protein	S:ENOG410XWQQ
JNUCC-1_02608	cobU|cobT	1071	Nicotinate-nucleotide-dimethylbenzimidazole phosphoribosyltransferase	L:COG0675
JNUCC-1_02609	paaI	417	hypothetical protein	Q:COG2050
JNUCC-1_02610		189	hypothetical protein	
JNUCC-1_02611		192	hypothetical protein	S:ENOG410ZQCY
JNUCC-1_02612		984	hypothetical protein	S:ENOG410ZAZJ
JNUCC-1_02613		1284	hypothetical protein	L:COG3547
JNUCC-1_02614		345	hypothetical protein	
JNUCC-1_02615		744	uncharacterized protein	Q:COG0500
JNUCC-1_02616		267	hypothetical protein	
JNUCC-1_02617	yrrT	627	Uncharacterized methyltransferase	S:ENOG4111K4C
JNUCC-1_02618		120	hypothetical protein	
JNUCC-1_02619		183	hypothetical protein	
JNUCC-1_02620		156	hypothetical protein	
JNUCC-1_02621		267	hypothetical protein	

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_02622		351	hypothetical protein	
JNUCC-1_02623		315	RNA polymerase sigma factor SigV	K:COG1595
JNUCC-1_02624		327	hypothetical protein	
JNUCC-1_02625		729	Alpha-glucoside transport ATP-binding protein AglK	G:COG3839
JNUCC-1_02626		774	hypothetical protein	S:COG1277
JNUCC-1_02627		267	hypothetical protein	S:ENOG4111WY0
JNUCC-1_02628		306	hypothetical protein	S:ENOG4111PCS
JNUCC-1_02629		198	Cold shock-like protein CspLB	K:COG1278
JNUCC-1_02630		645	hypothetical protein	
JNUCC-1_02631		297	hypothetical protein	
JNUCC-1_02632		993	Protein kintoun	S:ENOG41125I9
JNUCC-1_02633		1320	Cytosine permease	F:COG1457
JNUCC-1_02634	hyuA	1551	N-methylhydantoinase (ATP-hydrolyzing)	EQ:COG0145
JNUCC-1_02635		1074	hypothetical protein	EQ:COG0145
JNUCC-1_02636		477	hypothetical protein	
JNUCC-1_02637		1233	Transposase for insertion sequence element IS1557	L:COG3464
JNUCC-1_02638		459	hypothetical protein	
JNUCC-1_02639	mcrB	2466	5-methylcytosine-specific restriction enzyme	V:COG1401
JNUCC-1_02640		1053	Protein McrC	V:COG4268
JNUCC-1_02641		501	hypothetical protein	
JNUCC-1_02642		873	hypothetical protein	S:ENOG410YJ5R
JNUCC-1_02643		474	hypothetical protein	
JNUCC-1_02644	hsdR	2364	Type I site-specific deoxyribonuclease	V:COG4096
JNUCC-1_02645	hsdM	1473	Site-specific DNA-methyltransferase (adenine-specific)	V:COG0286
JNUCC-1_02646	hsdS	1431	Type I site-specific deoxyribonuclease	V:ENOG410ZKBR

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_02647		537	DNA-directed RNA polymerase	S:ENOG410XW7V
JNUCC-1_02648		228	hypothetical protein	
JNUCC-1_02649		174	hypothetical protein	
JNUCC-1_02650		723	hypothetical protein	S:ENOG41126P2
JNUCC-1_02651		327	hypothetical protein	
JNUCC-1_02652	dnaB	1290	DNA helicase	L:COG0305
JNUCC-1_02653		885	HTH-type transcriptional regulator XapR	K:ENOG410YMSV
JNUCC-1_02654	ilvB|ilvG|ilvI	1737	Acetolactate synthase	E:COG0028
JNUCC-1_02655	odh	1092	Opine dehydrogenase	C:ENOG410XS3N
JNUCC-1_02656		1128	Sarcosine oxidase	E:COG0665
JNUCC-1_02657		1665	Glutathione-binding protein GsiB	E:COG4166
JNUCC-1_02658		939	Oligopeptide transport system permease protein OppB	P:COG0601
JNUCC-1_02659		933	Dipeptide transport system permease protein DppC	P:COG1173
JNUCC-1_02660		1053	Dipeptide transport ATP-binding protein DppD	EP:COG0444
JNUCC-1_02661		858	Oligopeptide transport ATP-binding protein OppF	E:COG4608
JNUCC-1_02662		201	hypothetical protein	L:COG4584
JNUCC-1_02663		882	hypothetical protein	L:COG4584
JNUCC-1_02664		300	hypothetical protein	L:COG1484
JNUCC-1_02665		339	Insertion sequence IS408 putative ATP-binding protein	L:COG1484
JNUCC-1_02666		486	hypothetical protein	V:ENOG410ZZ4H
JNUCC-1_02667		216	hypothetical protein	
JNUCC-1_02668		1020	Sensory rhodopsin I transducer	S:COG0840
JNUCC-1_02669		324	hypothetical protein	
JNUCC-1_02670		1203	Transposase for insertion sequence element IS1111A	L:COG3547
JNUCC-1_02671		165	hypothetical protein	

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_02672		129	hypothetical protein	
JNUCC-1_02673		144	hypothetical protein	
JNUCC-1_02674		357	hypothetical protein	S:ENOG410ZZVF
JNUCC-1_02675		552	hypothetical protein	S:ENOG410Z9QX
JNUCC-1_02676		183	hypothetical protein	
JNUCC-1_02677		945	hypothetical protein	S:ENOG4111IJ6
JNUCC-1_02678		105	hypothetical protein	
JNUCC-1_02679		387	Glycerol-1-phosphatase	S:ENOG41122J1
JNUCC-1_02680		459	hypothetical protein	
JNUCC-1_02681		594	HTH-type transcriptional regulator BetI	K:ENOG4111ZCY
JNUCC-1_02682		1164	hypothetical protein	S:COG2311
JNUCC-1_02683	ltrA	1794	RNA-directed DNA polymerase	L:COG3344
JNUCC-1_02684		834	hypothetical protein	
JNUCC-1_02685		843	hypothetical protein	
JNUCC-1_02686		306	hypothetical protein	S:ENOG410YPU1
JNUCC-1_02687		267	hypothetical protein	S:ENOG410YPU1
JNUCC-1_02688		567	hypothetical protein	S:ENOG410XQCU
JNUCC-1_02689		387	hypothetical protein	S:ENOG410ZB73
JNUCC-1_02690		693	hypothetical protein	
JNUCC-1_02691		480	hypothetical protein	
JNUCC-1_02692		699	UPF0702 transmembrane protein YcaP	S:COG2323
JNUCC-1_02693	pepQ	1011	Xaa-Pro dipeptidase	E:COG0006
JNUCC-1_02694	K01436	1245	N-acyl-L-amino acid amidohydrolase	E:COG1473
JNUCC-1_02695	ALDH	1440	Aldehyde dehydrogenase (NAD(+))	C:COG1012
JNUCC-1_02696	ectB|dat	1008	Diaminobutyrate--2-oxoglutarate transaminase	E:COG0160

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_02697	ectB|dat	216	Diaminobutyrate-2-oxoglutarate transaminase	E:COG0160
JNUCC-1_02698		138	hypothetical protein	
JNUCC-1_02699		363	hypothetical protein	S:ENOG410YURJ
JNUCC-1_02700		648	hypothetical protein	S:COG4427
JNUCC-1_02701		387	hypothetical protein	S:COG4427
JNUCC-1_02702		360	hypothetical protein	S:ENOG410YJEY
JNUCC-1_02703		426	hypothetical protein	
JNUCC-1_02704		879	Uncharacterized MscS family protein YkuT	M:COG0668
JNUCC-1_02705		198	Cold shock-like protein CspLB	K:COG1278
JNUCC-1_02706	OTC|argF|argI	1020	Ornithine carbamoyltransferase	E:COG0078
JNUCC-1_02707		600	Putative HMP/thiamine-binding protein YkoF	S:ENOG4111NMW
JNUCC-1_02708		726	Autoinducer 2 import ATP-binding protein LsrA	V:COG1131
JNUCC-1_02709		768	Probable ABC transporter permease protein	P:COG0600
JNUCC-1_02710		1014	Formylaminopyrimidine-binding protein	P:COG0715
JNUCC-1_02711		252	hypothetical protein	
JNUCC-1_02712		138	hypothetical protein	
JNUCC-1_02713		366	hypothetical protein	
JNUCC-1_02714		234	hypothetical protein	
JNUCC-1_02715		135	hypothetical protein	
JNUCC-1_02716		411	uncharacterized protein	S:COG1714
JNUCC-1_02717		312	hypothetical protein	
JNUCC-1_02718	ipdC	1671	Indolepyruvate decarboxylase	GH:COG3961
JNUCC-1_02719		450	HTH-type transcriptional regulator PetP	K:ENOG4111G0I
JNUCC-1_02720		456	hypothetical protein	V:COG4767
JNUCC-1_02721		783	hypothetical protein	S:COG0596

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_02722		903	uncharacterized protein	O:COG5504
JNUCC-1_02723		198	hypothetical protein	
JNUCC-1_02724		759	Stage II sporulation protein SA	
JNUCC-1_02725		876	hypothetical protein	
JNUCC-1_02726	maa	495	Maltose O-acetyltransferase	S:COG0110
JNUCC-1_02727		243	Uncharacterized membrane protein YkoY	P:COG0861
JNUCC-1_02728		483	Uncharacterized membrane protein YkoY	P:COG0861
JNUCC-1_02729	frdA	1152	Fumarate reductase (quinol)	C:COG1902
JNUCC-1_02730		855	Putative ribonuclease-like protein YfkH	S:COG1295
JNUCC-1_02731		624	UPF0478 protein YtxG	S:COG4768
JNUCC-1_02732		363	hypothetical protein	S:COG4768
JNUCC-1_02733		207	hypothetical protein	
JNUCC-1_02734		2373	ABC transporter permease YtrF	V:ENOG410ZVWK
JNUCC-1_02735		180	hypothetical protein	
JNUCC-1_02736		693	Lipoprotein-releasing system ATP-binding protein LolD	V:COG1136
JNUCC-1_02737		417	hypothetical protein	S:ENOG410YYYD
JNUCC-1_02738	codA	1251	Cytosine deaminase	F:COG0402
JNUCC-1_02739		279	DNA base-flipping protein	L:COG3695
JNUCC-1_02740		705	Spore coat-associated protein	S:ENOG4111M2C
JNUCC-1_02741	dkgA	846	2,5-didehydrogluconate reductase (2-dehydro-L-gulonate-forming)	S:COG0656
JNUCC-1_02742		1011	hypothetical protein	S:COG4927
JNUCC-1_02743	ilvA|tdcB	945	Threonine ammonia-lyase	E:COG1171
JNUCC-1_02744		246	hypothetical protein	K:ENOG410ZI2Q
JNUCC-1_02745	mazF|ndoA|chpA	330	Endoribonuclease MazF	T:COG2337
JNUCC-1_02746		147	hypothetical protein	

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_02747	dadA	1113	D-amino acid dehydrogenase (quinone)	E:COG0665
JNUCC-1_02748	ppaC	930	Inorganic diphosphatase	C:COG1227
JNUCC-1_02749		1743	Sulfate transporter 3.2	P:COG0659
JNUCC-1_02750		258	hypothetical protein	S:ENOG410YURV
JNUCC-1_02751	menC	1116	o-succinylbenzoate synthase	M:COG4948
JNUCC-1_02752	tatD	861	Uncharacterized metal-dependent hydrolase	L:COG0084
JNUCC-1_02753		594	hypothetical protein	S:COG2102
JNUCC-1_02754		195	hypothetical protein	
JNUCC-1_02756		150	hypothetical protein	S:COG4636
JNUCC-1_02757		348	hypothetical protein	S:COG4636
JNUCC-1_02758		459	hypothetical protein	
JNUCC-1_02759		141	hypothetical protein	
JNUCC-1_02760		195	hypothetical protein	
JNUCC-1_02761		1332	Energy-coupling factor transporter ATP-binding protein EcfA1	S:COG1123
JNUCC-1_02762		774	hypothetical protein	S:ENOG4111FXW
JNUCC-1_02763	cysA	879	Sulfate-transporting ATPase	P:COG1121
JNUCC-1_02764		2532	hypothetical protein	S:ENOG410YYTS
JNUCC-1_02765		438	hypothetical protein	S:ENOG410XWEK
JNUCC-1_02766		762	hypothetical protein	S:ENOG410YGAT
JNUCC-1_02767	racD	690	Aspartate racemase	E:COG1794
JNUCC-1_02768		267	hypothetical protein	
JNUCC-1_02769		387	hypothetical protein	
JNUCC-1_02770		642	uncharacterized protein	S:COG2968
JNUCC-1_02771		474	hypothetical protein	
JNUCC-1_02772	surE	540	5′-nucleotidase	Q:ENOG4111I3F

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_02773		423	hypothetical protein	S:ENOG4111WNX
JNUCC-1_02774	ACSF2	1587	2-succinylbenzoate-CoA ligase	IQ:COG0318
JNUCC-1_02775		1209	Na(+)/H(+) antiporter NhaG	P:COG0025
JNUCC-1_02776		423	hypothetical protein	
JNUCC-1_02777		141	hypothetical protein	
JNUCC-1_02778		213	hypothetical protein	
JNUCC-1_02779		468	hypothetical protein	S:ENOG410Z3XV
JNUCC-1_02780		1023	Phosphate-binding protein PstS	P:COG0226
JNUCC-1_02781		957	Phosphate transport system permease protein PstC	P:COG0573
JNUCC-1_02782		888	Phosphate transport system permease protein PstA	P:COG0581
JNUCC-1_02783	aapP|bztD	825	Phosphate import ATP-binding protein PstB	P:COG1117
JNUCC-1_02784	tsdA	960	Thiosulfate dehydrogenase	C:COG3258
JNUCC-1_02785		240	Uncharacterized membrane protein YuzA	S:COG2155
JNUCC-1_02786	uvsE|UVE1	885	UV-damage endonuclease	L:COG4294
JNUCC-1_02787		810	Probable amino-acid-binding protein YxeM	E:COG0834
JNUCC-1_02788		441	hypothetical protein	
JNUCC-1_02789		666	Glutamine transport system permease protein	E:COG0765
JNUCC-1_02790	pstB	741	Phosphate-transporting ATPase	P:COG1117
JNUCC-1_02791		141	hypothetical protein	
JNUCC-1_02792		561	hypothetical protein	
JNUCC-1_02793		663	hypothetical protein	E:COG0253
JNUCC-1_02794	dmdB	1608	3-(methylthio)propionyl--CoA ligase	IQ:COG0318
JNUCC-1_02795		183	hypothetical protein	
JNUCC-1_02796	amiABC	858	N-acetylmuramoyl-L-alanine amidase	M:COG0860
JNUCC-1_02797	cynT|can	561	Carbonic anhydrase	P:COG0288

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_02798		201	Cold shock-like protein CspLB	K:COG1278
JNUCC-1_02799		258	hypothetical protein	S:ENOG410Y1M3
JNUCC-1_02800		1314	Recombination protein	S:COG2333
JNUCC-1_02801		504	hypothetical protein	
JNUCC-1_02802	trpB	780	Tryptophan synthase	E:COG0133
JNUCC-1_02803	trpB	348	Tryptophan synthase	E:COG0133
JNUCC-1_02804		378	HTH-type transcriptional regulator HmrR	K:COG0789
JNUCC-1_02805	cobU|cobT	1071	Nicotinate-nucleotide-dimethylbenzimidazole phosphoribosyltransferase	L:COG0675
JNUCC-1_02806		207	hypothetical protein	
JNUCC-1_02807		357	hypothetical protein	
JNUCC-1_02808		240	hypothetical protein	
JNUCC-1_02809		453	hypothetical protein	S:ENOG41128XM
JNUCC-1_02810		174	hypothetical protein	
JNUCC-1_02811		324	hypothetical protein	S:ENOG410XXT0
JNUCC-1_02812		1236	hypothetical protein	
JNUCC-1_02813		324	hypothetical protein	
JNUCC-1_02814		525	hypothetical protein	
JNUCC-1_02815		279	hypothetical protein	
JNUCC-1_02816		198	hypothetical protein	
JNUCC-1_02817		201	hypothetical protein	
JNUCC-1_02818		222	hypothetical protein	
JNUCC-1_02819		231	hypothetical protein	S:COG1983
JNUCC-1_02820		198	hypothetical protein	
JNUCC-1_02821		1194	Transposase for insertion sequence element IS905	L:COG3328
JNUCC-1_02822		222	hypothetical protein	S:ENOG410XWX0

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_02823		273	hypothetical protein	
JNUCC-1_02824		567	hypothetical protein	S:ENOG410YV3F
JNUCC-1_02825		150	hypothetical protein	
JNUCC-1_02826		189	hypothetical protein	
JNUCC-1_02827		165	hypothetical protein	
JNUCC-1_02828		465	hypothetical protein	
JNUCC-1_02829		381	hypothetical protein	S:ENOG4111PK9
JNUCC-1_02830		324	hypothetical protein	S:ENOG41127S6
JNUCC-1_02831	pflA|pflC|pflE	750	[Formate-C-acetyltransferase]-activating enzyme	O:COG1180
JNUCC-1_02832	pflD	2037	Formate C-acetyltransferase	C:COG1882
JNUCC-1_02833	serB-plsC	750	Phosphoserine phosphatase	E:COG0560
JNUCC-1_02834		456	hypothetical protein	S:ENOG4111XQ8
JNUCC-1_02835		714	Protein ORF73	S:ENOG4110JG7
JNUCC-1_02836		204	Small, acid-soluble spore protein	S:ENOG411226C
JNUCC-1_02837	cobU|cobT	1071	Nicotinate-nucleotide-dimethylbenzimidazole phosphoribosyltransferase	L:COG0675
JNUCC-1_02838		276	hypothetical protein	S:COG2071
JNUCC-1_02839		444	Protein NtpR	S:COG2071
JNUCC-1_02840	DPEP	948	Membrane dipeptidase	E:COG2355
JNUCC-1_02841		339	hypothetical protein	S:ENOG410YXBE
JNUCC-1_02842		1008	hypothetical protein	G:COG1085
JNUCC-1_02843		858	Glutamate synthase large subunit-like protein YerD	E:COG0069
JNUCC-1_02844	mgsC	732	Methylamine-glutamate N-methyltransferase	E:COG0069
JNUCC-1_02845		213	hypothetical protein	
JNUCC-1_02846		1506	Sodium/proline symporter	E:COG0591
JNUCC-1_02847	speB	981	Agmatinase	E:COG0010

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_02848	ansA|ansB	1029	Asparaginase	E:COG4448
JNUCC-1_02849	degP|htrA	957	Peptidase Do	O:COG0265
JNUCC-1_02850	ycsE|yitU|ywtE	783	5-amino-6-(5-phospho-D-ribitylamino)uracil phosphatase	S:COG0561
JNUCC-1_02851		1551	uncharacterized protein	C:COG1757
JNUCC-1_02852		345	hypothetical protein	C:COG3894
JNUCC-1_02853		1203	C4-dicarboxylate transport protein	C:COG1301
JNUCC-1_02854		363	hypothetical protein	
JNUCC-1_02855		279	hypothetical protein	
JNUCC-1_02856		855	uncharacterized protein	S:COG2996
JNUCC-1_02857		870	Solute carrier family 35 member G1	EG:COG0697
JNUCC-1_02858		666	hypothetical protein	
JNUCC-1_02859		888	Bacitracin transport ATP-binding protein BcrA	V:COG1132
JNUCC-1_02860		378	Uncharacterized HTH-type transcriptional regulator YhdI	K:COG1725
JNUCC-1_02861	speG|SAT	507	Diamine N-acetyltransferase	J:COG1670
JNUCC-1_02862		897	hypothetical protein	S:COG0679
JNUCC-1_02863		687	HTH-type transcriptional repressor RspR	K:COG1802
JNUCC-1_02864	dapA	930	4-hydroxy-tetrahydrodipicolinate synthase	E:COG0329
JNUCC-1_02865	aldA	1491	Lactaldehyde dehydrogenase	C:COG1012
JNUCC-1_02866	hpaB	1467	4-hydroxyphenylacetate 3-monooxygenase	Q:COG2368
JNUCC-1_02867	dmpB|xylE	984	Catechol 2,3-dioxygenase	E:COG0346
JNUCC-1_02868		1485	hypothetical protein	L:COG3666
JNUCC-1_02869	hpaC	480	Flavin reductase (NADH)	S:COG1853
JNUCC-1_02870		636	Leucine dehydrogenase	E:COG0334
JNUCC-1_02871	pdh	552	Phenylalanine dehydrogenase	E:COG0334
JNUCC-1_02872	hpaG	684	4-hydroxyphenylacetate degradation bifunctional isomerase/decarboxylase	Q:COG0179

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_02873	hpaG	759	4-hydroxyphenylacetate degradation bifunctional isomerase/decarboxylase	Q:COG0179
JNUCC-1_02874	hpaF|hpcD	387	5-carboxymethyl-2-hydroxymuconate Delta-isomerase	Q:COG3232
JNUCC-1_02875		168	hypothetical protein	
JNUCC-1_02876		816	Zinc transporter ZIP11	P:COG0428
JNUCC-1_02877		609	Putative membrane protein YtaF	S:COG1971
JNUCC-1_02878	topB	2169	DNA topoisomerase	L:COG0550
JNUCC-1_02879	ltrA	1317	RNA-directed DNA polymerase	L:COG3344
JNUCC-1_02880	ABC.FEV.A	1563	Iron-chelate-transporting ATPase	S:COG0488
JNUCC-1_02881		240	Ferredoxin 7Fe	C:COG1146
JNUCC-1_02882		144	hypothetical protein	S:ENOG410Z36V
JNUCC-1_02883		459	Probable flavodoxin-1	C:COG0716
JNUCC-1_02884		267	hypothetical protein	
JNUCC-1_02885		1317	Putative binding protein	G:COG1653
JNUCC-1_02886		411	Putative ABC transporter permease protein AmyD	P:COG1175
JNUCC-1_02887		363	Putative ABC transporter permease protein AmyD	P:COG1175
JNUCC-1_02888		747	L-arabinose transport system permease protein AraQ	G:COG0395
JNUCC-1_02889	nagZ	1569	Beta-N-acetylhexosaminidase	G:COG1472
JNUCC-1_02890	nagZ	1149	Beta-N-acetylhexosaminidase	S:COG3876
JNUCC-1_02891	murQ	903	N-acetylmuramic acid 6-phosphate etherase	S:COG2103
JNUCC-1_02892		870	Uncharacterized HTH-type transcriptional regulator YbbH	K:COG1737
JNUCC-1_02893	gspK	987	Glucosamine kinase	G:COG2971
JNUCC-1_02894	nagZ	975	Beta-N-acetylhexosaminidase	S:ENOG410ZPN5
JNUCC-1_02895	pbp4b	1050	Serine-type D-Ala-D-Ala carboxypeptidase	V:COG1680
JNUCC-1_02896		1506	hypothetical protein	S:ENOG410XPDK
JNUCC-1_02897		1170	hypothetical protein	S:ENOG410XSFI

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_02898		4152	hypothetical protein	S:ENOG410XQH8
JNUCC-1_02899		1317	hypothetical protein	S:ENOG4111FSC
JNUCC-1_02900		651	uncharacterized protein	S:COG1357
JNUCC-1_02901		1740	Methyl-accepting chemotaxis protein	S:COG0840
JNUCC-1_02902		468	hypothetical protein	S:ENOG4111PXW
JNUCC-1_02903	pcp	600	Pyroglutamyl-peptidase I	O:COG2039
JNUCC-1_02904		1170	Uncharacterized MFS-type transporter YttB	G:ENOG410ZVV9
JNUCC-1_02905	ycsE|yitU|ywtE	738	5-amino-6-(5-phospho-D-ribitylamino)uracil phosphatase	S:COG0561
JNUCC-1_02906		183	hypothetical protein	S:ENOG4112AHH
JNUCC-1_02907		1056	hypothetical protein	S:ENOG410XNPE
JNUCC-1_02908		444	hypothetical protein	S:ENOG41121CK
JNUCC-1_02909		447	hypothetical protein	S:ENOG41121CK
JNUCC-1_02910	ggt	1608	Gamma-glutamyltransferase	E:COG0405
JNUCC-1_02911		2022	Penicillin-binding protein	M:COG0768
JNUCC-1_02912		594	Transcriptional regulator LytR	K:COG1316
JNUCC-1_02913		351	Transcriptional regulator LytR	K:COG1316
JNUCC-1_02914	lexA	330	Repressor LexA	K:ENOG410XUC3
JNUCC-1_02915		420	hypothetical protein	S:COG5652
JNUCC-1_02916		150	hypothetical protein	
JNUCC-1_02917	nagA|AMDHD2	1173	N-acetylglucosamine-6-phosphate deacetylase	G:COG1820
JNUCC-1_02918	nagB|GNPDA	729	Glucosamine-6-phosphate deaminase	G:COG0363
JNUCC-1_02919	thyA|TYMS	642	Thymidylate synthase	S:COG1739
JNUCC-1_02920	degS	1131	Histidine kinase	T:ENOG410XNMH
JNUCC-1_02921		687	Chemotaxis response regulator protein-glutamate methylesterase	T:COG2201
JNUCC-1_02922		843	Protein DegV	S:COG1307

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_02923		1431	ComF operon protein	L:COG4098
JNUCC-1_02924		684	ComF operon protein	S:COG1040
JNUCC-1_02925		426	uncharacterized protein	S:ENOG4112242
JNUCC-1_02926		216	hypothetical protein	K:COG2747
JNUCC-1_02927		486	hypothetical protein	S:ENOG410ZY8E
JNUCC-1_02928		1452	Flagellar hook-associated protein	N:COG1256
JNUCC-1_02929		870	Flagellar hook-associated protein	N:COG1344
JNUCC-1_02930		552	uncharacterized protein	S:ENOG4111YHM
JNUCC-1_02931		492	Flagellar assembly factor FliW	S:COG1699
JNUCC-1_02932		228	Carbon storage regulator like protein	T:COG1551
JNUCC-1_02933		351	uncharacterized protein	N:COG1334
JNUCC-1_02934		1458	Flagellar hook-associated protein	N:COG1345
JNUCC-1_02935		402	Flagellar protein FliS	N:COG1516
JNUCC-1_02936		354	Flagellar protein FliT	N:ENOG410XZCW
JNUCC-1_02937		552	uncharacterized protein	J:COG1544
JNUCC-1_02938		1638	Protein translocase subunit SecA	U:COG0653
JNUCC-1_02939		876	Protein translocase subunit SecA	U:COG0653
JNUCC-1_02940		1053	Peptide chain release factor	J:COG1186
JNUCC-1_02941		360	Cytochrome c-551	C:COG2010
JNUCC-1_02942		687	Phosphonates import ATP-binding protein PhnC	D:COG2884
JNUCC-1_02943		456	Cell division protein	D:COG2177
JNUCC-1_02944		459	Cell division protein	D:COG2177
JNUCC-1_02945	prc|ctpA	801	C-terminal processing peptidase	M:COG0793
JNUCC-1_02946	prc|ctpA	675	C-terminal processing peptidase	M:COG0793
JNUCC-1_02947		1158	Cell division topological determinant MinJ	O:COG0265

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_02948	nirK	666	Nitrite reductase (NO-forming)	Q:COG2132
JNUCC-1_02949	nirK	381	Nitrite reductase (NO-forming)	Q:COG2132
JNUCC-1_02950		1983	UvrABC system protein	L:COG0556
JNUCC-1_02951		2883	UvrABC system protein	L:COG0178
JNUCC-1_02952		354	uncharacterized protein	S:ENOG4111UV1
JNUCC-1_02953	bshB2	675	Probable N-acetyl-alpha-D-glucosaminyl L-malate deacetylase	S:COG2120
JNUCC-1_02954		198	hypothetical protein	S:COG1983
JNUCC-1_02955		354	Uncharacterized membrane protein YvlD	S:COG1950
JNUCC-1_02956	hprK|ptsK	942	HPr kinase/phosphorylase	T:COG1493
JNUCC-1_02957	lgt|umpA	834	Phosphatidylglycerol-prolipoprotein diacylglyceryl transferase	M:COG0682
JNUCC-1_02958		963	Uncharacterized membrane protein YvoD	S:ENOG410XSJB
JNUCC-1_02959	ppaX	642	Inorganic diphosphatase	S:COG0546
JNUCC-1_02960	cysE	531	Serine O-acetyltransferase	S:COG0110
JNUCC-1_02961		135	hypothetical protein	
JNUCC-1_02962	glpA|glpD	1530	Glycerol-3-phosphate dehydrogenase	C:COG0578
JNUCC-1_02963		996	TPR repeat-containing protein YvcD	S:ENOG410XTC2
JNUCC-1_02964	trxB|TRR	954	Thioredoxin-disulfide reductase	O:COG0492
JNUCC-1_02965	mutT|NUDT15|MTH2	513	8-oxo-dGTP diphosphatase	L:COG0494
JNUCC-1_02966		888	Nucleotide-binding protein	S:COG1660
JNUCC-1_02967		963	Putative gluconeoproteinis factor	S:COG0391
JNUCC-1_02968		942	Putative sporulation transcription regulator WhiA	K:COG1481
JNUCC-1_02969		249	Phosphocarrier protein HPr	G:COG1925
JNUCC-1_02970		585	hypothetical protein	S:ENOG410Y714
JNUCC-1_02971		870	hypothetical protein	S:COG0456
JNUCC-1_02973	clpP|CLPP	588	Endopeptidase Clp	O:COG0740

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_02974		465	hypothetical protein	S:ENOG410Y60P
JNUCC-1_02975		258	Lipoprotein-releasing system ATP-binding protein LolD	EP:COG0444
JNUCC-1_02976		759	Oligopeptide transport ATP-binding protein	EP:COG0444
JNUCC-1_02977		969	Oligopeptide transport ATP-binding protein AppF	E:COG4608
JNUCC-1_02978		1686	Heme-binding protein	E:COG0747
JNUCC-1_02979		972	Dipeptide transport system permease protein DppB	P:COG0601
JNUCC-1_02980		906	Dipeptide transport system permease protein DppC	P:COG1173
JNUCC-1_02981		507	hypothetical protein	S:ENOG4111SZI
JNUCC-1_02982		591	SCO1 protein like protein	S:COG1999
JNUCC-1_02983		576	HTH-type transcriptional repressor YcnK	K:COG1349
JNUCC-1_02984		345	Multidrug resistance protein YkkC	P:COG2076
JNUCC-1_02985		315	Multidrug resistance protein YkkD	P:COG2076
JNUCC-1_02986		246	hypothetical protein	O:COG0526
JNUCC-1_02987		951	Central glycolytic protein regulator	K:COG2390
JNUCC-1_02988	GAPDH|gapA	1008	Glyceraldehyde-3-phosphate dehydrogenase (phosphorylating)	G:COG0057
JNUCC-1_02989	PGK|pgk	750	Phosphoglycerate kinase	G:COG0126
JNUCC-1_02990	PGK|pgk	435	Phosphoglycerate kinase	G:COG0126
JNUCC-1_02991	TPI|tpiA	759	Triose-phosphate isomerase	G:COG0149
JNUCC-1_02992	gpmI	1548	Phosphoglycerate mutase (2,3-diphosphoglycerate-independent)	G:COG0696
JNUCC-1_02993	ENO|eno	1287	Phosphopyruvate hydratase	G:COG0148
JNUCC-1_02994		915	Putative NAD(P)H nitroreductase YfhC	C:COG0778
JNUCC-1_02995		744	SkfA peptide export ATP-binding protein SkfE	V:COG0842
JNUCC-1_02996		861	Manganese transport system membrane protein MntC	P:COG1108
JNUCC-1_02997		933	Uncharacterized periplasmic metal-binding protein	P:COG0803
JNUCC-1_02998	PTS-EI.PTSI|ptsI	1719	Phosphoenolpyruvate--protein phosphotransferase	G:COG1080

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_02999	MGLL	921	Acylglycerol lipase	I:COG2267
JNUCC-1_03000		234	Protein translocase subunit SecG	U:ENOG410XVNV
JNUCC-1_03001	yvaK	747	Carboxylesterase	S:COG1647
JNUCC-1_03002	rnr|vacB	408	Ribonuclease	K:COG0557
JNUCC-1_03003	rnr|vacB	1815	Ribonuclease	K:COG0557
JNUCC-1_03004		465	SsrA-binding protein	O:COG0691
JNUCC-1_03005	argE	1629	Acetylornithine deacetylase	E:COG4187
JNUCC-1_03006		1053	Putative aminopeptidase YhfE	E:COG1363
JNUCC-1_03007		651	UPF0073 membrane protein	S:COG1272
JNUCC-1_03008		588	hypothetical protein	S:ENOG4111FII
JNUCC-1_03009	sppA	999	Putative signal peptide peptidase SppA	OU:COG0616
JNUCC-1_03010		495	Uncharacterized membrane protein YteJ	S:COG1714
JNUCC-1_03011		1020	UPF0421 protein	S:COG4129
JNUCC-1_03012	cwlO	1290	Peptidoglycan DL-endopeptidase CwlO	M:COG0791
JNUCC-1_03013	ltrA	1317	RNA-directed DNA polymerase	L:COG3344
JNUCC-1_03014		1488	Osmo-dependent choline transporter BetT2	P:COG1292
JNUCC-1_03015		1308	UPF0053 protein YhdP	P:COG1253
JNUCC-1_03016		804	uncharacterized protein	S:ENOG4111SXA
JNUCC-1_03017		414	Zinc-specific metallo-regulatory protein	K:COG0735
JNUCC-1_03018		765	29 kDa membrane protein in scaA 5′region	P:COG1108
JNUCC-1_03019		777	Fe(3+) ions import ATP-binding protein FbpC	S:COG0488
JNUCC-1_03020		939	High-affinity zinc uptake system protein ZnuA	P:COG0803
JNUCC-1_03021		294	Copper-sensing transcriptional repressor CsoR	S:COG1937
JNUCC-1_03022	copA|ATP7	792	Cu(+) exporting ATPase	P:COG2217
JNUCC-1_03023	copA|ATP7	1566	Cu(+) exporting ATPase	P:COG2217

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_03024		234	Small, acid-soluble spore protein H	M:ENOG410XY4N
JNUCC-1_03025		360	hypothetical protein	S:ENOG410ZDQ7
JNUCC-1_03026	fadN	2226	3-hydroxyacyl-CoA dehydrogenase	I:COG1250
JNUCC-1_03027	atoB	1176	Acetyl-CoA C-acetyltransferase	I:COG0183
JNUCC-1_03028	ACADS|bcd	1788	Short-chain acyl-CoA dehydrogenase	I:COG1960
JNUCC-1_03029	ARSC1|arsC	363	Arsenate reductase (glutaredoxin)	P:COG1393
JNUCC-1_03030		387	Glycine cleavage system H protein	E:COG0509
JNUCC-1_03031		354	uncharacterized protein	L:COG1658
JNUCC-1_03032		312	Thioredoxin-like protein YusE	O:ENOG410XWYJ
JNUCC-1_03033	nrtC|nasD	1038	Energy-coupling factor transporter ATP-binding protein EcfA2	P:COG1116
JNUCC-1_03034		669	Methionine import system permease protein MetP	P:COG2011
JNUCC-1_03035		855	Membrane lipoprotein TpN32	P:COG1464
JNUCC-1_03036		786	Probable ATP-dependent transporter ycf16	O:COG0396
JNUCC-1_03037		1314	FeS cluster assembly protein SufD	O:COG0719
JNUCC-1_03038	sufS	1221	Cysteine desulfurase	E:COG0520
JNUCC-1_03039		450	Zinc-dependent sulfurtransferase SufU	C:COG0822
JNUCC-1_03040		1398	UPF0051 protein	O:COG0719
JNUCC-1_03041		819	UPF0721 transmembrane protein YunE	S:COG0730
JNUCC-1_03042		1395	5′-nucleotidase	F:COG0737
JNUCC-1_03043		306	uncharacterized protein	S:COG3377
JNUCC-1_03044		777	Sporulation protein YunB	S:ENOG410ZYAS
JNUCC-1_03045		399	Uncharacterized sodium-dependent transporter YhdH	P:COG0733
JNUCC-1_03046		1134	Uncharacterized sodium-dependent transporter YhdH	P:COG0733
JNUCC-1_03047		105	hypothetical protein	
JNUCC-1_03048	lytH	978	L-Ala-D-Glu endopeptidase	M:COG0739

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_03049		603	Uncharacterized lipoprotein YutC	S:ENOG41123J4
JNUCC-1_03050		276	uncharacterized protein	S:COG4470
JNUCC-1_03051		279	hypothetical protein	S:ENOG410XXTH
JNUCC-1_03052	FAAH2	315	Fatty acid amide hydrolase	J:COG0154
JNUCC-1_03053	FAAH2	489	Fatty acid amide hydrolase	J:COG0154
JNUCC-1_03054	amiE	693	Amidase	J:COG0154
JNUCC-1_03055		750	hypothetical protein	S:ENOG4111MHE
JNUCC-1_03056		1134	hypothetical protein	U:COG4963
JNUCC-1_03057		297	hypothetical protein	U:COG4962
JNUCC-1_03058		1044	uncharacterized protein	U:COG4962
JNUCC-1_03059		930	hypothetical protein	U:ENOG4111NQ9
JNUCC-1_03060		936	hypothetical protein	U:COG2064
JNUCC-1_03061		219	hypothetical protein	
JNUCC-1_03062		804	uncharacterized protein	S:COG2304
JNUCC-1_03063		378	uncharacterized protein	S:COG2304
JNUCC-1_03064		288	hypothetical protein	S:COG2304
JNUCC-1_03065		189	hypothetical protein	
JNUCC-1_03066		1125	hypothetical protein	S:ENOG410YV3W
JNUCC-1_03067		834	hypothetical protein	
JNUCC-1_03068		279	hypothetical protein	
JNUCC-1_03069		717	hypothetical protein	S:ENOG410YYU5
JNUCC-1_03070		813	hypothetical protein	
JNUCC-1_03071		1428	hypothetical protein	S:ENOG410YV3W
JNUCC-1_03072		819	hypothetical protein	
JNUCC-1_03073		708	hypothetical protein	S:ENOG410YYU5

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_03074		822	hypothetical protein	
JNUCC-1_03075		498	hypothetical protein	
JNUCC-1_03076		825	hypothetical protein	
JNUCC-1_03077		819	hypothetical protein	
JNUCC-1_03078		822	hypothetical protein	
JNUCC-1_03079		396	hypothetical protein	S:ENOG4112CAJ
JNUCC-1_03080		717	hypothetical protein	S:ENOG410YW6N
JNUCC-1_03081		516	hypothetical protein	
JNUCC-1_03082		1347	hypothetical protein	S:ENOG410YV3W
JNUCC-1_03083		1299	hypothetical protein	S:ENOG410Y8P1
JNUCC-1_03084		270	hypothetical protein	S:ENOG411256J
JNUCC-1_03085		408	UPF0331 protein YutE	S:COG2445
JNUCC-1_03086		636	hypothetical protein	K:COG2345
JNUCC-1_03087		771	4-nitrophenylphosphatase	G:COG0647
JNUCC-1_03088	pgpA	516	Phosphatidylglycerophosphatase	I:COG1267
JNUCC-1_03089		969	Endospore coat-associated protein YutH	S:ENOG4111VIV
JNUCC-1_03090	gyaR|GOR1	966	Glyoxylate reductase	C:COG1052
JNUCC-1_03091		225	Putative nitrogen fixation protein YutI	O:COG0694
JNUCC-1_03092		327	Putative disulfide oxidoreductase YuzD	S:COG4837
JNUCC-1_03093		363	uncharacterized protein	S:COG0316
JNUCC-1_03094	fnr	987	Ferredoxin-NADP(+) reductase	O:COG0492
JNUCC-1_03095	ndh	531	NADH dehydrogenase	C:COG1252
JNUCC-1_03096	ndh	636	NADH dehydrogenase	C:COG1252
JNUCC-1_03097		312	Uncharacterized membrane protein YuiB	S:ENOG411296G
JNUCC-1_03098		681	uncharacterized protein	S:COG3584

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_03099		474	Uncharacterized membrane protein YuiD	S:COG1963
JNUCC-1_03100		753	Putative biotin transporter BioYB	S:COG1268
JNUCC-1_03101	deoD	708	Purine-nucleoside phosphorylase	F:COG0813
JNUCC-1_03102		276	Phosphocarrier protein HPr	G:COG1925
JNUCC-1_03103		489	uncharacterized protein	P:COG0490
JNUCC-1_03104		1179	Ammonium/H(+) antiporter subunit AmhT	P:COG0475
JNUCC-1_03105		399	Kinase-associated lipoprotein	S:ENOG41125VM
JNUCC-1_03106		210	hypothetical protein	S:ENOG410XWIQ
JNUCC-1_03107	SOD1	573	Superoxide dismutase	P:COG2032
JNUCC-1_03108	patB|malY	1176	Cystathionine beta-lyase	E:COG1168
JNUCC-1_03109	GPI|pgi	1347	Glucose-6-phosphate isomerase	G:COG0166
JNUCC-1_03110		369	Polyribonucleotide nucleotidyltransferase	J:COG1098
JNUCC-1_03111		1020	Putative potassium channel protein YugO	P:COG1226
JNUCC-1_03112		558	hypothetical protein	S:ENOG4111FEY
JNUCC-1_03113		1065	Cellulase	E:COG1363
JNUCC-1_03114	bpr	4170	Bacillopeptidase	O:COG1404
JNUCC-1_03115		585	Riboflavin transporter FmnP	S:COG3601
JNUCC-1_03116		393	hypothetical protein	
JNUCC-1_03117	menI|DHNAT	387	1,4-dihydroxy-2-naphthoyl-CoA hydrolase	Q:COG2050
JNUCC-1_03118	menA	933	UbiA prenyltransferase domain-containing protein	H:COG1575
JNUCC-1_03119		291	hypothetical protein	
JNUCC-1_03120	ltrA	1320	RNA-directed DNA polymerase	L:COG3344
JNUCC-1_03121	menF	1398	Isochorismate synthase	H:COG1169
JNUCC-1_03122	menD	1743	2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene-1-carboxylic-acidsynthase	H:COG1165
JNUCC-1_03123	menH	501	2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase	S:COG0596

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_03124	menB	894	1,4-dihydroxy-2-naphthoyl-CoA synthase	H:COG0447
JNUCC-1_03125	menE	1452	o-succinylbenzoate-CoA ligase	IQ:COG0318
JNUCC-1_03126		321	hypothetical protein	S:ENOG41121GJ
JNUCC-1_03127		540	hypothetical protein	S:ENOG410YSN2
JNUCC-1_03128	mutT|NUDT15|MTH2	477	8-oxo-dGTP diphosphatase	L:COG0494
JNUCC-1_03129		807	Uncharacterized ABC transporter permease protein YtlD	P:COG0600
JNUCC-1_03130		813	Lipoprotein-releasing system ATP-binding protein LolD	V:COG1136
JNUCC-1_03131		990	Putative binding protein YtlA	P:COG0715
JNUCC-1_03132	pckA	1677	Phosphoenolpyruvate carboxykinase (ATP)	C:COG1866
JNUCC-1_03133	metK	1200	Methionine adenosyltransferase	H:COG0192
JNUCC-1_03134		393	Uncharacterized transferase YtoA	S:COG0663
JNUCC-1_03135		1362	hypothetical protein	L:ENOG410XQ88
JNUCC-1_03136		657	Putative rRNA methylase YtqB	Q:COG0500
JNUCC-1_03137	LARS|leuS	2415	Leucine-tRNA ligase	J:COG0495
JNUCC-1_03138		753	hypothetical protein	
JNUCC-1_03142		573	Probable cell division protein YtgP	M:COG2244
JNUCC-1_03143		1014	Probable cell division protein YtgP	M:COG2244
JNUCC-1_03144	rsuA	735	16S rRNA pseudouridine(516) synthase	J:COG1187
JNUCC-1_03145	thpR	597	RNA 2′,3′-cyclic 3′-phosphodiesterase	J:COG1514
JNUCC-1_03146		921	RNA 2′,3′-cyclic phosphodiesterase	S:ENOG4111KVM
JNUCC-1_03147		231	hypothetical protein	
JNUCC-1_03148	dagK	777	Diacylglycerol kinase (ATP)	I:COG1597
JNUCC-1_03149		816	Putative phosphotransferase YtmP	M:COG0510
JNUCC-1_03150		288	hypothetical protein	S:ENOG41123PM
JNUCC-1_03151	trmB|METTL1|TRM8	654	tRNA (guanine(46)-N(7))-methyltransferase	S:COG0220

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_03152		858	Probable quorum-quenching lactonase YtnP	S:COG0491
JNUCC-1_03153		312	hypothetical protein	S:COG5584
JNUCC-1_03154	pepA	1074	Glutamyl aminopeptidase	E:COG1363
JNUCC-1_03155		501	Probable non-canonical purine NTP phosphatase	S:COG1986
JNUCC-1_03156		441	uncharacterized protein	S:ENOG4111IXG
JNUCC-1_03157		549	hypothetical protein	S:ENOG410ZH2Z
JNUCC-1_03158		804	UPF0354 protein	S:COG4848
JNUCC-1_03159		411	Putative tRNA-binding protein YtpR	J:COG0073
JNUCC-1_03160	pncB|NAPRT1	1128	Nicotinate phosphoribosyltransferase	H:COG1488
JNUCC-1_03161	murC	1311	UDP-N-acetylmuramate--L-alanine ligase	M:COG0773
JNUCC-1_03162		402	UPF0478 protein	S:COG4768
JNUCC-1_03163		477	uncharacterized protein	S:COG4980
JNUCC-1_03164		1026	hypothetical protein	D:COG0849
JNUCC-1_03165		1002	Cell division protein FtsA	D:COG0849
JNUCC-1_03166	pheA	1077	Chorismate mutase	E:COG1605
JNUCC-1_03167		246	Catabolite control protein A	K:COG1609
JNUCC-1_03168		738	Catabolite control protein A	K:COG1609
JNUCC-1_03169		825	Uncharacterized 29.3 kDa protein in ccpA 3′region	N:COG1291
JNUCC-1_03170		789	Uncharacterized 24.6 kDa protein in ccpA 3′region	N:COG1360
JNUCC-1_03171		1506	Myosin type-2 heavy chain	S:ENOG410XT8D
JNUCC-1_03172		225	hypothetical protein	
JNUCC-1_03173	racD	735	Aspartate racemase	E:COG1794
JNUCC-1_03174	murE	1482	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate-2,6-diaminopimelate ligase	M:COG0769
JNUCC-1_03175	asl	1188	D-aspartate ligase	S:COG3919
JNUCC-1_03176	murE	1491	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate-2,6-diaminopimelate ligase	M:COG0769

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_03177		1167	Acetoin utilization protein AcuC	BQ:COG0123
JNUCC-1_03178		651	Acetoin utilization protein AcuB	S:COG0517
JNUCC-1_03179	acuA	654	Acetoin utilization protein AcuA	S:ENOG410XRFR
JNUCC-1_03180		3117	Penicillin-binding protein 1A	M:COG0744
JNUCC-1_03181	YARS|tyrS	1278	Tyrosine-tRNA ligase	J:COG0162
JNUCC-1_03182		603	30S ribosomal protein S4	J:COG0522
JNUCC-1_03183	ydaM	1845	Diguanylate cyclase	T:ENOG410XNMH
JNUCC-1_03184	msrC	483	L-methionine (R)-S-oxide reductase	T:COG1956
JNUCC-1_03185		618	Probable HTH-type transcriptional regulator YttP	K:ENOG4111J0B
JNUCC-1_03186		1704	Septation ring formation regulator EzrA	D:COG4477
JNUCC-1_03187	iscS|NFS1	1140	Cysteine desulfurase	E:COG1104
JNUCC-1_03188	thiI	1140	tRNA uracil 4-sulfurtransferase	H:COG0301
JNUCC-1_03189		201	Small, acid-soluble spore protein	S:ENOG411226C
JNUCC-1_03190	ppnK|NADK	807	NAD(+) kinase	G:COG0061
JNUCC-1_03191		528	uncharacterized protein	S:ENOG41127TH
JNUCC-1_03192		456	Uncharacterized spore protein YtfJ	S:COG3874
JNUCC-1_03193	tpx	501	Peroxiredoxin	O:COG2077
JNUCC-1_03194		990	Site-specific DNA-methyltransferase (adenine-specific)	L:COG0827
JNUCC-1_03195	ackA	1188	Acetate kinase	C:COG0282
JNUCC-1_03196	moaB	516	Molybdopterin adenylyltransferase	H:COG0521
JNUCC-1_03197		438	Putative universal stress protein	T:COG0589
JNUCC-1_03198		162	hypothetical protein	S:ENOG410Z7MZ
JNUCC-1_03199	pepQ	1098	Xaa-Pro dipeptidase	E:COG0006
JNUCC-1_03200		681	Phage shock protein A like protein	KT:COG1842
JNUCC-1_03201		681	UPF0173 metal-dependent hydrolase	S:COG2220

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_03202		1224	hypothetical protein	L:COG3547
JNUCC-1_03203	comC	489	Type 4 prepilin-like protein leader peptide-processing enzyme	NOU:COG1989
JNUCC-1_03204	comC	318	Type 4 prepilin-like protein leader peptide-processing enzyme	NOU:COG1989
JNUCC-1_03205		228	hypothetical protein	S:ENOG410YSPX
JNUCC-1_03206		1311	uncharacterized protein	K:COG4109
JNUCC-1_03207		294	hypothetical protein	S:ENOG410Y8G4
JNUCC-1_03208	nrnA	948	3′(2′),5′-bisphosphate nucleotidase	S:COG0618
JNUCC-1_03209		504	Sporulation membrane protein YtrI	S:ENOG4111Q9Q
JNUCC-1_03210		333	Sporulation membrane protein YtrH	S:ENOG41121ZA
JNUCC-1_03211	dnaE2	3345	DNA-directed DNA polymerase	L:COG0587
JNUCC-1_03212	ME2|sfcA|maeA	1245	Malate dehydrogenase (oxaloacetate-decarboxylating)	C:COG0281
JNUCC-1_03213	accD	873	Acetyl-CoA carboxylase	I:COG0777
JNUCC-1_03214	accA	957	Acetyl-CoA carboxylase	I:COG0825
JNUCC-1_03215	pfkA|PFK	960	6-phosphofructokinase	G:COG0205
JNUCC-1_03216	PK|pyk	1767	Pyruvate kinase	G:COG0469
JNUCC-1_03217		390	UPF0716 protein YtzA	S:COG3030
JNUCC-1_03218		1128	UPF0118 membrane protein YtvI	S:COG0628
JNUCC-1_03219	CS|gltA	1116	Citrate (Si)-synthase	C:COG0372
JNUCC-1_03220	IDH1|IDH2|icd	1272	Isocitrate dehydrogenase (NADP(+))	C:COG0538
JNUCC-1_03221	mdh	939	Malate dehydrogenase	C:COG0039
JNUCC-1_03222		693	Response regulator ArlR	T:COG0745
JNUCC-1_03223	phoR	1362	Histidine kinase	T:ENOG410XNMH
JNUCC-1_03224	polA	612	DNA-directed DNA polymerase	L:COG0258
JNUCC-1_03225	polA	2055	DNA-directed DNA polymerase	L:COG0258
JNUCC-1_03226	mutM|fpg	828	DNA-formamidopyrimidine glycosylase	L:COG0266

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_03227	coaE	600	Dephospho-CoA kinase	H:COG0237
JNUCC-1_03228	GAPDH|gapA	1023	Glyceraldehyde-3-phosphate dehydrogenase (phosphorylating)	G:COG0057
JNUCC-1_03229		387	hypothetical protein	S:ENOG4111Y7X
JNUCC-1_03230		468	Transcriptional repressor NrdR	K:COG1327
JNUCC-1_03231		960	Replication initiation and membrane attachment protein	L:COG3611
JNUCC-1_03232		390	Replication initiation and membrane attachment protein	L:COG3611
JNUCC-1_03233		933	Primosomal protein DnaI	L:COG1484
JNUCC-1_03234		849	hypothetical protein	S:ENOG4111IPP
JNUCC-1_03235	TARS|thrS	1947	Threonine-tRNA ligase	J:COG0441
JNUCC-1_03236		504	Translation initiation factor IF-3, chloroplastic	J:COG0290
JNUCC-1_03237		198	50S ribosomal protein L35	J:COG0291
JNUCC-1_03238		357	50S ribosomal protein L20, chloroplastic	J:COG0292
JNUCC-1_03239		1689	hypothetical protein	L:COG3666
JNUCC-1_03240		270	uncharacterized protein	S:COG3326
JNUCC-1_03241		585	TVP38/TMEM64 family membrane protein YtxB	S:COG0398
JNUCC-1_03242		390	Sigma-w pathway protein YsdB	S:ENOG41120VU
JNUCC-1_03243		486	hypothetical protein	S:COG4508
JNUCC-1_03244	pepA	1086	Glutamyl aminopeptidase	E:COG1363
JNUCC-1_03245	mltC	594	Transglycosylase	M:COG0741
JNUCC-1_03246		1224	hypothetical protein	L:COG3547
JNUCC-1_03247		216	Small, acid-soluble spore protein	M:ENOG410XW06
JNUCC-1_03248		738	Uncharacterized tRNA/rRNA methyltransferase YsgA	J:COG0566
JNUCC-1_03249		111	hypothetical protein	
JNUCC-1_03250	FARSA|pheS	1035	Phenylalanine-tRNA ligase	J:COG0016
JNUCC-1_03251	FARSB|pheT	2427	Phenylalanine-tRNA ligase	J:COG0073

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_03252		261	Cell division protein ZapA	S:COG3027
JNUCC-1_03253		543	Uncharacterized transmembrane protein YshB	S:COG1286
JNUCC-1_03254		1722	DNA polymerase/3′-5′ exonuclease PolX	L:COG1796
JNUCC-1_03255		2343	Endonuclease MutS2	L:COG1193
JNUCC-1_03256		408	UPF0719 transmembrane protein YshE	S:COG3766
JNUCC-1_03257	ACSL|fadD	1680	Long-chain-fatty-acid--CoA ligase	IQ:COG0318
JNUCC-1_03258		606	Fatty acid metabolism regulator protein	K:ENOG410ZWA0
JNUCC-1_03259	fadN	774	3-hydroxyacyl-CoA dehydrogenase	I:COG1024
JNUCC-1_03260		447	hypothetical protein	L:COG3547
JNUCC-1_03261		897	hypothetical protein	L:COG3547
JNUCC-1_03262		774	Electron transfer flavoprotein subunit beta	C:COG2086
JNUCC-1_03263		543	Electron transfer flavoprotein subunit alpha	C:COG2025
JNUCC-1_03264		429	Electron transfer flavoprotein subunit alpha	C:COG2025
JNUCC-1_03265		315	Thioredoxin	O:COG0526
JNUCC-1_03266		216	UvrABC system protein	L:COG0322
JNUCC-1_03267		1548	UvrABC system protein	L:COG0322
JNUCC-1_03268		441	uncharacterized protein	S:ENOG41121J8
JNUCC-1_03269		378	Succinate dehydrogenase cytochrome b558 subunit	C:COG2009
JNUCC-1_03270	sdhA|frdA	1764	Succinate dehydrogenase (quinone)	C:COG1053
JNUCC-1_03271	sdhB|frdB	768	Succinate dehydrogenase (quinone)	C:COG0479
JNUCC-1_03272	ybgC	444	uncharacterized protein	S:COG0824
JNUCC-1_03273		225	Spore germination protein GerE	K:COG2771
JNUCC-1_03274		1410	K(+)/H(+) antiporter NhaP2	P:COG3263
JNUCC-1_03275		462	Uncharacterized HTH-type transcriptional regulator YsmB	K:COG1846
JNUCC-1_03276	murI	168	Glutamate racemase	M:COG0796

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_03277	murI	654	Glutamate racemase	M:COG0796
JNUCC-1_03278		1077	Spore germination protein GerM	S:COG5401
JNUCC-1_03279	rph	765	tRNA nucleotidyltransferase	J:COG0689
JNUCC-1_03280	rdgB	606	XTP/dITP diphosphatase	F:COG0127
JNUCC-1_03281		519	Putative metallophosphoesterase YsnB	S:COG0622
JNUCC-1_03284		978	TPR repeat-containing protein YsoA	S:ENOG4111TTB
JNUCC-1_03285		1287	Trigger factor	O:COG0544
JNUCC-1_03286		1281	ATP-dependent Clp protease ATP-binding subunit ClpX	O:COG1219
JNUCC-1_03287	lon	2100	Endopeptidase La	O:COG0466
JNUCC-1_03288	lon	219	Endopeptidase La	O:COG0466
JNUCC-1_03289		588	Probable GTP-binding protein EngB	S:COG0218
JNUCC-1_03290		480	Uncharacterized membrane protein YsxD	S:ENOG41121HT
JNUCC-1_03291	hemA	1374	Glutamyl-tRNA reductase	H:COG0373
JNUCC-1_03292		819	Protein HemX	O:COG0755
JNUCC-1_03293	hemC|HMBS	933	Hydroxymethylbilane synthase	H:COG0181
JNUCC-1_03294	hemD|UROS	780	Uroporphyrinogen-III synthase	H:COG1587
JNUCC-1_03295	hemB|ALAD	984	Porphobilinogen synthase	H:COG0113
JNUCC-1_03296	hemL	1293	Glutamate-1-semialdehyde 2,1-aminomutase	H:COG0001
JNUCC-1_03297		1113	Stage VI sporulation protein D	S:ENOG410XWF2
JNUCC-1_03298		1095	uncharacterized protein	S:ENOG410XXN8
JNUCC-1_03299		189	Uncharacterized membrane protein YszA	S:ENOG410Y86W
JNUCC-1_03300	VARS|valS	2076	Valine--tRNA ligase	J:COG0525
JNUCC-1_03301	VARS|valS	603	Valine--tRNA ligase	J:COG0525
JNUCC-1_03302	cofF	417	Coenzyme gamma-F420-2:alpha-L-glutamate ligase	HJ:COG0189
JNUCC-1_03303	cofF	447	Coenzyme gamma-F420-2:alpha-L-glutamate ligase	HJ:COG0189

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_03304	cofF	912	Coenzyme gamma-F420-2:alpha-L-glutamate ligase	HJ:COG0189
JNUCC-1_03305	folC	1290	Dihydrofolate synthase	H:COG0285
JNUCC-1_03306		1719	Adenylate cyclase	T:ENOG410XNMH
JNUCC-1_03307		909	hypothetical protein	S:ENOG410Y3N9
JNUCC-1_03308		690	UPF0758 protein	L:COG2003
JNUCC-1_03309		1191	Integrase	L:COG0582
JNUCC-1_03310		489	Phage-like element PBSX protein XkdA	S:ENOG4112AJI
JNUCC-1_03311		177	hypothetical protein	
JNUCC-1_03312		636	hypothetical protein	S:ENOG410YWXP
JNUCC-1_03313		345	hypothetical protein	K:ENOG410XUC3
JNUCC-1_03314		246	hypothetical protein	S:ENOG410XW1Q
JNUCC-1_03315		717	SPBc2 prophage-derived putative antirepressor protein YoqD	S:COG3646
JNUCC-1_03316		297	hypothetical protein	S:ENOG410Z7YW
JNUCC-1_03317		282	hypothetical protein	K:ENOG410Y3B7
JNUCC-1_03318		240	hypothetical protein	
JNUCC-1_03319		297	hypothetical protein	
JNUCC-1_03320		348	hypothetical protein	
JNUCC-1_03321		174	hypothetical protein	
JNUCC-1_03322		789	Replication protein 15	L:COG3935
JNUCC-1_03323		813	DNA replication protein DnaC	L:COG1484
JNUCC-1_03324		165	hypothetical protein	
JNUCC-1_03325		267	hypothetical protein	
JNUCC-1_03326		114	hypothetical protein	
JNUCC-1_03327		108	hypothetical protein	
JNUCC-1_03328		204	hypothetical protein	

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_03329		279	hypothetical protein	
JNUCC-1_03330		237	hypothetical protein	S:ENOG41124IT
JNUCC-1_03331		951	hypothetical protein	S:ENOG4111V3M
JNUCC-1_03332		258	hypothetical protein	
JNUCC-1_03333		480	hypothetical protein	S:ENOG4111TD0
JNUCC-1_03334		219	hypothetical protein	
JNUCC-1_03335		162	hypothetical protein	
JNUCC-1_03336		315	hypothetical protein	
JNUCC-1_03337		453	Uncharacterized phage-related protein	K:ENOG410XV79
JNUCC-1_03338		339	Probable integrase/recombinase YoeC	L:COG0582
JNUCC-1_03339		222	Probable integrase/recombinase YoeC	L:COG0582
JNUCC-1_03340		750	hypothetical protein	
JNUCC-1_03341		891	hypothetical protein	
JNUCC-1_03342		318	hypothetical protein	
JNUCC-1_03343	mcrA	348	hypothetical protein	V:COG1403
JNUCC-1_03344		531	hypothetical protein	S:COG3747
JNUCC-1_03345		1551	hypothetical protein	S:COG4626
JNUCC-1_03346		156	hypothetical protein	
JNUCC-1_03347		1197	Probable portal protein	S:COG4695
JNUCC-1_03348	clpP|CLPP	708	Endopeptidase Clp	O:COG0740
JNUCC-1_03349		1224	hypothetical protein	S:COG4653
JNUCC-1_03350		159	hypothetical protein	
JNUCC-1_03351		243	hypothetical protein	S:ENOG4111USG
JNUCC-1_03352		261	hypothetical protein	S:ENOG410XYQK
JNUCC-1_03353		351	hypothetical protein	

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_03354		387	hypothetical protein	
JNUCC-1_03355		387	hypothetical protein	
JNUCC-1_03356		561	hypothetical protein	S:ENOG410YG7B
JNUCC-1_03357		363	hypothetical protein	S:ENOG410ZCHZ
JNUCC-1_03358		3318	Protein ORF73	S:COG5283
JNUCC-1_03359		174	hypothetical protein	
JNUCC-1_03360		189	hypothetical protein	
JNUCC-1_03361		1443	hypothetical protein	S:ENOG410Z54F
JNUCC-1_03362		4020	hypothetical protein	S:ENOG410ZM95
JNUCC-1_03363		183	hypothetical protein	
JNUCC-1_03364		216	hypothetical protein	
JNUCC-1_03365		240	hypothetical protein	
JNUCC-1_03366		189	hypothetical protein	
JNUCC-1_03367		348	hypothetical protein	
JNUCC-1_03368		273	hypothetical protein	S:ENOG410YT2B
JNUCC-1_03369	amiABC	1023	N-acetylmuramoyl-L-alanine amidase	M:COG0860
JNUCC-1_03370		201	hypothetical protein	
JNUCC-1_03371		657	hypothetical protein	S:ENOG410YNYF
JNUCC-1_03372		456	hypothetical protein	S:ENOG410Y6AG
JNUCC-1_03373		336	hypothetical protein	
JNUCC-1_03374		285	hypothetical protein	
JNUCC-1_03375		1041	Rod shape-determining protein MreB	D:COG1077
JNUCC-1_03376		876	Cell shape-determining protein MreC	M:COG1792
JNUCC-1_03377		516	Rod shape-determining protein MreD	M:COG2891
JNUCC-1_03378		687	Probable septum site-determining protein MinC	D:COG0850

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_03379		801	Septum site-determining protein MinD	D:COG2894
JNUCC-1_03380		447	hypothetical protein	M:COG0739
JNUCC-1_03381		333	Stage IV sporulation protein FA	M:COG0739
JNUCC-1_03382	spoIVFB	864	Stage IV sporulation protein FB	S:ENOG41128PP
JNUCC-1_03383		309	50S ribosomal protein L21	J:COG0261
JNUCC-1_03384		330	uncharacterized protein	J:COG2868
JNUCC-1_03385		291	50S ribosomal protein L27	J:COG0211
JNUCC-1_03386	ltrA	1317	RNA-directed DNA polymerase	L:COG3344
JNUCC-1_03387	spo0B	531	Sporulation initiation phosphotransferase	S:ENOG410ZI52
JNUCC-1_03388	obgE|cgtA	1287	GTPase Obg	S:COG0536
JNUCC-1_03389		858	Spore coat assembly protein ExsA	S:ENOG41121ST
JNUCC-1_03390	nadE	741	NAD(+) synthase	H:COG0171
JNUCC-1_03391		537	hypothetical protein	
JNUCC-1_03392	glgC	732	Glucose-1-phosphate adenylyltransferase	K:COG0217
JNUCC-1_03393	ruvA	609	DNA helicase	L:COG0632
JNUCC-1_03394	ruvB	996	DNA helicase	L:COG2255
JNUCC-1_03395	ruvB	198	DNA helicase	S:ENOG410XV4S
JNUCC-1_03396	queA	1029	S-adenosylmethionine:tRNA ribosyltransferase-isomerase	J:COG0809
JNUCC-1_03397	tgt|QTRT1	1140	tRNA-guanine(34) transglycosylase	J:COG0343
JNUCC-1_03398		276	UPF0092 membrane protein	U:COG1862
JNUCC-1_03399		381	Uncharacterized membrane protein YrzE	S:ENOG4111WGR
JNUCC-1_03400		1278	P protein	P:COG1055
JNUCC-1_03401		1551	Stage V sporulation protein	M:COG2244
JNUCC-1_03402		294	Post-transcriptional regulator ComN	S:ENOG410XWPV
JNUCC-1_03403		2256	Protein translocase subunit SecDF	U:COG0341

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_03404		330	uncharacterized protein	S:COG5416
JNUCC-1_03405	recJ	2331	Single-stranded-DNA-specific exonuclease RecJ	L:COG0608
JNUCC-1_03406	APRT|apt	513	Adenine phosphoribosyltransferase	F:COG0503
JNUCC-1_03407	relA	2214	GTP diphosphokinase	KT:COG0317
JNUCC-1_03408	dtd|DTD	447	D-aminoacyl-tRNA deacylase	J:COG1490
JNUCC-1_03409	amiABC	1086	N-acetylmuramoyl-L-alanine amidase	S:COG3179
JNUCC-1_03410		174	hypothetical protein	S:ENOG410ZGC5
JNUCC-1_03411	HARS|hisS	228	Histidine-tRNA ligase	J:COG0124
JNUCC-1_03412	HARS|hisS	1065	Histidine-tRNA ligase	J:COG0124
JNUCC-1_03413	aspS	1773	Aspartate-tRNA ligase	J:COG0173
JNUCC-1_03414		708	Prespore-specific transcriptional regulator RsfA	K:ENOG4111JQ9
JNUCC-1_03415		1287	ATPase WRNIP1	L:COG2256
JNUCC-1_03416	iscS|NFS1	1161	Cysteine desulfurase	E:COG1104
JNUCC-1_03417	mnmA|trmU	1116	tRNA-uridine 2-sulfurtransferase	J:COG0482
JNUCC-1_03418		672	Probable UDP-N-acetylglucosamine-peptide N-acetylglucosaminyltransferase SEC	S:ENOG4111U03
JNUCC-1_03419	recD	2328	Exodeoxyribonuclease V	L:COG0507
JNUCC-1_03420		186	uncharacterized protein	S:ENOG410XUID
JNUCC-1_03421		1071	UPF0118 membrane protein YrrI	S:COG0628
JNUCC-1_03422	AARS|alaS	2643	Alanine--tRNA ligase	J:COG0013
JNUCC-1_03423	ruvX	270	UPF0297 protein	S:COG4472
JNUCC-1_03424	ruvX	414	Putative pre-16S rRNA nuclease	L:COG0816
JNUCC-1_03425		288	UPF0473 protein	S:COG3906
JNUCC-1_03426		1128	UPF0755 protein YrrL	S:COG1559
JNUCC-1_03427		639	Caffeoyl-CoA O-methyltransferase	S:COG4122
JNUCC-1_03428	udk|UCK	627	Uridine kinase	F:COG0572

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_03429		477	Transcription elongation factor GreA	K:COG0782
JNUCC-1_03430		684	uncharacterized protein	S:ENOG4111WW7
JNUCC-1_03431	mtnN|mtn|pfs	693	Adenosylhomocysteine nucleosidase	F:COG0775
JNUCC-1_03432		711	RNA polymerase sigma-K factor	K:COG1191
JNUCC-1_03433		372	Na(+)/H(+) antiporter subunit	P:ENOG411224K
JNUCC-1_03434		312	Na(+)/H(+) antiporter subunit F1	P:COG2212
JNUCC-1_03435		477	Na(+)/H(+) antiporter subunit	P:COG1863
JNUCC-1_03436		1479	Putative antiporter subunit mnhD2	CP:COG0651
JNUCC-1_03437		339	Na(+)/H(+) antiporter subunit	P:COG1006
JNUCC-1_03438		966	Na(+)/H(+) antiporter subunit A1	C:COG1009
JNUCC-1_03439		1389	Na(+)/H(+) antiporter subunit A1	C:COG1009
JNUCC-1_03440		147	Sporulation inhibitor sda	S:ENOG410ZA19
JNUCC-1_03441		516	uncharacterized protein	S:COG2179
JNUCC-1_03442		1101	uncharacterized protein	S:COG1161
JNUCC-1_03443	aroE	849	Shikimate dehydrogenase	E:COG0169
JNUCC-1_03444		291	Probable RNA-binding protein YqeI	J:COG1534
JNUCC-1_03445	nadD	513	Nicotinate-nucleotide adenylyltransferase	H:COG1057
JNUCC-1_03446	nadD	573	Nicotinate-nucleotide adenylyltransferase	H:COG1713
JNUCC-1_03447		372	Ribosomal silencing factor RsfS	S:COG0799
JNUCC-1_03448	ubiG	756	2-polyprenyl-6-hydroxyphenol methylase	Q:COG0500
JNUCC-1_03449		333	hypothetical protein	L:COG1555
JNUCC-1_03450		264	ComE operon protein	L:COG1555
JNUCC-1_03451	comEB	561	dCMP deaminase	F:COG2131
JNUCC-1_03452		2283	ComE operon protein	S:COG0658
JNUCC-1_03453		135	hypothetical protein	

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_03454	holA	1038	DNA-directed DNA polymerase	L:COG1466
JNUCC-1_03455		261	30S ribosomal protein S20	J:COG0268
JNUCC-1_03456	gpr	789	GPR endopeptidase	O:ENOG410XNXE
JNUCC-1_03457	gpr	390	GPR endopeptidase	O:ENOG410XNXE
JNUCC-1_03458		1173	Stage II sporulation protein	S:ENOG410ZNVS
JNUCC-1_03459		249	hypothetical protein	
JNUCC-1_03460		1809	Elongation factor	M:COG0481
JNUCC-1_03461	chuW	1158	Anaerobilin synthase	H:COG0635
JNUCC-1_03462		1032	Heat-inducible transcription repressor HrcA	K:COG1420
JNUCC-1_03463		567	Protein GrpE	O:COG0576
JNUCC-1_03464		1509	Chaperone protein DnaK	O:COG0443
JNUCC-1_03465		1122	Chaperone protein DnaJ	O:COG0484
JNUCC-1_03466	prmA	939	Ribosomal protein L11 methyltransferase	J:COG2264
JNUCC-1_03467	rsmE	765	16S rRNA (uracil(1498)-N(3))-methyltransferase	S:COG1385
JNUCC-1_03468	mtaB	1356	tRNA (N(6)-L-threonylcarbamoyladenosine(37)-C(2))-methylthiotransferase	J:COG0621
JNUCC-1_03469	deoC|DERA	672	Deoxyribose-phosphate aldolase	F:COG0274
JNUCC-1_03470		174	30S ribosomal protein S21	J:COG0828
JNUCC-1_03471		450	uncharacterized protein	S:COG1610
JNUCC-1_03472		243	hypothetical protein	
JNUCC-1_03473		1296	uncharacterized protein	O:COG1030
JNUCC-1_03474		615	UPF0365 protein	S:COG4864
JNUCC-1_03475		324	UPF0365 protein	S:COG4864
JNUCC-1_03476		504	hypothetical protein	S:ENOG410Z3C8
JNUCC-1_03477		282	uncharacterized protein	S:ENOG410XV43
JNUCC-1_03478		1212	Putative stage IV sporulation protein	S:ENOG410XR5M

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_03479		963	PhoH-like protein	T:COG1702
JNUCC-1_03480	pgpH	2133	uncharacterized protein	S:COG1480
JNUCC-1_03481		468	Endoribonuclease YbeY	S:COG0319
JNUCC-1_03482	dgkA	375	Undecaprenol kinase	M:COG0818
JNUCC-1_03483		903	GTPase Era	S:COG1159
JNUCC-1_03484		141	hypothetical protein	
JNUCC-1_03485		402	DNA repair protein RecO	L:COG1381
JNUCC-1_03486		348	DNA repair protein RecO	L:COG1381
JNUCC-1_03487	glyQ	879	Glycine-tRNA ligase	J:COG0752
JNUCC-1_03488	glyS	2085	Glycine-tRNA ligase	J:COG0751
JNUCC-1_03489		630	Transcriptional repressor CcpN	S:COG0517
JNUCC-1_03490	ppsR	804	([Pyruvate, water dikinase] phosphate) phosphotransferase	S:COG1806
JNUCC-1_03491	dnaG	1803	DNA primase	L:COG0358
JNUCC-1_03492		1122	RNA polymerase sigma factor SigA	K:COG0568
JNUCC-1_03493		375	hypothetical protein	C:COG2010
JNUCC-1_03494	trmK	702	tRNA (adenine(22)-N(1))-methyltransferase	S:COG2384
JNUCC-1_03495		291	GTP cyclohydrolase 1 type 2 like protein	S:COG3323
JNUCC-1_03496		852	GTP cyclohydrolase 1 type 2 like protein	S:COG3323
JNUCC-1_03497	DDX56|DBP9	276	RNA helicase	L:ENOG410XR15
JNUCC-1_03498	deaD|cshA	1092	RNA helicase	L:COG0513
JNUCC-1_03499	nfo	891	Deoxyribonuclease IV	L:COG0648
JNUCC-1_03500		282	hypothetical protein	S:ENOG410ZUQ0
JNUCC-1_03501		417	uncharacterized protein	S:ENOG410Y68H
JNUCC-1_03502		324	hypothetical protein	
JNUCC-1_03503		654	hypothetical protein	O:COG1030

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_03504		1629	uncharacterized protein	P:COG1283
JNUCC-1_03511	SOD2	612	Superoxide dismutase	P:COG0605
JNUCC-1_03512		1272	uncharacterized protein	G:ENOG410XQRZ
JNUCC-1_03513		2118	Penicillin-binding protein 2B	M:COG0768
JNUCC-1_03514		558	uncharacterized protein	S:ENOG410XVZA
JNUCC-1_03515		210	uncharacterized protein	S:ENOG410Y4H2
JNUCC-1_03516		150	50S ribosomal protein L33	J:COG0267
JNUCC-1_03517	MTHFS	576	5-formyltetrahydrofolate cyclo-ligase	H:COG0212
JNUCC-1_03518	thiF	1014	Sulfur carrier protein ThiS adenylyltransferase	H:COG0476
JNUCC-1_03519		177	hypothetical protein	
JNUCC-1_03520	gluP	1572	Rhomboid protease	S:COG0705
JNUCC-1_03521		1458	Stage V sporulation protein AF	S:ENOG410XNMP
JNUCC-1_03522		231	uncharacterized protein	S:COG4483
JNUCC-1_03523	glk	450	Glucokinase	G:COG1940
JNUCC-1_03524	glk	540	Glucokinase	G:COG1940
JNUCC-1_03525		189	hypothetical protein	
JNUCC-1_03526	gloB|gloC|HAGH	624	Hydroxyacylglutathione hydrolase	S:COG0491
JNUCC-1_03527		243	uncharacterized protein	S:ENOG41121FE
JNUCC-1_03528		699	hypothetical protein	K:COG2345
JNUCC-1_03529		396	hypothetical protein	
JNUCC-1_03530		444	hypothetical protein	
JNUCC-1_03531		351	hypothetical protein	S:ENOG410ZDGR
JNUCC-1_03532		432	hypothetical protein	S:ENOG410ZYJJ
JNUCC-1_03533		309	Type II secretion system protein	U:ENOG410ZYAQ
JNUCC-1_03534		1050	ComG operon protein	U:COG1459

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_03535		1011	ComG operon protein 1 like protein	U:COG2804
JNUCC-1_03536	aroK|aroL	501	Shikimate kinase	E:COG0703
JNUCC-1_03537		174	uncharacterized protein	S:ENOG410XVAB
JNUCC-1_03538		807	uncharacterized protein	S:ENOG4111PCH
JNUCC-1_03539	hepA	1665	Uncharacterized ATP-dependent helicase YqhH	L:COG0553
JNUCC-1_03540	gcvT|AMT	1110	Aminomethyltransferase	E:COG0404
JNUCC-1_03541	gcvPA	1353	Glycine dehydrogenase (aminomethyl-transferring)	E:COG0403
JNUCC-1_03542	gcvPB	1464	Glycine dehydrogenase (aminomethyl-transferring)	E:COG1003
JNUCC-1_03543	gloB|gloC|HAGH	366	Hydroxyacylglutathione hydrolase	P:COG0607
JNUCC-1_03544	nrdA|nrdE	2556	Ribonucleoside-diphosphate reductase	F:COG0209
JNUCC-1_03545		411	Transcriptional regulator MntR	K:COG1321
JNUCC-1_03546		885	uncharacterized protein	S:COG1752
JNUCC-1_03547		378	hypothetical protein	S:ENOG410ZN20
JNUCC-1_03548		531	uncharacterized protein	S:ENOG4111YFZ
JNUCC-1_03549	aroQ|qutE	465	3-dehydroquinate dehydratase	E:COG0757
JNUCC-1_03550	pepP	1068	Xaa-Pro aminopeptidase	E:COG0006
JNUCC-1_03551		558	Elongation factor P	J:COG0231
JNUCC-1_03552		1029	Stage III sporulation protein AA	S:COG3854
JNUCC-1_03553		342	Stage III sporulation protein	S:ENOG4111UDG
JNUCC-1_03554		207	Stage III sporulation protein AC	S:ENOG410ZXIN
JNUCC-1_03555		393	Stage III sporulation protein AD	S:ENOG4111UC5
JNUCC-1_03556		1176	Stage III sporulation protein AE	S:ENOG410XRMF
JNUCC-1_03557		621	Stage III sporulation protein AF	S:ENOG41126UT
JNUCC-1_03558		576	Stage III sporulation protein AG	S:ENOG41123Y1
JNUCC-1_03559		576	Stage III sporulation protein AH	S:ENOG4111V9K

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_03560		510	Biotin carboxyl carrier protein of acetyl-CoA carboxylase	I:COG0511
JNUCC-1_03561	accC	1359	Acetyl-CoA carboxylase	I:COG0439
JNUCC-1_03562		402	uncharacterized protein	S:COG1302
JNUCC-1_03563		381	N utilization substance protein B like protein	K:COG0781
JNUCC-1_03564	folD	849	Methylenetetrahydrofolate dehydrogenase (NADP(+))	H:COG0190
JNUCC-1_03565	xseA	1161	Exodeoxyribonuclease VII	L:COG1570
JNUCC-1_03566	xseB	234	Exodeoxyribonuclease VII	L:COG1722
JNUCC-1_03567	GGPS	885	Dimethylallyltranstransferase	H:COG0142
JNUCC-1_03568		759	hypothetical protein	S:ENOG4111TST
JNUCC-1_03569	tlyA	216	23S rRNA (cytidine(1920)-2′-O)-methyltransferase	J:COG1189
JNUCC-1_03570	tlyA	522	23S rRNA (cytidine(1920)-2′-O)-methyltransferase	J:COG1189
JNUCC-1_03571		1716	DNA repair protein RecN	L:COG0497
JNUCC-1_03572	spoIVB	291	SpoIVB peptidase	
JNUCC-1_03573	spoIVB	999	SpoIVB peptidase	M:COG0750
JNUCC-1_03574		777	Stage 0 sporulation protein	T:COG0784
JNUCC-1_03575		234	uncharacterized protein	S:ENOG4112AVA
JNUCC-1_03576		1095	Leucine dehydrogenase	E:COG0334
JNUCC-1_03577	DLD|lpd|pdhD	162	Dihydrolipoyl dehydrogenase	C:COG1249
JNUCC-1_03578	DLD|lpd|pdhD	1248	Dihydrolipoyl dehydrogenase	C:COG1249
JNUCC-1_03579	BCKDHA|bkdA1	702	3-methyl-2-oxobutanoate dehydrogenase (2-methylpropanoyl-transferring)	C:COG1071
JNUCC-1_03580	BCKDHA|bkdA1	276	3-methyl-2-oxobutanoate dehydrogenase (2-methylpropanoyl-transferring)	C:COG1071
JNUCC-1_03581	BCKDHB|bkdA2	984	3-methyl-2-oxobutanoate dehydrogenase (2-methylpropanoyl-transferring)	C:COG0022
JNUCC-1_03582	DBT|bkdB	1284	Dihydrolipoyllysine-residue (2-methylpropanoyl) transferase	C:COG0508
JNUCC-1_03583		432	UPF0403 protein	S:ENOG4111J34
JNUCC-1_03584		987	uncharacterized protein	S:COG4129

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_03585		135	hypothetical protein	
JNUCC-1_03586	mcmA1	1656	Methylmalonyl-CoA mutase	I:COG1884
JNUCC-1_03587	mcmA2	822	Methylmalonyl-CoA mutase	I:COG2185
JNUCC-1_03588	PCCB|pccB	1548	Propionyl-CoA carboxylase	I:COG4799
JNUCC-1_03589	pepT	1125	Tripeptide aminopeptidase	E:COG2195
JNUCC-1_03590	dinB	1239	DNA-directed DNA polymerase	L:COG0389
JNUCC-1_03591	ALDH	1368	Aldehyde dehydrogenase (NAD(+))	C:COG1012
JNUCC-1_03592	rnz	609	Ribonuclease Z	S:COG1234
JNUCC-1_03593	rnz	312	Ribonuclease Z	S:COG1234
JNUCC-1_03594	glpQ|ugpQ	756	Glycerophosphodiester phosphodiesterase	C:COG0584
JNUCC-1_03595		96	hypothetical protein	
JNUCC-1_03596	gloB|gloC|HAGH	870	Hydroxyacylglutathione hydrolase	S:COG0491
JNUCC-1_03597		882	Putative UV-damage repair protein UvrX	L:COG0389
JNUCC-1_03598		921	Pyridoxine 4-dehydrogenase	C:COG0667
JNUCC-1_03599	nudF	564	ADP-ribose diphosphatase	L:COG0494
JNUCC-1_03600		1179	uncharacterized protein	S:COG1379
JNUCC-1_03601		645	Stage II sporulation protein	S:COG1300
JNUCC-1_03602		456	Ferric uptake regulation protein	K:COG0735
JNUCC-1_03603		207	Uncharacterized membrane protein YqzK	S:ENOG410Y127
JNUCC-1_03604		894	Tyrosine recombinase XerD	L:COG4974
JNUCC-1_03605	deoB	1179	Phosphopentomutase	G:COG1015
JNUCC-1_03606	punA|PNP	819	Purine-nucleoside phosphorylase	F:COG0005
JNUCC-1_03607	pdp	1308	Pyrimidine-nucleoside phosphorylase	F:COG0213
JNUCC-1_03608	dacC|dacA|dacD	1191	Serine-type D-Ala-D-Ala carboxypeptidase	M:COG1686
JNUCC-1_03609		354	Anti-sigma F factor antagonist	T:COG1366

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_03610	spoIIAB	441	Non-specific serine/threonine protein kinase	T:COG2172
JNUCC-1_03611		750	RNA polymerase sigma-F factor	K:COG1191
JNUCC-1_03612		1224	hypothetical protein	L:COG3547
JNUCC-1_03613		603	Stage V sporulation protein AA	S:ENOG4111IFW
JNUCC-1_03614		429	Stage V sporulation protein	S:ENOG411245Y
JNUCC-1_03615		1488	Stage V sporulation protein AF	S:ENOG410XNMP
JNUCC-1_03616	lysA	1308	Diaminopimelate decarboxylase	E:COG0019
JNUCC-1_03617	PPIB|ppiB	435	Peptidylprolyl isomerase	O:COG0652
JNUCC-1_03618	rseP	459	hypothetical protein	S:ENOG410Z5HV
JNUCC-1_03619		366	Uncharacterized N-acetyltransferase in lysA 3′region	S:ENOG41121UC
JNUCC-1_03620		732	Segregation and condensation protein	S:COG1354
JNUCC-1_03621		582	Segregation and condensation protein	K:COG1386
JNUCC-1_03622	dacC|dacA|dacD	507	Serine-type D-Ala-D-Ala carboxypeptidase	M:COG1686
JNUCC-1_03623	dacC|dacA|dacD	543	Serine-type D-Ala-D-Ala carboxypeptidase	M:COG1686
JNUCC-1_03624		585	Spore maturation protein	S:COG2715
JNUCC-1_03625		273	Spore maturation protein	S:COG0700
JNUCC-1_03626		219	Spore maturation protein	S:COG0700
JNUCC-1_03627	rsuA	744	16S rRNA pseudouridine(516) synthase	J:COG1187
JNUCC-1_03628		573	Thiol-disulfide oxidoreductase ResA	O:COG0526
JNUCC-1_03629		1641	Cytochrome c bioproteinis protein ResB	O:COG1333
JNUCC-1_03630		1185	Cytochrome c bioproteinis protein ResC	O:COG0755
JNUCC-1_03631		717	Probable transcriptional regulator ycf27	T:COG0745
JNUCC-1_03632	resE	1758	Histidine kinase	T:ENOG410XNMH
JNUCC-1_03633		240	Ferredoxin	C:COG1141
JNUCC-1_03634		918	hypothetical protein	S:COG4955

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_03635	RECQL	1527	DNA helicase	L:COG0514
JNUCC-1_03636		588	uncharacterized protein	S:COG1266
JNUCC-1_03637		378	hypothetical protein	
JNUCC-1_03638	gudB|rocG	1275	Glutamate dehydrogenase	E:COG0334
JNUCC-1_03639	trxB|TRR	945	Thioredoxin-disulfide reductase	O:COG0492
JNUCC-1_03640		459	Protease PrsW	S:COG2339
JNUCC-1_03641		225	hypothetical protein	
JNUCC-1_03642	cwlJ|sleB	225	N-acetylmuramoyl-L-alanine amidase	M:COG3409
JNUCC-1_03643	cwlJ|sleB	627	N-acetylmuramoyl-L-alanine amidase	M:COG3409
JNUCC-1_03644		1344	Sporulation protein YpeB	S:ENOG410XR6R
JNUCC-1_03645		657	uncharacterized protein	M:COG5581
JNUCC-1_03646	cmk	681	(d)CMP kinase	F:COG0283
JNUCC-1_03647	plsC	591	1-acylglycerol-3-phosphate O-acyltransferase	I:COG0204
JNUCC-1_03648		1125	30S ribosomal protein S1 like protein	J:COG1185
JNUCC-1_03649		474	hypothetical protein	S:ENOG41124GU
JNUCC-1_03650		900	uncharacterized protein	S:ENOG410XTDQ
JNUCC-1_03651		108	hypothetical protein	
JNUCC-1_03652		1311	GTPase Der	S:COG1160
JNUCC-1_03653	gpsA	1032	Glycerol-3-phosphate dehydrogenase (NAD(P)(+))	C:COG0240
JNUCC-1_03654		261	Sporulation-specific transcription factor SpoVIF	S:ENOG4112CKD
JNUCC-1_03655		606	uncharacterized protein	S:ENOG4111JTI
JNUCC-1_03656		1479	Stage IV sporulation protein	S:ENOG410XQ51
JNUCC-1_03657		273	DNA-binding protein HU-1	L:COG0776
JNUCC-1_03658		222	Transcription attenuation protein MtrB	K:ENOG411234W
JNUCC-1_03659	hepST	789	Heptaprenyl diphosphate synthase	I:ENOG41124T5

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_03660	ubiE	708	Demethylmenaquinone methyltransferase	H:COG2226
JNUCC-1_03661	hepST	972	Heptaprenyl diphosphate synthase	H:COG0142
JNUCC-1_03662	ndk|NME	447	Nucleoside-diphosphate kinase	F:COG0105
JNUCC-1_03663	cheR	777	Protein-glutamate O-methyltransferase	T:ENOG410XNMH
JNUCC-1_03664	aroB	1065	3-dehydroquinate synthase	E:COG0337
JNUCC-1_03665		1266	TPR repeat-containing protein YpiA	S:COG0457
JNUCC-1_03666		570	UPF0302 protein	S:COG5582
JNUCC-1_03667		459	hypothetical protein	S:ENOG4111X5P
JNUCC-1_03668	MQCRA|qcrA|bfcA|petC	513	Menaquinol-cytochrome c reductase iron-sulfur subunit	C:COG0723
JNUCC-1_03669		675	Menaquinol-cytochrome c reductase cytochrome b subunit	C:COG1290
JNUCC-1_03670		780	Menaquinol-cytochrome c reductase cytochrome b/c subunit	C:COG1290
JNUCC-1_03671		582	uncharacterized protein	S:COG4347
JNUCC-1_03672		255	hypothetical protein	
JNUCC-1_03673		684	Putative membrane protease YugP	S:COG2738
JNUCC-1_03674		789	UPF0750 membrane protein YpjC	S:COG1284
JNUCC-1_03675	aroA	330	3-phosphoshikimate 1-carboxyvinyltransferase	S:COG1694
JNUCC-1_03676	dapB	717	4-hydroxy-tetrahydrodipicolinate reductase	E:COG0289
JNUCC-1_03677	mgsA	360	Methylglyoxal synthase	G:COG1803
JNUCC-1_03678	bshA	1131	N-acetyl-alpha-D-glucosaminyl L-malate synthase	M:COG0438
JNUCC-1_03679	cca	1197	CCA-adding enzyme	J:COG0617
JNUCC-1_03680	birA	990	Biotin--[biotin carboxyl-carrier protein] ligase	H:COG0340
JNUCC-1_03681	dinG	2799	DNA helicase	L:COG0847
JNUCC-1_03682		522	hypothetical protein	S:ENOG410YW5D
JNUCC-1_03683	aspB	1185	Aspartate transaminase	E:COG0436
JNUCC-1_03684	NARS|asnS	1293	Asparagine--tRNA ligase	J:COG0017

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_03685		681	DNA replication protein DnaD	L:COG3935
JNUCC-1_03686	mrcA	3402	Peptidoglycan glycosyltransferase	M:COG0744
JNUCC-1_03687		561	Holliday junction resolvase RecU	S:COG3331
JNUCC-1_03688		951	uncharacterized protein	S:ENOG4111GSD
JNUCC-1_03689		114	hypothetical protein	
JNUCC-1_03690		222	hypothetical protein	
JNUCC-1_03691		393	hypothetical protein	S:ENOG410YN3F
JNUCC-1_03692	cdd|CDA	405	Cytidine deaminase	F:COG0295
JNUCC-1_03693		309	Cell cycle protein GpsB	D:COG3599
JNUCC-1_03694	ypsC	984	Putative RNA methyltransferase YpsC	L:COG0116
JNUCC-1_03695	ypsC	150	Putative RNA methyltransferase YpsC	L:COG0116
JNUCC-1_03696		588	hypothetical protein	S:COG1999
JNUCC-1_03697	coxA|ctaD	225	Cytochrome-c oxidase	C:COG0843
JNUCC-1_03698	coxA|ctaD	1428	Cytochrome-c oxidase	C:COG0843
JNUCC-1_03699	coxB|ctaC	483	Cytochrome-c oxidase	C:COG1622
JNUCC-1_03700		147	hypothetical protein	
JNUCC-1_03701		1086	1,3,6,8-tetrahydroxynaphthalene synthase	Q:COG3424
JNUCC-1_03702		510	uncharacterized protein	S:COG1755
JNUCC-1_03703		201	Cold shock protein	K:COG1278
JNUCC-1_03704	fhs	1719	Formate-tetrahydrofolate ligase	F:COG2759
JNUCC-1_03705		597	uncharacterized protein	S:COG1418
JNUCC-1_03706		1068	hypothetical protein	M:COG0791
JNUCC-1_03707	thyA|TYMS	954	Thymidylate synthase	F:COG0207
JNUCC-1_03708	DHFR|folA	495	Dihydrofolate reductase	H:COG0262
JNUCC-1_03709	mobA	585	Molybdenum cofactor guanylyltransferase	H:COG0746

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_03710		177	Sec-independent protein translocase protein TatA	U:ENOG410XUF0
JNUCC-1_03711		747	Sec-independent protein translocase protein TatCd	U:COG0805
JNUCC-1_03712		222	UPF0346 protein	S:COG4479
JNUCC-1_03713		330	SPBc2 prophage-derived uncharacterized protein YolD	S:ENOG410XYPA
JNUCC-1_03714		450	uncharacterized protein	S:ENOG410XYUH
JNUCC-1_03715	msrA	957	Peptide-methionine (S)-S-oxide reductase	O:COG0225
JNUCC-1_03716		210	uncharacterized protein	S:ENOG41125J7
JNUCC-1_03717		240	Ferredoxin 7Fe	C:COG1146
JNUCC-1_03718	acyP	273	Acylphosphatase	C:COG1254
JNUCC-1_03719	dmpA|dap	966	D-stereospecific aminopeptidase	EQ:COG3191
JNUCC-1_03720	puuB|ordL	1542	Putative Rieske 2Fe-2S iron-sulfur protein YhfW	C:COG0723
JNUCC-1_03721	puuB|ordL	1509	Putative Rieske 2Fe-2S iron-sulfur protein YhfW	C:COG0723
JNUCC-1_03722		480	hypothetical protein	S:ENOG4111VZF
JNUCC-1_03723	polA	867	DNA-directed DNA polymerase	L:COG0258
JNUCC-1_03724		165	hypothetical protein	
JNUCC-1_03725		3510	uncharacterized protein	S:COG0699
JNUCC-1_03726	pip	423	Prolyl aminopeptidase	S:COG0596
JNUCC-1_03727	pip	639	Prolyl aminopeptidase	S:COG0596
JNUCC-1_03728		249	hypothetical protein	
JNUCC-1_03729	PCCB|pccB	1530	Propionyl-CoA carboxylase	I:COG4799
JNUCC-1_03730	crt	831	Enoyl-CoA hydratase	I:ENOG410XTHX
JNUCC-1_03731		210	Oxaloacetate decarboxylase alpha chain	I:COG0511
JNUCC-1_03732	accC	1347	Acetyl-CoA carboxylase	I:COG0439
JNUCC-1_03733	ACADS|bcd	1143	Short-chain acyl-CoA dehydrogenase	I:COG1960
JNUCC-1_03734	parC	2448	DNA gyrase subunit	L:COG0188

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_03735	gyrB	1953	DNA topoisomerase (ATP-hydrolyzing)	L:COG0187
JNUCC-1_03736		420	uncharacterized protein	S:COG1832
JNUCC-1_03737	plsY	582	Glycerol-3-phosphate 1-O-acyltransferase	S:COG0344
JNUCC-1_03738		249	Putative membrane protein insertion efficiency factor	S:COG0759
JNUCC-1_03739	nadE	255	NAD(+) synthase	S:ENOG4111VDS
JNUCC-1_03740	ybgC	429	Putative acyl-CoA thioesterase YneP	S:COG0824
JNUCC-1_03741		231	Small, acid-soluble spore protein Tlp	M:ENOG411284T
JNUCC-1_03742		144	hypothetical protein	
JNUCC-1_03743	ACO|acnA	2706	Aconitate hydratase	C:COG1048
JNUCC-1_03744	kinA	1083	Histidine kinase	T:ENOG410XNMH
JNUCC-1_03745		207	uncharacterized protein	S:ENOG410YK2T
JNUCC-1_03746		375	Protein CcdC	O:COG4846
JNUCC-1_03747	evgS|bvgS	363	Histidine kinase	T:COG2197
JNUCC-1_03748		297	Na(+)/H(+) antiporter subunit B1	P:COG2111
JNUCC-1_03749		132	Putative antiporter subunit mnhB2	P:COG2111
JNUCC-1_03750		717	Cytochrome c-type bioproteinis protein CcdA	O:COG0785
JNUCC-1_03751		222	UPF0154 protein	S:COG3763
JNUCC-1_03752		453	hypothetical protein	S:ENOG410YYXD
JNUCC-1_03753	tktA|tktB	2007	Transketolase	G:COG0021
JNUCC-1_03754		234	UPF0291 protein	S:COG4224
JNUCC-1_03755		639	Resolvase like protein YneB	L:COG1961
JNUCC-1_03756	lexA	624	Repressor LexA	K:COG1974
JNUCC-1_03757	glnA|GLUL	1338	Glutamine synthetase	E:COG0174
JNUCC-1_03758	CTH	1275	Cystathionine gamma-lyase	P:COG4100
JNUCC-1_03759		825	GTPase HflX	S:COG2262

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_03760		420	GTPase HflX	S:COG2262
JNUCC-1_03761		939	Stage V sporulation protein	O:COG0464
JNUCC-1_03762		231	RNA-binding protein Hfq	T:COG1923
JNUCC-1_03763	miaA|TRIT1	936	tRNA dimethylallyltransferase	J:COG0324
JNUCC-1_03764		450	General stress protein 20U	P:COG0783
JNUCC-1_03765		1422	DNA mismatch repair protein HexB	L:COG0323
JNUCC-1_03766		468	DNA mismatch repair protein MutL	L:COG0323
JNUCC-1_03767		2574	DNA mismatch repair protein MutS	L:COG0249
JNUCC-1_03768		564	Spore coat protein	M:ENOG4111JGI
JNUCC-1_03769	ABC.PA.A	432	Polar-amino-acid-transporting ATPase	S:COG4550
JNUCC-1_03770	miaB	1560	tRNA-2-methylthio-N(6)-dimethylallyladenosine synthase	J:COG0621
JNUCC-1_03771		261	Stage V sporulation protein	S:COG2359
JNUCC-1_03772		798	uncharacterized protein	S:COG1692
JNUCC-1_03773	rny	1677	Ribonuclease	S:COG1418
JNUCC-1_03774		1032	Protein RecA	L:COG0468
JNUCC-1_03775	pncC	909	Nicotinamide-nucleotide amidase	H:COG1058
JNUCC-1_03776	pncC	339	Nicotinamide-nucleotide amidase	H:COG1058
JNUCC-1_03777	pgsA|PGS1	579	CDP-diacylglycerol--glycerol-3-phosphate 1-phosphatidyltransferase	I:COG0558
JNUCC-1_03778		915	Uncharacterized membrane protein YmfM	S:COG1426
JNUCC-1_03779		789	uncharacterized protein	S:ENOG410XSRB
JNUCC-1_03780		252	uncharacterized protein	S:ENOG411237P
JNUCC-1_03781	fabG	726	3-oxoacyl-[acyl-carrier-protein] reductase	S:ENOG410XNW1
JNUCC-1_03782	IDE|ide	1284	Insulysin	O:COG0612
JNUCC-1_03783	pqqL	1278	Probable inactive metalloprotease YmfF	O:COG0612
JNUCC-1_03784		999	DNA translocase FtsK	D:COG1674

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_03785		1041	DNA translocase FtsK	D:COG1674
JNUCC-1_03786		213	hypothetical protein	S:ENOG410Y52J
JNUCC-1_03787	clpP|CLPP	297	Endopeptidase Clp	O:COG0740
JNUCC-1_03788	clpP|CLPP	372	Endopeptidase Clp	O:COG0740
JNUCC-1_03789	dapA	879	4-hydroxy-tetrahydrodipicolinate synthase	E:COG0329
JNUCC-1_03790	lysC	1233	Aspartate kinase	E:COG0527
JNUCC-1_03791	asd	1020	Aspartate-semialdehyde dehydrogenase	E:COG0136
JNUCC-1_03792		621	Dipicolinate synthase subunit	H:COG0452
JNUCC-1_03793		870	Dipicolinate synthase subunit	S:ENOG4111H6E
JNUCC-1_03794		243	uncharacterized protein	S:COG1873
JNUCC-1_03795	pqqL	1218	uncharacterized zinc protease YmxG	O:COG0612
JNUCC-1_03796	pdaA	603	uncharacterized protein	G:COG0726
JNUCC-1_03797		414	uncharacterized protein	G:COG0726
JNUCC-1_03798	pnp|PNPT1	2106	Polyribonucleotide nucleotidyltransferase	J:COG1185
JNUCC-1_03799		270	30S ribosomal protein S15	J:COG0184
JNUCC-1_03800	ribF	951	Riboflavin kinase	H:COG0196
JNUCC-1_03801	truB|PUS4|TRUB1	891	tRNA pseudouridine(55) synthase	J:COG0130
JNUCC-1_03802		342	Ribosome-binding factor	J:COG0858
JNUCC-1_03803		279	uncharacterized protein	S:COG1550
JNUCC-1_03804		2118	Translation initiation factor IF-2	J:COG0532
JNUCC-1_03805		306	Probable ribosomal protein in infB 5′region	J:COG1358
JNUCC-1_03806		351	uncharacterized protein	K:COG2740
JNUCC-1_03807		1107	Transcription termination/antitermination protein NusA	K:COG0195
JNUCC-1_03808		471	Ribosome maturation factor RimP	S:COG0779
JNUCC-1_03809	polC	4293	DNA-directed DNA polymerase	L:COG2176

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_03810	rseP	1266	Probable protease eep	M:COG0750
JNUCC-1_03811	CDS1|CDS2|cdsA	777	Phosphatidate cytidylyltransferase	I:COG0575
JNUCC-1_03812	uppS	762	Ditrans,polycis-undecaprenyl-diphosphate synthase ((2E,6E)-farnesyl-diphosphate specific)	I:COG0020
JNUCC-1_03813		558	Ribosome-recycling factor	J:COG0233
JNUCC-1_03814	pyrH	723	UMP kinase	F:COG0528
JNUCC-1_03815		885	Elongation factor Ts	J:COG0264
JNUCC-1_03816		780	30S ribosomal protein S2	J:COG0052
JNUCC-1_03817		438	hypothetical protein	S:ENOG410XXUM
JNUCC-1_03818		288	hypothetical protein	S:ENOG410Y47W
JNUCC-1_03819		1377	hypothetical protein	L:COG1315
JNUCC-1_03820		783	RNA polymerase sigma-D factor	K:COG1191
JNUCC-1_03821	cheD	501	Protein-glutamine glutaminase	NT:COG1871
JNUCC-1_03822		636	CheY-P phosphatase CheC	N:COG1776
JNUCC-1_03823		468	Chemotaxis protein	NT:COG0835
JNUCC-1_03824	cheA	2007	Histidine kinase	T:COG0643
JNUCC-1_03825	cheB	1062	Protein-glutamate methylesterase	T:COG2197
JNUCC-1_03826		864	Flagellum site-determining protein YlxH	D:COG0455
JNUCC-1_03827		1110	Flagellar biosynthesis protein FlhF	N:COG1419
JNUCC-1_03828		2034	Flagellar biosynthesis protein FlhA	N:COG1298
JNUCC-1_03829		1083	Flagellar biosynthetic protein FlhB	N:COG1377
JNUCC-1_03830		780	Flagellar biosynthetic protein FliR	N:COG1684
JNUCC-1_03831		270	Flagellar biosynthetic protein FliQ	N:COG1987
JNUCC-1_03832		666	Flagellar biosynthetic protein FliP	N:COG1338
JNUCC-1_03833		249	hypothetical protein	
JNUCC-1_03834		348	hypothetical protein	N:COG3190

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_03835		363	Virulence factors putative positive transcription regulator BvgA	T:COG0784
JNUCC-1_03836		648	Flagellar motor switch phosphatase FliY	N:COG1776
JNUCC-1_03837		552	Flagellar motor switch phosphatase FliY	N:COG1776
JNUCC-1_03838		996	Flagellar motor switch protein FliM	N:COG1868
JNUCC-1_03839		420	Flagellar protein FliL	N:COG1580
JNUCC-1_03840		240	uncharacterized protein	N:COG1582
JNUCC-1_03841		801	Flagellar hook protein FlgE	N:COG4786
JNUCC-1_03842		378	hypothetical protein	N:ENOG41121WS
JNUCC-1_03843		456	FlaA locus uncharacterized protein YlxG	N:COG1843
JNUCC-1_03844		1296	hypothetical protein	N:ENOG410XUTY
JNUCC-1_03845		606	hypothetical protein	S:ENOG410ZY87
JNUCC-1_03846		441	Flagellar FliJ protein	N:COG2882
JNUCC-1_03847	yscN|sctN|hrcN|ssaN	396	H(+)-transporting two-sector ATPase	NU:COG1157
JNUCC-1_03848	fliI	948	H(+)-transporting two-sector ATPase	NU:COG1157
JNUCC-1_03849		753	Probable flagellar assembly protein FliH	N:COG1317
JNUCC-1_03850		1011	Flagellar motor switch protein FliG	N:COG1536
JNUCC-1_03851		1599	Flagellar M-ring protein	N:COG1766
JNUCC-1_03852		306	Flagellar hook-basal body complex protein FliE	N:COG1677
JNUCC-1_03853		453	Flagellar basal-body rod protein FlgC	N:COG1558
JNUCC-1_03854		399	Flagellar basal body rod protein FlgB	N:COG1815
JNUCC-1_03855		780	GTP-sensing transcriptional pleiotropic repressor CodY	K:COG4465
JNUCC-1_03856		1398	ATP-dependent protease ATPase subunit HslU	O:COG1220
JNUCC-1_03857	hslV|clpQ	423	HslU--HslV peptidase	O:COG5405
JNUCC-1_03858		918	Tyrosine recombinase XerC	L:COG4973
JNUCC-1_03859	topA	2079	DNA topoisomerase	L:COG0550

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_03860		912	Protein smf	L:COG0758
JNUCC-1_03861	mtkB	903	Malate-CoA ligase	C:COG0074
JNUCC-1_03862	sucC	1161	Succinate-CoA ligase (ADP-forming)	C:COG0045
JNUCC-1_03863		279	uncharacterized protein	S:COG2257
JNUCC-1_03864		1764	hypothetical protein	S:ENOG4112AGN
JNUCC-1_03865	rnhB	510	Ribonuclease H	L:COG0164
JNUCC-1_03866	rnhB	255	Ribonuclease H	L:COG0164
JNUCC-1_03867		849	Ribosome bioproteinis GTPase	S:COG1161
JNUCC-1_03868	lepB	549	Signal peptidase I	U:COG0681
JNUCC-1_03869		345	50S ribosomal protein L19	J:COG0335
JNUCC-1_03870	trmD	747	tRNA (guanine(37)-N(1))-methyltransferase	J:COG0336
JNUCC-1_03871		390	uncharacterized protein	S:ENOG41120S0
JNUCC-1_03872		228	UPF0109 protein	S:COG1837
JNUCC-1_03873		267	30S ribosomal protein S16	J:COG0228
JNUCC-1_03874	SRP54|ffh	1344	Signal-recognition-particle GTPase	U:COG0541
JNUCC-1_03875		321	UPF0122 protein	S:COG2739
JNUCC-1_03876		993	Signal recognition particle receptor FtsY	U:COG0552
JNUCC-1_03877		3387	Chromosome partition protein Smc	D:COG1196
JNUCC-1_03878		225	hypothetical protein	D:COG1196
JNUCC-1_03879		225	UPF0435 protein	S:COG4840
JNUCC-1_03880	rnc|DROSHA|RNT1	681	Ribonuclease III	K:COG0571
JNUCC-1_03881		237	Acyl carrier protein	I:COG0236
JNUCC-1_03882	phbB	741	Acetoacetyl-CoA reductase	S:ENOG410XNW1
JNUCC-1_03883	fabD	951	[Acyl-carrier-protein] S-malonyltransferase	I:COG0331
JNUCC-1_03884	plsX	543	Glycerol-3-phosphate 1-O-acyltransferase	I:COG0416

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_03885	plsX	528	Glycerol-3-phosphate 1-O-acyltransferase	I:COG0416
JNUCC-1_03886		594	Transcription factor FapR	Q:COG2050
JNUCC-1_03887	recG	2034	DNA helicase	L:COG1200
JNUCC-1_03888	sdaA|sdaB|tdcG	876	L-serine ammonia-lyase	E:COG1760
JNUCC-1_03889	sdaA|sdaB|tdcG	663	L-serine ammonia-lyase	E:COG1760
JNUCC-1_03890		1656	uncharacterized protein	S:COG1461
JNUCC-1_03891		363	uncharacterized protein	S:COG1302
JNUCC-1_03892		189	50S ribosomal protein L28	J:COG0227
JNUCC-1_03893		1464	hypothetical protein	S:ENOG410XPWT
JNUCC-1_03894	ltrA	1317	RNA-directed DNA polymerase	L:COG3344
JNUCC-1_03895		129	hypothetical protein	
JNUCC-1_03896	thiN|TPK1|THI80	660	Thiamine diphosphokinase	H:COG1564
JNUCC-1_03897	rpe|RPE	663	Ribulose-phosphate 3-epimerase	G:COG0036
JNUCC-1_03898	rsgA|engC	882	Putative ribosome bioproteinis GTPase RsgA	S:COG1162
JNUCC-1_03899	prkC|stkP	1989	Non-specific serine/threonine protein kinase	T:COG0515
JNUCC-1_03900	prpC|phpP	759	Protein-serine/threonine phosphatase	T:COG0631
JNUCC-1_03901	rsmB|sun	1347	16S rRNA (cytosine(967)-C(5))-methyltransferase	J:COG0144
JNUCC-1_03902	MTFMT|fmt	936	Methionyl-tRNA formyltransferase	J:COG0223
JNUCC-1_03903	priA	2409	Primosomal protein N′	L:COG1198
JNUCC-1_03904	coaBC|dfp	1206	Phosphopantothenoylcysteine decarboxylase	H:COG0452
JNUCC-1_03905	rpoZ	198	DNA-directed RNA polymerase	K:COG1758
JNUCC-1_03906	gmk	621	Guanylate kinase	F:COG0194
JNUCC-1_03907		261	UPF0296 protein	S:COG2052
JNUCC-1_03908		2655	Calcium-transporting ATPase	P:COG0474
JNUCC-1_03909		1716	uncharacterized protein	K:COG1293

Table. 3. 10. Continue.

CDS Name	Gene	Length	Product	EggNOG
JNUCC-1_03910		435	hypothetical protein	K:COG0583
JNUCC-1_03911		447	HTH-type transcriptional regulator TsaR	K:ENOG410YPSC
JNUCC-1_03912	pyrE	615	Orotate phosphoribosyltransferase	F:COG0461
JNUCC-1_03913	pyrF	714	Orotidine-5′-phosphate decarboxylase	F:COG0284
JNUCC-1_03914	pyrDI	936	Dihydroorotate dehydrogenase (NAD(+))	F:COG0167
JNUCC-1_03915		783	Dihydroorotate dehydrogenase B (NAD(+)), electron transfer subunit	C:COG0543
JNUCC-1_03916	URA4|pyrC	618	Dihydroorotase	F:COG0044

감사의 글

저에게 있어서 이번 박사과정은 다양한 경험과 그 동안 접해보지 못하였던 새로운 것을 배울 수 있는 시기였으며, 앞으로 제 인생에 많은 도움을 주리라 생각을 가져 봅니다. 오랜 대학원 생활을 거치며 부족하나마 이 논문을 완성하게 되었습니다. 이 박사학위 논문은 주위의 많은 분들이 도와주셨기에 가능했습니다. 그러하기에 일일이 찾아뵈어 감사의 인사를 전하지 못하는 대신 지면으로나마 감사하다는 말씀을 드리고 싶습니다.

많이 부족한 저를 지도하시어 지금까지 이끌어 주신 현창구 교수님께 존경과 감사의 마음을 표하며, 항상 건강하시길 바랍니다. 또한 많은 지식과 가르침을 주시고 바쁜 시간을 쪼개어 미흡한 논문을 지적해주시고 다듬어 주신 김덕수 교수님, 이남호 교수님, 임희정 교수님, 그리고 김기옥 연구위원님께 감사의 인사를 올립니다. 그리고 박사과정 동안 많은 가르침과 격려를 아끼지 않으신 강창희 교수님, 김원형 교수님, 윤경섭 교수님께도 감사의 인사를 드립니다.

박사과정 동안 관심과 조언으로 많은 도움을 준 실험실을 거쳐 간 모든 구성원에게 감사의 말을 전합니다. 특히 같이 고민을 나누고 힘을 북돋아 준 정유철, 이나리 박사과정과 현수빈 석사과정을 비롯한 실험실 학생들에게도 고맙다는 말을 전합니다.

마지막으로 박사과정을 잘 마칠 수 있도록 옆에서 묵묵히 도와준 평생의 반려자 사랑하는 명지와 건강하게 잘 자라주는 아들 준서에게 고맙다는 말을 전합니다. 그리고 못난 자식을 항상 믿어주시고, 챙겨주시는 부모님과 늘 격려를 아끼지 않으시며 믿음을 주시는 장인, 장모님께 감사의 말씀을 드립니다.

감사의 글에 다 표현 못한 분들이 많습니다. 지면상 다 나열하지 못하여 죄송한 마음이 듭니다. 이 글을 쓰며 많은 분들에게 직간접적으로 도움을 받고 있다는 것을 느낄 수 있었습니다. 이에 조금이나마 보답하기 위하여 저는 더욱 더 노력하여 많은 사람에게 선한 영향력을 미칠 수 있는 사람이 되도록 하겠습니다. 항상 감사드립니다. 건강하시고 행복하시길 바랍니다.

변후돈 드림