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(54) Title: GENOMICS OF ACTINOPLANES UTAHENSIS

(57) Abstract: The present invention describes the DNA-sequence of the wild type genome as well as all genetic modifications which were introduced into the wild type-and further developed strains, based thereon. Thereby the first genotypic characterization of the developed strains, including the latest production strain, has been accomplished, accounting for the major part of the invention. Furthermore, on the basis of the determined DNA-sequences, potential genes were identified and account, combined with their functional annotation, for another part of the invention. In particular, the gene-and DNA-sequences, as well as protein-sequences derived there out, contribute to the invention which were affected by mutagenic modifications throughout the strain development process, potentially contributing to the increased production yield.



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GENOMICS OF ACTINOPLANES UTAHENSIS

DESCRIPTION OF THE INVENTION

The gram-positive prokaryote *Actinoplanes utahensis* was described for the first time by John Couch in 1963 (Couch, J. N., Elisha Mitchell Sci. Soc., 1963, 79:53-70). Thereafter, in the year 1977, acarbose and its homologues were first found in the supernatant of an *Actinoplanes utahensis* culture (Schmidt *et al.*, Naturwissenschaften, 1977, 64:535-536). Two years later, the medical effect of acarbose as an α -glucosidase-inhibitor within the human intestine was discovered (Caspary *et al.*, Res. Exp. Med., 1979, 175:1-6) and within the same year, its potential application for the treatment of type-2 diabetes mellitus was propagated (Frommer *et al.*, J. Med. Plant Res., 1979, 35:195-217).

Since 1990 the α -glucosidase-inhibitor acarbose is produced and marketed for the treatment of type-2 diabetes mellitus. Starting from the *A. utahensis* wild type strain the production has been continuously improved with regard to an ever increasing acarbose yield by optimization of the fermentation process as well as the production strain itself. The strain development has been driven by a multitude of mutagenesis experiments, which are primarily responsible for the raising acarbose production.

The genetic modifications in the organism, triggered by the mutagenesis experiments have so far only been recognizable by phenotypic characteristics (e.g. the increase of acarbose yield). More precisely, the genetic bases for the raising production yields have, until now, been completely unknown. However, this knowledge is of fundamental interest for the understanding of the mechanisms, leading to the rise in production. Furthermore it forms the most important prerequisite for the process of further, targeted genetic modification of the organism, optimizing *A. utahensis* to an even greater extend.

The present invention describes the DNA-sequence of the wild type genome as well as all genetic modifications which were introduced into the wild type- and further developed strains, based thereon. Thereby the first genotypic characterization of the developed strains, including the latest production strain, has been accomplished, accounting for the major part of the invention. Furthermore, on the basis of the determined DNA-sequences, potential genes were identified and account, combined with their functional annotation, for another part of the invention. In particular, the gene- and DNA-sequences, as well as protein-sequences derived there out which were affected by mutagenic modifications throughout the strain development process, potentially contributing to the increased production yield, contribute to the invention.

Material and Methods

As briefly described above, a series of mutagenesis experiments has been performed on the *Actinoplanes utahensis* wild type strain SE50-100, originally isolated from a soil sample. These experiments were aimed at the identification of mutants with an improved production of acarbose as well as other parameters, relevant for industrial production by fermentation such as high growth rate, optimized nutrient needs and consumption as well as low formation of cumbersome byproducts. Initially based on the wild type strain, further mutagenesis experiments were continuously performed on the mutant strains selected from the previous experiments. During the course of the strain development, several mutants with outstanding attributes were selected as new production strains and transferred into large scale production. Of these, seven strains were selected, including the latest production strain as well as the wild type strain, to be sequenced by Bielefeld University's Center for Biotechnology (CeBiTec) Universitätsstrasse 27, 33615 Bielefeld, Germany. Table 1 lists all seven strains that have been used during this project in the chronological order of their development.

Table 1 list all *A. utahensis* strains used in this study in their chronological order.

Strain Symbol	Development Order	Remark
SE50-100	(1)	wild type strain
SN223-29-47	2	
C445-P47	3	
SN12755-48	4	
SC3687-18-43	5	
SC7177-40-17	6	
SN19910-37-21	7	latest production strain

Strain Cultivation

Cultivation of strains in order to check their acarbose productivity was done as described previously (Schmidt *et al.*, Naturwissenschaften, 1977, 64:535-536). In order to isolate DNA, the *Actinoplanes* strains were cultivated in a two-step shake flask system. Beside inorganic salts the medium contained starch hydrolysate as carbon source and yeast extract as nitrogen source. Preculture and main culture were run for 3 days and 4 days, respectively, on a rotary shaker at 28°C. Then the biomass was collected by centrifugation.

Strain Mutagenesis

The strain development of the Acarbose producer was performed by the method of stepwise selection of higher producing strains. This method uses the process of random mutation by chemical or physical means. Chemicals used to induce mutations were either alkylating agents or intercalating dyes that serve as frameshift mutagens. Physical treatment of cells to induce mutagenesis was done with UV light of 365 nm. Fragments of the mycelium were used for mutagenesis treatment in appropriate buffer systems. After the treatment the biological material was grown for a short period in liquid medium to allow phenotypic expression of the induced alterations and then plated on agar plates. A random selection of clones that survived the mutagenesis treatment was checked for their acarbose productivity in small scale shake flask experiments. The best mutant clones obtained during a mutation cycle of this kind were chosen for the next mutation step. Several such steps of mutation and selection resulted in a gradual increase of productivity.

Preparation of Genomic DNA

The preparation of genomic DNA of *A. utahensis* strain SE50-110 was performed by a modification of the general described procedure (Maniatis T., Fritsch E.F., Sambrook J., Molecular Cloning – A Laboratory Manual, Cold Spring Harbor Press, 1982). The mycel of 50 mL of freshly grown culture was harvested by centrifugation (10 min., 4.000 rpm, 4 °C) in a Christ centrifuge. The pellet was washed 4 times in a buffer containing 15 % sucrose (Merck KGaA, Darmstadt, Germany, cat. 7651), 25 mM TrisHCl pH 7.2 (Merck KGaA, Darmstadt, Germany, cat. 1.08382.1000), and 25 mM EDTA (Merck KGaA, Darmstadt, Germany, cat. 8418) under the same conditions. Finally the pellet was resuspended in 4.5 mL of the same buffer and lysozyme (Merck KGaA, Darmstadt, Germany, cat. 1.05281.0010) and RNase (Qiagen, Hilden, Germany, cat. 19101) were added to final concentrations of 5 mg/mL and 50 µg/mL respectively and the mixture was incubated at 37 °C for 45 minutes. After the addition of SDS (Serva, Heidelberg, Germany, cat. 20767) and proteinase K (Qiagen, Hilden, Germany, cat. 19133) to 0.5 % and 2 µg/mL final concentrations respectively, the incubation was continued at 50 °C for 5 minutes. NaCl (Merck KGaA, Darmstadt, Germany, cat.1.06404.1000) was added to a final concentration of 300 mM and the volume adjusted with WFI to 8 mL. The lysate was subjected to three successive phenol/SEVAG extractions (SEVAG is a mixture of 24 parts chloroform [Merck KGaA, Darmstadt, Germany, cat. 1.02445.1000] and 1 part isoamylalcohol [Merck KGaA, Darmstadt, Germany, cat. 1.979.1000]) and the phenol was removed by washing the DNA solution with 10 mL SEVAG. The DNA was precipitated by the addition of 0.1 volume of 3 M sodium acetate (pH 4.8) (Merck KGaA, Darmstadt, Germany, cat. 6268) and 1 volume of cold isopropanol (Merck KGaA, Darmstadt, Germany, cat. 1.09634.1011). The DNA was pelleted by centrifugation (25 minutes, 4.000 rpm, 4 °C; Christ centrifuge) and the DNA pellet was washed thoroughly (5 x) with 70 % ethanol (Merck KGaA, Darmstadt, Germany, cat. 1.00983.1011) (10 minutes, 4000 rpm, 4 °C; Christ centrifuge) and air-dried. Finally the pellet was resuspended in 200 µL Tris pH 8.5 over night at 4 °C and the DNA concentration was determined by measuring the optical density at 260 nm and 280 nm. The size of the prepared DNA was analysed by subjecting an aliquot (10 µL) of the DNA solution to electrophoresis through a 1 % agarose gel as quality check.

Fosmid-Library Construction

Fosmids are commonly used for preparing genomic libraries when a smaller insert size is desired. The inserts have an average size of 40 kb and are produced by random shearing, yielding a more uniform coverage of the genome than other library types. Fosmids are excellent candidates for closing gaps in a whole genome sequencing projects due to their uniform coverage. The fosmid-library construction for *Actinoplanes utahensis* wild type has been carried out on genomic DNA by IIT Biotech GmbH, Universitätsstr. 25, 33615 Bielefeld, Germany. For construction in *E. coli* EPI300 cells, the CopyControl™ Cloning System (EPICENTRE Biotechnologies, 726 Post Road, Madison, WI 53713, USA) has been used. The kit was obtained from Biozym Scientific GmbH, Steinbrinksweg 27, 31840 Hessisch Oldendorf, Germany.

Fosmid-Library Sequencing

Fosmid-library sequencing for *Actinoplanes utahensis* wild type has been carried out on a 3730xl DNA-Analyzer (Applied Biosystems, 850 Lincoln Centre Drive, Foster City, CA 94404, USA) by IIT Biotech GmbH, Universitätsstr. 25, 33615 Bielefeld, Germany. The device performs parallel Sanger-sequencing in 96 capillaries (Sanger *et al.*, J. Mol. Biol., 1975, 94 (3):441-448). The resulting flowgram files were base called and stored in FASTA format. Both files were later used for gap-closure and quality assessment.

High-Throughput Genome Sequencing Genome Sequencer FLX

The Genome Sequencer FLX (GS FLX) system (454 Life Sciences, 15 Commercial Street, Branford, CT 06405, USA) has been used for pyrosequencing of the *A. utahensis* wild type strain SE50-100 as well as the latest production strain SN19910-37-21. Two different protocols and reagent series were used on the GS FLX platform:

1. Standard series with long paired end (PE) protocol. The genome-DNA fragment size for the PE-library construction was 2.5 – 3.0 kb. The protocol yields an average read length of 2 x 100 bases and a total number of sequenced bases of about 100Mb.
2. Titanium series with whole genome shotgun (WGS) protocol. The genome-DNA fragment size for the WGS-library construction was 500 - 800 bp. The protocol yields a read length of 400 – 500 bases and a total number of sequenced bases ranging from 400 – 600 Mb.

Details on the protocols are provided in the manufacturers manuals, namely the *GS FLX Sequencing Method Manual* (December 2007), *GS FLX Paired End DNA Library Preparation Method Manual* (December 2007), *GS FLX Titanium Sequencing Method Manual* (October 2008) and the *GS FLX Titanium General Library Preparation Method Manual* (October 2008)

Genome Analyzer IIx

The Genome Analyzer IIx (GA IIx) system (Illumina, Inc., 9885 Towne Centre Drive, San Diego, CA 92121, USA) including Cluster-Station and Paired-End-Module has been used for sequencing-by-synthesis of the five former productions strains SN223-29-47, C445-P47, SN12755-48, SC3687-18-43 and SC7177-40-17. For all five strains, the paired end protocol with a genome-DNA fragment size of approximately 330 bp and a read length of 2 x 36 bases was used. Library preparation, cluster generation and sequencing were performed according to the manufacturers manuals *Paired-End sequencing Sample Preparation Guide* (Part # 1005063 Rev. B September 2009), *Using the Paired-End Cluster Generation Kit v2 on the Cluster Station and Paired-End Module* (Part # 1005629 Rev. C February 2009) and *Using SBS Sequencing Kit v3 on the Genome Analyzer* (Part # 1005637 Rev. A November 2008).

Wild Type Draft Genome Assembly

The automated assembly of all *Actinoplanes utahensis* wild type reads generated by the GS FLX platform was performed with the Newbler assembler software (gsAssembler version 2.0.00.22, 454 Life Science). For detailed information on the assembly algorithm see the *Genome Sequencer FLX System Software Manual Part C*, version 2.3 (October 2009).

Wild Type Genome Finishing

In order to close remaining gaps between contiguous sequences (contigs) still present after the automated *de novo* assembly by the Newbler program, the visual assembly software package Consed (Gordon *et al.*, Genome Research, 1998, 8:195-202) was utilized. Within the graphical user interface, primer pairs at the ends of contiguous contigs were selected. These primer pairs were then used to amplify desired sequences from clones originating from the previously constructed fosmid-library in order to bridge the gaps between contiguous contigs.

After the DNA sequence of these fosmid-reads had been determined, manual assembly of all applicable reads was performed with the aid of different program features. In detail, a fosmid-read is first aligned to the 5' end of a contig, extending it by its 5' remainder. Afterwards, the 3' end of the neighboring contig is aligned to this extension, spanning the previously existing gap and joining the two contigs.

In cases where the length or quality of one fosmid-read was not sufficient to span the gap, multiple rounds of primer selection, sequencing and manual assembly were performed.

Wild Type Genome Annotation Identification of Coding Sequences (CDS)

The potential genes and partial gene sequences on the wild type genome (see Appendix) were identified by a series of computational analysis. All utilized programs are part of the GenDB annotation-pipeline (Meyer *et al.*, Nucleic Acids Research, 2003, 31(8):2187-95). For the identification of CDSs intrinsic, extrinsic and combined methods were applied in order to achieve optimal results.

The program responsible for the intrinsic prediction of CDSs is Glimmer (Delcher *et al.*, Nucleic Acid Research, 1999, 27:4636-41). It first constructs a training set from CDSs with optimal characteristics taken from the genome to be analyzed. Based upon this set, an interpolated Markov Model is calculated, which is used in the actual search-run to identify all CDSs of the genomic sequence. Glimmer tends to calculate more CDSs as are actually there.

The extrinsic CDS-prediction has been carried out by CRITICA (Badger *et al.*, Mol. Biol. Evol., 1999, 16:512-24). CRITICA first makes use of the BLASTN algorithm (Altschul *et al.*, J. Mol. Biol., 1990, 215(3):403-10) in order to determine a list of genomic sequences which show at least slight similarity to sequences from public DNA-databases. If the translated amino acid sequence possesses a higher similarity than it would be expected based on the DNA-similarities, this is interpreted as evidence for being a conserved coding sequence. CRITICA combines these results with intrinsic analysis based on the distribution of hexa nucleotides to improve the prediction of previously unknown sequences. Despite this, CRITICA still tends to predict fewer CDS in cases where no homolog sequence is already stored in a public database.

The Reganor software (McHardy *et al.*, Bioinformatics, 2004, 20(10):1622-31) has been used to optimize the results calculated by Glimmer and CRITICA. It combines the results of both programs and thus minimizes their respective shortcomings. Moreover, the CDS predicted by CRITICA form the basis of the combined results, complemented by the intrinsic predictions calculated by Glimmer.

Annotation and Functional Prediction

The identified open reading frames were analyzed through a variety of different software packages in order to draw conclusions from their RNA- and/or amino acid-sequences regarding their potential function. Besides their functional prediction, further characteristics and structural features have also been calculated.

Homology-based searches were applied to identify conserved sequences by means of comparison to public and/or proprietary nucleotide- and protein-databases. If a significant sequence similarity was found throughout the major section of a gene, it was concluded that the gene should have a similar function in *A. utahensis*. The homology-based method, which was used to annotate the gene list of *Actinoplanes utahensis*, is termed BLASTX (Coulson, Trends in Biotechnology, 1994, 12:76-80). BLASTX translates a given nucleotide sequence

into three forward and three reverse complementary reading frames before it compares them against protein databases (e.g. the public, non-redundant protein database (nr-aa) at the National Center for Biotechnology Information (NCBI)).

Enzymatic classification has been performed on the basis of *enzyme commission* (EC) numbers (Webb, Edwin C., San Diego: Published for the International Union of Biochemistry and Molecular Biology by Academic Press, 1992, ISBN 0-12-227164-5. For further functional gene prediction, the *cluster* of orthologous groups of proteins (COG) classification system has been applied (Tatusov et al., Science, 1997, 278(5338):631-7 and Tatusov et al., Nucleic Acids Res. 2001, 29(1):22-8).

To identify potential transmembrane proteins, the software TMHMM (Krogh et al., J. Mol. Biol., 2001, 305(3):567-80 and Sonnhammer et al., Proc. Int. Conf. Intell. Syst. Mol. Biol., 1998, 6:175-82) has been utilized. It makes use of Hidden Markov Models to predict transmembrane helices and other characteristics of transmembrane proteins. With information gained thereof, membrane associated functional predictions obtain significantly stronger conclusiveness.

The software SignalP (Bendtsen et al., J. Mol. Biol., 2004, 340:783-95 and Nielsen et al., protein Engineering, 1997, 10:1-6) was used to predict the secretion capability of the identified CDSs. This is done by means of Hidden Markov Models and neural networks, searching for the appearance and position of potential signal peptide cleavage sites within the amino acid sequence. The resulting score can be interpreted as a probability measure for the secretion of the translated protein. SignalP retrieves only those proteins which are secreted by the classical signal-peptide-bound mechanisms.

In order to identify further proteins from *Actinoplanes utahensis* which are not secreted via the classical way, the software SecretomeP has been applied (Bendtsen et al., BMC Microbiology, 2005, 5:58). The underlying neural network has been trained with secreted proteins, known to lack signal peptides despite their occurrence in the exoproteome. The final secretion capability of the translated genes was been derived by the combined results of SignalP and SecretomeP predictions.

To reveal polycistronic transcriptional units, proprietary software has been developed which predicts jointly transcribed genes by their orientation and proximity to neighboring genes (adopted from Salgado et al., Proc. Natl. Acad. Sci. USA, 2000, 97(12):6652-7). In light of these predictions, operon structures can be determined and based upon them further sequence regions can be derived with high probability of contained promoter and operator elements.

Secondary structures of single-stranded DNA- respective RNA-molecules were calculated by the RNashapes software (Steffen et al., Bioinformatics, 2006, 22(4):500-503). The results were used for the intrinsic prediction of transcriptional terminators which indicate operon and gene ends, respectively.

Production Strain Reference Assembly

The assembly of reads obtained for all six production strains has been achieved by mapping them onto the wild type reference genome. For this task, two different software programs were utilized, taking the two read types into account which originated from the Genome Sequencer FLX (read-length 400 - 500 bases WGS) and Genome Analyzer IIx (read length 2x36 bases PE) system, respectively.

The gsMapper software (version 2.3, 454 Life Science) was used to align the reads from the Genome Sequencer FLX platform against the wild type reference genome. The program implements a heuristic to find the best alignment position for each read within the reference sequence. After all reads have been aligned, multiple alignments for the reads that align contiguously to the reference are performed in order to form contigs. From the contigs' multiple alignments, consensus basecall sequences are produced using the flow-signals of the reads in the multiple alignments, resulting in quality and confidence values for each base. For detailed information on the mapping algorithm see the *Genome Sequencer FLX System Software Manual Part C*, version 2.3 (October 2009).

As part of the CLC Genomics Workbench (CLC bio, Finlandsgade 10-12, Katrinebjerg, 8200 Aarhus N, Denmark), the short read assembly algorithm with PE information has been used to align reads from the Genome Analyzer IIx platform against the reference genome. For detailed information on the mapping algorithm see the *CLC Genomics Workbench User Manual 3.7.1*.

Identification of Mutations in the Production Strains

Genetic variations between the wild type strain SE50-100 and the latest production strain SN19910-37-2 have been automatically determined during the reference assembly process by means of the gsAssembler software (version 2.3, 454 Life Science). The details of the algorithm, determining single nucleotide polymorphisms (SNPs) as well as structural variations, can be found in the *Genome Sequencer FLX System Software Manual Part C*, version 2.3 (October 2009).

Mutations between the wild type strain and the five former production strains have been determined using the CLC Genomics Workbench (CLC bio, Finlandsgade 10-12 Katrinebjerg, 8200 Aarhus N, Denmark). Specialized algorithms for high-throughput data analysis of SNPs and deletion/insertion polymorphisms (DIPs) have been used, described in detail in *CLC Genomics Workbench User Manual 3.7.1*.

Sequencing, Assembly and Annotation of the *Actinoplanes utahensis* Wild Type Strain

The draft genome sequence of the *Actinoplanes utahensis* wild type strain SE50-100 has been determined by a combination of sequencing information from three high-throughput runs. These were carried out on a Genome Sequencer FLX system, using two paired-end (PE) and one whole genome shotgun (WGS) approaches. The sequencings resulted in the successful nucleotide sequence determination of about 2 million reads, accounting for approximately 407 million sequenced bases in total (see table 2 for detailed information on the outcomes of each run).

Table 2 shows the results of the three high-throughput sequencing runs for the *A. utahensis* wild type strain SE50-100. Two paired-end (PE) and one whole genome shotgun (WGS) run were performed.

Run	454 Technology	Reads	Paired Reads	Bases
1	Standard, PE	742,169	259,260	103,840,588
2	Standard, PE	751,570	265,457	105,329,378
3	Titanium, WGS	481,602	-	197,732,895
Total		1,975,341	524,717	406,902,861

The sequenced reads were then successfully (99.65%) assembled into 476 contiguous sequences (contigs) exceeding 500 bases in length. Considering the resulting draft genome size of 9,122,632 bases, a genome coverage of 43.88-fold has been accomplished. Due to 480,030 (91.48%) successfully mapped paired-end reads, these contigs could already be ordered and oriented into eleven scaffolds (multiple contigs whose order and orientation are known from paired-end information). Table 3 gives further inside into the success- and error-rates of the assembly process leading to the preliminary draft genome sequence of the *Actinoplanes utahensis* wild type strain SE50-100.

Table 3 displays the results of successfully assembled reads, bases and the inferred read error. The inferred read error is calculated from mismatches between the reads and the consensus sequence of the final assembled contigs and measures the frequency of incorrectly called bases.

Run	454 Technology	Assembled Reads	Assembled Bases	Inferred Read Error
1	Standard, PE	99.58% (739,079)	98.08% (101,847,643)	0.36% (370,520)
2	Standard, PE	99.59% (748,526)	98.18% (103,411,267)	0.35% (364,397)
3	Titanium, WGS	99.85% (480,863)	99.33% (196,416,109)	0.52% (1,018,256)
Total		99.65% (1,968,468)	98.72% (401,675,019)	0.44% (1,753,173)

Interestingly, the genome sequence of the previously published acarbose cluster (Wehmeier, Biocat. Biotrans., 2003, 21:279–285 and Wehmeier and Piepersberg, Appl. Microbiol. Biotechnol., 2004, 63:613–625) was not identical to the sequencing results described above. In total, 37 single nucleotide polymorphisms (SNPs) and 24 deletion/insertion polymorphisms (DIPs) were found to be artificially introduced into the wild type sequence by the former sequencing attempt (see figure 1). The correction of these flawed sequencings lead to a minor elongation (42 bases) of the *acbC* gene as well as to the

correction of several temporary frameshifts within the *acbE* gene. This however, had no consequence on overall annotation of the gene and the whole acarbose cluster.

Figure 1 shows former false sequencings of the acarbose cluster which were corrected by the performed high-throughput sequencing described here.

Finishing of the Draft Genome Sequence by Fosmid Library Sequencing

In order to obtain a whole genome scaffold of the wild type strain SE50-100, terminal insert sequences of 999 randomly selected fosmid clones have been determined (figure 2). No inconsistencies between the eleven paired-end-based scaffolds and the fosmid-library-based whole genome scaffold were found, corroborating the quality of the sequencing runs as well as the accuracy of the assembly process. In total 600 Sanger reads were derived from selected clones covering most of the remaining gaps of the draft genome. By manual assembly of these reads, 411 gaps between contigs could be bridged and closed respectively. The remaining 64 contigs form a single, circular scaffold and could not be bridged with this method due to long repetitive DNA-sequences and/or uncovered regions within the fosmid library. The resulting improved genome sequence of the *A. utahensis* wild type strain SE50-100 and is deposited in the appendix of this document.

Figure 2 depicts the circular mapping of the fosmid clones (grey) used to build the genomic scaffold. The eleven scaffolds, which were based on the paired-end information, are marked in black.

Based on the improved genome sequence, a guanine-cytosine (G+C) content of 71.29% has been calculated which is typical for actinobacteria closely related to the *Actinoplanes* genus (Ventura *et al.*, Microbiol. Mol. Biol. Rev., 2007, 71(3): 495–548).

Annotation of the *Actinoplanes utahensis* Wild Type Genome

On the foundation of the improved genome sequence, a full genome annotation has been performed, resulting in the determination of 8,027 putative coding sequences (CDS) with an average gene length of 985 nucleotides. Based thereon, *Actinoplanes utahensis* exhibits a coding density of 86.35% with notable G+C content difference of about 3% between coding (71.68%) and non-coding (68.70%) DNA regions. By examining the structural gene composition, 1,793 putative polycistronic transcriptional units were predicted, hosting 5,980 genes (74.50%) with an average number of 3.34 genes per operon. All nucleotide sequences as well as their amino acid translations are deposited in the appendix of this document. Table 4 summarizes the outcomes of the gene prediction process.

Table 4 shows the results of the gene prediction software for the A. utahensis wild type strain.

Gene Prediction Parameter	Value
Coding sequences	8,027
Coding bases	7,904,275 (86.35%)
Average gene length (bp)	985
Coding G+C content (%)	71.68
Non-coding G+C content (%)	68.70
Putative monocistronic transcriptional units	2,047

Putative polycistronic transcriptional units (PTU)	1,793
Average number of genes per PTU	3.34

A variety of different programs were used to perform the functional annotation of the identified open reading frames. Due to extrinsic protein database comparisons 2,839 CDSs (35.67%) could be enzymatically characterized with an enzyme commission (EC) number. In addition 701 CDSs (8.73%), possessing typical transmembrane spanning regions, have been identified and classified as membrane-associated proteins. For a total number of 600 proteins signal peptides, and thus a high probability of being secreted into the extracellular medium, have been predicted. For additional 657 proteins, other secretion mechanisms were proposed. However, these predictions would result in an unusual high number of secreted proteins. Furthermore, the *cluster of orthologous groups of proteins* (COG) classification system has been applied and revealed an assignment of 3,983 (49.62%) CDSs to one or multiple COG-categories. Appendix table 9 offers a more comprehensive outline of the COG-categories and its subdivisions whereas the results of the general annotation are summarized in table 5. After full annotation, 2,684 genes (33.44%) had still no associated function. However, distant similarities to other sequences were found in public databases. For 434 (5.41%) orphan genes, not even distant related sequences were found in the databases.

Table 5 lists the results of the functional gene annotation for the *A. utahensis* wild type strain.

Functional Annotation Parameter	Value
CDSs with annotated function	4,909 (61.16%)
↳ CDSs with EC-number	2,839 (35.67%)
↳ CDSs with COG-category	3,983 (49.62%)
CDSs with unknown function	2,684 (33.44%)
Orphan CDSs	434 (5.41%)
Membrane associated proteins	701 (8.73%)
Signal peptide predicted (75% confidence)	600 (7.47%)
Other secretion mechanism predicted (95% conf.)	657 (8.18%)

The annotated wild type genome is shown as a circular plot in figure 3. In addition to the depicted genes on the forward (outmost circle) and reverse strand (second circle), the G+C content (third circle) as well as the G+C skew (forth circle) is drawn in. Furthermore, several sites of high importance are marked, including the origin of replication, the previously described trehalose (Lee *et al.*, Appl. Microbiol. Biotechnol., 2008, 80:767–778) and acarbose clusters, an interesting protein cluster consisting of about 25 contiguous ribosomal proteins as well as the location of an integrative and conjugative element (ICE). Table 6 lists the general features of the *Actinoplanes utahensis* wild type genome.

Figure 3 shows a circular genome plot of the *Actinoplanes utahensis* SE50-100 wild type chromosome. On the outmost circle, genes in forward orientation are depicted. The second circle hosts genes on the reverse strand. The G+C content and the G+C skew are shown on the third and fourth circle, respectively.

Table 6 lists the general features of the *A. utahensis* SE50-100 genome.

Feature	Genome
Total size (bp)	9,122,632

G+C content (%)	71.29
No. of CDS	8,027
No. of orphans	434
Coding density (%)	86.35
Average gene length (bp)	985
No. of rRNAs	4 x 16S-23S-5S
No. of transposase genes	39

By means of further extrinsic database searches, the most homologous gene and the organism it originates from have been assigned to each open reading frame. Together with the detailed annotations described above, this information is listed for each CDS in appendix table 10.

For many genes, an even more detailed manual annotation has been added to the (semi-) automated information described above. These genes include, but are not limited to all elements of the acarbose cluster (Wehmeier and Pipersberg, Appl. Microbiol. Biotechnol., 2004, 63: 613-625), the trehalose cluster (Lee *et al.*, Appl. Microbiol. Biotechnol., 2008, 80:767-778) as well as certain classes of proteins such as starch degrading- and synthesizing-enzymes, sugar epimerases, genes involved in the uptake, transport and metabolism of maltose, secreted proteins, cellulases and genes involved in nitrogen metabolism and sporulation associated genes and their protein translations.

Metabolic Potential of the *A. utahensis* Wild Type Strain

Through the use of annotated EC numbers, it was possible to analyze the metabolic capabilities of *Actinoplanes utahensis*. Mapping of the EC numbers onto canonical pathways of the Kyoto Encyclopedia of Genes and Genomes (KEGG) revealed the availability of all major pathways regarding the central metabolism such as the glycolysis, the TCA cycle and the pentose-phosphate-pathway. For the utilization of the Entner-Dudoroff-pathway however, the key enzyme phosphogluconate dehydratase is missing for the catalysis of 6-Phospho-D-gluconate to 2-Dehydro-3-deoxy-D-gluconate-6P.

Genome Sequencing of the *A. utahensis* Production Strains

In addition to the wild type strain SE50-100, the latest production strain SN19910-37-21 as well as five former strains were sequenced in order to reveal genetic differences responsible for the increased acarbose production in these strains. The latest strain has been sequenced on the Genome Sequencer FLX (GS FLX) system, whereas the former strains were sequenced using the Genome Analyzer IIx (GA IIx) platform solely based on paired-end data. The results are summarized in table 7. In total, 5.6 billion bases were sequenced.

Table 7 lists all sequenced A. utahensis production strains in the order of their acarbose production.

Strain Symbol	Platform	Protocol	Reads	Bases	Coverage
SN223-29-47	GA IIx	PE	34,571,040	1,209,986,400	132.64
C445-P47	GA IIx	PE	30,360,960	1,062,633,600	116.48
SN12755-48	GA IIx	PE	29,292,960	1,025,253,600	112.39
SC3687-18-43	GA IIx	PE	28,105,200	983,682,000	107.83
SC7177-40-17	GA IIx	PE	27,332,400	956,634,000	104.86
SN19910-37-21	GS FLX	Titanium, WGS	776,085	297,036,826	32.56

Identification of Genetic Variations between the Mutated Strains and the Wild Type

Consequent reference mapping against the previously finished wild type genome lead to the assembly of all six production strains. In addition, all genetic variations between the production strains and the wild type strain could be determined. Interestingly, no major deletion mutations had taken place, as the wild type genome is generally completely covered by the reads originating from the production strains. However, 1,826 single nucleotide polymorphisms (SNPs) and 128 deletion/insertion polymorphisms (DIPs) were discovered between the wild type genome and the latest production strain. The number of SNPs introduced into each genome, as listed in table 8, rises with the chronological development of the strain. All mutations and their exact transitions are listed in appendix table 11 together with the production strains, showing their first occurrence.

Table 8 lists the number of single nucleotide polymorphisms (SNPs) and deletion/insertion polymorphisms (DIPs) that were detected between the corresponding production strain and the *A. utahensis* wild type genome.

Strain Symbol	SNPs	DIPs
SN223-29-47	428	7
C445-P47	1,040	6
SN12755-48	1,204	6
SC3687-18-43	1,331	5
SC7177-40-17	1,533	7
SN19910-37-21	1,826	128

The SNP based nucleotide transitions were not gaussian distributed but show a more than 100-fold preference for the two transition G→A and C→T. Figure 4 depicts these findings.

Figure 4 shows the transition frequency of SNP mutations between the wild type and the latest production strain.

By comparison of annotated gene loci against positions where SNPs and DIPs were introduced, it was found that 1,896 genes (23.62%) were affected by these mutations on the nucleotide level as can be seen in figure 5. Of these, 376 genes were still coding for the identical protein sequence, holding only silent mutations. On the other side, the protein sequence of 816 genes changed on individual positions, leaving the amino acid sequence unchanged for the most part. However, the 704 residuary genes were hit by mutations changing their length and/or reading frame. In detail, 429 genes were predicted to have an increased length compared to the wild type whereas 275 genes were shortened.

Figure 5 visualizes only the 1,896 genes which were hit by a mutation event. On the outmost circle, forward oriented genes are listed. On the second circle, backward genes are depicted. The third and forth circles represent the G+C content and the G+C skew, respectively.

Modifications of the Central Metabolism

The enzyme encoding genes which were affected by mutagenesis events are likely to have an impact on the overall metabolism as well as special pathways like the one encoding for the formation of acarbose. For this reason, these genes were mapped according to their EC numbers onto canonical pathways of the KEGG database to identify loss of functionality introduced by the mutagenesis experiments. While several enzymes of the central metabolism were affected by SNPs, only few genes were hit by mutations leading to a probable loss of function. In addition, for each of these severely changed genes at least one other gene, annotated with the same EC number, was still available, probably assisting for the knocked out version.

Modifications of the Acarbose Cluster and the Use of Former Production Strains

By sequencing of the former production strains, it was possible to trace mutations back through time to the strain they were first introduced into. This analysis was especially enlightening on the sequence of the acarbose cluster as depicted in figure 6. The 13 SNPs which hit the cluster were sequentially introduced as mutation experiments were executed. Two SNPs were introduced into the intragenic region between genes *acbW* and *acbV*. Furthermore, two SNPs were introduced to the *acbD* gene. The *acbD* encoding protein, an acarviosyltransferase is believed to load acarbose with maltodextrins in the extracellular space prior to reimport through the acarbose importer complex. Another mutation is located in the *acbH* gene which encodes the subject binding protein of the acarbose importer complex.

Figure 6 shows the acarbose cluster in conjunction with the mutations which were introduced therein during the development of the depicted former production strains.

Claims

1. A DNA having essentially the sequence of SEQ ID 16053 or fragments thereof characterized in that it contains at least one of the mutations depicted in table 9.
2. A microorganism comprising the DNA according to claim 1.
3. A method for producing Acarbose comprising the steps:
 - a) cultivating the microorganism of claim 2 and
 - b) harvesting the Acarbose produced by the microorganism.

LIST OF ALL MUTATIONS

Table 9 lists all mutations introduced into the Actinoplanes utahensis wild type strain SE50-100 by the corresponding production strains.

Position in reference wild type strain	Base in Reference strain	Occurrence in Strain						Affected Gene ID
		SN19910-37-21	SC7177-40-17	SC3687-18-43	SN12755-48	C445-P47	SN223-29-47	
SE50-100								
7102	G		A	A	A	A	A	cds_wt_4
11919	G	A	A	A	A	A	A	cds_wt_7
12285	G	A	A	A	A	A	A	cds_wt_7
12651	G	A	A	A	A	A	A	cds_wt_7
13511	G	A	A	A	A	A	A	cds_wt_7
46974	C	T	T	T	T	T	T	cds_wt_41
62542	C		T	T	T	T	T	cds_wt_52
64957	C	T	T	T	T	T	T	cds_wt_54
65055	C	T	T	T	T	T	T	cds_wt_54
65455	C	C/T					T/C	-
65460	C	C/T					T	-
65882	G	A	A	A	A	A	A	cds_wt_55
72685	A						A/G	-
72693	A						A/G	-
72701	A						A/G	-
73373	C		T	T	T	T	T	cds_wt_61
73467	C		T	T	T	T	T	cds_wt_61
76845	C	T	T	T	T	T	T	cds_wt_64
78965	C	T	T	T	T	T	T	cds_wt_66
80653	G		A	A	A	A	A	cds_wt_67
85503	G		A	A	A	A	A	cds_wt_70
88269	G		A	A	A	A	A	cds_wt_72
88369	G		A	A	A	A	A	cds_wt_72
89368	C	T	T	T	T	T	T	cds_wt_72
89901	C		T	T	T	T	T	cds_wt_72
90029	C		T	T	T	T	T	cds_wt_72
91949	C	T	T	T	T	T	T	cds_wt_74

93427	C	T	T	T	T	T	T	-
101351	G		A	A	A	A	A	cds_wt_82
103967	C						T	cds_wt_84
104063	C	T		T	T	T	T	cds_wt_84
110857	C		T	T	T	T	T	cds_wt_88
112637	G		A	A	A	A	A	cds_wt_90
114499	G		A	A	A	A	A	cds_wt_90
115250	G		A	A	A	A	A	cds_wt_92
115873	C		T	T	T	T	T	cds_wt_92
115983	C			T			T	cds_wt_93
117494	C		T	T	T	T	T	cds_wt_93
119344	G		A	A	A	A	A	cds_wt_94
134489	C	T	T	T	T	T	T	cds_wt_106
139515	C		T	T	T	T	T	-
146767	C	T	T	T	T	T	T	cds_wt_119
161035	G		A	A	A	A	A	cds_wt_133
172303	G		A	A	A	A	A	cds_wt_143
176176	G					A	A	cds_wt_146
178880	G						G/A	cds_wt_148
180754	C			T	T		T	cds_wt_150
180925	C			T			T	cds_wt_150
184674	G			A	A	A	A	cds_wt_154
190568	C		T	T	T	T	T	cds_wt_159
190644	C		T	T	T	T	T	cds_wt_159
191971	C		T	T	T	T	T	cds_wt_161
193584	G		A	A	A	A	A	cds_wt_162
196028	C		T	T	T	T	T	cds_wt_164
196338	C		T	T	T	T	T	-
214992	G		A	A	A	A	A	-
222841	G					A	A	cds_wt_187
222924	C					T	T	cds_wt_187
228543	C						T	cds_wt_193
247200	C				T	T	T	cds_wt_205
248952	C	T	T	T	T	T	T	cds_wt_206
253299	G						A	cds_wt_209
254551	G						A	cds_wt_210
259829	C			T	T		T	-
268705	C		T	T	T	T	T	cds_wt_224
270822	G	A	A	A	A	A	A	cds_wt_227
273723	G	A		A	A		A	cds_wt_229
276430	C		T	T	T	T	T	cds_wt_232
276561	C			T	T	T	T	cds_wt_232
283007	G	A	A	A	A	A	A	-
283062	G	A	A	A	A	A	A	-
287132	C				T	T	T	cds_wt_247
294767	G					A	A	cds_wt_253

295356	C	T	T	T	T	T	T	cds_wt_254
300028	C						T	cds_wt_256
303810	G					A	A	cds_wt_259
313837	C					T	T	cds_wt_271
316698	G					A	A	cds_wt_273
316929	G		A	A	A	A	A	cds_wt_273
325503	C		T	T	T	T	T	cds_wt_283
331088	G				A	A	A	-
340040	G			A	A		A	cds_wt_297
342987	G		A	A	A	A	A	cds_wt_299
343915	G	A	A	A	A	A	A	cds_wt_300
352688	C	T	T	T	T	T	T	cds_wt_308
353668	G		A	A	A	A	A	cds_wt_308
361019	G		A	A	A	A	A	cds_wt_314
362742	G		A	A	A	A	A	cds_wt_315
375835	C	T	T	T	T	T	T	cds_wt_329
381358	G			A	A		A	cds_wt_335
382029	G		A	A	A	A	A	cds_wt_335
391677	C	T		T	T	T	T	cds_wt_345
400166	C		T	T	T	T	T	cds_wt_350
406413	G				A	A	A	cds_wt_355
409544	G		A	A	A	A	A	cds_wt_358
416199	G						A	cds_wt_364
419938	C	T	T	T	T	T	T	cds_wt_369
425067	G					A	A	cds_wt_374
425419	G					A	A	cds_wt_374
426464	G		A	A	A	A	A	cds_wt_376
438324	C		T	T	T	T	T	cds_wt_385
446368	G		A	A	A	A	A	cds_wt_390
446984	G		A	A	A	A	A	cds_wt_392
447392	G		A	A	A	A	A	-
450492	G						A	cds_wt_395
458678	C		T	T	T	T	T	cds_wt_403
459753	C						T	-
459833	A	G		G		G	G	cds_wt_405
466505	G		A	A	A	A	A	cds_wt_416
474923	G						A	cds_wt_423
482599	G			A	A	A	A	cds_wt_430
494993	G		A	A	A	A	A	cds_wt_445
500358	C	T	T	T	T	T	T	cds_wt_449
510408	C			T	T	T	T	cds_wt_459
511515	G		A	A	A	A	A	cds_wt_460
512816	G						A	cds_wt_463
513902	C	T	T	T	T	T	T	cds_wt_464
515197	G						A	cds_wt_465
518156	G		A	A	A	A	A	cds_wt_468

533618	G	A	A	A	A	A	A	cds_wt_485
536327	C	T		T	T		T	cds_wt_488
542891	G		A	A	A	A	A	cds_wt_493
548989	C		T	T	T	T	T	cds_wt_496
553081	G		A	A	A	A	A	cds_wt_500
553332	G		A	A	A	A	A	cds_wt_500
557884	G						A	cds_wt_502
557907	G						A	cds_wt_502
567026	C	T	T	T	T	T	T	-
587166	A	G	G	G	G	G	G	cds_wt_528
590721	G						A	cds_wt_530
602225	C	T	T	T	T	T	T	cds_wt_543
604184	C						T	cds_wt_544
605918	C	T	T	T	T	T	T	cds_wt_546
621774	C					T	T	-
624361	C	T	T	T	T	T	T	-
625600	C	T	T	T	T	T	T	-
626283	G		A	A	A	A	A	-
629283	G		A	A	A	A	A	cds_wt_565
636108	C					T	T	-
648981	G		A	A	A	A	A	cds_wt_582
684062	G		A	A	A	A	A	cds_wt_613
702171	C					T	T	cds_wt_627
702650	C					T	T	cds_wt_627
703452	C			T	T	T	T	cds_wt_628
706109	C						T	cds_wt_631
711168	G			A	A	A	A	-
712462	A						A/G	cds_wt_637
714678	G			A	A	A	A	cds_wt_639
714785	G		A	A	A	A	A	cds_wt_639
717602	G			A	A	A	A	cds_wt_641
719600	G			A	A	A	A	cds_wt_643
724097	G			A	A	A	A	cds_wt_646
738525	C					T	T	cds_wt_655
744594	G						A	cds_wt_662
746362	G			A	A	A	A	cds_wt_664
750285	C		T	T	T	T	T	cds_wt_667
752663	G		A	A	A	A	A	cds_wt_670
763762	C						C/G	-
763785	G						G/C	-
763792	C						C/G	-
763951	C						C/G	-
765635	G	A	A	A	A	A	A	cds_wt_682
766073	G		A	A	A	A	A	cds_wt_682
769289	G		A	A	A	A	A	cds_wt_686
776043	C			T	T	T	T	cds_wt_692

780677	C					T	T	-
781916	C			T	T	T	T	cds_wt_698
783900	C			T	T	T	T	cds_wt_699
786653	G	A	A	A	A	A	A	cds_wt_702
795572	C	T	T	T	T	T	T	cds_wt_709
796824	G			A	A	A	A	cds_wt_710
798663	G			A	A	A	A	cds_wt_712
810530	G						A	cds_wt_724
810533	C						G	-
810556	T						T/C	cds_wt_725
810557	G						G/C	cds_wt_725
810563	C						C/T	cds_wt_725
810576	A						A/G	cds_wt_725
819250	G		A	A	A	A	A	cds_wt_730
829153	C	T	T	T	T	T	T	cds_wt_739
830171	C						T	cds_wt_740
831404	G		A	A	A	A	A	cds_wt_741
838352	G						A	cds_wt_748
842068	G		A	A	A	A	A	cds_wt_750
847887	G					A	A	cds_wt_753
861775	C	T	T	T	T	T	T	cds_wt_768
870304	G		A	A	A	A	A	cds_wt_776
880820	C	T	T	T	T	T	T	cds_wt_785
897424	C	T	T	T	T	T	T	cds_wt_794
907842	G	A	A	A	A	A	A	cds_wt_799
908987	C	T	T	T	T	T	T	-
921289	G		A	A	A	A	A	cds_wt_813
941088	G	A	A	A	A	A	A	cds_wt_829
945666	G				A	A	A	cds_wt_834
959932	C						T	cds_wt_847
964504	G		A	A	A	A	A	cds_wt_850
964558	C					T	T	cds_wt_850
970334	C	T	T	T	T	T	T	cds_wt_857
972781	C		T	T	T		T	cds_wt_860
995285	G		A	A	A	A	A	cds_wt_879
1004653	C						T	-
1006503	C	T	T	T	T	T	T	cds_wt_889
1008680	G						A	cds_wt_890
1009674	G	A	A	A	A	A	A	cds_wt_893
1009813	G						A	cds_wt_893
1023301	C		T	T	T	T	T	cds_wt_902
1028963	G		A	A	A	A	A	cds_wt_908
1030345	C	T	T	T	T	T	T	cds_wt_910
1030822	G		A	A	A	A	A	cds_wt_911
1037262	G		A	A	A	A	A	cds_wt_917
1041811	C		T	T	T	T	T	cds_wt_919

1054013	C		T	T	T	T	T	-
1055406	C	T	T	T	T	T	T	-
1082623	G			A	A		A	cds_wt_952
1085482	C					T	T	cds_wt_953
1085499	C		T	T	T	T	T	cds_wt_953
1088995	C	T	T	T	T	T	T	cds_wt_956
1097530	C			T	T	T	T	cds_wt_967
1107807	T						A	-
1117905	C					T	T	-
1119169	G					A	A	cds_wt_987
1120103	G	A					A	cds_wt_989
1120852	G	A	A	A	A	A	A	cds_wt_990
1122832	C					T	T	cds_wt_990
1123080	C		T	T	T	T	T	cds_wt_990
1128153	G		A	A	A	A	A	cds_wt_993
1130585	G		A	A	A	A	A	cds_wt_999
1145784	C					T	T	cds_wt_1014
1146897	G		A	A	A	A	A	cds_wt_1015
1153166	C						T	cds_wt_1021
1163219	C					T	T	cds_wt_1027
1163309	G		A	A	A	A	A	cds_wt_1027
1163538	G			A	A		A	cds_wt_1027
1169629	C				T	T	T	cds_wt_1032
1169882	C					T	T	cds_wt_1032
1170591	C				T	T	T	cds_wt_1032
1172808	C					T	T	cds_wt_1035
1172940	C		T	T	T	T	T	cds_wt_1035
1173551	C		T	T	T	T	T	cds_wt_1035
1179238	C		T	T	T	T	T	-
1192548	C					T	T	cds_wt_1050
1194346	C		T	T	T	T	T	cds_wt_1051
1194637	G	A	A	A	A	A	A	cds_wt_1051
1196403	C	T	T	T	T	T	T	cds_wt_1053
1208932	C						T	cds_wt_1065
1221399	C					T	T	cds_wt_1081
1222202	C		T	T	T	T	T	cds_wt_1083
1225212	C					T	T	cds_wt_1086
1242677	G		A	A	A	A	A	cds_wt_1101
1249095	C					T	T	cds_wt_1105
1250477	G						A	-
1255855	C	T	T	T	T	T	T	-
1260719	C	T		T	T		T	cds_wt_1114
1261347	C						T	cds_wt_1114
1261926	C	T	T	T	T	T	T	cds_wt_1115
1262307	G		A	A	A	A	A	cds_wt_1115
1262367	G		A	A	A	A	A	cds_wt_1115

1267545	C					T	T	cds_wt_1120
1270664	C					T	T	cds_wt_1122
1272928	C					T	T	cds_wt_1123
1273797	C					T	T	cds_wt_1124
1277491	G	A		A	A		A	cds_wt_1127
1282245	G						A	cds_wt_1131
1284346	C					T	T	cds_wt_1134
1285883	C	T	T	T	T	T	T	cds_wt_1136
1291340	C					T	T	cds_wt_1144
1300654	G		A	A	A	A	A	cds_wt_1155
1306705	C					T	T	-
1307526	C	T	T	T	T	T	T	-
1308200	C	T	T	T	T	T	T	cds_wt_1161
1315876	C					T	T	cds_wt_1170
1317961	G	A	A	A	A	A	A	cds_wt_1172
1321981	C				T	T	T	cds_wt_1176
1322304	C					T	T	cds_wt_1176
1325473	C				T	T	T	cds_wt_1179
1325983	G	A	A	A	A	A	A	cds_wt_1180
1327837	C					T	T	cds_wt_1183
1329364	C				T	T	T	cds_wt_1185
1330802	G		A	A	A	A	A	cds_wt_1186
1335338	C		T	T	T		T	cds_wt_1189
1342390	C					T	T	cds_wt_1195
1343472	A				C	C	C	cds_wt_1196
1344261	C					T	T	cds_wt_1196
1346995	C					T	T	-
1348395	G					A	A	cds_wt_1202
1351344	C					T	T	cds_wt_1204
1352745	C				T	T	T	cds_wt_1206
1356389	C				T	T	T	-
1359105	G		A	A	A	A	A	cds_wt_1210
1359182	C					T	T	cds_wt_1210
1362032	C					T	T	cds_wt_1212
1370065	G		A	A	A	A	A	cds_wt_1221
1370088	C	T	T	T	T	T	T	cds_wt_1221
1379821	C						T	cds_wt_1228
1382638	G		A	A	A	A	A	cds_wt_1232
1388800	C		T	T	T	T	T	cds_wt_1238
1404278	C	T					T	cds_wt_1248
1409508	G					A	A	cds_wt_1254
1410045	G					A	A	-
1413757	G					A	A	cds_wt_1259
1415711	G					A	A	cds_wt_1262
1415773	G					A	A	cds_wt_1262
1418132	C					T	T	cds_wt_1264

1419671	G					A	A	cds_wt_1265
1420016	C					T	T	cds_wt_1265
1428228	C		T	T	T	T	T	cds_wt_1270
1428233	C	T	T	T	T	T	T	cds_wt_1270
1435884	C					T	T	cds_wt_1279
1438355	C					T	T	cds_wt_1282
1440872	G				A	A	A	cds_wt_1282
1443149	C						T	cds_wt_1285
1450678	G		A	A	A	A	A	cds_wt_1294
1453590	G		A	A	A	A	A	cds_wt_1296
1454075	C						T	cds_wt_1297
1455191	G		A	A	A	A	A	cds_wt_1298
1463521	C			T	T	T	T	cds_wt_1303
1473239	C		T	T	T	T	T	cds_wt_1311
1474775	G					A	A	cds_wt_1312
1482297	C				T	T	T	cds_wt_1318
1494980	G					A	A	cds_wt_1326
1502729	G	A	A	A	A	A	A	cds_wt_1332
1514463	C	T					T	-
1525258	G						A	cds_wt_1357
1533361	C						T	cds_wt_1364
1545597	T						T/C	-
1563822	C		T	T	T	T	T	cds_wt_1394
1563854	C	T	T	T	T	T	T	cds_wt_1394
1565818	C						T	cds_wt_1396
1566866	C					T	T	cds_wt_1397
1570236	G					A	A	cds_wt_1398
1570636	C	T	T	T	T	T	T	cds_wt_1399
1581033	T		C	C	C	C	C	cds_wt_1411
1594972	G	A	A	A	A	A	A	cds_wt_1426
1614616	C		T	T	T	T	T	cds_wt_1441
1615586	C		T	T	T	T	T	cds_wt_1441
1616152	C		T	T	T	T	T	cds_wt_1442
1616981	C			T	T	T	T	cds_wt_1443
1617561	C			T		T	T	cds_wt_1443
1617928	C	T	T	T	T	T	T	cds_wt_1444
1622589	G	A	A	A	A	A	A	cds_wt_1447
1641656	C	T					T	cds_wt_1457
1641711	C						T	cds_wt_1457
1641953	C			T		T	T	cds_wt_1458
1648653	G		A	A	A	A	A	cds_wt_1466
1648676	G		A	A	A	A	A	cds_wt_1466
1649444	C					T	T	-
1650400	G	A	A	A	A	A	A	-
1658589	G					A	A	cds_wt_1467
1661376	G						A	cds_wt_1469

1664324	C					T	T	cds_wt_1474
1680524	C	T	T	T	T	T	T	cds_wt_1485
1682349	G			A	A	A	A	cds_wt_1485
1682842	C					T	T	cds_wt_1486
1686608	C				T	T	T	cds_wt_1490
1695571	C		T	T	T	T	T	cds_wt_1495
1699167	G		A	A	A	A	A	cds_wt_1499
1700705	G						A	cds_wt_1501
1715788	T						C	cds_wt_1517
1727072	G		A	A	A	A	A	cds_wt_1526
1747963	C	T	T	T	T	T	T	cds_wt_1546
1748448	C					T	T	cds_wt_1547
1778278	C					T	T	cds_wt_1569
1779396	C		T	T	T	T	T	cds_wt_1570
1779723	C		T	T	T	T	T	cds_wt_1570
1792608	G		A	A	A	A	A	cds_wt_1583
1793069	C					T	T	cds_wt_1584
1795610	C					T	T	cds_wt_1588
1803172	C		T	T	T	T	T	-
1805902	C	T	T	T	T	T	T	cds_wt_1595
1815104	C	T	T	T	T	T	T	cds_wt_1601
1848170	G						A	cds_wt_1640
1858054	C				T	T	T	cds_wt_1649
1874864	G		A	A	A	A	A	cds_wt_1664
1878368	C		T	T	T	T	T	cds_wt_1669
1878456	C		T	T	T	T	T	cds_wt_1669
1881797	G		A	A	A	A	A	cds_wt_1671
1881821	G		A	A	A	A	A	cds_wt_1671
1883780	G		A	A	A	A	A	cds_wt_1673
1886024	G	A	A	A	A	A	A	cds_wt_1677
1886177	G		A	A	A	A	A	cds_wt_1677
1886499	G	A	A	A	A	A	A	cds_wt_1677
1888003	G						A	cds_wt_1678
1888277	G		A	A	A	A	A	-
1891012	G		A	A	A	A	A	cds_wt_1680
1891205	C	T	T	T	T	T	T	cds_wt_1681
1891493	G		A	A	A	A	A	cds_wt_1682
1891608	G		A	A	A	A	A	cds_wt_1682
1895230	C						T	cds_wt_1683
1896121	G		A	A	A	A	A	cds_wt_1684
1898465	G		A	A	A	A	A	cds_wt_1686
1904126	G		A	A	A	A	A	cds_wt_1689
1904415	G		A	A	A	A	A	cds_wt_1689
1918600	G					A	A	cds_wt_1702
1926767	G					A	A	cds_wt_1710
1930239	G	A	A	A	A	A	A	-

1933689	G		A	A	A	A	A	cds_wt_1718
1935111	G			A	A	A	A	cds_wt_1721
1938524	G		A	A	A	A	A	cds_wt_1725
1941158	G		A	A	A	A	A	cds_wt_1729
1950155	C				T		T	cds_wt_1737
1961896	C				T	T	T	cds_wt_1749
1964247	C						T	-
1971635	A					C	C	cds_wt_1755
1973884	G		A	A	A	A	A	cds_wt_1756
1985968	G	A	A	A	A	A	A	cds_wt_1769
1986215	C						T	cds_wt_1769
1987891	C					T	T	cds_wt_1770
1987907	C					T	T	cds_wt_1770
1993612	G		A	A	A	A	A	cds_wt_1778
1997079	C		T	T	T	T	T	cds_wt_1783
2043866	G					A	A	cds_wt_1830
2043889	G					A	A	cds_wt_1830
2048938	C						T	cds_wt_1835
2058063	G		A	A	A	A	A	cds_wt_1841
2058998	G	A	A	A	A	A	A	cds_wt_1841
2060664	G		A	A	A	A	A	cds_wt_1843
2060796	G		A	A	A	A	A	cds_wt_1843
2067415	G						A	-
2067911	G	A	A	A	A	A	A	cds_wt_1851
2071535	G						A	cds_wt_1854
2077305	A						G/A	-
2077309	T						C/T	-
2077321	A						G/A	-
2077324	G						A/G	-
2077336	A						G/A	-
2077351	C						T/C	-
2077353	A						G/A	-
2077369	C						T/C	-
2077383	G	G/A	G/A	G/A	G/A	G/A	A/G	-
2077384	C	C/G	C/G	C/G	C/G	C/G	G/C	-
2077398	G	G/C	G/C	G/C	G/C	G/C	G/C	-
2077432	T						C/T	-
2077603	A						G/A	cds_wt_1862
2077615	C						A/C	cds_wt_1862
2077618	G						A/G	cds_wt_1862
2077636	T						C/T	cds_wt_1862
2077645	G						C/G	cds_wt_1862
2077651	G						C/G	cds_wt_1862
2077652	A						G/A	cds_wt_1862
2077654	A						G/A	cds_wt_1862
2077663	C						A/C	cds_wt_1862

2077669	G						C/G	cds_wt_1862
2077671	T						C/T	cds_wt_1862
2077682	C						G/C	cds_wt_1862
2077688	G						A/G	cds_wt_1862
2077691	C						G/C	cds_wt_1862
2077694	A						C/A	cds_wt_1862
2077697	G						C/G	cds_wt_1862
2077703	T						G/T	cds_wt_1862
2077715	G						A/G	cds_wt_1862
2077724	A						G/A	cds_wt_1862
2077726	C						T/C	cds_wt_1862
2077730	G						C/G	cds_wt_1862
2077733	G						A/G	cds_wt_1862
2077736	C						C/T	cds_wt_1862
2077742	G						C/G	cds_wt_1862
2077745	A						G/A	cds_wt_1862
2077751	G						A/G	cds_wt_1862
2077762	T						C/T	cds_wt_1862
2077769	T						C/T	cds_wt_1862
2077772	A						G/A	cds_wt_1862
2077775	G						A/G	cds_wt_1862
2077793	G						C/G	cds_wt_1862
2077794	A						G/A	cds_wt_1862
2077795	C						T/C	cds_wt_1862
2077805	C						T/C	cds_wt_1862
2080486	C						T	cds_wt_1864
2086608	G		A	A	A	A	A	cds_wt_1866
2096915	G		A	A	A	A	A	cds_wt_1878
2098836	C	T	T	T	T	T	T	cds_wt_1880
2099830	G						A	cds_wt_1880
2126265	C		T	T	T	T	T	-
2131730	G		A	A	A	A	A	cds_wt_1909
2135109	C						T	cds_wt_1912
2136848	C		T	T	T	T	T	-
2144528	G	A	A	A	A	A	A	cds_wt_1918
2147486	G		A	A	A	A	A	cds_wt_1921
2154132	C	T	T	T	T	T	T	cds_wt_1927
2154136	C	T	T	T	T	T	T	cds_wt_1927
2188490	C				T	T	T	cds_wt_1959
2191494	C	T	T	T	T	T	T	cds_wt_1960
2199567	G		A	A	A	A	A	cds_wt_1969
2208975	G	A	A	A	A	A	A	cds_wt_1977
2212324	G				A	A	A	cds_wt_1979
2212659	G		A	A	A	A	A	cds_wt_1980
2230643	G		A	A	A	A	A	cds_wt_1996
2235434	G		A	A	A	A	A	cds_wt_2000

2250499	C	T	T	T	T	T	T	cds_wt_2012
2259118	C			T	T		T	cds_wt_2019
2260582	G						A	cds_wt_2019
2266821	C	T	T		T	T	T	cds_wt_2023
2271223	G	A	A	A	A	A	A	cds_wt_2027
2273696	C	T	T	T	T	T	T	-
2277990	C	T					T	cds_wt_2031
2291798	C		T	T	T	T	T	cds_wt_2032
2293101	C						C/T	cds_wt_2033
2293102	G						G/T	cds_wt_2033
2293121	G	C/G	C/G	C/G	C/G	C/G	G/C	cds_wt_2033
2293139	A	C/A	C/A	C/A	C/A	C/A	A/C	cds_wt_2033
2293157	G	G/A	G/A	G/A	G/A	G/A	G/A	cds_wt_2033
2293169	G						G/C	cds_wt_2033
2293175	G						G/A	cds_wt_2033
2293176	A						A/T	cds_wt_2033
2293184	C						C/G	cds_wt_2033
2293185	G						G/A	cds_wt_2033
2293187	A						A/G	cds_wt_2033
2293196	G						A/G	cds_wt_2033
2293202	G						G/C	cds_wt_2033
2293205	G						C/G	cds_wt_2033
2293214	G						G/C	cds_wt_2033
2293219	A						A/T	cds_wt_2033
2293220	G						G/C	cds_wt_2033
2293226	G						C/G	cds_wt_2033
2293228	G						G/A	cds_wt_2033
2293234	A						A/T	cds_wt_2033
2293235	G						G/C	cds_wt_2033
2293238	G						G/C	cds_wt_2033
2293244	G						G/C	cds_wt_2033
2293247	G						A/G	cds_wt_2033
2293253	G	G/A	A	G/A	G/A	A/G	A/G	cds_wt_2033
2293268	G	G/C	C	C	C	C	C/G	cds_wt_2033
2293310	G						G/A	cds_wt_2033
2293313	G						G/C	cds_wt_2033
2293316	G						G/A	cds_wt_2033
2293319	G						G/A	cds_wt_2033
2293328	G						G/C	cds_wt_2033
2293337	G						G/C	cds_wt_2033
2293346	G						G/C	cds_wt_2033
2293352	C						C/G	cds_wt_2033
2293367	G	G/C	C/G	G/C			G/C	cds_wt_2033
2293376	C	G/C	G/C	C/G	C/G	C/G	C/G	cds_wt_2033
2293403	C						C/G	cds_wt_2033
2293463	C						C/G	cds_wt_2033

2302130	G						A	cds_wt_2039
2312744	C					T	T	cds_wt_2051
2313183	G			A	A		A	cds_wt_2051
2315988	C	T	T	T	T	T	T	cds_wt_2052
2323085	C	T	T	T	T	T	T	cds_wt_2057
2329242	C	T	T	T	T	T	T	cds_wt_2063
2332081	G		A	A	A	A	A	cds_wt_2066
2341627	C				T		T	cds_wt_2073
2347673	C	T	T	T	T	T	T	cds_wt_2076
2348681	G	A	A	A	A	A	A	cds_wt_2077
2359598	G		A	A	A	A	A	cds_wt_2088
2362060	A						G	cds_wt_2091
2368326	G					A	A	cds_wt_2097
2376154	G	A	A	A	A	A	A	cds_wt_2107
2380176	C		T	T	T	T	T	cds_wt_2113
2382542	C		T	T	T	T	T	cds_wt_2115
2382567	C		T	T	T	T	T	cds_wt_2115
2382748	C		T	T	T	T	T	-
2389975	C				T	T	T	-
2392147	C				T	T	T	cds_wt_2122
2396255	G					A	A	cds_wt_2123
2415101	G		A	A	A		A	cds_wt_2140
2422620	C				T	T	T	cds_wt_2147
2437185	G		A	A	A	A	A	cds_wt_2158
2448470	G		A	A	A	A	A	cds_wt_2169
2452760	G		A	A	A	A	A	cds_wt_2173
2456608	C				T	T	T	cds_wt_2175
2459347	C				T	T	T	cds_wt_2177
2459641	G					A	A	cds_wt_2178
2460824	C				T	T	T	cds_wt_2180
2463427	C						T	cds_wt_2182
2482048	C	T	T	T	T	T	T	cds_wt_2197
2482381	G	A	A	A	A	A	A	cds_wt_2197
2483453	C		T	T	T	T	T	cds_wt_2199
2487377	G	A	A	A	A	A	A	cds_wt_2203
2489641	G		A	A	A	A	A	cds_wt_2206
2492054	G					A	A	-
2502775	G					A	A	-
2515457	G					A	A	cds_wt_2228
2518872	G			A	A	A	A	cds_wt_2232
2530466	G		A	A	A	A	A	cds_wt_2252
2532233	G		A	A	A	A	A	cds_wt_2256
2533237	G		A	A	A	A	A	cds_wt_2259
2536306	G		A	A	A	A	A	-
2538874	G		A	A	A	A	A	cds_wt_2265
2542087	G		A	A	A	A	A	cds_wt_2270

2544720	C					T	T	cds_wt_2270
2553277	G						A	cds_wt_2277
2556662	C					T	T	cds_wt_2283
2559280	G	A	A	A	A	A	A	-
2562212	G					A	A	cds_wt_2288
2564253	G					A	A	-
2564620	G					A	A	-
2566353	G					A	A	cds_wt_2290
2572994	G		A	A	A	A	A	cds_wt_2297
2573153	C		T	T	T	T	T	cds_wt_2297
2575327	G				A		A	cds_wt_2299
2599645	G					A	A	cds_wt_2323
2599894	G					A	A	cds_wt_2324
2601319	G					A	A	cds_wt_2324
2606340	G					A	A	cds_wt_2330
2608948	G					A	A	cds_wt_2334
2610422	C					T	T	-
2614778	G						A	cds_wt_2339
2617082	G					A	A	cds_wt_2340
2618776	C		T	T	T	T	T	cds_wt_2342
2618805	C		T	T	T	T	T	cds_wt_2342
2620558	G					A	A	cds_wt_2344
2626414	A			G	G	G	G	cds_wt_2350
2636037	C					T	T	cds_wt_2357
2639682	G					A	A	cds_wt_2361
2642753	G		A	A	A	A	A	cds_wt_2364
2644984	C					T	T	cds_wt_2364
2651718	C		T	T	T	T	T	cds_wt_2367
2652733	C					T	T	cds_wt_2368
2653074	C					T	T	cds_wt_2368
2653159	C	T	T	T	T	T	T	cds_wt_2368
2653337	G		A	A	A	A	A	cds_wt_2369
2655271	C						T	cds_wt_2371
2655308	C						T	cds_wt_2371
2657059	C					T	T	cds_wt_2371
2658261	G					A	A	cds_wt_2372
2659295	C					T	T	cds_wt_2373
2663775	C					T	T	cds_wt_2376
2670944	C					T	T	cds_wt_2378
2671043	C					T	T	cds_wt_2378
2672551	C					T	T	cds_wt_2380
2676880	C	T	T	T	T	T	T	cds_wt_2382
2677056	G		A	A	A	A	A	cds_wt_2382
2677196	C	T	T	T	T	T	T	cds_wt_2382
2678066	G		A	A	A	A	A	cds_wt_2382
2679900	C					T	T	cds_wt_2383

2686364	C					T	T	cds_wt_2390
2687028	C					T	T	cds_wt_2391
2688632	C					T	T	cds_wt_2392
2694405	G						A	cds_wt_2396
2701281	G					A	A	cds_wt_2403
2712327	G					A	A	-
2720850	C	T	T	T	T	T	T	cds_wt_2418
2728435	G					A	A	cds_wt_2425
2731397	G		A	A	A	A	A	cds_wt_2428
2735550	G	G/A	G/A	G/A	G/A	G/A	G/A	-
2735576	G						G/C	-
2738768	C			T	T	T	T	cds_wt_2433
2744600	C	T	T	T	T	T	T	cds_wt_2438
2748694	C	T	T	T	T	T	T	cds_wt_2442
2756873	C		T	T	T	T	T	cds_wt_2449
2760595	G					A	A	-
2762887	G			A	A	A	A	cds_wt_2453
2763137	G		A	A	A	A	A	cds_wt_2453
2764279	C		T	T	T	T	T	cds_wt_2454
2766645	C			T	T	T	T	cds_wt_2456
2770562	C					T	T	-
2773173	C	T	T	T	T	T	T	cds_wt_2462
2774095	G		A	A	A	A	A	cds_wt_2464
2774734	G		A	A	A	A	A	cds_wt_2465
2774874	G		A	A	A	A	A	cds_wt_2465
2776314	C					T	T	cds_wt_2466
2776919	C		T	T	T	T	T	cds_wt_2467
2778598	G					A	A	cds_wt_2468
2779539	G					A	A	-
2782696	C					T	T	cds_wt_2473
2783578	C					T	T	-
2783738	C					T	T	cds_wt_2474
2785372	C					T	T	cds_wt_2475
2785531	C					T	T	cds_wt_2475
2787379	G		A	A	A	A	A	cds_wt_2476
2788015	C					T	T	cds_wt_2477
2788247	C					T	T	cds_wt_2477
2789216	C		T	T	T	T	T	cds_wt_2478
2790626	C		T	T	T	T	T	cds_wt_2479
2791577	C					T	T	cds_wt_2480
2792510	C					T	T	cds_wt_2481
2792715	G	A	A	A	A	A	A	cds_wt_2481
2797814	C	T	T	T	T	T	T	cds_wt_2487
2799953	C		T	T	T	T	T	cds_wt_2489
2800033	C					T	T	cds_wt_2489
2802765	C					T	T	-

2803789	C		T	T	T	T	T	cds_wt_2493
2804694	C		T	T	T	T	T	cds_wt_2494
2806670	C		T	T	T	T	T	cds_wt_2496
2814611	G						A	-
2815199	C						C/T	cds_wt_2502
2816239	G						A	cds_wt_2503
2821693	G				A	A	A	cds_wt_2509
2838356	C					T	T	-
2841171	T						T/A	cds_wt_2526
2841177	C						C/G	cds_wt_2526
2841183	C						C/G	cds_wt_2526
2841213	T						T/C	cds_wt_2526
2841228	C						C/G	cds_wt_2526
2841237	G						G/C	cds_wt_2526
2841251	G						G/T	cds_wt_2526
2841255	C						C/G	cds_wt_2526
2841258	G						G/T	cds_wt_2526
2841276	C	G/C		G	G	G	C/G	cds_wt_2526
2841293	C						C/G	cds_wt_2526
2841297	C						C/A	cds_wt_2526
2841303	C						C/T	cds_wt_2526
2841306	G						G/A	cds_wt_2526
2841312	T						C/T	cds_wt_2526
2841315	C						G/C	cds_wt_2526
2841322	A						A/T	cds_wt_2526
2841323	G						G/T	cds_wt_2526
2841327	C						G/C	cds_wt_2526
2841335	G						C/G	cds_wt_2526
2841357	G						C/G	cds_wt_2526
2841360	G						C/G	cds_wt_2526
2841369	G						C/G	cds_wt_2526
2841376	T						T/C	cds_wt_2526
2841377	G						T/G	cds_wt_2526
2841384	G						C/G	cds_wt_2526
2841389	T						T/C	cds_wt_2526
2841397	G						G/T	cds_wt_2526
2841398	A						C/A	cds_wt_2526
2841402	G						A/G	cds_wt_2526
2841403	G						C/G	cds_wt_2526
2841409	T						A/T	cds_wt_2526
2841413	G						T/G	cds_wt_2526
2841423	C						G/C	cds_wt_2526
2841444	G						C/G	cds_wt_2526
2841451	C						T/C	cds_wt_2526
2841477	C						G/C	cds_wt_2526
2841514	G						T/G	cds_wt_2526

2841531	A						G/A	cds_wt_2526
2841534	G						C/G	cds_wt_2526
2841536	T						A/T	cds_wt_2526
2841540	C						C/G	cds_wt_2526
2841546	G						C/G	cds_wt_2526
2841552	G						C	cds_wt_2526
2841554	T						C/T	cds_wt_2526
2841555	C						T/C	cds_wt_2526
2841562	C						T/C	cds_wt_2526
2841563	A						C/A	cds_wt_2526
2841569	A						C/A/T	cds_wt_2526
2841575	C						T/C	cds_wt_2526
2841585	C						C/G	cds_wt_2526
2841588	G						C/G	cds_wt_2526
2841594	G						A/G	cds_wt_2526
2841605	C						C/A	cds_wt_2526
2841609	C						C/G	cds_wt_2526
2841617	T						G/T	cds_wt_2526
2841636	G	C		C	C		C/G	cds_wt_2526
2841656	A						C/A	cds_wt_2526
2841660	G						C/G	cds_wt_2526
2841668	C						T/C	cds_wt_2526
2841690	G						C/G	-
2841700	G						T	-
2841701	C						T	-
2841708	G						A/G	-
2841734	T						C	-
2841735	C						T	-
2841738	G						C	-
2841744	C						G/C	-
2841747	G						A	-
2841756	C						G	-
2841759	G						C	-
2841762	C						G	-
2841776	G						T	-
2841778	T						G	-
2841783	G						C	-
2841786	A						T	-
2841789	C						T	-
2845157	G		A	A	A	A	A	cds_wt_2528
2850318	G			A	A	A	A	cds_wt_2533
2851372	G						A	cds_wt_2534
2853353	C		T	T	T	T	T	cds_wt_2535
2853817	G						A	cds_wt_2535
2868405	C	T	T	T	T	T	T	cds_wt_2548
2874011	C		T	T	T	T	T	cds_wt_2551

2875055	G		A	A	A	A	A	-
2875488	G				A	A	A	-
2876911	G	A					A	cds_wt_2553
2882407	C		T	T	T	T	T	cds_wt_2558
2888545	C		T	T	T	T	T	cds_wt_2562
2890510	C	T	T	T	T	T	T	cds_wt_2565
2892791	G						A	cds_wt_2566
2896239	G	A					A	cds_wt_2568
2896828	G	A	A	A	A	A	A	cds_wt_2568
2896833	G	A	A	A	A	A	A	cds_wt_2568
2899845	C	T	T	T	T	T	T	-
2899865	C	T	T	T	T	T	T	-
2901123	C		T	T	T	T	T	cds_wt_2572
2905469	C		T	T	T	T	T	cds_wt_2574
2912026	G	A	A	A	A	A	A	cds_wt_2580
2921100	C					T	T	cds_wt_2587
2934976	G	A	A	A	A	A	A	-
2935134	G						A	-
2935223	G				A	A	A	-
2945715	G		A	A	A	A	A	cds_wt_2611
2953167	C	T	T	T	T	T	T	cds_wt_2616
2956464	C	T	T	T	T	T	T	cds_wt_2620
2965167	G						A	cds_wt_2630
2971031	C	T	T	T	T	T	T	cds_wt_2633
2971761	C	T	T	T	T	T	T	cds_wt_2633
2973653	C	T	T	T	T	T	T	cds_wt_2634
2976296	C	T					T	cds_wt_2637
2978371	C	T	T	T	T	T	T	cds_wt_2638
2983351	G		A	A	A	A	A	cds_wt_2644
2986416	C	T	T	T	T	T	T	cds_wt_2649
2987675	C	T	T	T	T	T	T	cds_wt_2650
2988967	C	T	T	T	T	T	T	cds_wt_2650
2992035	C					T	T	cds_wt_2651
2993614	A						G	cds_wt_2652
2994097	G	A	A	A	A	A	A	cds_wt_2652
3000921	G	A	A	A	A	A	A	cds_wt_2658
3002748	G				A	A	A	cds_wt_2659
3003382	G					A	A	-
3005352	G				A	A	A	cds_wt_2662
3006201	C				T		T	cds_wt_2662
3021497	G		A	A	A	A	A	cds_wt_2674
3026718	C					T	T	-
3027132	G				A	A	A	-
3031683	C		T	T	T	T	T	-
3032969	C		T	T	T	T	T	-
3044082	G						A	cds_wt_2679

3045579	G	A	A	A	A	A	A	cds_wt_2679
3049857	G						A	cds_wt_2681
3066905	C					T	T	cds_wt_2697
3079916	T						A/T	-
3079923	C						C/T	-
3079936	G						A/G	-
3079950	A	T/A					T/A	-
3080004	C						C/T	-
3080006	A						T/A	-
3080035	C	C/T					C/T	cds_wt_2713
3080043	A	C/A	C/A	C/A	C/A	C/A	C/A	cds_wt_2713
3080063	G	C/G	C/G	C/G	C/G	C/G	C/G	cds_wt_2713
3080084	C	C/T	C/T	C/T	C/T	C/T	C/T	cds_wt_2713
3080087	G	G/C/T	G/C/T	C/G/T	G/C/T	G/T/C	C/T/G	cds_wt_2713
3080098	C					C/A	C/A	cds_wt_2713
3080128	C					T/C	T/C	cds_wt_2713
3080136	A					G/A	G/A	cds_wt_2713
3080160	C						G/C	cds_wt_2713
3080161	T						C/T	cds_wt_2713
3080163	T						C/T	cds_wt_2713
3080183	T	T/C	T/C	T/C	T/C	T/C	C/T	cds_wt_2713
3080192	G	C/G	C/G	C/G	C/G	C/G	C/G	cds_wt_2713
3080204	G	C/G	C/G	C/G	C/G	C/G	C/G	cds_wt_2713
3080237	G						C/G	cds_wt_2713
3080288	G						C/G	cds_wt_2713
3080294	G						T/G	cds_wt_2713
3080316	C						C/T	-
3080321	T		T/C	T/C	T/C	T/C	T/C	-
3080325	G	G/T	G/T	G/T	G/T	G/T	T/G	-
3080326	C	C/T	C/T	C/T	C/T	C/T	T/C	-
3080355	A	A/T	A/T	A/T	A/T	A/T	T/A	-
3080356	A						A/G	-
3080357	A	A/G	A/G	A/G	A/G	A/G	A/G	-
3080359	A						A/G	-
3080372	A	A/G	A/G	A/G	A/G	A/G	A/G	-
3080375	A						A/C	-
3080382	G						G/A	-
3080391	A						A/G	-
3080393	C						C/T	-
3080394	G						G/A	-
3080402	A						A/G	-
3080406	A						A/G	-
3080418	A						A/G	-
3080447	C						C/T	-
3080465	T						T/C	-
3080472	C						C/T	-

3080482	A						A/G	-
3080485	C						C/T	-
3080496	T						T/C	-
3082062	G						A	-
3084014	G	A	A	A	A	A	A	cds_wt_2717
3087970	C		T	T	T	T	T	cds_wt_2721
3089578	G			A	A	A	A	-
3090231	G						G/C	cds_wt_2723
3101153	G		A	A	A	A	A	cds_wt_2729
3120006	C			T	T	T	T	-
3121040	C		T	T	T	T	T	-
3125035	C		T	T	T	T	T	cds_wt_2746
3125407	C						T	cds_wt_2746
3128098	C		T	T	T	T	T	cds_wt_2749
3131738	C		T	T	T	T	T	cds_wt_2753
3133651	C		T	T	T	T	T	cds_wt_2755
3133766	G	A	A	A	A	A	A	cds_wt_2755
3137673	C					T	T	cds_wt_2759
3138173	G	A	A	A	A	A	A	cds_wt_2760
3147694	C				T	T	T	cds_wt_2765
3148142	C		T	T	T	T	T	cds_wt_2766
3148342	C		T	T	T	T	T	cds_wt_2766
3148452	C		T	T	T	T	T	cds_wt_2766
3148777	C		T	T	T	T	T	cds_wt_2766
3148960	C		T	T	T	T	T	cds_wt_2766
3149335	C		T	T	T	T	T	cds_wt_2766
3151547	C						T	-
3152279	C		T	T	T	T	T	-
3153365	G	A	A	A	A	A	A	-
3156844	C				T	T	T	cds_wt_2777
3175067	G	A	A	A	A	A	A	cds_wt_2796
3176311	C			T		T	T	cds_wt_2797
3180510	C			T	T	T	T	cds_wt_2801
3181134	C		T	T	T	T	T	cds_wt_2803
3196810	C						T	cds_wt_2815
3198674	G	A	A	A	A	A	A	cds_wt_2817
3203788	G						A	cds_wt_2823
3204764	G						A	cds_wt_2823
3208464	G			A	A	A	A	cds_wt_2826
3213080	C		T	T	T	T	T	cds_wt_2831
3214059	C					T	T	cds_wt_2832
3216019	C			T	T		T	cds_wt_2834
3216133	C						T	cds_wt_2834
3218109	C			T	T	T	T	cds_wt_2834
3226281	C					T	T	cds_wt_2841
3229241	G				A	A	A	cds_wt_2845

3230387	G				A	A	A	cds_wt_2847
3235932	C		T	T	T	T	T	cds_wt_2851
3237109	C	T	T	T	T	T	T	cds_wt_2851
3238700	C		T	T	T	T	T	cds_wt_2854
3241279	C		T	T	T	T	T	cds_wt_2857
3241643	G				A	A	A	cds_wt_2857
3245145	C				T	T	T	cds_wt_2860
3247705	G		A	A	A	A	A	cds_wt_2861
3248186	G		A	A	A	A	A	cds_wt_2862
3249319	C		T	T	T	T	T	cds_wt_2862
3251559	G		A	A	A	A	A	-
3253347	C		T	T	T	T	T	-
3253453	C		T	T	T	T	T	cds_wt_2867
3253884	G				A	A	A	-
3254464	G				A	A	A	-
3258028	G			A	A	A	A	cds_wt_2872
3258094	G			A	A		A	-
3258637	C		T	T	T	T	T	-
3259667	C			T	T		T	cds_wt_2874
3261792	G			A	A	A	A	cds_wt_2876
3262978	C	T	T	T	T	T	T	cds_wt_2876
3266668	G		A	A	A	A	A	cds_wt_2879
3266806	C	T	T	T	T	T	T	cds_wt_2879
3267341	G			A	A	A	A	cds_wt_2880
3267927	C		T	T	T	T	T	cds_wt_2880
3268140	T		C	C	C	C	C	cds_wt_2880
3269676	G		A	A	A	A	A	cds_wt_2882
3270548	G			A	A	A	A	cds_wt_2882
3275254	A		G	G	G	G	G	cds_wt_2885
3276870	C		T	T	T	T	T	cds_wt_2888
3277187	C	T	T	T	T	T	T	-
3279932	C		T	T	T	T	T	-
3285105	C		T	T	T	T	T	cds_wt_2902
3289175	C						T	cds_wt_2903
3289533	C			T	T	T	T	cds_wt_2903
3290417	G				A		A	cds_wt_2904
3290880	C			T	T	T	T	-
3291408	C	T	T	T	T	T	T	cds_wt_2906
3294618	C		T	T	T	T	T	cds_wt_2909
3295292	C		T	T	T	T	T	-
3296150	C		T	T	T	T	T	-
3296689	C		T	T	T	T	T	cds_wt_2910
3297254	C		T	T	T	T	T	cds_wt_2910
3297593	G						A	cds_wt_2910
3297802	C		T	T	T	T	T	cds_wt_2910
3297816	G						A	cds_wt_2910

3299219	C		T	T	T	T	T	-
3300457	C		T	T	T	T	T	cds_wt_2914
3300838	C	T		T	T	T	T	cds_wt_2914
3300849	C	T	T	T	T	T	T	cds_wt_2914
3307410	G		A	A	A	A	A	-
3307738	G		A	A	A	A	A	-
3309205	C		T	T	T	T	T	cds_wt_2919
3309441	G						A	cds_wt_2919
3313410	C		T	T	T	T	T	cds_wt_2923
3314734	C		T	T	T	T	T	cds_wt_2925
3315483	C		T	T	T	T	T	cds_wt_2925
3316995	C						T	cds_wt_2926
3318906	C		T	T	T	T	T	cds_wt_2927
3319964	C			T	T	T	T	cds_wt_2928
3321895	G		A	A	A	A	A	cds_wt_2929
3326784	G		A	A	A	A	A	cds_wt_2933
3327191	G		A	A	A	A	A	cds_wt_2934
3328753	C		T	T	T	T	T	cds_wt_2934
3336319	C		T	T	T	T	T	cds_wt_2941
3337206	G					A	A	cds_wt_2941
3338688	C		T	T	T	T	T	cds_wt_2943
3345311	C		T	T	T	T	T	cds_wt_2947
3346757	G					A	A	cds_wt_2947
3347355	C				T	T	T	cds_wt_2947
3347540	C				T	T	T	cds_wt_2947
3347560	C				T	T	T	cds_wt_2947
3348860	C		T	T	T	T	T	-
3349015	C				T	T	T	cds_wt_2949
3349651	C				T	T	T	cds_wt_2949
3350820	C		T	T	T	T	T	cds_wt_2951
3351613	C		T	T	T	T	T	cds_wt_2953
3353030	C			T	T	T	T	cds_wt_2954
3354271	C				T	T	T	cds_wt_2954
3354637	C				T	T	T	cds_wt_2955
3358411	G						G/A	-
3358883	G					A	A	-
3361525	G	A	A	A	A	A	A	cds_wt_2960
3363657	C		T	T	T	T	T	-
3368167	C		T	T	T	T	T	-
3368381	C						C/T	cds_wt_2966
3375301	C		T	T	T	T	T	cds_wt_2971
3381507	C						T	cds_wt_2978
3383846	C		T	T	T	T	T	cds_wt_2982
3386322	C			T	T	T	T	cds_wt_2985
3386914	G		A	A	A	A	A	cds_wt_2986
3388650	C		T	T	T	T	T	cds_wt_2988

3388663	C			T	T	T	T	cds_wt_2988
3388840	G	A	A	A	A	A	A	cds_wt_2988
3390202	G			A	A	A	A	cds_wt_2990
3391187	C		T	T	T	T	T	cds_wt_2991
3394129	C		T	T	T	T	T	cds_wt_2995
3395838	C		T	T	T	T	T	cds_wt_2996
3396692	C						T	cds_wt_2997
3397717	C		T	T	T	T	T	cds_wt_2998
3400152	C		T	T	T	T	T	cds_wt_3000
3402866	G		A	A	A	A	A	cds_wt_3004
3403044	C					T	T	cds_wt_3004
3403253	C		T	T	T	T	T	cds_wt_3004
3404959	C		T	T	T	T	T	cds_wt_3006
3405078	C	T	T	T	T	T	T	-
3409620	G				A		A	cds_wt_3009
3412544	G		A	A	A	A	A	cds_wt_3012
3415574	A	G	G	G	G	G	G	cds_wt_3016
3418558	C			T	T	T	T	-
3418906	G		A	A	A	A	A	-
3420004	C		T	T	T	T	T	cds_wt_3019
3420345	C					T	T	cds_wt_3019
3429994	C					T	T	cds_wt_3030
3430020	G	A	A	A	A	A	A	cds_wt_3030
3431269	C		T	T	T	T	T	cds_wt_3032
3432683	G				A	A	A	-
3433788	G				A	A	A	-
3434662	C		T	T	T	T	T	cds_wt_3034
3435439	G				A	A	A	cds_wt_3035
3435661	G				A	A	A	cds_wt_3035
3440357	G				A	A	A	cds_wt_3039
3441404	C					T	T	-
3453288	C						T	cds_wt_3048
3454769	G				A	A	A	cds_wt_3048
3456480	C		T	T	T	T	T	-
3457161	C				T	T	T	cds_wt_3050
3461043	C	T	T	T	T	T	T	cds_wt_3053
3461116	G		A	A	A	A	A	cds_wt_3053
3464902	C	T	T	T	T	T	T	cds_wt_3057
3469479	C		T	T	T	T	T	-
3473066	G	A		A	A		A	cds_wt_3065
3474749	C		T	T	T	T	T	-
3484337	G		A	A	A	A	A	cds_wt_3076
3484696	C		T	T	T	T	T	cds_wt_3077
3490633	G	A	A	A	A	A	A	cds_wt_3080
3511395	C			T	T	T	T	-
3517523	G	A	A	A	A	A	A	-

3518338	C		T	T	T	T	T	cds_wt_3100
3519210	C	T	T	T	T	T	T	cds_wt_3102
3519280	C	T	T	T	T	T	T	cds_wt_3102
3526212	G	A	A	A	A	A	A	cds_wt_3108
3526229	G	A	A				A	cds_wt_3108
3532172	C					T	T	cds_wt_3117
3532281	C			T	T	T	T	cds_wt_3117
3539856	C		T	T	T	T	T	cds_wt_3124
3540438	C				T	T	T	cds_wt_3124
3540952	C			T	T	T	T	cds_wt_3125
3553678	G					A	A	cds_wt_3135
3558780	G		A	A	A	A	A	cds_wt_3138
3559503	G	A	A	A	A	A	A	cds_wt_3139
3560298	T		C	C	C	C	C	cds_wt_3140
3572036	C		T	T	T	T	T	cds_wt_3152
3587529	C		T	T	T	T	T	-
3590513	C		T	T	T	T	T	cds_wt_3168
3590937	C		T	T	T	T	T	cds_wt_3168
3596971	C						T	cds_wt_3175
3601304	C		T	T	T	T	T	-
3610733	G			A	A	A	A	-
3613460	C						T	cds_wt_3186
3617806	G		A	A	A	A	A	cds_wt_3189
3618063	C	T	T	T	T	T	T	cds_wt_3189
3618082	G						A	cds_wt_3189
3621113	G		A	A	A	A	A	cds_wt_3191
3625554	C		T	T	T	T	T	cds_wt_3196
3626449	C				T	T	T	cds_wt_3198
3626548	C				T	T	T	cds_wt_3198
3627377	C	T	T	T	T	T	T	cds_wt_3199
3627686	C				T	T	T	cds_wt_3199
3628977	C		T	T	T	T	T	cds_wt_3199
3632788	C					T	T	cds_wt_3200
3647003	C			T	T	T	T	cds_wt_3215
3650159	G						A	cds_wt_3219
3658514	C					T	T	cds_wt_3227
3659174	C	T	T	T	T	T	T	cds_wt_3228
3672218	G	A	A	A	A	A	A	cds_wt_3242
3695232	G	A	A	A	A	A	A	cds_wt_3263
3702963	C		T	T	T	T	T	cds_wt_3268
3704185	C		T	T	T	T	T	cds_wt_3269
3704278	G						G/C	cds_wt_3269
3704281	T						T/G	cds_wt_3269
3704282	C						C/T	cds_wt_3269
3704293	T						T/G	cds_wt_3269
3704327	G						A/G	cds_wt_3269

3704335	C						T/C	cds_wt_3269
3704338	C						G/C	cds_wt_3269
3704340	A						C/A	cds_wt_3269
3704371	G						C/G	cds_wt_3269
3704386	T						C/T	cds_wt_3269
3704389	C						G/C	cds_wt_3269
3704395	G						C/G	cds_wt_3269
3704404	G						C/G	cds_wt_3269
3704415	C						T/C	cds_wt_3269
3704427	G	G/A	G/A	G/A	G/A	G/A	A/G	cds_wt_3269
3704428	C	C/T	T/C	C/T	C/T	C/T	T/C	cds_wt_3269
3704464	C	C/T	C/T	C/T	C/T	C/T	T/C	cds_wt_3269
3704484	A						C/A	cds_wt_3269
3704485	C						G/C	cds_wt_3269
3704491	G						C/G	cds_wt_3269
3704512	G						C/G	cds_wt_3269
3704519	A						G/A	cds_wt_3269
3704531	A						G/A	cds_wt_3269
3704534	G						C/G	cds_wt_3269
3704536	C						G/C	cds_wt_3269
3704543	C						G/C	cds_wt_3269
3704544	T						C/T	cds_wt_3269
3704554	T						T/G	cds_wt_3269
3704563	C						G/C	cds_wt_3269
3704573	A						G/A	cds_wt_3269
3704574	A						G/A	cds_wt_3269
3704577	G						C/G	cds_wt_3269
3704584	C						G/C	cds_wt_3269
3704587	G						A/G	cds_wt_3269
3704590	G						C/G	cds_wt_3269
3704605	T						C/T	cds_wt_3269
3704608	C						G/C	cds_wt_3269
3704617	T						G/T	cds_wt_3269
3704619	A						C/A	cds_wt_3269
3704620	C						A/C	cds_wt_3269
3704629	C						G/C	cds_wt_3269
3704638	C						G/C	cds_wt_3269
3704641	G						C/G	cds_wt_3269
3704647	C						G/C	cds_wt_3269
3704650	G						C/G	cds_wt_3269
3704660	C						A/C	cds_wt_3269
3704662	G						A/G	cds_wt_3269
3704668	T						C/T	cds_wt_3269
3704669	G						A/G	cds_wt_3269
3704670	T						C/T	cds_wt_3269
3704680	C						G/C	cds_wt_3269

3704684	C						G/C	cds_wt_3269
3704686	G						C/G	cds_wt_3269
3704746	G	G/C	G/C	G/C	G/C	G/C	C/G	cds_wt_3269
3704755	C	C/G	C/G	C/G	C/G	C/G	C/G	cds_wt_3269
3704767	A	A/G	A/G	A/G	A/G	A/G	A/G	cds_wt_3269
3704782	T						T/C	cds_wt_3269
3704789	A						A/G	cds_wt_3269
3704791	C						C/G	cds_wt_3269
3704806	C						C/T	cds_wt_3269
3704815	T						T/C	cds_wt_3269
3704822	C						C/G	cds_wt_3269
3704844	C						C/A	cds_wt_3269
3704851	A						A/G	cds_wt_3269
3704852	C						C/A	cds_wt_3269
3704866	T						T/C	cds_wt_3269
3704869	C						C/G	cds_wt_3269
3704875	C						C/G	cds_wt_3269
3704906	G					A	A	cds_wt_3269
3706589	C						C/G	cds_wt_3270
3706625	G						G/C	cds_wt_3270
3706641	G						G/T	cds_wt_3270
3706652	G						G/A	cds_wt_3270
3706655	C						C/G	cds_wt_3270
3706679	T						T/C	cds_wt_3270
3706715	C						C/G	cds_wt_3270
3706735	C						C/G	cds_wt_3270
3706737	A						A/G	cds_wt_3270
3706739	G						G/C	cds_wt_3270
3706784	C						C/T	cds_wt_3270
3706790	T						T/C	cds_wt_3270
3706794	A						A/G	cds_wt_3270
3706805	G						G/C	cds_wt_3270
3706822	A						A/G	cds_wt_3270
3706862	C	C/G	C/G	C/G	C/G	C/G	C/G	cds_wt_3270
3706926	G						G/T	cds_wt_3270
3706932	A						A/C	cds_wt_3270
3706940	G						G/A	cds_wt_3270
3706945	G						G/C	cds_wt_3270
3706950	T						T/A	cds_wt_3270
3706951	C						C/G	cds_wt_3270
3706958	T						T/C	cds_wt_3270
3706960	A						A/G	cds_wt_3270
3706967	C						C/G	cds_wt_3270
3706983	C						C/G	cds_wt_3270
3706985	G						G/C	cds_wt_3270
3706994	G						G/C	cds_wt_3270

3706996	A						A/C	cds_wt_3270
3707006	G						G/C	cds_wt_3270
3707012	C						C/A	cds_wt_3270
3707013	A						A/G	cds_wt_3270
3707036	C						C/G	cds_wt_3270
3711369	G					A	A	cds_wt_3273
3713575	C						T	cds_wt_3274
3724878	G		A	A	A	A	A	cds_wt_3284
3724955	G		A	A	A	A	A	cds_wt_3285
3727102	G						A	cds_wt_3287
3727130	G						A	cds_wt_3287
3727909	C		T	T	T	T	T	cds_wt_3288
3732046	C					T	T	cds_wt_3292
3733052	G	A	A	A	A	A	A	cds_wt_3293
3740023	G					A	A	cds_wt_3297
3741710	G					A	A	cds_wt_3299
3744813	G					A	A	cds_wt_3301
3750360	G					A	A	cds_wt_3306
3756113	C	T	T	T	T	T	T	cds_wt_3312
3762328	G						A	cds_wt_3318
3763755	G					A	A	cds_wt_3319
3764788	G		A	A	A	A	A	cds_wt_3320
3771690	C	T	T	T	T	T	T	cds_wt_3327
3775098	G						A	cds_wt_3331
3775718	G					A	A	cds_wt_3332
3776484	G					A	A	cds_wt_3333
3783703	T		C	C	C	C	C	cds_wt_3342
3786947	G					A	A	cds_wt_3346
3788243	C					T	T	-
3798429	G					A	A	cds_wt_3363
3799202	G		A	A	A	A	A	cds_wt_3364
3799222	G		A	A	A	A	A	cds_wt_3364
3802171	C	T	T	T	T	T	T	cds_wt_3368
3806580	C					T	T	cds_wt_3371
3825163	C						T	cds_wt_3394
3828141	G					A	A	-
3831054	G					A	A	cds_wt_3401
3831114	G		A	A	A	A	A	cds_wt_3401
3831589	C					T	T	-
3831701	G					A	A	-
3837175	G					A	A	cds_wt_3406
3841387	G					A	A	cds_wt_3410
3843222	C	T	T	T	T	T	T	cds_wt_3413
3843509	G					A	A	cds_wt_3414
3843815	G	A	A	A	A	A	A	cds_wt_3414
3844238	G					A	A	cds_wt_3414

3846121	G						A	cds_wt_3417
3846452	G					A	A	cds_wt_3417
3852914	T			C	C	C	C	cds_wt_3423
3873931	G						A	cds_wt_3442
3879758	G					A	A	cds_wt_3449
3883035	C	T	T	T	T	T	T	cds_wt_3453
3905636	C					T	T	cds_wt_3478
3919216	C		T	T	T	T	T	cds_wt_3488
3920191	G					A	A	cds_wt_3489
3928659	C		T	T	T	T	T	cds_wt_3496
3935704	C						C/T	cds_wt_3503
3941486	G				A	A	A	cds_wt_3508
3964297	G					A	A	cds_wt_3529
3965972	G			A	A	A	A	cds_wt_3530
3968608	C		T	T	T	T	T	cds_wt_3533
3983198	C		T	T	T	T	T	cds_wt_3545
3993744	G						G/A	cds_wt_3554
4002370	G		A	A	A	A	A	cds_wt_3560
4004770	C			T	T	T	T	cds_wt_3562
4006580	C		T	T	T	T	T	cds_wt_3562
4006932	G		A	A	A	A	A	cds_wt_3562
4013932	G	A	A	A	A	A	A	cds_wt_3571
4014337	T				C	C	C	cds_wt_3572
4017638	C				T	T	T	cds_wt_3574
4019106	G		A	A	A	A	A	cds_wt_3576
4020770	C		T	T	T	T	T	cds_wt_3577
4025302	C	T	T	T	T	T	T	cds_wt_3582
4027304	G				A	A	A	cds_wt_3584
4034139	G						G/T	cds_wt_3588
4043320	A					G	G	cds_wt_3599
4063459	G		A	A	A	A	A	cds_wt_3621
4072648	C		T	T	T	T	T	cds_wt_3630
4073198	C						T	cds_wt_3630
4073446	G						A	cds_wt_3630
4074524	C		T	T	T	T	T	cds_wt_3631
4081747	C				T	T	T	cds_wt_3639
4086210	A	G	G	G	G	G	G	cds_wt_3643
4089001	C			T	T		T	cds_wt_3647
4102977	C					T	T	cds_wt_3657
4104004	C					T	T	cds_wt_3658
4114649	G		A	A	A	A	A	cds_wt_3670
4117981	G		A	A	A	A	A	cds_wt_3673
4118234	C		T	T	T	T	T	-
4121337	G		A	A	A	A	A	-
4124406	G		A	A	A	A	A	cds_wt_3680
4130087	C		T	T	T	T	T	cds_wt_3683

4148633	C					T	T	cds_wt_3698
4150599	C					T	T	cds_wt_3700
4152842	C		T	T	T	T	T	cds_wt_3703
4156366	G	A	A	A	A	A	A	cds_wt_3707
4156524	G					A	A	cds_wt_3707
4157742	G	A	A	A	A	A	A	cds_wt_3708
4157795	G	A	A	A	A	A	A	cds_wt_3708
4158022	G	A	A	A	A	A	A	cds_wt_3708
4160265	G	A		A	A		A	-
4170648	C		T	T	T	T	T	cds_wt_3719
4186914	C				T		T	cds_wt_3734
4187188	G				A		A	cds_wt_3735
4192330	C		T	T	T	T	T	cds_wt_3740
4192395	C	T	T	T	T	T	T	cds_wt_3740
4194086	C	T		T	T		T	cds_wt_3741
4196729	C	T	T	T	T	T	T	cds_wt_3743
4205330	C						T	cds_wt_3752
4218066	G	A	A	A	A	A	A	cds_wt_3764
4220842	G		A	A	A	A	A	cds_wt_3768
4231722	C		T	T	T	T	T	cds_wt_3782
4251577	C		T	T	T	T	T	-
4253562	G				A	A	A	-
4255089	G		A	A	A	A	A	cds_wt_3798
4268915	C	T	T	T	T	T	T	cds_wt_3809
4284264	C	T	T	T	T	T	T	cds_wt_3820
4285070	G						A	cds_wt_3821
4286615	G						A	cds_wt_3823
4299670	C		T	T	T	T	T	-
4302785	G		A	A	A	A	A	cds_wt_3840
4302812	C						T	cds_wt_3840
4312528	G		A	A	A	A	A	cds_wt_3851
4312875	C					T	T	cds_wt_3851
4314885	G		A	A	A	A	A	cds_wt_3852
4314896	C	T	T	T	T	T	T	cds_wt_3852
4314899	G		A	A	A	A	A	cds_wt_3852
4316350	C	T	T	T	T	T	T	cds_wt_3853
4318874	C		T	T	T	T	T	-
4319625	C				T	T	T	-
4324089	G			A	A	A	A	cds_wt_3859
4325174	G		A	A	A	A	A	cds_wt_3860
4325955	G		A	A	A	A	A	cds_wt_3860
4327176	C		T	T	T	T	T	cds_wt_3861
4328372	C		T	T	T	T	T	cds_wt_3861
4329685	C		T	T	T	T	T	cds_wt_3862
4329867	C		T	T	T	T	T	cds_wt_3862
4331851	C		T	T	T	T	T	cds_wt_3862

4331916	C		T	T	T	T	T	cds_wt_3862
4334253	C						T	-
4335755	C				T	T	T	-
4340706	C					T	T	-
4343282	T						C	cds_wt_3868
4347901	C				T	T	T	cds_wt_3875
4352755	G	A	A	A	A	A	A	cds_wt_3879
4360959	G	A	A	A	A	A	A	cds_wt_3884
4361293	C				T	T	T	cds_wt_3884
4362371	C		T	T	T	T	T	cds_wt_3885
4365880	G					A	A	cds_wt_3888
4376161	C			T	T	T	T	cds_wt_3893
4376238	C		T	T	T	T	T	cds_wt_3893
4378853	G		A	A	A	A	A	-
4395837	G					A	A	cds_wt_3904
4396016	C		T	T	T	T	T	cds_wt_3904
4402736	C		T	T	T	T	T	cds_wt_3911
4406151	G					A	A	cds_wt_3914
4414580	G	A	A	A	A	A	A	-
4414632	C		T	T	T	T	T	-
4420655	C					T	T	cds_wt_3928
4433146	G						A	cds_wt_3940
4438071	G		A	A	A	A	A	-
4440571	T		C	C	C	C	C	cds_wt_3948
4440772	G					A	A	cds_wt_3949
4443633	G					A	A	cds_wt_3952
4444731	C						T	cds_wt_3953
4446487	T		C	C	C	C	C	cds_wt_3954
4463567	C	T			T		T	cds_wt_3967
4463766	G			A			A	cds_wt_3967
4467838	G						A	cds_wt_3969
4474494	G		A	A	A	A	A	cds_wt_3976
4481185	G				A	A	A	cds_wt_3981
4486135	C		T	T	T	T	T	cds_wt_3985
4487769	G						A	cds_wt_3986
4490385	G		A	A	A	A	A	cds_wt_3989
4496083	G		A	A	A	A	A	cds_wt_3998
4499876	C		T	T	T	T	T	cds_wt_4002
4503563	C	T	T	T	T	T	T	cds_wt_4006
4504062	C	T	T	T	T	T	T	cds_wt_4006
4517204	G	A	A	A	A	A	A	cds_wt_4018
4524639	G				A		A	cds_wt_4025
4524706	G						A	cds_wt_4025
4529241	G		A	A	A	A	A	cds_wt_4028
4529778	G		A	A	A	A	A	cds_wt_4029
4531772	G	A	A	A	A	A	A	cds_wt_4032

4532547	G	A	A	A	A	A	A	cds_wt_4032
4532943	G	A	A	A	A	A	A	cds_wt_4033
4533824	G	A	A	A	A	A	A	cds_wt_4034
4535251	G		A	A	A	A	A	cds_wt_4035
4537480	G		A	A	A	A	A	cds_wt_4036
4537859	G	A	A	A	A	A	A	-
4543587	G	A	A	A	A	A	A	cds_wt_4041
4547764	C					T	T	cds_wt_4046
4558815	C		T	T	T	T	T	-
4558914	C		T	T	T	T	T	cds_wt_4060
4564648	G	A	A	A	A	A	A	cds_wt_4064
4564991	G	A	A	A	A	A	A	cds_wt_4064
4573497	C		T	T	T	T	T	cds_wt_4073
4573536	C		T	T	T	T	T	cds_wt_4073
4575408	C					T	T	cds_wt_4075
4577334	C	T	T	T	T	T	T	cds_wt_4076
4580403	G						A	cds_wt_4079
4582642	T				C	C	C	-
4588387	C	A	A	A	A	A	A	cds_wt_4086
4588663	G			A	A	A	A	cds_wt_4087
4597434	C					T	T	-
4598262	C		T	T	T	T	T	cds_wt_4091
4601247	G						G/C	cds_wt_4093
4601248	T						T/C	cds_wt_4093
4603166	C					T	T	cds_wt_4094
4611131	C		T	T	T	T	T	cds_wt_4099
4614475	C		T	T	T	T	T	cds_wt_4103
4616665	G		A	A	A	A	A	cds_wt_4104
4617801	G						A	cds_wt_4106
4619989	C			T	T		T	cds_wt_4108
4621439	G	A	A	A	A	A	A	cds_wt_4109
4626601	G	A		A	A	A	A	cds_wt_4114
4630752	C			T	T	T	T	cds_wt_4116
4649811	A						A/G	cds_wt_4135
4650590	C				T	T	T	cds_wt_4136
4669551	C		T	T	T	T	T	cds_wt_4157
4670815	G						A	cds_wt_4158
4674426	G			A	A	A	A	cds_wt_4162
4677968	C		T	T	T	T	T	cds_wt_4168
4688341	C						T	cds_wt_4174
4697092	C		T	T	T	T	T	cds_wt_4179
4700003	G	A	A	A	A	A	A	cds_wt_4181
4702254	C	T	T	T	T	T	T	cds_wt_4183
4704691	C	T	T	T	T	T	T	cds_wt_4185
4704704	C	T	T	T	T	T	T	cds_wt_4185
4713174	C		T	T	T	T	T	-

4727776	G	A	A	A	A	A	A	cds_wt_4209
4736024	C						T	cds_wt_4219
4766839	C	T	T	T	T	T	T	cds_wt_4240
4769655	C	T		T	T	T	T	cds_wt_4243
4776927	G		A	A	A	A	A	cds_wt_4247
4788381	C					T	T	cds_wt_4255
4794373	C	T	T	T	T	T	T	cds_wt_4264
4799012	G	A	A	A	A	A	A	cds_wt_4268
4812357	C						T	cds_wt_4277
4813704	G						G/T	-
4813710	G						G/T	-
4813711	A						A/C	-
4814060	C				T/C		C/T	-
4814078	C						C/T	-
4814081	C						C/T	-
4814082	G						G/C	-
4814087	T						T/C	-
4818340	G					A	A	-
4820651	C					T	T	cds_wt_4283
4821863	G	A	A	A	A	A	A	-
4852073	T						T/C	-
4852080	T						C/T	cds_wt_4318
4852093	T						C/T	cds_wt_4318
4852131	G						A/G	cds_wt_4318
4852238	T				C/T	C/T	C/T	cds_wt_4318
4852271	T						T/C	cds_wt_4318
4852348	G		G/A	G/A	G/A	G/A	G/A	cds_wt_4318
4852373	T						T/C	cds_wt_4318
4858842	C	T	T	T	T	T	T	cds_wt_4320
4859921	G	A	A	A	A	A	A	cds_wt_4321
4860949	G		A	A	A	A	A	cds_wt_4321
4872907	G				A	A	A	cds_wt_4325
4879205	C					T	T	cds_wt_4332
4886810	C					T	T	cds_wt_4337
4889101	G	A	A	A	A	A	A	cds_wt_4340
4891956	C					T	T	cds_wt_4341
4896797	C		T	T	T	T	T	cds_wt_4345
4903124	G						A	cds_wt_4350
4904325	A						A/G	-
4904344	C						C/G	-
4904345	C						C/T	-
4904355	A						G	-
4904359	G						G/C	-
4904360	T						T/C	-
4908341	C		T	T	T	T	T	-
4908687	C						T	-

4911304	C						T	cds_wt_4356
4916472	C		T	T	T	T	T	cds_wt_4359
4920831	C						T	cds_wt_4362
4924034	C		T	T	T	T	T	cds_wt_4363
4924484	C		T	T	T	T	T	cds_wt_4363
4927068	C		T	T	T	T	T	cds_wt_4367
4927798	C		T	T	T	T	T	cds_wt_4367
4929941	C		T	T	T	T	T	cds_wt_4370
4930693	C			T	T	T	T	cds_wt_4370
4932671	C						T	cds_wt_4373
4933447	T						T/C	cds_wt_4374
4948234	G					A	A	cds_wt_4390
4950870	C	T	T	T	T	T	T	cds_wt_4393
4951932	C	T	T	T	T	T	T	cds_wt_4394
4953821	C	T			T		T	-
4978515	G	A					A	cds_wt_4414
4981742	C						T	cds_wt_4416
4984320	A		G	G	G	G	G	cds_wt_4417
4987021	G	A	A	A	A	A	A	cds_wt_4421
4987606	G		A	A	A	A	A	cds_wt_4421
4991441	G		A	A	A	A	A	cds_wt_4424
4992870	G	A	A	A	A	A	A	cds_wt_4425
5014441	C	T	T	T	T	T	T	cds_wt_4442
5016187	C	T	T	T	T	T	T	cds_wt_4443
5016773	C	T	T	T	T	T	T	cds_wt_4443
5025119	G						A	cds_wt_4454
5030757	C						T	cds_wt_4459
5053257	C		T	T	T	T	T	cds_wt_4482
5056010	C		T	T	T	T	T	-
5056241	C		T	T	T	T	T	cds_wt_4487
5058845	C					T	T	-
5058850	C					T	T	-
5060436	C		T	T	T	T	T	cds_wt_4489
5061245	C		T	T	T	T	T	cds_wt_4489
5062621	C		T	T	T	T	T	cds_wt_4490
5063656	C		T	T	T	T	T	cds_wt_4492
5063753	A						A/G	cds_wt_4492
5063759	T						T/G	cds_wt_4492
5063766	C						C/T	cds_wt_4492
5063772	A						A/G	cds_wt_4492
5063775	T						T/C	cds_wt_4492
5063777	A						A/G	cds_wt_4492
5063883	T						T/C	cds_wt_4492
5063900	G	G/A	G/A	G/A	G/A	G/A	G/A	cds_wt_4492
5063967	T						C/T	cds_wt_4492
5063994	C						C/G	cds_wt_4492

5063997	T						C/T	cds_wt_4492
5064000	G						C/G	cds_wt_4492
5064054	C	C/G	C/G		C/G	C/G	C/G	cds_wt_4492
5064140	T	T/A	T/A	T/A		T/A	A/T	cds_wt_4492
5064188	G	G/C	G/C	G/C	G/C	G/C	G/C	-
5064199	G	G/A	G/A	G/A	G/A	G/A	A/G	-
5064223	T	T/C	T/C	T/C	T/C	T/C	C/T	-
5064318	G	G/A		G/A	G/A	G/A	G/A	-
5064363	G						G/A	-
5064364	C						C/G	-
5064368	T	T/C	T/C	T/C	T/C	C/T	C/T	-
5066806	C		T	T	T	T	T	cds_wt_4496
5079654	C						T	cds_wt_4505
5080712	C		T	T	T	T	T	cds_wt_4505
5080760	G		A	A	A	A	A	-
5083716	C		T	T	T	T	T	cds_wt_4508
5085149	C		T	T	T	T	T	cds_wt_4509
5087053	C		T	T	T	T	T	cds_wt_4509
5089288	G		A	A	A	A	A	cds_wt_4511
5095356	C		T	T	T	T	T	cds_wt_4517
5096131	C		T	T	T	T	T	cds_wt_4517
5099106	C					T	T	cds_wt_4520
5099331	C					T	T	cds_wt_4521
5099501	C						T	cds_wt_4521
5104316	C		T	T	T	T	T	cds_wt_4525
5104896	C		T	T	T	T	T	cds_wt_4525
5105840	C		T	T	T	T	T	cds_wt_4526
5107273	C		T	T	T	T	T	cds_wt_4528
5107438	G						A	cds_wt_4528
5110964	G						A	cds_wt_4534
5111341	G			A			A	cds_wt_4534
5111525	G	A		A			A	cds_wt_4534
5113971	C		T	T	T	T	T	cds_wt_4535
5114926	C						T/C	-
5114933	C						T/C	-
5116995	G				A	A	A	cds_wt_4538
5117622	G				A	A	A	cds_wt_4538
5126463	G				A	A	A	-
5128522	G				A	A	A	cds_wt_4545
5131328	G		A	A	A	A	A	cds_wt_4547
5132598	C		T	T	T	T	T	cds_wt_4548
5133033	C		T	T	T	T	T	cds_wt_4548
5134996	G		A	A	A	A	A	cds_wt_4551
5136119	C		T	T	T	T	T	cds_wt_4552
5139533	C	T	T	T	T	T	T	cds_wt_4555
5141709	G		A	A	A	A	A	cds_wt_4556

5147647	C		T	T	T	T	T	cds_wt_4560
5158997	C		T	T	T	T	T	cds_wt_4571
5171223	G	A	A	A	A	A	A	-
5189948	C		T	T	T	T	T	cds_wt_4598
5196838	C		T	T	T	T	T	cds_wt_4603
5203530	G						A	cds_wt_4610
5204859	C		T	T	T	T	T	cds_wt_4612
5213315	G						A	cds_wt_4621
5216015	G		A	A	A	A	A	cds_wt_4624
5221083	C		T	T	T	T	T	cds_wt_4628
5229965	G		A	A	A	A	A	cds_wt_4633
5233924	G						A	cds_wt_4635
5246591	G				A	A	A	cds_wt_4645
5247914	C	T	T	T	T	T	T	cds_wt_4646
5253451	C	T					T	cds_wt_4650
5255901	C		T	T	T	T	T	cds_wt_4652
5259871	G		A	A	A	A	A	cds_wt_4654
5270798	G	A	A	A	A	A	A	cds_wt_4667
5277822	G	A		A	A		A	cds_wt_4674
5280936	C		T	T	T	T	T	cds_wt_4680
5283902	G					A	A	cds_wt_4682
5292603	C	T	T	T	T	T	T	cds_wt_4692
5309793	G		A	A	A	A	A	cds_wt_4713
5317263	G				A	A	A	cds_wt_4720
5323245	G					A	A	cds_wt_4725
5323289	C					T	T	cds_wt_4725
5323708	G					A	A	cds_wt_4726
5326705	G						A	cds_wt_4730
5339380	G	A					A	cds_wt_4742
5349635	C	T	T	T	T	T	T	cds_wt_4752
5350111	G		A	A	A	A	A	cds_wt_4752
5356868	C		T	T	T	T	T	cds_wt_4756
5363828	C					T	T	cds_wt_4763
5385564	C	T	T	T	T	T	T	cds_wt_4780
5391456	G		A	A	A	A	A	cds_wt_4787
5404805	G					A	A	cds_wt_4798
5415953	G	A	A	A	A	A	A	cds_wt_4808
5416207	C	T	T	T	T	T	T	cds_wt_4808
5419045	C		T	T	T	T	T	cds_wt_4811
5438747	G	A	A	A	A	A	A	cds_wt_4833
5457995	G		A	A	A	A	A	cds_wt_4849
5465469	C					T	T	cds_wt_4855
5481386	G					A	A	cds_wt_4866
5485106	C		T	T	T	T	T	cds_wt_4869
5500846	G		A	A	A	A	A	cds_wt_4887
5514802	C		T	T	T	T	T	cds_wt_4901

5516464	C						T	cds_wt_4902
5530664	C		T	T	T	T	T	cds_wt_4914
5537010	G	A	A	A	A	A	A	cds_wt_4920
5540526	G	A					A	-
5541233	C		T	T	T	T	T	cds_wt_4926
5543634	C		T	T	T	T	T	cds_wt_4929
5545010	C						T	cds_wt_4929
5545574	G					A	A	cds_wt_4929
5548499	C				T	T	T	cds_wt_4933
5557711	G	A		A	A		A	cds_wt_4941
5574966	C	T	T	T	T	T	T	cds_wt_4961
5576016	C		T	T	T	T	T	-
5579654	C				T	T	T	cds_wt_4970
5582215	C						C/T	cds_wt_4972
5590781	T						T/A	-
5590796	C						C/T	-
5590809	T						T/C	-
5590810	G						G/A	-
5590823	G	G/A	G/A	G/A	G/A	G/A	G/A	-
5590828	A						A/G	-
5590847	G	G/T	G/T	G/T	G/T	G/T	G/T	-
5590861	G	G/C	G/C	G/C	G/C	G/C	G/C	-
5590867	A	A/C	A/C	A/C	A/C	A/C	A/C	-
5590868	A						A/G	-
5590886	G	G/A	G/A	G/A	G/A	G/A	A/G	cds_wt_4977
5590889	T	T/C	T/C	T/C		T/C	C/T	cds_wt_4977
5590903	A						G/A	cds_wt_4977
5590909	G						T/G	cds_wt_4977
5590910	C						G/C	cds_wt_4977
5590912	G						T/G	cds_wt_4977
5590918	G						A/G	cds_wt_4977
5590923	A						G/A	cds_wt_4977
5590927	T						G/T	cds_wt_4977
5590933	G						A/G	cds_wt_4977
5590945	C						G/C	cds_wt_4977
5590960	T						C/T	cds_wt_4977
5590961	C						T/C	cds_wt_4977
5590972	T						C/T	cds_wt_4977
5590978	T						C/T	cds_wt_4977
5590981	G						C/G	cds_wt_4977
5590987	T						C/T	cds_wt_4977
5590993	C	C/G					G/C	cds_wt_4977
5591002	G						G/A	cds_wt_4977
5591008	T	C/T	T/C	T/C	C/T	T/C	C/T	cds_wt_4977
5591026	C						G/C	cds_wt_4977
5591035	C						G/C	cds_wt_4977

5591054	C	A/C	C/A	C/A	C/A	C/A	A/C	cds_wt_4977
5591063	T						C/T	cds_wt_4977
5591065	C						G/C	cds_wt_4977
5591069	A						A/G	cds_wt_4977
5591074	A						G/A	cds_wt_4977
5591077	C						A/C	cds_wt_4977
5591092	A						G/A	cds_wt_4977
5591095	G						C/G	cds_wt_4977
5591098	T						C/T	cds_wt_4977
5591115	G						A/G	cds_wt_4977
5591158	G	T/G	T/G	T/G	T/G	T/G	T/G	cds_wt_4977
5591179	G						T/G	cds_wt_4977
5591220	C			G/C	G/C	G/C	G/C	cds_wt_4977
5591226	A				G/A	G/A	G/A	cds_wt_4977
5591268	T						C/T	cds_wt_4977
5591361	C						G/C	cds_wt_4977
5591442	G						A/G	cds_wt_4977
5591445	C						T/C	cds_wt_4977
5591457	G						C/G	cds_wt_4977
5591458	A						C/A	cds_wt_4977
5591466	G						C/G	cds_wt_4977
5591469	G						A/G	cds_wt_4977
5591472	C						G/C	cds_wt_4977
5591476	A						A/G	cds_wt_4977
5591496	G						C/G	cds_wt_4977
5591499	A						C/A	cds_wt_4977
5591505	G						C/G	cds_wt_4977
5591508	T						G/T	cds_wt_4977
5591520	A						G/A	cds_wt_4977
5591532	C						T/C	cds_wt_4977
5591541	C						T/C	cds_wt_4977
5591553	G						A/G	cds_wt_4977
5591562	G						T/G	cds_wt_4977
5591565	G						C/G	cds_wt_4977
5591571	A						G/A	cds_wt_4977
5591577	A						C/A	cds_wt_4977
5591596	C						T/C	cds_wt_4977
5591598	G						C/G	cds_wt_4977
5591607	C	C/T	C/T	C/T	C/T	C/T	T/C	cds_wt_4977
5591613	T	T/C	T/C	T/C	T/C	T/C	C/T	cds_wt_4977
5591632	C						A/C	cds_wt_4977
5591635	G						G/T	cds_wt_4977
5591640	T						T/C	cds_wt_4977
5591643	C						C/T	cds_wt_4977
5591654	A						A/C	cds_wt_4977
5591656	A						A/G	-

5604643	G		A	A	A	A	A	cds_wt_4993
5612009	C				T	T	T	cds_wt_5000
5626626	C		T	T	T	T	T	-
5629121	C		T	T	T	T	T	cds_wt_5011
5631426	C					T	T	cds_wt_5015
5636810	G		A	A	A	A	A	cds_wt_5021
5657449	C	T	T	T	T	T	T	cds_wt_5035
5659036	G		A	A	A	A	A	cds_wt_5036
5692125	C			T	T	T	T	cds_wt_5065
5694507	C			T	T	T	T	cds_wt_5069
5696833	C					T	T	cds_wt_5070
5698190	C		T	T	T	T	T	-
5705110	C			T	T	T	T	cds_wt_5076
5708625	C			T	T	T	T	cds_wt_5079
5709728	C		T	T	T	T	T	cds_wt_5079
5724677	C			T	T		T	cds_wt_5088
5727195	C						T	cds_wt_5090
5728510	C					T	T	cds_wt_5091
5732980	C			T	T	T	T	cds_wt_5094
5738712	G						A	cds_wt_5097
5738846	C						T	cds_wt_5097
5745077	C						T	cds_wt_5099
5751489	C			T	T	T	T	cds_wt_5101
5751716	C						T	cds_wt_5101
5753910	C			T	T	T	T	cds_wt_5103
5755351	C						T	cds_wt_5105
5756752	C						T	cds_wt_5107
5756803	C						T	cds_wt_5107
5760058	C						G	cds_wt_5110
5760301	C						T	cds_wt_5110
5763377	C		T	T	T	T	T	cds_wt_5111
5764363	C			T	T	T	T	cds_wt_5111
5765100	C			T	T	T	T	cds_wt_5111
5765446	C			T	T	T	T	cds_wt_5111
5767623	C	T	T	T	T	T	T	cds_wt_5113
5779664	C					T	T	cds_wt_5122
5780052	C					T	T	cds_wt_5122
5781808	C			T	T	T	T	cds_wt_5123
5783477	G		A	A	A	A	A	-
5788208	C			T	T	T	T	cds_wt_5131
5790337	C			T	T	T	T	cds_wt_5133
5791404	C			T	T	T	T	cds_wt_5133
5793414	G	A	A	A	A	A	A	cds_wt_5134
5795059	C			T	T	T	T	-
5795465	G		A	A	A	A	A	cds_wt_5136
5799803	G						A	cds_wt_5140

5803395	C			T	T	T	T	cds_wt_5141
5803716	G			A	A	A	A	cds_wt_5141
5805398	G		A	A	A	A	A	cds_wt_5143
5805735	G		A	A	A	A	A	cds_wt_5143
5807160	C	T	T	T	T	T	T	cds_wt_5145
5809295	G						A	cds_wt_5147
5810587	G					A	A	-
5811908	C						T	cds_wt_5148
5813504	C			T			T	cds_wt_5149
5813556	C		T	T	T	T	T	cds_wt_5149
5834083	C						T	cds_wt_5170
5842153	G						C	cds_wt_5173
5843698	T						T/C	cds_wt_5173
5843724	C						C/A	cds_wt_5173
5843727	C						C/T	cds_wt_5173
5843751	G						G/A	cds_wt_5173
5843752	G						G/C	cds_wt_5173
5843766	A						A/G	cds_wt_5173
5843783	A						A/G	cds_wt_5173
5843786	G						G/C	cds_wt_5173
5843787	C						C/G	cds_wt_5173
5843795	G						G/C	cds_wt_5173
5843796	T						T/A	cds_wt_5173
5843797	G						G/T	cds_wt_5173
5843804	C						C/G	cds_wt_5173
5843810	C						C/T	cds_wt_5173
5843818	T						T/C	cds_wt_5173
5843819	T						T/G	cds_wt_5173
5843831	C						C/T	cds_wt_5173
5843863	G						G/T	cds_wt_5173
5843878	C						C/T	cds_wt_5173
5843881	G						G/T	cds_wt_5173
5843888	G						G/A	cds_wt_5173
5843890	G						G/C	cds_wt_5173
5843897	C						C/G	cds_wt_5173
5843899	G						G/T	cds_wt_5173
5843902	C						C/T	cds_wt_5173
5843942	C						C/T	cds_wt_5173
5843965	G						G/C	cds_wt_5173
5843980	C						C/G	cds_wt_5173
5843981	C						C/T	cds_wt_5173
5843987	C						C/G	cds_wt_5173
5843988	C						C/T	cds_wt_5173
5843992	C						C/T	cds_wt_5173
5857131	C		T	T	T	T	T	cds_wt_5188
5858663	C				T	T	T	cds_wt_5190

5879695	G		A	A	A	A	A	cds_wt_5201
5880188	T						T/C	cds_wt_5201
5880203	G						G/C	cds_wt_5201
5880223	C						C/T	cds_wt_5201
5880241	A						A/C	cds_wt_5201
5880306	C						C/T	cds_wt_5201
5880307	T						T/C	cds_wt_5201
5880349	A						A/T	cds_wt_5201
5880412	G						G/A	cds_wt_5201
5880421	C						C/T	cds_wt_5201
5880430	A						A/G	cds_wt_5201
5880517	T	T/C	T/C	T/C	T/C	T/C	T/C	cds_wt_5201
5882826	G		A	A	A	A	A	cds_wt_5202
5887657	G						C/G	cds_wt_5205
5887660	G						C/G	cds_wt_5205
5887684	T						C/T	cds_wt_5205
5887693	T						C/T	cds_wt_5205
5887696	G						C/G	cds_wt_5205
5887718	G						G/A	cds_wt_5205
5887732	G						G/C	cds_wt_5205
5887734	G						G/A	cds_wt_5205
5887765	A	G/A	G/A	G/A	G/A	G/A	A/G/C	cds_wt_5205
5887771	G						G/C	cds_wt_5205
5887774	G						G/A	cds_wt_5205
5887775	C	T/C	T/C	T/C	T/C	T/C	C/T	cds_wt_5205
5887784	T				T/C		T/C	cds_wt_5205
5887792	T	T/C	T/C		T/C		T/C	cds_wt_5205
5887810	G						G/C	cds_wt_5205
5887813	G						G/C	cds_wt_5205
5887816	G						G/C	cds_wt_5205
5887820	G	G/C	G/C	G/C	G/C	G/C	G/C	cds_wt_5205
5887824	C	C/G	C/G	C/G	C/G	C/G	C/G	cds_wt_5205
5887831	G						G/C	cds_wt_5205
5887837	C						C/T	cds_wt_5205
5887843	C						C/G	cds_wt_5205
5887892	G		A/G	A/G	A/G	A/G	A/G	cds_wt_5205
5887931	G	G/A/C	A/G	G/A	G/A	G/A	G/A/C	cds_wt_5205
5887937	G						G/C	cds_wt_5205
5887938	C						C/G	cds_wt_5205
5887942	C						C/G	cds_wt_5205
5887945	G						G/C	cds_wt_5205
5887951	G						C/G	cds_wt_5205
5887960	G						G/C	cds_wt_5205
5887969	G						G/C	cds_wt_5205
5887970	C						C/G	cds_wt_5205
5887971	A						A/G	cds_wt_5205

5887974	G						G/T	cds_wt_5205
5887975	C						C/T	cds_wt_5205
5887977	T						T/A	cds_wt_5205
5887982	C						C/A/T	cds_wt_5205
5887988	G						G/T	cds_wt_5205
5887990	C						C/G	cds_wt_5205
5888003	A						A/C	cds_wt_5205
5888004	A						A/G	cds_wt_5205
5888005	A						A/G	cds_wt_5205
5888026	C						C/T	cds_wt_5205
5888050	G						G/C	cds_wt_5205
5888053	G						G/C	cds_wt_5205
5888056	G						G/C	cds_wt_5205
5888083	G						G/C	cds_wt_5205
5888092	C						C/G	cds_wt_5205
5888095	C						C/G	cds_wt_5205
5888102	G						G/A	cds_wt_5205
5888103	T						T/C	cds_wt_5205
5888122	C						C/T	cds_wt_5205
5888143	G						G/C	cds_wt_5205
5890782	G						G/C	cds_wt_5206
5890839	T	T/C	T/C	T/C	T/C	T/C	C/T	cds_wt_5206
5890849	T						A/T	cds_wt_5206
5890851	C						G/C	cds_wt_5206
5890863	C						G/C	cds_wt_5206
5890864	G						A/G	cds_wt_5206
5890869	G						T/G	cds_wt_5206
5890872	C						T/C	cds_wt_5206
5890893	C						T/C	cds_wt_5206
5890899	C						T/C	cds_wt_5206
5890906	G						A/G	cds_wt_5206
5890908	G						G/A	cds_wt_5206
5890914	C						T/C	cds_wt_5206
5890920	C						G/C	cds_wt_5206
5890923	C						T/C	cds_wt_5206
5890926	C						G/C	cds_wt_5206
5890971	C		C/T	C/T	C/T	C/T	C/T	cds_wt_5206
5890992	C	T/C	T/C	T/C	T/C	T/C	C/T	cds_wt_5206
5891058	G						C/G	cds_wt_5206
5891061	G						C/G	cds_wt_5206
5891070	C						T/C	cds_wt_5206
5891094	T						C/T	cds_wt_5206
5891097	C						C/G	cds_wt_5206
5891100	C						C/T	cds_wt_5206
5891121	C						T/C	cds_wt_5206
5891142	G						G/C	cds_wt_5206

5891145	C						C/G	cds_wt_5206
5891148	G						C/G	cds_wt_5206
5891187	G		G/C	G/C	G/C	G/C	G/C	cds_wt_5206
5891220	G						G/C	cds_wt_5206
5891247	T						T/C	cds_wt_5206
5891250	C						C/T	cds_wt_5206
5891263	T						T/C	cds_wt_5206
5892300	C						C/T	cds_wt_5206
5892304	A						A/C	cds_wt_5206
5892312	C						C/G	cds_wt_5206
5892330	C						C/T	cds_wt_5206
5892370	A						A/G	cds_wt_5206
5892413	C						C/T	cds_wt_5206
5892414	T						T/C	cds_wt_5206
5892456	A						A/T	cds_wt_5206
5892519	G	G/A	G/A	G/A	G/A	G/A	G/A	cds_wt_5206
5894264	G						A	cds_wt_5207
5894322	G						A	cds_wt_5207
5894986	A						A/G	cds_wt_5207
5894989	T						T/C	cds_wt_5207
5895041	G						G/A	cds_wt_5207
5895043	C						C/G	cds_wt_5207
5895049	C						C/G	cds_wt_5207
5895054	T						T/C	cds_wt_5207
5895058	G						G/C	cds_wt_5207
5895073	C	C/G	C/G	C/G	C/G	C/G	C/G	cds_wt_5207
5895100	G	G/C	G/C	G/C			G/C	cds_wt_5207
5895106	C						G/C	cds_wt_5207
5895108	T						C/T	cds_wt_5207
5895115	C						G/C	cds_wt_5207
5895118	A						C/A	cds_wt_5207
5895127	C						G/C	cds_wt_5207
5895130	C						G/C	cds_wt_5207
5895137	A						T/A	cds_wt_5207
5895142	T						C/T	cds_wt_5207
5895147	G						C/G	cds_wt_5207
5895181	C	C/T	C/T	C/T	C/T	C/T	T/C	cds_wt_5207
5895254	A						G/A	cds_wt_5207
5895280	T	T/C	C/T	T/C	T/C	T/C	C/T	cds_wt_5207
5895283	G	G/C	G/C	G/C	G/C	G/C	C/G	cds_wt_5207
5895298	C	C/G	C/G	C/G	C/G	C/G	G/C	cds_wt_5207
5895299	G	G/A	G/A	G/A	G/A	G/A	A/G	cds_wt_5207
5895319	C						G/C	cds_wt_5207
5895328	C						T/C	cds_wt_5207
5895334	C						T/C	cds_wt_5207
5895340	G						C/G	cds_wt_5207

5895346	G						G/C	cds_wt_5207
5895349	C						T/C	cds_wt_5207
5895358	C						T/C	cds_wt_5207
5895361	C						G/C	cds_wt_5207
5895370	C						C/T	cds_wt_5207
5895391	C						T/C	cds_wt_5207
5895436	G						C/G	cds_wt_5207
5895437	A						G/A	cds_wt_5207
5895439	C						G/C	cds_wt_5207
5895493	G		G/C	G/C	G/C	G/C	C/G	cds_wt_5207
5895496	G		G/C	G/C	G/C	G/C	C/G	cds_wt_5207
5895505	C						T/C	cds_wt_5207
5895529	T	T/C	C/T	T/C	T/C	T/C	C/T	cds_wt_5207
5895532	C	C/G	G/C	C/G	C/G	C/G	G/C	cds_wt_5207
5895577	G						C/G	cds_wt_5207
5895580	C						G/C	cds_wt_5207
5895628	T						C/T/G	cds_wt_5208
5895629	T						C/T	cds_wt_5208
5895661	C						C/G	cds_wt_5208
5895847	C	C/G	C/G	C/G	C/G	C/G	C/G	cds_wt_5208
5895878	G	G/A		G/A	G/A	G/A	G/A	cds_wt_5208
5895898	C		C/T	C/T	C/T	C/T	C/T	cds_wt_5208
5895899	A		A/C	A/C		A/C	A/C	cds_wt_5208
5895915	A	A/G	A/G	A/G	A/G	A/G	G/A	cds_wt_5208
5895949	C						T/C	cds_wt_5208
5896081	C	C/G	C/G	C/G	C/G	C/G	G/C	cds_wt_5208
5896085	C	C/T	C/T	C/T	C/T		T/C	cds_wt_5208
5896090	C	C/T	C/T	C/T	C/T		T/C	cds_wt_5208
5896115	C						C/T	cds_wt_5208
5896120	A						A/G	cds_wt_5208
5896123	G						G/C	cds_wt_5208
5896126	T						T/C	cds_wt_5208
5896147	T						T/G	cds_wt_5208
5896148	T						T/C	cds_wt_5208
5896154	T						T/C	cds_wt_5208
5896156	G						G/C	cds_wt_5208
5896159	G						G/C	cds_wt_5208
5896246	T						T/C	cds_wt_5208
5896279	C						T/C	cds_wt_5208
5896312	A						A/G	cds_wt_5208
5896324	A						A/G	cds_wt_5208
5896333	G						G/A	cds_wt_5208
5896381	G						G/C	cds_wt_5208
5900925	C						C/G	cds_wt_5209
5900943	G						G/T	cds_wt_5209
5900949	C						C/G	cds_wt_5209

5900955	C						C/T	cds_wt_5209
5900958	C						C/G	cds_wt_5209
5900965	T						T/C	cds_wt_5209
5900971	G						G/C	cds_wt_5209
5900972	C						C/G	cds_wt_5209
5900997	C						C/T	cds_wt_5209
5901000	C						C/T	cds_wt_5209
5901015	A						A/C	cds_wt_5209
5901034	C						C/A	cds_wt_5209
5901048	C						C/T	cds_wt_5209
5901050	G						G/A	cds_wt_5209
5901057	C						C/T	cds_wt_5209
5901068	G						G/A	cds_wt_5209
5901071	A						A/G	cds_wt_5209
5901078	G	G/T	G/T			G/T	G/T	cds_wt_5209
5901099	C	C/T	C/T	C/T	C/T	C/T	C/T	cds_wt_5209
5901123	T						T/A	cds_wt_5209
5901135	G						C/G	cds_wt_5209
5901172	G						A/G	cds_wt_5209
5901186	G						G/A	cds_wt_5209
5901195	T						T/C	cds_wt_5209
5901204	G						G/A	cds_wt_5209
5901219	C						A/C	cds_wt_5209
5901342	T	T/C	T/C	T/C	T/C	T/C	C/T	cds_wt_5209
5901345	T						T/G	cds_wt_5209
5901346	T						T/C	cds_wt_5209
5901354	C						C/G	cds_wt_5209
5901615	C	T/C	T/C	T/C	T/C	T/C	T/C	cds_wt_5209
5901617	G	C/G	C/G	C/G	C/G	C/G	C/G	cds_wt_5209
5901660	C						C/G	cds_wt_5209
5901664	T	T/G	T/G	T/G	T/G	T/G	T/G	cds_wt_5209
5901669	C	C/A	C/A		C/A	C/A	A/C	cds_wt_5209
5901673	T						A/T	cds_wt_5209
5901675	C						G/C	cds_wt_5209
5901679	C						C/T	cds_wt_5209
5901688	C						T/C	cds_wt_5209
5901689	T						A/T	cds_wt_5209
5901690	G						C/G	cds_wt_5209
5901698	C						A/C	cds_wt_5209
5901712	G						A/G	cds_wt_5209
5901713	T						A/T	cds_wt_5209
5901714	T						T/C	cds_wt_5209
5901719	G						G/C	cds_wt_5209
5901726	G						G/C	cds_wt_5209
5901729	C						C/G	cds_wt_5209
5901732	C						C/T	cds_wt_5209

5901733	G						G/A	cds_wt_5209
5901738	C						C/G	cds_wt_5209
5901752	C						C/T	cds_wt_5209
5901757	G						G/A	cds_wt_5209
5901764	T						C/T	cds_wt_5209
5901767	C						G/C	cds_wt_5209
5901771	G						C/G	cds_wt_5209
5901790	C						G/C	cds_wt_5209
5901791	G						C/G	cds_wt_5209
5901793	G						A/G	cds_wt_5209
5901807	G						C/G	cds_wt_5209
5901824	G						A/G	cds_wt_5209
5901826	G						G/A	cds_wt_5209
5901830	T						T/G	cds_wt_5209
5901840	A						A/C	cds_wt_5209
5902914	C	T	T	T	T	T	T	cds_wt_5209
5905708	G		A	A	A	A	A	cds_wt_5211
5925008	C	T	T	T	T	T	T	-
5925517	G		A	A	A	A	A	cds_wt_5227
5926357	G						A	cds_wt_5228
5928875	C					T	T	cds_wt_5231
5930205	C	T	T	T	T	T	T	cds_wt_5232
5933164	G	A	A	A	A	A	A	-
5947433	C	T	T	T	T	T	T	cds_wt_5246
5957471	G			A	A	A	A	-
5960825	C		T	T	T	T	T	cds_wt_5274
5961809	T	G/T			G/T	G/T	G/T	cds_wt_5275
5961866	T						T/A	-
5970914	C		T	T	T	T	T	cds_wt_5279
5975910	A	A/G	A/G	A/G	A/G	A/G	G/A	cds_wt_5283
5975911	A	A/G	A/G	A/G	A/G	A/G	G/A	-
5975926	A	A/G	A/G	A/G	A/G	A/G	G/A	-
5978267	C	T	T	T	T	T	T	cds_wt_5286
6005749	C		T	T	T	T	T	cds_wt_5311
6009383	G	A	A	A	A	A	A	cds_wt_5315
6010024	C			T	T	T	T	cds_wt_5316
6026234	C		T	T	T	T	T	-
6033950	C	T	T	T	T	T	T	cds_wt_5324
6042035	C						T	-
6050103	C					C/T	C/T	cds_wt_5343
6050112	A						C/A	cds_wt_5343
6050115	G						G/C	cds_wt_5343
6050116	C						C/G	cds_wt_5343
6050118	G						G/A	cds_wt_5343
6050509	G	G/A	A/G	A/G	A/G	A/G	A/G	cds_wt_5343
6050536	G						G/C	cds_wt_5343

6050556	G						C/G	cds_wt_5343
6050557	C						A/C	cds_wt_5343
6050584	T						T/A	cds_wt_5343
6050694	T						T/C	cds_wt_5343
6050727	A			G/A	G/A	G/A	G/A	cds_wt_5343
6050730	G		C/G	C/G	C/G	C/G	C/G	cds_wt_5343
6050769	G						G/A	cds_wt_5343
6050820	A						A/C	cds_wt_5343
6050822	T						T/C	cds_wt_5343
6050824	C						C/T	cds_wt_5343
6050947	T						C/T	cds_wt_5343
6050949	A						G/A	cds_wt_5343
6050952	T						T/C	cds_wt_5343
6050958	G						A/G	cds_wt_5343
6050965	A						C/A	cds_wt_5343
6050971	T						C/T	cds_wt_5343
6051079	A	G/A	G/A	G/A	G/A	G/A	A/G	cds_wt_5343
6051571	G	A	A	A	A	A	A	-
6072579	C				T	T	T	-
6074412	G	A	A	A	A	A	A	-
6075058	G	A	A	A	A	A	A	-
6083188	C					T	T	-
6085177	C					T	T	cds_wt_5373
6090298	C		T	T	T	T	T	cds_wt_5376
6094419	C	T	T	T	T	T	T	cds_wt_5383
6095825	C	T	T	T	T	T	T	cds_wt_5386
6098808	C	T	T	T	T	T	T	cds_wt_5388
6099142	C	T	T	T	T	T	T	cds_wt_5388
6099801	C	T	T	T	T	T	T	-
6100131	C	T	T	T	T	T	T	cds_wt_5389
6100928	C	T	T	T	T	T	T	cds_wt_5389
6114598	C		T	T	T	T	T	cds_wt_5399
6129757	G	A	A	A	A	A	A	-
6151020	G	A	A	A	A	A	A	cds_wt_5451
6157309	C		T	T	T	T	T	cds_wt_5456
6157376	C		T	T	T	T	T	cds_wt_5456
6178150	G		A	A	A	A	A	cds_wt_5472
6188180	C		T	T	T	T	T	cds_wt_5481
6191683	G	A			A		A	cds_wt_5487
6207945	G	A	A	A	A	A	A	cds_wt_5501
6216366	C			T	T		T	cds_wt_5511
6230439	A			G	G	G	G	cds_wt_5526
6251389	G		A	A	A	A	A	cds_wt_5542
6251652	G		A	A	A	A	A	cds_wt_5542
6255100	G		A	A	A	A	A	cds_wt_5546
6264179	G			A	A	A	A	cds_wt_5554

6265855	G		A	A	A	A	A	-
6267856	G			A	A		A	cds_wt_5556
6278700	G	A	A	A	A	A	A	-
6281103	C					T	T	cds_wt_5566
6282875	C		T	T	T	T	T	cds_wt_5567
6286620	C						T	cds_wt_5571
6288364	C			T	T	T	T	cds_wt_5571
6291716	C		T	T	T	T	T	cds_wt_5574
6297821	C		T	T	T	T	T	cds_wt_5578
6303632	G					A	A	cds_wt_5583
6306219	C		T	T	T	T	T	cds_wt_5586
6309112	G					A	A	cds_wt_5588
6322894	G						A	-
6328731	C	T	T	T	T	T	T	cds_wt_5605
6331035	G	A	A	A	A	A	A	cds_wt_5607
6338677	G	A	A	A	A	A	A	cds_wt_5615
6339429	C					T	T	-
6344180	C				T	T	T	cds_wt_5619
6346415	C				T		T	cds_wt_5622
6361477	C		T	T	T	T	T	cds_wt_5639
6362282	G			A	A	A	A	cds_wt_5639
6366940	C	T			T		T	cds_wt_5641
6368217	G					A	A	cds_wt_5643
6369699	G					A	A	cds_wt_5644
6375315	G	A	A	A	A	A	A	cds_wt_5648
6381431	C		T	T	T	T	T	cds_wt_5654
6401947	G	A	A			A	A	-
6403645	C				T	T	T	cds_wt_5675
6437676	C	T	T	T	T	T	T	cds_wt_5697
6439389	G					A	A	cds_wt_5698
6450624	C		T	T	T	T	T	-
6454248	C		T	T	T	T	T	cds_wt_5708
6454843	C					T	T	-
6456678	C					T	T	cds_wt_5711
6456912	C		T	T	T	T	T	cds_wt_5712
6459047	G						A	cds_wt_5715
6460584	T		C	C	C	C	C	-
6471884	G					A	A	cds_wt_5729
6485358	C		T	T	T	T	T	cds_wt_5741
6499172	G				A	A	A	cds_wt_5757
6500551	G						A	cds_wt_5760
6507389	C	T	T	T	T	T	T	cds_wt_5765
6517707	C			T	T		T	-
6525706	G					A	A	cds_wt_5775
6538378	C					T	T	cds_wt_5786
6542765	C		T	T	T	T	T	cds_wt_5790

6543445	C		T	T	T	T	T	cds_wt_5791
6543579	C		T	T	T	T	T	cds_wt_5791
6545779	C		T	T	T	T	T	cds_wt_5792
6550507	C					T	T	cds_wt_5797
6553219	G		A	A	A	A	A	cds_wt_5800
6553546	G			A			A	cds_wt_5800
6553589	G		A	A	A	A	A	cds_wt_5800
6555594	G		A	A	A	A	A	cds_wt_5804
6556192	C						T	cds_wt_5804
6560301	C		T	T	T	T	T	-
6561416	G		A	A	A	A	A	cds_wt_5810
6563658	C			T	T		T	cds_wt_5812
6564054	C		T	T	T	T	T	cds_wt_5812
6564511	C			T	T	T	T	cds_wt_5813
6564827	C		T	T	T	T	T	cds_wt_5813
6567102	C		T	T	T	T	T	cds_wt_5815
6567313	C					T	T	cds_wt_5816
6568360	C				T		T	cds_wt_5817
6569524	C		T	T	T	T	T	cds_wt_5819
6569696	G		A	A	A	A	A	cds_wt_5819
6570943	C		T	T	T	T	T	cds_wt_5820
6572188	C			T	T		T	cds_wt_5821
6572441	C			T	T		T	cds_wt_5821
6580904	G		A	A	A	A	A	cds_wt_5830
6581219	G						G/A	cds_wt_5830
6589934	C		T	T	T	T	T	cds_wt_5837
6595494	C	T		T	T		T	-
6604343	C						T	cds_wt_5851
6615272	C						T	cds_wt_5859
6617190	G	A	A	A	A	A	A	cds_wt_5861
6619058	C						T	cds_wt_5862
6622561	G	A	A	A	A	A	A	cds_wt_5864
6629950	C				T	T	T	cds_wt_5870
6632292	C	T	T	T	T	T	T	cds_wt_5872
6656015	C	T				T	T	cds_wt_5891
6669477	G					A	A	cds_wt_5901
6690831	C		T	T	T	T	T	cds_wt_5923
6690855	G					A	A	cds_wt_5923
6696960	G					A	A	-
6705369	G		A	A	A	A	A	cds_wt_5935
6716231	G		A	A	A	A	A	-
6729998	G		A	A	A	A	A	cds_wt_5955
6734341	C				T	T	T	cds_wt_5960
6758247	G					A	A	cds_wt_5984
6759384	C						T	cds_wt_5985
6767085	G					A	A	cds_wt_5990

6769984	C				T	T	T	cds_wt_5994
6780798	A			G	G	G	G	cds_wt_6005
6801699	G	A	A	A	A	A	A	cds_wt_6025
6805336	G	A	A	A	A	A	A	cds_wt_6026
6805990	G	A	A	A	A	A	A	cds_wt_6026
6808471	C		T	T	T	T	T	-
6818998	G		A	A	A	A	A	cds_wt_6038
6830990	G					A	A	cds_wt_6049
6843179	C						T	cds_wt_6061
6847192	G						A	cds_wt_6063
6854404	C						T	cds_wt_6068
6858684	G		A	A	A	A	A	cds_wt_6073
6883984	C		T	T	T	T	T	cds_wt_6092
6884717	G					A	A	cds_wt_6092
6890659	G		A	A	A	A	A	cds_wt_6098
6892977	G		A	A	A	A	A	cds_wt_6100
6898871	C		T	T	T	T	T	cds_wt_6107
6902839	A	T	T	T	T	T	T	cds_wt_6112
6911746	G		A	A	A	A	A	cds_wt_6117
6916561	G	A	A	A	A	A	A	cds_wt_6122
6916943	C		T	T	T	T	T	cds_wt_6122
6927456	G	A		A	A		A	cds_wt_6133
6960103	G			A	A	A	A	cds_wt_6158
6961070	C					T	T	cds_wt_6159
6968534	C	T	T	T	T	T	T	-
6973392	G		A	A	A	A	A	-
6987945	G		A	A	A	A	A	cds_wt_6176
6993597	G				A	A	A	cds_wt_6181
6995391	C		T	T	T	T	T	cds_wt_6182
6996621	C						T	cds_wt_6183
6999127	C		T	T	T	T	T	cds_wt_6187
6999520	C					T	T	cds_wt_6187
6999817	C		T	T	T	T	T	cds_wt_6188
7000264	C		T	T	T	T	T	cds_wt_6188
7002458	G		A	A	A	A	A	cds_wt_6190
7003486	G					A	A	cds_wt_6192
7003496	G					A	A	cds_wt_6192
7004068	C	T	T	T	T	T	T	cds_wt_6193
7009952	C					T	T	-
7010119	C					T	T	cds_wt_6198
7010712	C					T	T	cds_wt_6199
7015917	G		A	A	A	A	A	cds_wt_6203
7019067	C		T	T	T	T	T	-
7019437	C		T	T	T	T	T	cds_wt_6206
7020227	C			T	T	T	T	cds_wt_6207
7021026	C		T	T	T	T	T	cds_wt_6209

7023202	C		T	T	T	T	T	cds_wt_6212
7024113	C					T	T	cds_wt_6213
7026584	C		T	T	T	T	T	cds_wt_6217
7028273	C		T	T	T	T	T	cds_wt_6218
7028622	C					T	T	cds_wt_6218
7029812	C						T	cds_wt_6219
7031076	C						T	cds_wt_6219
7040546	C	T	T	T	T	T	T	cds_wt_6233
7053643	C		T	T	T	T	T	cds_wt_6243
7065316	C		T	T	T	T	T	cds_wt_6252
7075215	C		T	T	T	T	T	cds_wt_6264
7098642	C		T	T	T	T	T	cds_wt_6283
7099792	C		T	T	T	T	T	cds_wt_6284
7100617	C			T	T	T	T	cds_wt_6285
7101023	C		T	T	T	T	T	cds_wt_6285
7103392	C		T	T	T	T	T	-
7104098	C		T	T	T	T	T	cds_wt_6288
7109594	C		T	T	T	T	T	cds_wt_6291
7110600	C		T	T	T	T	T	cds_wt_6293
7110641	C		T	T	T	T	T	cds_wt_6293
7112833	C		T	T	T	T	T	cds_wt_6295
7116801	C	T	T	T	T	T	T	cds_wt_6297
7135624	G	A	A	A	A	A	A	cds_wt_6314
7135635	G	A					A	cds_wt_6314
7146220	G		A	A	A	A	A	-
7160415	C		T	T	T		T	-
7161529	G		A	A	A	A	A	cds_wt_6338
7162249	G		A	A	A	A	A	cds_wt_6338
7165660	C				T	T	T	-
7176091	G	A	A	A	A		A	cds_wt_6348
7177869	G	A	A	A	A	A	A	cds_wt_6350
7185280	G						A	cds_wt_6354
7186525	C		T	T	T	T	T	cds_wt_6355
7211965	G						G/C	cds_wt_6378
7211966	A						A/T	cds_wt_6378
7211975	C						C/T	cds_wt_6378
7211983	G						G/T	cds_wt_6378
7211992	G						G/T	cds_wt_6378
7211994	G						G/A	cds_wt_6378
7212006	T						T/C	cds_wt_6378
7212047	C						C/G	cds_wt_6378
7212067	T						T/A	cds_wt_6378
7212068	G						G/C	cds_wt_6378
7212075	G						G/C	cds_wt_6378
7212088	A						A/T	cds_wt_6378
7212097	T						T/C	cds_wt_6378

7212113	T						T/C	cds_wt_6378
7212121	G						G/T	cds_wt_6378
7212122	T						T/C	cds_wt_6378
7212142	T						T/C	cds_wt_6378
7212144	C						C/G	cds_wt_6378
7212151	T						T/G	cds_wt_6378
7212156	G						G/C	cds_wt_6378
7212180	C						C/G	cds_wt_6378
7212182	G						G/C	cds_wt_6378
7212183	T						T/C	cds_wt_6378
7212206	T						T/C	cds_wt_6378
7216330	G	A	A	A	A	A	A	cds_wt_6380
7218939	G	A	A	A	A	A	A	-
7219494	G					A	A	-
7224067	G						A	cds_wt_6388
7228023	G						A	-
7240925	G	A		A	A		A	cds_wt_6398
7241497	C			T	T		T	cds_wt_6399
7264121	G		A	A	A	A	A	cds_wt_6416
7266647	G	A	A	A	A	A	A	cds_wt_6419
7283171	C	T	T	T	T	T	T	cds_wt_6434
7294161	A		G	G	G	G	G	-
7303836	C	T	T	T	T	T	T	cds_wt_6454
7310019	G		A	A	A	A	A	cds_wt_6461
7314132	C		T	T	T	T	T	cds_wt_6463
7314146	C		T	T	T	T	T	cds_wt_6463
7319151	G	A	A	A	A	A	A	cds_wt_6467
7319658	G		A	A	A	A	A	cds_wt_6467
7321495	G						A	cds_wt_6470
7329181	G		A	A	A	A	A	cds_wt_6478
7330808	G		A	A	A	A	A	cds_wt_6480
7362245	C					T	T	cds_wt_6510
7369374	C					T	T	cds_wt_6518
7371536	C					T	T	cds_wt_6520
7377855	C		T	T	T	T	T	cds_wt_6527
7384932	G	A	A	A	A	A	A	cds_wt_6533
7385124	C		T	T	T	T	T	cds_wt_6533
7386113	G		A	A	A	A	A	cds_wt_6533
7389303	C		T	T	T	T	T	cds_wt_6535
7394213	C		T	T	T	T	T	cds_wt_6540
7394997	C					T	T	cds_wt_6540
7400636	C					T	T	-
7401592	C		T	T	T	T	T	cds_wt_6544
7422484	G		A	A	A	A	A	cds_wt_6563
7446288	G						A	-
7451085	C		T	T	T	T	T	-

7452627	C		T	T	T	T	T	cds_wt_6589
7453489	C	T	T	T	T	T	T	cds_wt_6590
7453910	C		T	T	T	T	T	cds_wt_6591
7460642	C		T	T	T	T	T	cds_wt_6600
7462223	G	A	A	A	A	A	A	cds_wt_6601
7484067	C	T	T	T	T	T	T	-
7490770	G					A	A	cds_wt_6634
7492384	G						A	cds_wt_6634
7498836	G		A	A	A	A	A	cds_wt_6639
7511194	G						A	cds_wt_6648
7517188	G		A	A	A	A	A	cds_wt_6653
7518982	C	T	T	T	T	T	T	cds_wt_6654
7524203	G		A	A	A	A	A	cds_wt_6659
7525798	C		T	T	T	T	T	cds_wt_6660
7546077	C		T	T	T	T	T	-
7583090	G			A	A	A	A	-
7588792	C		T	T	T	T	T	cds_wt_6730
7598819	G		A	A	A	A	A	-
7600514	G					A	A	cds_wt_6738
7604996	G						A	cds_wt_6743
7607903	G		A	A	A	A	A	cds_wt_6746
7622689	G		A	A	A	A	A	cds_wt_6763
7627683	G						G/T	cds_wt_6770
7630530	G	A	A	A	A	A	A	cds_wt_6772
7639840	G					A	A	cds_wt_6784
7641043	G						A	cds_wt_6785
7646004	G	A	A	A	A	A	A	cds_wt_6788
7648704	G	A	A	A	A	A	A	cds_wt_6791
7652691	G	A	A	A	A	A	A	cds_wt_6794
7654254	G	A	A	A	A	A	A	-
7655513	G	A	A	A	A	A	A	-
7662521	G		A		A		A	-
7671626	C				T	T	T	cds_wt_6808
7672126	G						A	cds_wt_6808
7687061	G						A	cds_wt_6826
7689723	G		A	A	A	A	A	cds_wt_6829
7714246	C		T	T	T	T	T	cds_wt_6856
7718521	G		A	A	A	A	A	cds_wt_6860
7719226	G		A	A	A	A	A	cds_wt_6861
7719430	G		A	A	A	A	A	cds_wt_6861
7720998	G		A	A	A	A	A	cds_wt_6862
7731353	G		A	A	A	A	A	cds_wt_6874
7733376	G					A	A	cds_wt_6876
7736672	C						C/T	cds_wt_6879
7740086	C	T	T	T	T	T	T	cds_wt_6883
7740896	G				A	A	A	cds_wt_6884

7765137	G		A	A	A	A	A	cds_wt_6902
7772239	G		A	A	A	A	A	cds_wt_6912
7789263	G	A	A	A	A	A	A	cds_wt_6933
7790304	G						A	cds_wt_6933
7801751	G		A	A	A	A	A	cds_wt_6947
7802623	T						T/C	-
7802638	T						T/C	-
7802639	C						C/T	-
7802682	A		T	T	T	T	T	-
7809752	G					A	A	cds_wt_6953
7809834	G					A	A	cds_wt_6953
7823754	C	T	T	T	T	T	T	cds_wt_6968
7825882	G				A	A	A	cds_wt_6969
7832540	G	A	A	A	A	A	A	cds_wt_6976
7838339	C		T	T	T	T	T	cds_wt_6980
7841392	C		T	T	T	T	T	cds_wt_6983
7841997	C		T	T	T	T	T	cds_wt_6983
7842274	C		T	T	T	T	T	cds_wt_6984
7844241	G		A	A	A	A	A	cds_wt_6985
7855301	C		T	T	T	T	T	cds_wt_6993
7864327	G	A	A	A	A	A	A	-
7874843	C						T	cds_wt_7008
7883195	A						G	cds_wt_7018
7889441	G		A	A	A	A	A	cds_wt_7022
7909245	G	A	A	A	A	A	A	cds_wt_7036
7912017	A						G	cds_wt_7038
7917279	G		A	A	A	A	A	cds_wt_7040
7926998	G	A		A	A	A	A	cds_wt_7045
7931764	G		A	A	A	A	A	cds_wt_7049
7934819	G		A	A	A	A	A	cds_wt_7051
7948630	C	T	T	T	T	T	T	cds_wt_7068
7963950	G			A	A	A	A	cds_wt_7082
7967045	G			A	A	A	A	cds_wt_7086
7969374	G	A	A	A	A	A	A	cds_wt_7089
7984213	G		A	A	A	A	A	cds_wt_7101
7984254	G		A	A	A	A	A	cds_wt_7101
7985275	G	A		A			A	cds_wt_7103
8009877	C	T	T	T	T	T	T	cds_wt_7127
8026754	C	T					T	cds_wt_7145
8036245	C		T	T	T	T	T	cds_wt_7152
8042744	G				A	A	A	cds_wt_7156
8051051	G	A	A	A	A	A	A	cds_wt_7165
8053700	C						T	cds_wt_7169
8062905	A						T	-
8062911	C						T	-
8075410	C	T	T	T	T	T	T	cds_wt_7189

8077440	G		A	A	A	A	A	cds_wt_7191
8087405	G	A	A	A	A	A	A	cds_wt_7205
8094018	G		A	A	A	A	A	cds_wt_7211
8095401	G	A					A	cds_wt_7213
8096270	C	T					T	cds_wt_7214
8122172	G						A	cds_wt_7240
8123295	G		A	A	A	A	A	cds_wt_7241
8123721	G		A	A	A	A	A	cds_wt_7241
8136640	C		T	T	T	T	T	cds_wt_7254
8161493	C		T	T	T	T	T	cds_wt_7274
8165695	A						A/T	cds_wt_7279
8165703	A						A/G	cds_wt_7279
8165704	C						C/G	cds_wt_7279
8167086	G		A	A	A	A	A	cds_wt_7280
8171741	G	A	A	A	A	A	A	cds_wt_7283
8179169	G				A	A	A	cds_wt_7288
8181933	G	A	A	A	A	A	A	cds_wt_7290
8186618	C	T	T	T	T	T	T	cds_wt_7297
8193241	C			T	T	T	T	cds_wt_7306
8195170	C		T	T	T	T	T	cds_wt_7307
8195310	C		T	T	T	T	T	cds_wt_7307
8199221	G	A	A	A	A	A	A	cds_wt_7312
8202704	C						C/T	cds_wt_7315
8205853	G	A	A	A	A	A	A	cds_wt_7319
8212158	C	T	T	T	T	T	T	cds_wt_7324
8212583	G					A	A	cds_wt_7324
8214951	C		T	T	T	T	T	cds_wt_7328
8221459	G	A	A	A	A	A	A	cds_wt_7335
8227017	G						A	cds_wt_7340
8233448	C					T	T	cds_wt_7347
8237580	G						A	cds_wt_7349
8239310	G						A	cds_wt_7349
8240439	G					A	A	cds_wt_7350
8241289	G		A	A	A	A	A	cds_wt_7350
8243590	G	A	A	A	A	A	A	-
8247542	G		A	A	A	A	A	cds_wt_7357
8248207	C						T	cds_wt_7357
8256006	G		A	A	A	A	A	cds_wt_7367
8263792	G		A	A	A	A	A	cds_wt_7373
8267543	G		A	A	A	A	A	cds_wt_7377
8272330	G						A	cds_wt_7379
8273351	C		T	T	T	T	T	cds_wt_7380
8278809	G				A	A	A	cds_wt_7384
8282707	G						A	cds_wt_7387
8298405	T	T/A	T/A		T/A		T/A	cds_wt_7401
8298413	C	C/G		C/G	C/G	C/G	C/G	cds_wt_7401

8302281	G	A	A	A	A	A	A	cds_wt_7405
8311927	T		C	C	C	C	C	cds_wt_7413
8323622	C		T	T	T	T	T	cds_wt_7423
8325049	G						G/C	cds_wt_7424
8325050	A						G/A	cds_wt_7424
8325073	C	C/G	C/G	C/G	C/G	C/G	C/G	cds_wt_7424
8325095	G						G/C	cds_wt_7424
8325096	G						G/T	cds_wt_7424
8325102	C						C/G	cds_wt_7424
8325109	T						C/T	cds_wt_7424
8325115	C						G/C	cds_wt_7424
8325118	C						C/G	cds_wt_7424
8325121	G						G/C	cds_wt_7424
8325127	G						G/C	cds_wt_7424
8325133	C						G/C	cds_wt_7424
8325203	T				T/C		T/C	cds_wt_7424
8325210	A	A/G	A/G	A/G	A/G	A/G	G/A	cds_wt_7424
8325277	C						C/G	cds_wt_7424
8325286	C						C/G	cds_wt_7424
8349257	G				A	A	A	cds_wt_7444
8351616	G				A	A	A	cds_wt_7445
8355565	C					T	T	cds_wt_7448
8355924	C		T	T	T	T	T	cds_wt_7448
8363036	G	A	A	A	A	A	A	cds_wt_7452a
8364757	C	T	T	T	T	T	T	cds_wt_7454
8365293	G	A	A	A	A	A	A	cds_wt_7454
8368404	G			A	A	A	A	cds_wt_7457
8378911	G		A	A	A	A	A	cds_wt_7464
8379977	G			A	A	A	A	-
8380006	C						T	-
8381094	G			A	A	A	A	cds_wt_7465
8384806	G				A	A	A	cds_wt_7468
8389000	C					T	T	cds_wt_7470
8389283	A	G	G	G	G	G	G	cds_wt_7470
8393915	G		A	A	A	A	A	cds_wt_7472
8396831	G						A	cds_wt_7476
8397563	G				A	A	A	cds_wt_7476
8402662	G		A	A	A	A	A	-
8411820	C			T	T	T	T	cds_wt_7490
8413318	C		T	T	T	T	T	cds_wt_7491
8414872	C		T	T	T	T	T	cds_wt_7491
8431655	T	A/T	A/T	A/T	A/T	A/T	T/A	-
8441210	C	T			T	T	T	cds_wt_7510
8449495	G						G/A	cds_wt_7513
8453858	G				A		A	cds_wt_7514
8463714	G					A	A	cds_wt_7525

8466767	G		A	A	A	A	A	cds_wt_7529
8491536	G	A	A	A	A	A	A	-
8497636	C						T	cds_wt_7552
8506267	G			A	A	A	A	cds_wt_7561
8509227	G						A	cds_wt_7562
8515828	G		A	A	A	A	A	cds_wt_7566
8529144	G		A	A	A	A	A	cds_wt_7572
8544731	G		A	A	A	A	A	-
8546526	C	T	T	T	T	T	T	cds_wt_7591
8556565	G		A				A	-
8559522	G	A	A	A	A	A	A	cds_wt_7602
8560241	C						T	cds_wt_7603
8567608	C		T	T	T	T	T	cds_wt_7607
8572238	C					T	T	-
8576774	G	A		A	A	A	A	-
8582623	C					T	T	cds_wt_7615
8589455	C					T	T	cds_wt_7621
8589459	C					T	T	cds_wt_7621
8595339	C	T	T	T	T	T	T	cds_wt_7627
8610015	C		T	T	T	T	T	cds_wt_7640
8622039	C	T	T	T	T	T	T	cds_wt_7652
8631175	G	A	A	A	A	A	A	cds_wt_7660
8640526	C		T	T	T	T	T	cds_wt_7667
8646416	G		A	A	A	A	A	cds_wt_7674
8647802	G		A	A	A	A	A	cds_wt_7675
8648408	G				A	A	A	cds_wt_7676
8655581	C	T	T	T	T	T	T	cds_wt_7683
8658688	G		A	A	A	A	A	cds_wt_7685
8668191	C		T	T	T	T	T	cds_wt_7693
8668196	G		A	A	A	A	A	cds_wt_7693
8669919	G	A	A	A	A	A	A	-
8674137	C	T	T	T	T	T	T	cds_wt_7700
8678961	G		A	A	A	A	A	cds_wt_7704
8682722	G	A	A	A	A	A	A	-
8690364	C	T	T	T	T	T	T	cds_wt_7711
8691972	C						T	cds_wt_7712
8699652	G		A	A	A	A	A	cds_wt_7716
8699708	G		A	A	A	A	A	cds_wt_7716
8709561	C		T	T	T	T	T	-
8720459	G	A	A	A	A	A	A	cds_wt_7731
8731485	G					A	A	cds_wt_7745
8737851	G	A	A	A	A	A	A	cds_wt_7749
8737859	G	A	A	A	A	A	A	cds_wt_7749
8742265	C		T		T	T	T	cds_wt_7750
8743148	C			T	T		T	cds_wt_7751
8754468	G		A	A	A	A	A	-

8754501	G		A	A	A	A	A	-
8759529	G						A	cds_wt_7757
8761290	C		T	T	T	T	T	cds_wt_7757
8769464	T					C	C	-
8792629	G		A	A	A	A	A	cds_wt_7788
8793001	C	T	T	T	T	T	T	cds_wt_7788
8809351	C		T	T	T	T	T	cds_wt_7801
8813761	C		T	T	T	T	T	cds_wt_7803
8813866	C		T	T	T	T	T	cds_wt_7803
8816396	G	A	A	A	A	A	A	cds_wt_7805
8821923	G		A	A	A	A	A	cds_wt_7810
8825490	G		A	A	A	A	A	cds_wt_7813
8828064	C		T	T	T	T	T	cds_wt_7815
8841828	G	A	A	A	A	A	A	cds_wt_7827
8842797	G					A	A	cds_wt_7828
8843541	G						A	cds_wt_7828
8845199	T		C	C	C	C	C	cds_wt_7829
8848419	G	A	A	A	A	A	A	cds_wt_7832
8849052	G	A	A	A	A	A	A	cds_wt_7833
8854017	C			T	T	T	T	cds_wt_7839
8854256	G		A	A	A	A	A	cds_wt_7839
8858030	G		A	A	A	A	A	cds_wt_7843
8859328	G						A	cds_wt_7844
8860995	G			A			A	cds_wt_7846
8861382	G		A	A	A	A	A	-
8871894	C	T	T	T	T	T	T	-
8872344	C						C/T	cds_wt_7854
8875526	G		A	A	A	A	A	cds_wt_7858
8881555	G				A	A	A	cds_wt_7864
8889242	G						A	cds_wt_7871
8893686	G	A	A	A	A	A	A	cds_wt_7877
8894581	G	A	A	A	A	A	A	-
8896018	G	A	A	A	A	A	A	cds_wt_7879
8901982	G	A	A	A	A	A	A	cds_wt_7883
8902511	G		A	A	A	A	A	cds_wt_7883
8902844	G		A	A	A	A	A	cds_wt_7884
8902903	G		A	A	A	A	A	cds_wt_7884
8907784	G	A	A	A	A	A	A	-
8927137	G						A	-
8929703	G	A	A	A	A	A	A	cds_wt_7911
8931762	C	T	T	T	T	T	T	cds_wt_7914
8934108	G					A	A	cds_wt_7916
8937518	C						T	cds_wt_7919
8943513	C						T	cds_wt_7925
8943676	C						T	cds_wt_7925
8944024	C						T	-

8945415	C			T	T	T	T	-
8946251	C			T	T	T	T	cds_wt_7927
8948806	G		A	A	A	A	A	cds_wt_7930
8950622	C	T	T	T	T	T	T	cds_wt_7931
8951908	C		T	T	T	T	T	cds_wt_7932
8953417	G	A		A	A		A	cds_wt_7935
8955117	G					A	A	cds_wt_7936
8956021	C						T	cds_wt_7937
8956608	C						T	cds_wt_7937
8958843	C	T			T	T	T	cds_wt_7939
8959688	G			A	A	A	A	cds_wt_7940
8974326	G		A	A	A	A	A	cds_wt_7953
8979884	C			T	T	T	T	cds_wt_7957
8982938	G	G/C	G/C				G/C	cds_wt_7963
8982956	G	G/C	G/C	G/C	G/C	G/C	G/C	cds_wt_7963
8982975	G						G/C	cds_wt_7963
8983002	G	G/A	G/A	G/A	G/A	G/A	G/A	-
8983053	C	C/T	C/T	C/T	C/T	C/T	C/T	cds_wt_7964
8983087	G						A/G	cds_wt_7964
8983088	G						G/C	cds_wt_7964
8983102	A	A/G	A/G	A/G	A/G	A/G	G/A	cds_wt_7964
8983134	G	G/C	G/C	G/C	G/C	G/C	G/C	cds_wt_7964
9008254	C						T	cds_wt_7977
9028349	G	A	A	A	A	A	A	cds_wt_7991
9029056	C					T	T	cds_wt_7991
9045846	G		A	A	A	A	A	cds_wt_7996
9049564	C						T	cds_wt_7998
9052240	C	T	T	T	T	T	T	cds_wt_8000
9052265	G			A	A	A	A	cds_wt_8000
9053107	G	A	A	A	A	A	A	-
9058239	G	A	A	A	A	A	A	cds_wt_8006
9060181	C		T	T	T	T	T	cds_wt_8008
9064090	C	T	T	T	T	T	T	cds_wt_8011
9072129	C						C/T	cds_wt_8017

Summary of Identified COG Categories

Table 10 shows details on COG-classified genes of the *A. utahensis* wild type strain SE50-100. For each COG category and its subcategories, the number of annotated genes and the absolute percentage is listed.

COG-Categories	Population
CDS with COG-category	3,983 (49.62%)
↳ Information storage and processing	1240 (15.45%)
↳ Translation. ribosomal structure and biogenesis	200 (2.49%)
↳ RNA processing and modification	2 (0.02%)
↳ Transcription	771 (9.61%)
↳ Replication. recombination and repair	266 (3.31%)
↳ Chromatin structure and dynamics	1 (0.01%)
↳ Cellular processes and signaling	1398 (17.42%)
↳ Cell cycle control. cell division. chromosome partitioning	49 (0.61%)
↳ Nuclear structure	0 (0.00%)
↳ Defense mechanisms	84 (1.05%)
↳ Signal transduction mechanisms	592 (7.38%)
↳ Cell wall/membrane/envelope biogenesis	302 (3.76%)
↳ Cell motility	104 (1.30%)
↳ Cytoskeleton	8 (0.10%)
↳ Extracellular structures	0 (0.00%)
↳ Intracellular trafficking. secretion. and vesicular transport	89 (1.11%)
↳ Posttranslational modification. protein turnover. chaperones	170 (2.12%)
↳ Metabolism	2409 (30.01%)
↳ Energy production and conversion	308 (3.84%)
↳ Carbohydrate transport and metabolism	575 (7.16%)
↳ Amino acid transport and metabolism	521 (6.49%)
↳ Nucleotide transport and metabolism	82 (1.02%)
↳ Coenzyme transport and metabolism	187 (2.33%)
↳ Lipid transport and metabolism	234 (2.92%)
↳ Inorganic ion transport and metabolism	257 (3.20%)
↳ Secondary metabolites biosynthesis. transport and catabolism	245 (3.05%)

ALL GENES WITH ANNOTATION

Table 11 lists all annotated genes of the *Actinoplanes utahensis* wild type strain SE50-100.

Gene ID	Gene Symbol	Annotation
		HTH-type transcriptional repressor purR; Purine nucleotide synthesis repressor; Pur regulon repressor;
cds_wt_0	-	
cds_wt_1	smpB	SsrA-binding protein;
cds_wt_2	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3	-	Putative membrane protein actII-3;
cds_wt_4	glcF	glycolate oxidase subunit (Fe-S) protein
cds_wt_5	glcE	glycolate oxidase subunit
cds_wt_6	glcD	glycolate oxidase subunit GlcD
cds_wt_7	ppdK	pyruvate, orthophosphate dikinase
cds_wt_8	-	Protein phnB;
		Platelet-activating factor acetylhydrolase; PAF acetylhydrolase; PAF 2-acylhydrolase; LDL-associated phospholipase A2; LDL-PLA
cds_wt_9	-	
		Platelet-activating factor acetylhydrolase; PAF acetylhydrolase; PAF 2-acylhydrolase; LDL-associated phospholipase A2; LDL-PLA
cds_wt_10	-	
cds_wt_11	recQ	DNA helicase
cds_wt_12	rsbU	Uncharacterized protein Rv1364c/MT1410;
cds_wt_13	toxB	GTP cyclohydrolase II
cds_wt_14	ribG	riboflavin-specific deaminase
cds_wt_15	-	hypothetical protein
cds_wt_16	-	hypothetical protein
cds_wt_17	lpg2	Glycogen synthase 2; Starch
		6-pyruvoyl tetrahydrobiopterin synthase; PTP synthase; PTPS; Sepiapterin synthase A; Protein purple;
cds_wt_18	-	
cds_wt_19	adh7	hypothetical protein
cds_wt_20	-	hypothetical protein
cds_wt_21	potD	Vitamin B12-binding protein;
cds_wt_22	estA	hydrolase, alpha/beta fold family
cds_wt_23	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_24	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_25	-	hypothetical protein predicted by Glimmer/Critica
		Chaperone protein htpG; Heat shock protein htpG;
cds_wt_26	htpG	High temperature protein G;
cds_wt_27	-	putative membrane protein
cds_wt_28	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_29	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_30	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_31	-	Multidrug resistance protein B;
		HTH-type transcriptional regulator tcmR;
cds_wt_32	tcmR	Tetracenomycin C transcriptional repressor;

cds_wt_33	sitS	putative dehydrogenase
cds_wt_34	acpD	acyl carrier protein phosphodiesterase, putative
cds_wt_35	-	HTH-type transcriptional regulator mhqR;
cds_wt_36	gntP	Uncharacterized permease yojA;
cds_wt_37	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_38	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_39	-	hypothetical cytosolic protein
cds_wt_40	-	LexA repressor;
cds_wt_41	tetV	Uncharacterized MFS-type transporter yfiS;
cds_wt_42	-	HTH-type transcriptional regulator betI;
cds_wt_43	-	Multidrug resistance protein B homolog;
cds_wt_44	folP	dihydropteroate synthase
cds_wt_45	tlpB	Methyl-accepting chemotaxis protein III; MCP-III;
cds_wt_46	-	Ribose and galactose chemoreceptor protein;
cds_wt_47	cydC	HTH-type transcriptional regulator betI;
cds_wt_48	cydD	transport ATP-binding protein CydC
cds_wt_49	cydA	ABC transporter, ATP-binding protein
cds_wt_50	-	putative cytochrome oxidase subunit I
cds_wt_51	-	hypothetical protein
cds_wt_52	-	Probable protease htpX homolog;
cds_wt_53	ruvB	Uncharacterized protein yibP;
cds_wt_54	-	Cell division cycle protein 48 homolog AF_1297;
cds_wt_55	-	hypothetical protein
cds_wt_56	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_57	-	hypothetical protein
cds_wt_58	yvoA	Tyrosine-protein phosphatase;
cds_wt_59	trpB	Mannosyl-D-glycerate transport/metabolism system
cds_wt_60	lolA	repressor mngR; Fatty acyl-responsive regulator;
cds_wt_61	tcrA	Protein P30;
cds_wt_62	tctE	tryptophan synthase beta chain
cds_wt_63	ycnI	hypothetical protein
cds_wt_64	-	Transcriptional regulatory protein yycF;
cds_wt_65	-	sensor histidine kinase
cds_wt_66	xysA	Uncharacterized protein ycnI;
cds_wt_67	-	hypothetical protein
cds_wt_68	celD	hypothetical protein predicted by Glimmer/Critica
cds_wt_69	xysA	endo-1,4-beta-xylanase
cds_wt_70	aglA	hypothetical protein
cds_wt_71	xynD	endo-1,4-beta-xylanase
cds_wt_72	glcI	cellulase., cellulose 1,4-beta-cellobiosidase
cds_wt_73	abfB	endo-1,4-beta-xylanase
cds_wt_74	-	putative alpha-galactosidase
cds_wt_75	xylI	Arabinoxylan arabinofuranohydrolase; AXH; AXH-m2,3; AXH-m23; Alpha-L-arabinofuranosidase; AF;
		Glucan endo-1,3-beta-glucosidase;
		putative endo-1,4-beta-glucanase
		RNA polymerase sigma-H factor; Sigma-30;
		Arabinofuranosidase/B-xylosidase; Includes: Alpha-N-arabinofuranosidase; Arabinosidase; Includes: Beta-xylosidase; 1,4-beta-D-xylan xylohydrolase; Xylan 1,4-beta-xylosidase;

cds_wt_76	xysA	endo-1,4-beta-xylanase
cds_wt_77	abfB	Alpha-N-arabinofuranosidase B; Arabinosidase B; ABF B;
cds_wt_78	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_79	-	hypothetical protein
cds_wt_80	-	Uncharacterized protein yhdN;
cds_wt_81	-	beta-galactosidase
cds_wt_82	-	Otogelin;
cds_wt_83	-	putative cholesterol esterase
cds_wt_84	hpkA	sensory transduction histidine kinase
cds_wt_85	lctP	L-lactate permease;
cds_wt_86	lldP	L-lactate permease;
cds_wt_87	aepA	hypothetical protein
cds_wt_88	-	Pre-mRNA cleavage complex 2 protein Pcf11; Pre-mRNA cleavage complex II protein Pcf11;
cds_wt_89	-	Probable transposase for insertion sequence element ISRM3-like;
cds_wt_90	-	Inter-alpha-trypsin inhibitor heavy chain H3; Inter-alpha-inhibitor heavy chain 3; ITI heavy chain H3; ITI-HC3;
cds_wt_91	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_92	-	hypothetical protein
cds_wt_93	shpl	Neutral metalloprotease;
cds_wt_94	-	Putrescine importer;
cds_wt_95	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_96	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_97	-	dipeptidase 1 (renal)
cds_wt_98	-	Endoglucanase H; Endo-1,4-beta-glucanase H; EgH; Cellulase H;
cds_wt_99	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_100	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_101	yycA	Undecaprenyl phosphate-alpha-4-amino-4-deoxy-L-arabinose arabinosyl transferase; Undecaprenyl phosphate-alpha-L-Ara4N transferase; 4-amino-4-deoxy-L-arabinose lipid A transferase;
cds_wt_102	pgi	glucose-6-phosphate isomerase
cds_wt_103	-	hypothetical protein
cds_wt_104	chiA	extracellular exochitinase Chi36
cds_wt_105	-	Riboflavin biosynthesis protein ribD; Includes: Diaminohydroxyphosphoribosylaminopyrimidine deaminase; DRAP deaminase; Riboflavin-specific deaminase; Includes: 5-amino-6-
cds_wt_106	sps1	serine/threonine protein kinase
cds_wt_107	-	Alkanesulfonate monooxygenase; FMNH2-dependent aliphatic sulfonate monooxygenase;
cds_wt_108	msuE	putative oxidoreductase
cds_wt_109	-	Filamentous hemagglutinin;
cds_wt_110	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_111	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_112	-	hypothetical protein predicted by Glimmer/Critica

cds_wt_113	-	HTH-type transcriptional regulator betI; Uncharacterized HTH-type transcriptional regulator
cds_wt_114	ybjK	ybjK;
cds_wt_115	emrE	Multidrug resistance protein mmr;
cds_wt_116	-	hypothetical protein predicted by Glimmer/Critica
		Bifunctional protein NCOAT; Nuclear cytoplasmic O-GlcNAcase and acetyltransferase; Meningioma-expressed antigen 5; Includes: Beta-hexosaminidase; N-acetyl-beta-glucosaminidase; Beta-N-acetylhexosaminidase; Hexosaminidase C; N-acetyl-beta-D-glucosaminidase; O-GlcNAcase; Includes:
cds_wt_117	-	Histone acetyltransferase; HAT;
		Voltage-dependent P/Q-type calcium channel subunit alpha-1A; Voltage-gated calcium channel subunit alpha Cav2.1; Calcium channel, L type, alpha-1 polypeptide isoform 4; Brain calcium channel I; BI;
cds_wt_118	-	
cds_wt_119	kaiC	Circadian clock protein kinase kaiC;
cds_wt_120	cheY	Transcriptional regulatory protein resD;
cds_wt_121	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_122	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_123	dppA	Glutathione-binding protein gsiB;
cds_wt_124	-	Nickel transport system permease protein nikB;
		Oligopeptide transport system permease protein
cds_wt_125	dppC	appC;
		Phosphate import ATP-binding protein pstB;
cds_wt_126	-	Phosphate-transporting ATPase; ABC phosphate transporter;
		Phosphate import ATP-binding protein pstB;
cds_wt_127	-	Phosphate-transporting ATPase; ABC phosphate transporter;
cds_wt_128	-	hypothetical protein
cds_wt_129	-	Uncharacterized protein Mb1584;
cds_wt_130	-	hypothetical protein
cds_wt_131	-	hypothetical protein
cds_wt_132	-	transcriptional regulator, ROK family
cds_wt_133	manB	beta-mannosidase
		HTH-type transcriptional repressor purR; Purine nucleotide synthesis repressor; Pur regulon
cds_wt_134	lacI	repressor;
cds_wt_135	-	Collagen alpha-4
		HTH-type transcriptional repressor purR; Purine nucleotide synthesis repressor; Pur regulon
cds_wt_136	-	repressor;
cds_wt_137	-	beta-glucosidase
cds_wt_138	gpm2	putative phosphoglycerate mutase family protein
cds_wt_139	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_140	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_141	-	hypothetical protein predicted by Glimmer/Critica

		Beta-hexosaminidase subunit beta; N-acetyl-beta-glucosaminidase subunit beta; Beta-N-acetylhexosaminidase subunit beta; Hexosaminidase subunit B;
cds_wt_142	Hexb	
cds_wt_143	-	triacylglycerol lipase
cds_wt_144	acrA	Macrolide-specific efflux protein macA;
		Response regulator mprA; Mycobacterial persistence regulator A;
cds_wt_145	phoP	
cds_wt_146	phoR	sensor histidine kinase
cds_wt_147	macA	Macrolide-specific efflux protein macA;
cds_wt_148	-	putative ABC transporter ATP-binding protein
		Macrolide export ATP-binding/permease protein
cds_wt_149	-	macB;
cds_wt_150	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_151	-	hypothetical protein predicted by Glimmer/Critica
		HTH-type transcriptional regulator malT; ATP-dependent transcriptional activator malT;
cds_wt_152	-	
cds_wt_153	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_154	terC	Uncharacterized membrane protein STKORF319;
cds_wt_155	DODA	4,5-DOPA dioxygenase extradiol;
cds_wt_156	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_157	iolC	putative carbohydrate kinase
		5-deoxy-glucuronate isomerase; 5DG isomerase; EC=5.3.1.n1;
cds_wt_158	iolB	
cds_wt_159	iolD	putative acetolactate synthase
		Inosose dehydratase; 2-keto-myo-inositol dehydratase; 2KMI dehydratase;
cds_wt_160	iolE	HTH-type transcriptional repressor purR; Purine nucleotide synthesis repressor; Pur regulon repressor;
cds_wt_161	-	
		Autoinducer 2 import system permease protein lsrC;
cds_wt_162	-	AI-2 import system permease protein lsrC;
cds_wt_163	-	putative sugar ABC transporter ATP-binding protein
cds_wt_164	iolG	myo-inositol 2-dehydrogenase
		Uncharacterized HTH-type transcriptional regulator
cds_wt_165	-	yvaF;
cds_wt_166	paaZ	putative oxidoreductase
cds_wt_167	paaA	Phenylacetic acid degradation protein paaA;
cds_wt_168	paaC	Phenylacetic acid degradation protein paaC;
cds_wt_169	paaD	Phenylacetic acid degradation protein paaD;
		Probable phenylacetic acid degradation NADH oxidoreductase paaE;
cds_wt_170	paaE	
cds_wt_171	-	putative methyltransferase
cds_wt_172	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_173	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_174	pepD	putative protease
		Multidrug resistance protein 3; ATP-binding cassette sub-family B member 1A; P-glycoprotein 3; MDR1A;
cds_wt_175	ywjA	Putative metallophosphoesterase FLJ45032
cds_wt_176	-	homolog;

cds_wt_177	-	hypothetical protein
cds_wt_178	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_179	-	hypothetical protein predicted by Glimmer/Critica
		Bifunctional heparan sulfate N-deacetylase/N-sulfotransferase 3; Glucosaminyl N-deacetylase/N-sulfotransferase 3; NDST-3; hNDST-3; N-heparan sulfate sulfotransferase 3; N-HSST 3; Includes: Heparan sulfate N-deacetylase 3; Includes: Heparan sulfate N-sulfotransferase 3;
cds_wt_180	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_181	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_182	pknA	serine/threonine protein kinase
cds_wt_183	-	Uncharacterized amino acid permease yfnA;
		Anti-sigma F factor antagonist; Stage II sporulation protein AA;
cds_wt_184	-	hypothetical protein
cds_wt_185	-	hypothetical protein
cds_wt_186	biol	probable cytochrome p450 140 CYP140
cds_wt_187	egl2	cellulase
		D-alanine--D-alanine ligase; D-alanylalanine synthetase; D-Ala-D-Ala ligase;
cds_wt_188	-	Enterochelin esterase; Ferric enterobactin esterase;
cds_wt_189	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_190	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_191	-	Uncharacterized signaling protein CC_0091;
cds_wt_192	-	probable helicase HelZ
cds_wt_193	helZ	probable helicase HelZ
cds_wt_194	helZ	probable helicase HelZ
cds_wt_195	-	hypothetical protein
cds_wt_196	-	Collagen alpha-5
cds_wt_197	-	Uncharacterized protein R665;
cds_wt_198	-	Putative membrane protein mmpL3;
cds_wt_199	-	hypothetical protein predicted by Glimmer/Critica
		FK506-binding protein 4; Peptidyl-prolyl cis-trans isomerase; PPlase; Rotamase;
cds_wt_200	fkbp	UPF0246 protein VV1_0535;
cds_wt_201	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_202	-	Uncharacterized HTH-type transcriptional regulator MJ0272;
cds_wt_203	lanR	hypothetical protein
cds_wt_204	-	hypothetical protein
cds_wt_205	copD	Copper resistance protein D;
cds_wt_206	pgm	phosphoglucomutase
cds_wt_207	-	Uncharacterized signaling protein PA3311;
cds_wt_208	-	hypothetical protein predicted by Glimmer/Critica
		Membrane-bound lytic murein transglycosylase F; EC=4.2.2.n1; Murein lyase F;
cds_wt_209	glnH	hypothetical protein
cds_wt_210	-	hypothetical protein
cds_wt_211	prpF	Phosphoserine phosphatase rsbP;
cds_wt_212	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_213	gnd	6-phosphogluconate dehydrogenase
cds_wt_214	-	putative acetyltransferase
cds_wt_215	-	Probable disease resistance protein At5g43740;
cds_wt_216	PDR1	Pleiotropic drug resistance protein 1; NtPDR1;

cds_wt_217	-	Spermidine/putrescine import ATP-binding protein potA;
cds_wt_218	nrdG	anaerobic ribonucleoside-triphosphate reductase activating protein
cds_wt_219	-	Endonuclease/exonuclease/phosphatase family domain-containing protein 1;
cds_wt_220	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_221	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_222	-	Uncharacterized AAA domain-containing protein ycf46;
cds_wt_223	-	hypothetical protein
cds_wt_224	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_225	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_226	-	Cyanoglobin; Hemoglobin; Hb;
cds_wt_227	ereB	hypothetical protein
cds_wt_228	LIP6	Lipase 6;
cds_wt_229	mocA	K ⁺ channel beta subunit
cds_wt_230	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_231	-	Putative multidrug resistance protein mdtD;
cds_wt_232	glgX	putative glycosyl hydrolase
cds_wt_233	-	Amino-acid acetyltransferase; N-acetylglutamate synthase; AGS; NAGS;
cds_wt_234	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_235	-	hypothetical protein
cds_wt_236	scrB	Beta-fructofuranosidase, insoluble isoenzyme 1; Sucrose hydrolase 1; Invertase 1; Cell wall beta-fructosidase 1; OsCIN1;
cds_wt_237	-	hypothetical protein
cds_wt_238	-	Uncharacterized protein yecE;
cds_wt_239	-	hypothetical protein
cds_wt_240	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_241	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_242	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_243	-	hypothetical protein
cds_wt_244	-	Uncharacterized protein Mb2600;
cds_wt_245	Cuta	Protein CutA; Brain acetylcholinesterase putative membrane anchor;
cds_wt_246	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_247	phoD	phosphodiesterase/alkaline phosphatase D
cds_wt_248	-	hypothetical protein
cds_wt_249	-	hypothetical membrane protein
cds_wt_250	lamA	Beta-1,3-glucan-binding protein; BGBP; Beta-1,3-glucan recognition protein; BetaGRP;
cds_wt_251	-	Uncharacterized signaling protein PA1727;
cds_wt_252	-	monooxygenase, DszC family
cds_wt_253	-	Uncharacterized protein ML0378;
cds_wt_254	-	Signaling protein ykoW;
cds_wt_255	PHOA	acid phosphatase
cds_wt_256	-	Uncharacterized MFS-type transporter MJ1317;
cds_wt_257	-	Protein tolB;

cds_wt_258	-	Uncharacterized protein DR_1314;
cds_wt_259	fabG	3-oxoacyl-
cds_wt_260	polA	putative 5'-3' exonuclease
cds_wt_261	bcd1	butyryl-CoA dehydrogenase
cds_wt_262	lrp	Uncharacterized HTH-type transcriptional regulator PH1519;
cds_wt_263	-	hypothetical protein
cds_wt_264	-	hypothetical protein
cds_wt_265	-	Laminin subunit beta-2; S-laminin; Laminin chain B3;
cds_wt_266	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_267	-	hypothetical protein
cds_wt_268	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_269	-	hypothetical protein
cds_wt_270	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_271	kamA	lysine 2,3-aminomutase
cds_wt_272	-	L-threonine 3-dehydrogenase;
cds_wt_273	aepA	Putative amidohydrolase ytcJ;
cds_wt_274	kamD	D-lysine 5,6-aminomutase, alpha subunit
cds_wt_275	kamE	D-lysine 5,6-aminomutase beta subunit
cds_wt_276	-	hypothetical protein
cds_wt_277	mutL	methylaspartate mutase
cds_wt_278	ppm1	putative apolipoprotein N-acyltransferase
cds_wt_279	ppm1	putative glycosyl transferase
cds_wt_280	-	UPF0716 protein ytzA;
cds_wt_281	-	hypothetical protein
cds_wt_282	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_283	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_284	Ttn	Titin; Connectin;
cds_wt_285	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_286	-	Uncharacterized MFS-type transporter yfiS;
cds_wt_287	-	putative transcriptional regulator
cds_wt_288	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_289	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_290	-	Uncharacterized HTH-type transcriptional regulator MJ1325;
cds_wt_291	-	hypothetical protein
cds_wt_292	-	hypothetical protein
cds_wt_293	-	putative nitroreductase
cds_wt_294	ssuD	alkanesulfonate monooxygenase
cds_wt_295	-	Putative sensory transducer protein;
cds_wt_296	-	Spermidine/putrescine import ATP-binding protein potA;
cds_wt_297	xyIR	Xylose repressor;
cds_wt_298	araG	ribose ABC transporter ATP-binding protein
cds_wt_299	araH	Xylose transport system permease protein xyIH;
cds_wt_300	chvE	Multiple sugar-binding periplasmic receptor chvE;
cds_wt_301	-	hypothetical protein
cds_wt_302	-	putative oxidoreductase
cds_wt_303	-	Putative xanthine dehydrogenase yagS FAD-binding subunit;

cds_wt_304	pucE	oxidoreductase
cds_wt_305	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_306	-	Sensor protein fixL;
cds_wt_307	-	Laminin subunit beta-1; Laminin B1 chain;
cds_wt_308	-	Uncharacterized signaling protein CC_0091;
cds_wt_309	-	hypothetical protein
cds_wt_310	-	putative short chain dehydrogenase
cds_wt_311	-	hypothetical protein predicted by Glimmer/Critica
Replicase polyprotein 1ab; pp1ab; ORF1ab polyprotein; Contains: Non-structural protein 1; nsp1; p28; Contains: Non-structural protein 2; nsp2; p65; Contains: Non-structural protein 3; nsp3; Papain-like proteinases 1/2; PL1-PRO/PL2-PRO; p210; Contains: Non-structural protein 4; nsp4; Peptide HD2; p44; Contains: 3C-like proteinase; 3CL-PRO; 3CLp; M-PRO; p27; nsp5; Contains: Non-structural protein 6; nsp6; Contains: Non-structural protein 7; nsp7; p10; Contains: Non-structural protein 8; nsp8; p22; Contains: Non-structural protein 9; nsp9; p12; Contains: Non-structural protein 10; nsp10; Growth factor-like peptide; GFL; p15; Contains: RNA-directed RNA polymerase; RdRp; Pol; p100; nsp12; Contains: Helicase; Hel; p67; nsp13; Contains: Exoribonuclease; ExoN; nsp14; Contains: Uridylate- specific endoribonuclease; NendoU; nsp15; p35; Contains: Putative 2'-O-methyl transferase; nsp16;		
cds_wt_312	-	
cds_wt_313	fhuF	hypothetical protein
cds_wt_314	tse	Methyl-accepting chemotaxis serine transducer;
cds_wt_315	pfpl	Pfpl
Translocator protein; Peripheral-type benzodiazepine receptor; PBR; PKBS; Mitochondrial benzodiazepine receptor;		
cds_wt_316	tspO	
cds_wt_317	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_318	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_319	-	Alanine racemase 1;
cds_wt_320	hspX	17.5 kDa class I heat shock protein; HSP 17.5-E; Putative ABC transporter ATP-binding protein TTE1589;
cds_wt_321	-	
cds_wt_322	-	Catechol 1,2-dioxygenase; Uncharacterized HTH-type transcriptional regulator ywbl;
cds_wt_323	stmR	
cds_wt_324	pcaF	beta-ketoadipyl CoA thiolase
cds_wt_325	pcaI	3-oxoadipate CoA-transferase subunit A
cds_wt_326	pcaJ	3-oxoadipate CoA-transferase subunit B
cds_wt_327	ssuD	hypothetical protein
High-affinity branched-chain amino acid transport system permease protein livM; LIV-I protein M;		
cds_wt_328	-	
Autoinducer 2 import system permease protein lsrC; AI-2 import system permease protein lsrC;		
cds_wt_329	livH	

		Phosphate import ATP-binding protein pstB; Phosphate-transporting ATPase; ABC phosphate transporter;
cds_wt_330	livF	
cds_wt_331	livG	Sulfate/thiosulfate import ATP-binding protein cysA; Sulfate-transporting ATPase;
cds_wt_332	-	Leu/Ile/Val-binding protein homolog 2;
cds_wt_333	bdhA	D-beta-hydroxybutyrate dehydrogenase
cds_wt_334	-	hydrolase, alpha/beta fold family
cds_wt_335	tetV	High-affinity glucose transporter SNF3;
cds_wt_336	-	HTH-type transcriptional regulator glxA;
cds_wt_337	-	Collagen alpha-5
cds_wt_338	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_339	abfB	Alpha-N-arabinofuranosidase B; Arabinosidase B; ABF B;
cds_wt_340	gntR	Uncharacterized HTH-type transcriptional regulator ydfH;
cds_wt_341	kipA	hypothetical protein
cds_wt_342	kipl	hypothetical protein
cds_wt_343	-	Putative proline/betaine transporter;
cds_wt_344	-	Virginiamycin B lyase; Streptogramin B lyase;
cds_wt_345	-	Uncharacterized HTH-type transcriptional regulator ydeS;
cds_wt_346	ramA	alfa-L-rhamnosidase
cds_wt_347	cheB	protein-glutamate methylesterase
cds_wt_348	-	Anti-sigma F factor antagonist; Stage II sporulation protein AA;
cds_wt_349	cheB	protein-glutamate methylesterase
cds_wt_350	cheR	methyltransferase
cds_wt_351	-	UPF0718 protein ycgR;
cds_wt_352	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_353	rtcB	UPF0027 protein TK0358;
cds_wt_354	-	Anti-sigma F factor antagonist; Stage II sporulation protein AA;
cds_wt_355	-	RNA polymerase sigma factor rpoD; Sigma-70;
cds_wt_356	-	Phytochrome-like protein cph2; Bacteriophytochrome cph2;
cds_wt_357	-	putative glutathione-dependent aldehyde dehydrogenase
cds_wt_358	topI	DNA topoisomerase 1B; TopIB; DNA topoisomerase type IB;
cds_wt_359	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_360	-	Uncharacterized methyltransferase C25B8.09;
cds_wt_361	-	possible bifunctional enzyme: 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase (HhdD isomerase) + cyclase/dehydrase
cds_wt_362	aspC	aspartate aminotransferase
cds_wt_363	-	hypothetical protein
cds_wt_364	ctaD	putative cytochrome c oxidase subunit I
cds_wt_365	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_366	-	hypothetical protein predicted by Glimmer/Critica

cds_wt_367	ltrA	Uncharacterized protein RA0937; Diflavin flavoprotein A 1; NADH:oxygen oxidoreductase; SsATF573;
cds_wt_368	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_369	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_370	-	polypeptide deformylase
cds_wt_371	def2	Zinc transporter 9; ZnT-9; Solute carrier family 30 member 9;
cds_wt_372	catA	pectate lyase II
cds_wt_373	pel1	oxidoreductase, short chain dehydrogenase/reductase family
cds_wt_374	-	DNA protection during starvation protein;
cds_wt_375	dps	hypothetical protein predicted by Glimmer/Critica
cds_wt_376	-	Probable RuBisCO transcriptional regulator;
cds_wt_377	oxyR	hypothetical protein predicted by Glimmer/Critica
cds_wt_378	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_379	-	pyruvate oxidase
cds_wt_380	-	hypothetical protein
cds_wt_381	-	hypothetical protein
cds_wt_382	-	hypothetical protein
cds_wt_383	-	narrowly conserved hypothetical protein with duf54
cds_wt_384	-	Holliday junction ATP-dependent DNA helicase ruvB;
cds_wt_385	moxR	Translation initiation factor IF-2;
cds_wt_386	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_387	-	Myosin-1; Class I unconventional myosin; Type I myosin;
cds_wt_388	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_389	-	Uncharacterized signaling protein PA3311;
cds_wt_390	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_391	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_392	-	Uncharacterized amino-acid permease P7G5.06;
cds_wt_393	-	hypothetical protein
cds_wt_394	amdA	hypothetical protein predicted by Glimmer/Critica
cds_wt_395	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_396	-	Uncharacterized protein ydfG;
cds_wt_397	-	Uncharacterized protein yxiA;
cds_wt_398	abnA	hypothetical protein predicted by Glimmer/Critica
cds_wt_399	-	Helicase IV;
cds_wt_400	-	Uncharacterized protein ypaA;
cds_wt_401	-	UPF0061 protein MAP_3154;
cds_wt_402	-	Cholinesterase; Acylcholine acylhydrolase; Choline esterase II; Butyrylcholine esterase;
cds_wt_403	lipI	Pseudocholinesterase; Transcription elongation regulator 1; TATA box- binding protein-associated factor 2S; Transcription factor CA150;
cds_wt_404	-	Putative transposase for insertion sequence element IS6501;
cds_wt_405	-	putative transposase
cds_wt_406	-	Uncharacterized protein y4sN;
cds_wt_407	-	

cds_wt_408	-	nucleotidyltransferase domain protein
cds_wt_409	-	hypothetical protein
cds_wt_410	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_411	ssuD	Alkanesulfonate monooxygenase; FMNH2-dependent aliphatic sulfonate monooxygenase;
cds_wt_412	phaB	Poly
cds_wt_413	-	Anti-sigma F factor antagonist; Stage II sporulation protein AA;
cds_wt_414	-	Cytochrome b-c1 complex subunit Rieske, mitochondrial; Ubiquinol-cytochrome c reductase iron-sulfur subunit; Rieske iron-sulfur protein; RISP; Complex III subunit 5; Contains: Cytochrome b-c1 complex subunit 11; Ubiquinol-cytochrome c reductase 8 kDa protein; Complex III subunit IX;
cds_wt_415	-	hypothetical protein
cds_wt_416	-	RNA polymerase sigma factor rpoD;
cds_wt_417	pimH	Uncharacterized MFS-type transporter yfml; Polypeptide N-acetylgalactosaminyltransferase 1; Protein-UDP acetylgalactosaminyltransferase 1; UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase 1; Polypeptide GalNAc transferase 1; pp-GaNTase 1; GalNAc-T1; Contains: Polypeptide N-acetylgalactosaminyltransferase 1 soluble form;
cds_wt_418	-	aldehyde dehydrogenase family 1, subfamily A3
cds_wt_419	betB	hypothetical protein predicted by Glimmer/Critica
cds_wt_420	-	carbamoyltransferase
cds_wt_421	-	Uncharacterized 55.3 kDa protein in thcA 5' region; ORF1;
cds_wt_422	-	Epoxide hydrolase 2; Soluble epoxide hydrolase; SEH; Epoxide hydratase; Cytosolic epoxide hydrolase; CEH;
cds_wt_423	-	glycosyltransferase
cds_wt_424	rfaG	putative transferase
cds_wt_425	-	phosphoheptose isomerase
cds_wt_426	lpcA	ADP-heptose synthase
cds_wt_427	rfaE	3-oxoacyl-
cds_wt_428	-	ADP-heptose--LPS heptosyltransferase 2; ADP-heptose--LPS heptosyltransferase II;
cds_wt_429	-	Calcium-gated potassium channel mthK;
cds_wt_430	-	hypothetical protein
cds_wt_431	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_432	-	hypothetical protein
cds_wt_433	-	hypothetical protein
cds_wt_434	-	2,3-bisphosphoglycerate-dependent phosphoglycerate mutase; Phosphoglyceromutase; PGAM; BPG-dependent PGAM; dPGM;
cds_wt_435	-	putative metalloprotease
cds_wt_436	prt1	hypothetical protein predicted by Glimmer/Critica
cds_wt_437	-	UPF0118 membrane protein sll0063;
cds_wt_438	-	Tetracycline repressor protein class H;
cds_wt_439	tetR	

cds_wt_440	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_441	spcT	Uncharacterized protein Mb1288c;
cds_wt_442	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_443	-	Uncharacterized protein ycf39; ORF319;
cds_wt_444	-	hypothetical protein
cds_wt_445	-	HTH-type transcriptional regulator betI;
cds_wt_446	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_447	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_448	-	possible peroxidase, putative
cds_wt_449	sgcA	putative adenylate cyclase
cds_wt_450	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_451	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_452	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_453	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_454	yjfF	UPF0060 membrane protein Mmwy1_1139;
		Spermidine/putrescine-binding periplasmic protein;
cds_wt_455	potD	SPBP;
cds_wt_456	yhfO	Uncharacterized N-acetyltransferase MJ1207;
		Laminin subunit gamma-3; Laminin 12 gamma 3
cds_wt_457	-	subunit;
cds_wt_458	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_459	-	hypothetical protein predicted by Glimmer/Critica
		Probable inorganic polyphosphate/ATP-NAD kinase;
cds_wt_460	-	Poly
cds_wt_461	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_462	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_463	-	hypothetical protein
cds_wt_464	-	RNA pyrophosphohydrolase;
cds_wt_465	lysX	lysyl-tRNA synthetase
cds_wt_466	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_467	-	Uncharacterized protein Cgl0967/cg1104; ORF2;
cds_wt_468	srfJ	glycosyl hydrolase
cds_wt_469	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_470	-	putative secreted protein
cds_wt_471	-	hypothetical protein
cds_wt_472	map	methionine aminopeptidase
cds_wt_473	-	putative DNA-binding protein
cds_wt_474	-	Uncharacterized protein yegE;
cds_wt_475	-	Uncharacterized protein MJ1623;
cds_wt_476	biol	putative cytochrome P450
		Alkanal monooxygenase alpha chain; Bacterial
cds_wt_477	luxA	luciferase alpha chain;
cds_wt_478	-	Uncharacterized protein Mb1292c;
cds_wt_479	fliQ	Flagellar biosynthetic protein fliQ;
cds_wt_480	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_481	-	Uncharacterized transporter yoaV;
cds_wt_482	-	Probable RuBisCO transcriptional regulator;
cds_wt_483	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_484	-	DnaJ homolog subfamily C member 22;

cds_wt_485	-	Putative S-adenosyl-L-methionine-dependent methyltransferase MAV_4444;
cds_wt_486	-	Beta-lactamase ROB-1;
cds_wt_487	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_488	-	Heat shock 70 kDa protein 1A; HSP70.1;
cds_wt_489	hibD	6-phosphogluconate dehydrogenase NAD-binding domain-containing protein
cds_wt_490	-	Putative ribosome maturation factor rimN;
cds_wt_491	-	putative secreted protein
cds_wt_492	cpbD	GlcNAc-binding protein A;
cds_wt_493	celY	Exoglucanase-2; Exoglucanase II; Exocellobiohydrolase II; 1,4-beta-cellobiohydrolase II; Avicelase II;
cds_wt_494	celD	Endoglucanase E-4; Endo-1,4-beta-glucanase E-4;
cds_wt_495	ugd	Cellulase E-4; Cellulase E4;
cds_wt_496	aglE	UDP-glucose dehydrogenase
cds_wt_497	aglF	Alpha-glucosides-binding periplasmic protein aglE;
cds_wt_498	aglG	Alpha-glucoside transport system permease protein aglF;
cds_wt_499	-	Probable ABC transporter permease protein yurM;
cds_wt_500	lolD	Methionine import ATP-binding protein metN;
cds_wt_501	-	Spermidine/putrescine import ATP-binding protein potA;
cds_wt_502	-	putative membrane protein
cds_wt_503	-	putative membrane protein
cds_wt_504	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_505	bag	hypothetical protein predicted by Glimmer/Critica
cds_wt_506	narK	IgA FC receptor; Beta antigen; B antigen;
cds_wt_507	CAO	Probable nitrate transporter narT;
cds_wt_508	nirB	Chlorophyllide a oxygenase, chloroplastic;
cds_wt_509	sirB	Chlorophyll a oxygenase; Chlorophyll b synthase;
cds_wt_510	yjjA	nitrite reductase
cds_wt_511	-	Sirohydrochlorin ferrochelataase;
cds_wt_512	-	hypothetical protein
cds_wt_513	ethA	Uncharacterized protein Rv0885/MT0908;
cds_wt_514	-	Fatty acid metabolism regulator protein;
cds_wt_515	acoC	monooxygenase, flavin-binding family
cds_wt_516	-	probable short-chain dehydrogenase
cds_wt_517	-	putative hydrolase
cds_wt_518	cisZ	hypothetical protein predicted by Glimmer/Critica
cds_wt_519	citA	Iodotyrosine dehalogenase 1; IYD-1;
cds_wt_520	-	citrate synthase
cds_wt_521	novA	citrate synthase
cds_wt_522	yusO	Ubiquinone/menaquinone biosynthesis methyltransferase ubiE;
cds_wt_523	-	Lipid A export ATP-binding/permease protein msbA;
		Multiple antibiotic resistance protein marR;
		Probable UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase SEC; Protein SECRET AGENT;

cds_wt_524	-	HTH-type transcriptional regulator hpr; Protease production regulatory protein hpr;
cds_wt_525	-	Putative membrane protein actII-3;
cds_wt_526	ssuD	alkanesulfonate monooxygenase
cds_wt_527	-	hypothetical protein predicted by Glimmer/Critica
		HTH-type transcriptional repressor purR; Purine nucleotide synthesis repressor; Pur regulon repressor;
cds_wt_528	rbsR	
cds_wt_529	aglA	putative alpha-glucosidase
cds_wt_530	-	Uncharacterized protein Mb1389c;
cds_wt_531	tauB	ABC transporter ATP-binding protein
		Taurine-binding periplasmic protein; Sulfate starvation-induced protein 1; SSI1;
cds_wt_532	tauA	
cds_wt_533	tauC	Nitrate transport permease protein nrtB;
cds_wt_534	-	amino acid ABC transporter, permease protein
cds_wt_535	atrC	putative ABC transporter ATP-binding protein
		Membrane-bound lytic murein transglycosylase F; EC=4.2.2.n1; Murein lyase F;
cds_wt_536	fliY	
cds_wt_537	-	Uncharacterized protein ML0378;
cds_wt_538	-	Nephrocystin-3;
cds_wt_539	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_540	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_541	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_542	-	putative DNA-binding protein
cds_wt_543	-	Voltage-gated potassium channel subunit beta-1; K
cds_wt_544	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_545	-	putative transcriptional regulator
		Uncharacterized 36.0 kDa protein in kdgK 5' region; K1 ORF;
cds_wt_546	-	
		Uncharacterized HTH-type transcriptional regulator ydeP;
cds_wt_547	-	
cds_wt_548	adh	NADPH:quinone reductase
cds_wt_549	yvbT	Uncharacterized protein yddN;
cds_wt_550	luxA	putative monooxygenase
cds_wt_551	-	putative FMNH ₂ -utilizing oxygenase
cds_wt_552	-	Putative monooxygenase yxeK;
cds_wt_553	oppD	Glutathione import ATP-binding protein gsiA;
cds_wt_554	dppC	Dipeptide transport system permease protein dppC;
cds_wt_555	oppB	Glutathione transport system permease protein gsiC;
cds_wt_556	oppA	Periplasmic oligopeptide-binding protein;
cds_wt_557	-	putative membrane protein
cds_wt_558	prpE	possible acyl-CoA synthetase
cds_wt_559	-	Sensor protein vraS;
		Transcriptional regulatory protein degU; Protease production enhancer protein;
cds_wt_560	-	
cds_wt_561	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_562	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_563	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_564	-	hypothetical protein predicted by Glimmer/Critica

cds_wt_565	-	Tetratricopeptide repeat protein 28; TPR repeat protein 28;
cds_wt_566	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_567	pcrA	UvrD/REP helicase family protein
cds_wt_568	-	hypothetical protein
cds_wt_569	-	hypothetical protein
cds_wt_570	-	HTH-type transcriptional regulator betI;
cds_wt_571	-	acyl-CoA dehydrogenase
cds_wt_572	fadA	acetyl-CoA acyltransferase
cds_wt_573	fadB	enoyl-CoA hydratase / 3-hydroxyacyl-CoA dehydrogenase / 3-hydroxybutyryl-CoA epimerase
cds_wt_574	mcr	alpha-methylacyl-CoA racemase
cds_wt_575	-	Uncharacterized protein yneF;
cds_wt_576	tlpB	Methyl-accepting chemotaxis protein mcpB; H3;
cds_wt_577	-	hypothetical protein
cds_wt_578	ytfH	Uncharacterized HTH-type transcriptional regulator ydeP;
cds_wt_579	ytfG	Prestalk A differentiation protein A;
cds_wt_580	-	Prolyl-tRNA synthetase; Proline--tRNA ligase; ProRS;
cds_wt_581	-	hypothetical protein
cds_wt_582	-	hypothetical protein
cds_wt_583	-	Uncharacterized protein ML1167;
cds_wt_584	-	Uncharacterized protein ML1167;
cds_wt_585	tlpB	Methyl-accepting chemotaxis protein mcpA; H1;
cds_wt_586	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_587	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_588	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_589	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_590	-	Sulfatase-modifying factor 1; C-alpha-formylglycine-generating enzyme 1;
cds_wt_591	-	hypothetical protein
cds_wt_592	lacI	HTH-type transcriptional repressor purR; Purine nucleotide synthesis repressor; Pur regulon repressor;
cds_wt_593	-	Probable ABC transporter permease protein yurM;
cds_wt_594	ugpA	Probable ABC transporter permease protein yurN;
cds_wt_595	-	Uncharacterized ABC transporter extracellular-binding protein yurO;
cds_wt_596	-	putative beta-xylosidase
cds_wt_597	-	Nif-specific regulatory protein;
cds_wt_598	-	putative aldehyde dehydrogenase
cds_wt_599	gabT	4-aminobutyrate aminotransferase
cds_wt_600	asnC	Leucine-responsive regulatory protein;
cds_wt_601	-	Dimethylglycine dehydrogenase, mitochondrial; ME2GLYDH;
cds_wt_602	PHYB	Phytochrome B;
cds_wt_603	yqjL	Uncharacterized protein yqjL;
cds_wt_604	soxR	HTH-type transcriptional regulator hmrR; Copper efflux regulator; Copper export regulator;
cds_wt_605	bioA	putative aminotransferase

cds_wt_606	-	Gamma-glutamylputrescine oxidoreductase; Gamma-glutamylputrescine oxidase; Gamma-Glu-Put oxidase;
cds_wt_607	potC	Spermidine/putrescine transport system permease protein potC;
cds_wt_608	potH	Spermidine/putrescine transport system permease protein potB;
cds_wt_609	potD	Spermidine/putrescine-binding periplasmic protein 2; SPBP;
cds_wt_610	potA	spermidine/putrescine ABC transporter ATP-binding subunit
cds_wt_611	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_612	-	aldehyde dehydrogenase
cds_wt_613	-	putative aminotransferase
cds_wt_614	mmsA	methylmalonate-semialdehyde dehydrogenase
cds_wt_615	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_616	-	putative serine/threonine protein kinase
cds_wt_617	suhB	inositol-1-monophosphatase
cds_wt_618	-	Membrane-associated guanylate kinase, WW and PDZ domain-containing protein 3; Membrane-associated guanylate kinase inverted 3; MAGI-3;
cds_wt_619	-	Scaffolding-like protein;
cds_wt_620	-	putative integral membrane protein
cds_wt_621	rbsA	Autoinducer 2-binding protein lsrB; AI-2-binding protein lsrB;
cds_wt_622	lsrC	ABC-type sugar (aldose) transport system, ATPase component
cds_wt_623	lsrC	Autoinducer 2 import system permease protein lsrC;
cds_wt_624	xylA	AI-2 import system permease protein lsrC;
cds_wt_625	-	Autoinducer 2 import system permease protein lsrC;
cds_wt_626	cyaC	AI-2 import system permease protein lsrC;
cds_wt_627	PHYB	putative sugar isomerase
cds_wt_628	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_629	-	two-component response regulator
cds_wt_630	-	two-component hybrid sensor and regulator
cds_wt_631	phoR	Methyl-accepting chemotaxis protein III; MCP-III;
cds_wt_632	cbiM	Ribose and galactose chemoreceptor protein;
cds_wt_633	cbiM	hypothetical protein predicted by Glimmer/Critica
cds_wt_634	cbiQ	hypothetical protein
cds_wt_635	cbiO	sensory box histidine kinase PhoR
cds_wt_636	-	Protein cbiM;
cds_wt_637	xpk	putative membrane protein
cds_wt_638	-	Uncharacterized protein MJ1089;
		Phosphate import ATP-binding protein pstB;
		Phosphate-transporting ATPase; ABC phosphate transporter;
		Probable N-acetylmuramoyl-L-alanine amidase; Cell wall hydrolase; Autolysin; ORFL3;
		putative phosphoketolase
		enoyl-CoA hydratase/isomerase family protein

cds_wt_639	-	putative transcriptional regulator
cds_wt_640	-	putative integral membrane protein
cds_wt_641	yicl	putative glycosyl hydrolase
cds_wt_642	-	sn-glycerol-3-phosphate transport system permease protein <i>ugpE</i> ;
cds_wt_643	lacF	sn-glycerol-3-phosphate transport system permease protein <i>ugpA</i> ;
cds_wt_644	-	Uncharacterized ABC transporter extracellular-binding protein <i>yurO</i> ; HTH-type transcriptional repressor <i>purR</i> ; Purine nucleotide synthesis repressor; Pur regulon repressor;
cds_wt_645	malR	glucan 1,4-beta-glucosidase
cds_wt_646	-	NADH oxidase
cds_wt_647	nox	similar to Tripeptidyl-peptidase II (TPP-II) (Tripeptidyl aminopeptidase)
cds_wt_648	TPP2	hypothetical protein predicted by Glimmer/Critica
cds_wt_649	-	Chitooligosaccharide deacetylase; Nodulation protein B;
cds_wt_650	nodB	HTH-type transcriptional activator <i>tipA</i> ;
cds_wt_651	-	Uncharacterized MFS-type transporter <i>y4rN</i> ;
cds_wt_652	-	hypothetical protein
cds_wt_653	-	acyl-CoA dehydrogenase
cds_wt_654	-	3-oxoacyl-
cds_wt_655	fabG	putative acyl-CoA dehydrogenase
cds_wt_656	acdA	Tetracycline repressor protein class E;
cds_wt_657	tetR	hypothetical protein
cds_wt_658	-	Bifunctional protein <i>hldE</i> ; Includes: D-beta-D-heptose 7-phosphate kinase; D-beta-D-heptose 7-phosphotransferase; Includes: D-beta-D-heptose 1-phosphate adenosyltransferase;
cds_wt_659	pfkB	tRNA
cds_wt_660	-	Uncharacterized HAD-hydrolase PH1655;
cds_wt_661	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_662	-	hypothetical protein
cds_wt_663	yggC	Alkanal monooxygenase alpha chain; Bacterial luciferase alpha chain;
cds_wt_664	luxA	Spore protein <i>ykuD</i> homolog;
cds_wt_665	-	ATP synthase subunit beta; F-ATPase subunit beta;
cds_wt_666	rho	ATP synthase F1 sector subunit beta;
cds_wt_667	-	putative DNA-binding protein
cds_wt_668	-	Uncharacterized protein Rv1996/MT2052;
cds_wt_669	GLN1	glutamine synthetase
cds_wt_670	-	Anti-sigma F factor antagonist; Stage II sporulation protein AA;
cds_wt_671	prsR	hypothetical protein
cds_wt_672	prpF	Phosphoserine phosphatase <i>rsbP</i> ;
cds_wt_673	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_674	phoB	Probable transcriptional regulator <i>ycf27</i> ; OmpR-like protein;

cds_wt_675	sidE	Vibriobactin utilization protein viuB;
cds_wt_676	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_677	-	hypothetical protein
cds_wt_678	hemN	oxygen-independent coproporphyrinogen III oxidase
cds_wt_679	TRIO	Triple functional domain protein; PTPRF-interacting protein;
cds_wt_680	-	Inosine-5'-monophosphate dehydrogenase; IMP dehydrogenase; IMPDH; IMPD;
cds_wt_681	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_682	-	putative monooxygenase
cds_wt_683	-	taurine dioxygenase
cds_wt_684	-	Putative aliphatic sulfonates transport permease protein ssuC;
cds_wt_685	ssuB	putative taurine transport system ATP-binding protein
cds_wt_686	-	Nitrate transport ATP-binding protein nrtC;
cds_wt_687	-	Sporulation-control protein spo0M; Stage 0 sporulation protein M;
cds_wt_688	-	hypothetical protein
cds_wt_689	mdh	malate dehydrogenase
cds_wt_690	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_691	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_692	cckA	two-component hybrid sensor and regulator
cds_wt_693	expR	Transcriptional activator protein expR;
cds_wt_694	-	Uncharacterized hemerythrin-like protein C869.06c;
cds_wt_695	-	Putative membrane protein SCO5905;
cds_wt_696	-	Transmembrane 9 superfamily member 2;
cds_wt_697	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_698	plcN	non-hemolytic phospholipase C precursor
cds_wt_699	pcaC	4-carboxymuconolactone decarboxylase
cds_wt_700	pcaB	3-carboxy-cis,cis-muconate cycloisomerase
cds_wt_701	pcaG	protocatechuate 3,4-dioxygenase alpha subunit
cds_wt_702	pcaH	protocatechuate 3,4-dioxygenase, beta subunit
cds_wt_703	allR	HTH-type transcriptional repressor allR; Negative regulator of allantoin and glyoxylate utilization operons;
cds_wt_704	pobA	p-hydroxybenzoate hydroxylase
cds_wt_705	-	Uncharacterized membrane protein bbp_130;
cds_wt_706	-	hypothetical protein
cds_wt_707	-	Uncharacterized methyltransferase MJ1487;
cds_wt_708	-	hypothetical protein
cds_wt_709	-	hypothetical protein
cds_wt_710	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_711	kdgR	Pectin degradation repressor protein kdgR;
cds_wt_712	tauC	Translation initiation factor IF-2;
cds_wt_713	ssuC	Bicarbonate transport system permease protein cmpB;
cds_wt_714	ssuB	ABC transporter, ATP-binding protein
cds_wt_715	-	Uncharacterized protein Mb2247c;
cds_wt_716	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_717	padR	putative transcriptional regulator

cds_wt_718	-	Methionine import ATP-binding protein metN;
cds_wt_719	PDR1	Pleiotropic drug resistance protein 1; NtPDR1;
cds_wt_720	-	Protein piccolo; Aczonin; Multidomain presynaptic
cds_wt_721	-	cytomatrix protein; Brain-derived HLMN protein;
cds_wt_722	-	Dynamin-3; Dynamin, testicular; T-dynamin;
cds_wt_723	-	putative secreted protein
		putative secreted protein
		Chromodomain-helicase-DNA-binding protein 4;
cds_wt_724	CHD4	CHD-4; ATP-dependent helicase CHD4; Mi-2
cds_wt_725	-	autoantigen 218 kDa protein; Mi2-beta;
cds_wt_726	-	DNA polymerase IV; Pol IV;
cds_wt_727	aap	hypothetical protein predicted by Glimmer/Critica
cds_wt_728	-	Collagen alpha-4
		Collagen alpha-5
cds_wt_729	-	glutamate-1-semialdehyde 2,1-aminomutase,
		putative
		Uncharacterized WD repeat-containing protein
cds_wt_730	-	alr2800;
		Cell surface glycoprotein 1; Outer layer protein B; S-
cds_wt_731	-	layer protein 1;
cds_wt_732	menC	N-acylamino acid racemase
		Uncharacterized HTH-type transcriptional regulator
cds_wt_733	-	CPE0189;
cds_wt_734	-	hypothetical protein
cds_wt_735	cpg2	putative peptidase
cds_wt_736	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_737	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_738	-	hypothetical protein predicted by Glimmer/Critica
		Macrolide export ATP-binding/permease protein
cds_wt_739	macB	macB;
cds_wt_740	-	ABC transporter, ATP-binding protein
		DNA-directed RNA polymerase subunit beta; RNAP
		subunit beta; Transcriptase subunit beta; RNA
cds_wt_741	hlyD	polymerase subunit beta;
		Multidrug resistance protein mdtA; Multidrug
cds_wt_742	ybjY	transporter mdtA;
cds_wt_743	-	Hybrid signal transduction histidine kinase A;
		Probable transcriptional regulator ycf27; OmpR-like
cds_wt_744	rpaA	protein;
cds_wt_745	-	signal transduction histidine kinase
cds_wt_746	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_747	-	UPF0707 protein yvbY;
cds_wt_748	ykgF	Uncharacterized electron transport protein ykgF;
cds_wt_749	rhaB	putative rhamnose kinase
cds_wt_750	yuxG	Uncharacterized oxidoreductase yuxG; ORF2;
cds_wt_751	Fn1	Fibronectin; FN;
cds_wt_752	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_753	-	Putative multidrug resistance protein mdtD;
cds_wt_754	-	Protein nirD;
cds_wt_755	-	hypothetical protein predicted by Glimmer/Critica

		HTH-type transcriptional repressor purR; Purine nucleotide synthesis repressor; Pur regulon repressor;
cds_wt_756	rbsR	
cds_wt_757	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_758	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_759	gshA	putative glutamylcysteine synthetase
		SON protein; SON3; Negative regulatory element-binding protein; NRE-binding protein; DBP-5; Bax antagonist selected in saccharomyces 1; BASS1;
cds_wt_760	-	
cds_wt_761	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_762	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_763	-	hypothetical protein
cds_wt_764	-	hypothetical protein
cds_wt_765	-	putative acetyltransferase
cds_wt_766	fbp	FKBP-type peptidyl-prolyl cis-trans isomerase
cds_wt_767	yjdF	Uncharacterized protein yjdF;
cds_wt_768	-	putative DNA-binding protein
cds_wt_769	-	NADPH:quinone reductase
cds_wt_770	arsR	Arsenical resistance operon repressor;
cds_wt_771	-	hypothetical protein
cds_wt_772	-	3-oxoacyl-
cds_wt_773	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_774	-	transposase, IS4
cds_wt_775	-	transposase, IS4
cds_wt_776	-	Glycogen synthase; Starch
cds_wt_777	-	hypothetical protein
cds_wt_778	csd1	putative aminotransferase
cds_wt_779	-	hypothetical protein
cds_wt_780	dapE	succinyl-diaminopimelate desuccinylase
cds_wt_781	-	2',3'-cyclic-nucleotide 2'-phosphodiesterase;
cds_wt_782	-	Probable sugar efflux transporter;
		Ubiquinone/menaquinone biosynthesis
cds_wt_783	-	methyltransferase ubiE;
cds_wt_784	eglA	Endoglucanase; Endo-1,4-beta-glucanase; Cellulase;
cds_wt_785	-	two-component hybrid sensor and regulator
cds_wt_786	-	histidine kinase/response regulator hybrid protein
cds_wt_787	-	Sensor histidine kinase malK; Malate kinase sensor;
cds_wt_788	-	hypothetical protein
		Protein piccolo; Aczonin; Multidomain presynaptic cytomatrix protein;
cds_wt_789	Pclo	
		Neurogenic locus notch homolog protein 3; Notch 3; Contains: Notch 3 extracellular truncation; Contains: Notch 3 intracellular domain;
cds_wt_790	-	
cds_wt_791	-	hypothetical protein
cds_wt_792	moxR	Holliday junction ATP-dependent DNA helicase ruvB;
		Neuronal cell adhesion molecule; Nr-CAM; NgCAM-related cell adhesion molecule; Ng-CAM-related;
cds_wt_793	TTN	hBravo;
cds_wt_794	-	Collagen alpha-2
cds_wt_795	-	Uncharacterized protein y4bA/y4pH;

cds_wt_796	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_797	rsbU	Uncharacterized protein Rv1364c/MT1410;
		two-component system sensor histidine
		kinase/response regulator, hybrid ('one-component
		system')
cds_wt_798	cyaC	
cds_wt_799	sigF	RNA polymerase sigma factor rpoD;
		Cytosolic non-specific dipeptidase; CNDP
cds_wt_800	-	dipeptidase 2;
cds_wt_801	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_802	rsbU	Uncharacterized protein Rv1364c/MT1410;
cds_wt_803	xylS	XylIDLEGF operon transcriptional activator;
cds_wt_804	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_805	cheB	protein-glutamate methylesterase
cds_wt_806	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_807	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_808	-	hypothetical protein
		Anti-sigma F factor antagonist; Stage II sporulation
cds_wt_809	-	protein AA;
cds_wt_810	-	Carboxylate-amine ligase Bcep1808_0078;
cds_wt_811	-	putative recombinase
cds_wt_812	-	Sensor protein gacS;
cds_wt_813	-	putative two-component system sensor kinase
		Modification methylase BabI; M.BabI; Adenine-
		specific methyltransferase BabI; DNA
cds_wt_814	-	methyltransferase ccrM; M.CcrMI ortholog;
cds_wt_815	-	Protein grpE; HSP-70 cofactor;
cds_wt_816	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_817	-	hypothetical protein
cds_wt_818	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_819	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_820	-	hypothetical protein
cds_wt_821	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_822	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_823	-	hypothetical protein
cds_wt_824	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_825	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_826	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_827	-	Protein STU1;
cds_wt_828	-	Uncharacterized protein yebA;
cds_wt_829	-	Holliday junction ATP-dependent DNA helicase ruvB;
cds_wt_830	-	hypothetical protein predicted by Glimmer/Critica
		Protein transport protein Sec24D; SEC24-related
cds_wt_831	-	protein D;
cds_wt_832	-	hypothetical protein
cds_wt_833	-	hypothetical protein
cds_wt_834	-	hypothetical protein
cds_wt_835	-	hypothetical protein
cds_wt_836	-	hypothetical protein
cds_wt_837	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_838	-	hypothetical protein

cds_wt_839	lysM	Uncharacterized protein DR_0888;
cds_wt_840	-	hypothetical protein
cds_wt_841	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_842	W	Baseplate assembly protein W; GpW;
cds_wt_843	-	hypothetical protein
cds_wt_844	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_845	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_846	X	Uncharacterized protein X;
cds_wt_847	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_848	arlS	sensor histidine kinase
cds_wt_849	tcrA	Response regulator mprA; Mycobacterial persistence regulator A;
cds_wt_850	-	hypothetical protein
cds_wt_851	cheW	Chemotaxis protein cheW;
cds_wt_852	luxB	monooxygenase
cds_wt_853	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_854	-	hypothetical protein
cds_wt_855	-	Sensor histidine kinase yvfT;
cds_wt_856	nreC	Oxygen regulatory protein nreC; Nitrogen regulation protein C;
cds_wt_857	mmyE	12-oxophytodienoate reductase 1; 12-oxophytodienoate-10,11-reductase 1; OPDA-reductase 1; AtOPR1; FS-AT-I;
cds_wt_858	mmyE	NADPH dehydrogenase; Xenobiotic reductase;
cds_wt_859	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_860	tcaB	Bicyclomycin resistance protein; Sulfonamide resistance protein;
cds_wt_861	tlpB	Methyl-accepting chemotaxis protein mcpB; H3;
cds_wt_862	-	HTH-type transcriptional repressor acnR;
cds_wt_863	tcsA	Two-component system protein A;
cds_wt_864	oppA	Periplasmic oligopeptide-binding protein;
cds_wt_865	oppD	Glutathione import ATP-binding protein gsiA;
cds_wt_866	oppC	Oligopeptide transport system permease protein appC;
cds_wt_867	oppB	Oligopeptide transport system permease protein appB;
cds_wt_868	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_869	butB	S-layer-related protein;
cds_wt_870	-	L-asparagine oxygenase; EC=1.14.11.n1; L-asparagine 3-hydroxylase;
cds_wt_871	Hao1	(S)-2-hydroxy-acid oxidase, peroxisomal, putative / glycolate oxidase, putative / short chain alpha-hydroxy acid oxidase, putative
cds_wt_872	cyc	Cytochrome P450 2C39; CYP11C39;
cds_wt_873	-	Collagen alpha-4
cds_wt_874	spcT	Uncharacterized MFS-type transporter y4rN;
cds_wt_875	yusZ	3-oxoacyl-
cds_wt_876	-	Putative uncharacterized transporter ygaY;
cds_wt_877	-	hypothetical protein

cds_wt_878	ntaB	Diflavin flavoprotein A 1; NADH:oxygen oxidoreductase; SsATF573;
cds_wt_879	otsA	alpha,alpha-trehalose-phosphate synthase
cds_wt_880	tdh	L-threonine 3-dehydrogenase;
cds_wt_881	mmfH	Short-chain specific acyl-CoA dehydrogenase, mitochondrial; SCAD; Butyryl-CoA dehydrogenase;
cds_wt_882	-	Probable transposase for insertion sequence element IS701;
cds_wt_883	-	glucose-methanol-choline oxidoreductase
cds_wt_884	pepN	putative metallopeptidase
cds_wt_885	-	hypothetical protein
cds_wt_886	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_887	WWP2	NEDD4-like E3 ubiquitin-protein ligase WWP2; WW domain-containing protein 2; Atrophin-1-interacting protein 2; AIP2;
cds_wt_888	nodB	Chitooligosaccharide deacetylase; Nodulation protein B;
cds_wt_889	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_890	PHYB	Phytochrome B;
cds_wt_891	-	Alcohol dehydrogenase class-3; Alcohol dehydrogenase class-III; Alcohol dehydrogenase 5; S-
cds_wt_892	-	hypothetical protein
cds_wt_893	-	Putative metallophosphoesterase MTH_1774;
cds_wt_894	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_895	-	HTH-type transcriptional repressor purR; Purine nucleotide synthesis repressor; Pur regulon repressor;
cds_wt_896	-	Neuropilin-1; A5 protein;
cds_wt_897	tas	Methyl-accepting chemotaxis aspartate transducer;
cds_wt_898	Cpa1	similar to Carboxypeptidase A2 precursor
cds_wt_899	-	putative transcriptional regulator
cds_wt_900	-	Uncharacterized MFS-type transporter ydeE;
cds_wt_901	NAGK	hypothetical protein
cds_wt_902	celF	6-phospho-beta-glucosidase
cds_wt_903	-	L-arabinose transport system permease protein araQ;
cds_wt_904	malF	sn-glycerol-3-phosphate transport system permease protein ugpA;
cds_wt_905	-	Maltotriose-binding protein; MMBP; Maltodextrin-binding protein;
cds_wt_906	xylR	Putative xylose repressor;
cds_wt_907	csn	putative chitosanase
cds_wt_908	lexA	SOS regulatory protein
cds_wt_909	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_910	bfrA	Bacterioferritin; BFR; Cytochrome b-1; Cytochrome b-557;
cds_wt_911	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_912	celA	putative endo-1,4-beta-glucanase
cds_wt_913	cypA	Cytochrome P450 2C39; CYP11C39;
cds_wt_914	-	hypothetical protein predicted by Glimmer/Critica

cds_wt_915	-	Carbohydrate diacid regulator; Sugar diacid regulator;
cds_wt_916	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_917	hemL	glutamate-1-semialdehyde 2,1-aminomutase
cds_wt_918	xylB	xylulose kinase
cds_wt_919	-	Regulator of nonsense transcripts 1 homolog;
cds_wt_920	-	GTP-binding protein lepA;
cds_wt_921	-	hypothetical protein
cds_wt_922	-	hypothetical protein
cds_wt_923	-	Phytochrome A1;
cds_wt_924	-	putative secreted protein
cds_wt_925	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_926	-	hypothetical protein
Polypeptide N-acetylgalactosaminyltransferase 3; Polypeptide GalNAc transferase 3; pp-GaNTase 3; GalNAc-T3; Protein-UDP acetylgalactosaminyltransferase 3; UDP-GalNAc;polypeptide N-acetylgalactosaminyltransferase 3;		
cds_wt_927	-	acetylgalactosaminyltransferase 3;
cds_wt_928	wbpH	Glycogen synthase; Starch
cds_wt_929	rfaG	Glycogen synthase; Starch
cds_wt_930	-	hypothetical protein
cds_wt_931	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_932	acd3	acyl-CoA dehydrogenase
cds_wt_933	-	Negative transcription regulator padR;
Lysophospholipase NTE1; Neuropathy target esterase homolog; Intracellular phospholipase B;		
cds_wt_934	-	oxidoreductase, molybdopterin-binding
cds_wt_935	-	pyridoxamine 5'-phosphate oxidase
cds_wt_936	pdxH	Putative tyrosine-protein phosphatase H16_A0669;
cds_wt_937	-	Ribosomal-protein-alanine acetyltransferase; Acetylating enzyme for N-terminal of ribosomal protein S5;
cds_wt_938	-	HTH-type transcriptional regulator hmrR; Copper
cds_wt_939	merR	efflux regulator; Copper export regulator;
cds_wt_940	-	hypothetical protein predicted by Glimmer/Critica
Cardiolipin synthetase; Cardiolipin synthase; CL synthase;		
cds_wt_941	comA	Uncharacterized metalloprotease HI0409;
cds_wt_942	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_943	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_944	-	Uncharacterized signaling protein PA3311;
cds_wt_945	-	Ribosomal-protein-serine acetyltransferase; Acetylating enzyme for N-terminal of ribosomal protein L7/L12;
cds_wt_946	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_947	-	YME1-like 1 (S. cerevisiae)
cds_wt_948	-	Anti-sigma F factor antagonist; Stage II sporulation protein AA;
cds_wt_949	-	UPF0721 transmembrane protein HI0198;
cds_wt_950	-	

cds_wt_951	-	Nigrin b; Agglutinin V; SNAV; Contains: Nigrin b A chain; rRNA N-glycosidase; Contains: Nigrin b B chain;
cds_wt_952	yjiZ	Probable glucarate transporter; D-glucarate permease;
cds_wt_953	-	hypothetical protein
cds_wt_954	-	putative secreted protein
cds_wt_955	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_956	-	Blue-light-activated protein; Includes: Blue-light-activated histidine kinase; Includes: Response regulator;
cds_wt_957	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_958	moaA	Coenzyme PQQ synthesis protein E; Pyrroloquinoline quinone biosynthesis protein E;
cds_wt_959	ppe2	Uncharacterized protein Rv2577/MT2654;
cds_wt_960	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_961	-	hypothetical protein
cds_wt_962	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_963	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_964	-	Mediator of RNA polymerase II transcription subunit 14; Mediator complex subunit 14;
cds_wt_965	-	Nucleoporin NUP159; Nuclear pore protein NUP159;
cds_wt_966	ag84	Laminin subunit beta-2; S-laminin; S-LAM;
cds_wt_967	ltrA	Uncharacterized protein RA0937;
cds_wt_968	pitA	Probable low-affinity inorganic phosphate transporter;
cds_wt_969	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_970	-	hypothetical protein
cds_wt_971	purU	formyltetrahydrofolate deformylase
cds_wt_972	aes2	hypothetical protein
cds_wt_973	cbp	Replicase polyprotein 1a; pp1a; ORF1a polyprotein; Contains: Non-structural protein 1; nsp1; p28; Contains: Non-structural protein 2; nsp2; p65; Contains: Non-structural protein 3; nsp3; Papain-like proteinases 1/2; PL1-PRO/PL2-PRO; p210; Contains: Non-structural protein 4; nsp4; Peptide HD2; p44; Contains: 3C-like proteinase; 3CL-PRO; 3CLp; M-PRO; p27; nsp5; Contains: Non-structural protein 6; nsp6; Contains: Non-structural protein 7; nsp7; p10; Contains: Non-structural protein 8; nsp8; p22; Contains: Non-structural protein 9; nsp9; p12; Contains: Non-structural protein 10; nsp10; Growth factor-like peptide; GFL; p15; Contains: Non-structural protein 11; nsp11;
cds_wt_974	-	putative DNA-binding protein
cds_wt_975	yhdN	putative aldo/keto reductase
cds_wt_976	-	hypothetical protein
cds_wt_977	nodB	Chitooligosaccharide deacetylase; Nodulation protein B;
cds_wt_978	-	Uncharacterized protein Rv0966c/MT0994;
cds_wt_979	-	3-oxoacyl-

cds_wt_980	-	aminotransferase, class I
cds_wt_981	-	UPF0118 membrane protein Rv0205/MT0215;
cds_wt_982	-	homogentisate 1,2-dioxygenase
cds_wt_983	-	hypothetical protein
cds_wt_984	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_985	hmgB	putative fumarylacetoacetase
cds_wt_986	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_987	-	hypothetical protein
cds_wt_988	pra	Proline-rich antigen; 36 kDa antigen;
cds_wt_989	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_990	hstK	serine/threonine kinase with two-component sensor domain
cds_wt_991	-	hypothetical protein
cds_wt_992	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_993	yjhE	hypothetical protein
cds_wt_994	-	hypothetical protein
cds_wt_995	-	Uncharacterized protein yrhO;
cds_wt_996	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_997	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_998	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_999	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1000	czcD	Zinc transporter 8; ZnT-8; Solute carrier family 30 member 8;
cds_wt_1001	-	hypothetical protein
cds_wt_1002	-	Uncharacterized protein Mb0093;
cds_wt_1003	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1004	mprF	Probable lysylphosphatidylglycerol synthetase; LPG synthetase; Multiple peptide resistance factor;
cds_wt_1005	lpd	dihydrolipoamide dehydrogenase
cds_wt_1006	-	Collagen alpha-5
cds_wt_1007	-	Glycogen synthase; Starch
cds_wt_1008	-	Polypeptide N-acetylgalactosaminyltransferase 5; pp-GaNTase 5; Protein-UDP
cds_wt_1009	-	acetylgalactosaminyltransferase 5; UDP-GalNAc:polypeptide N-
cds_wt_1010	-	acetylgalactosaminyltransferase 5;
cds_wt_1011	-	Membrane-bound protein lytR;
cds_wt_1012	marR	selenoprotein W-related protein
cds_wt_1013	-	Pyruvoyl-dependent arginine decarboxylase; PvlArgDC; Contains: Pyruvoyl-dependent arginine decarboxylase subunit beta; Contains: Pyruvoyl-dependent arginine decarboxylase subunit alpha;
cds_wt_1014	rbsC	Multiple antibiotic resistance protein marR;
cds_wt_1015	-	Putative esterase yheT;
cds_wt_1016	rbsA	Autoinducer 2 import system permease protein lsrC; AI-2 import system permease protein lsrC;
		Ribose transport system permease protein rbsC;
		putative sugar uptake ABC transporter ATP-binding protein

		HTH-type transcriptional repressor purR; Purine nucleotide synthesis repressor; Pur regulon repressor;
cds_wt_1017	rbsB	
cds_wt_1018	ptlJ	Uncharacterized protein yetH;
		HTH-type transcriptional activator rhaS; L-rhamnose operon regulatory protein rhaS;
cds_wt_1019	ptlR	
cds_wt_1020	yagE	putative dihydrodipicolinate synthase
cds_wt_1021	-	hypothetical protein
cds_wt_1022	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1023	noIO	putative carbamoyl transferase
cds_wt_1024	-	proline rich protein (putative membrane protein)
		1,4-alpha-glucan-branching enzyme; Glycogen-branching enzyme; BE; 1,4-alpha-D-glucan:1,4-alpha-D-glucan 6-glucosyl-transferase;
cds_wt_1025	-	
cds_wt_1026	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1027	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1028	-	hypothetical protein
cds_wt_1029	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1030	tas1	putative aldo/keto reductase
cds_wt_1031	-	Uncharacterized protein yhjA;
cds_wt_1032	-	Uncharacterized protein C4H3.03c;
cds_wt_1033	-	putative methyltransferase
cds_wt_1034	-	Camphene synthase, chloroplastic; EC=4.2.3.n4;
cds_wt_1035	srpl	Major membrane protein I; MMP-I; 35 kDa antigen;
cds_wt_1036	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1037	ETR1	sensor histidine kinase
cds_wt_1038	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1039	tetR	Tetracycline repressor protein class H;
		Tetracycline resistance protein from transposon Tn4351/Tn4400;
cds_wt_1040	tetX	
cds_wt_1041	PHYB	histidine kinase/response regulator hybrid protein
cds_wt_1042	-	hypothetical protein
		3-methyl-2-oxobutanoate hydroxymethyltransferase;
cds_wt_1043	-	Ketopantoate hydroxymethyltransferase; KPHMT;
cds_wt_1044	-	Autoinducer 2 sensor kinase/phosphatase luxQ;
cds_wt_1045	phy	Sensor protein kinase walk;
cds_wt_1046	phy	two-component hybrid sensor and regulator
		Uncharacterized ABC transporter extracellular-binding protein yurO;
cds_wt_1047	yurO	
		sn-glycerol-3-phosphate transport system permease protein ugpA;
cds_wt_1048	yurN	
cds_wt_1049	msmG	Probable ABC transporter permease protein yesQ;
cds_wt_1050	-	hypothetical protein
cds_wt_1051	fdhF	formate dehydrogenase A chain
cds_wt_1052	-	hypothetical protein
cds_wt_1053	-	Prestalk A differentiation protein A;
		55.5 kDa and 49.5 kDa sporulation proteins;
cds_wt_1054	-	ORF1590 and ORF1422;
cds_wt_1055	-	hypothetical protein
cds_wt_1056	-	Uncharacterized protein y4IL;

cds_wt_1057	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1058	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1059	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1060	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1061	-	Sialidase; Neuraminidase;
cds_wt_1062	-	Laminin subunit beta-2; S-laminin; Laminin chain B3;
cds_wt_1063	ysiA	UPF0053 protein yrkA;
cds_wt_1064	arsB	Arsenical pump membrane protein; Arsenic efflux pump protein;
cds_wt_1065	mtrR	HTH-type transcriptional regulator mtrR;
cds_wt_1066	-	Uncharacterized protein C2A9.02;
cds_wt_1067	-	Uncharacterized protein YLL056C;
cds_wt_1068	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1069	-	Uncharacterized protein yuxI;
cds_wt_1070	-	HTH-type transcriptional regulator betI;
cds_wt_1071	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1072	fabH	3-oxoacyl- Glucomannan 4-beta-mannosyltransferase 9; Glucomannan synthase; Mannan synthase 9; Cellulose synthase-like protein A9; AtCslA9; Protein RESISTANT TO AGROBACTERIUM TRANSFORMATION 4;
cds_wt_1073	-	Acetyl-coenzyme A synthetase; Acetate--CoA ligase;
cds_wt_1074	-	Acyl-activating enzyme;
cds_wt_1075	-	Acetyl-coenzyme A synthetase; Acetate--CoA ligase; Acyl-activating enzyme;
cds_wt_1076	-	Polypeptide N-acetylgalactosaminyltransferase 5; pp- GaNTase 5; Protein-UDP acetylgalactosaminyltransferase 5; UDP- GalNAc:polypeptide N- acetylgalactosaminyltransferase 5;
cds_wt_1077	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1078	-	Cytochrome P450 3A5; CYP11A5; P450-PCN3; HLp2;
cds_wt_1079	cdh	UDP-N-acetylglucosamine 4-epimerase; UDP- GlcNAc 4-epimerase;
cds_wt_1080	srpR	HTH-type transcriptional regulator srpR; Solvent efflux pump srpABC operon corepressor;
cds_wt_1081	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1082	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1083	-	HTH-type transcriptional regulator betI;
cds_wt_1084	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1085	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1086	ctaD	cytochrome c oxidase subunit I
cds_wt_1087	dinX	DNA polymerase IV
cds_wt_1088	lldA	hypothetical protein
cds_wt_1089	-	Translation initiation factor IF-2;
cds_wt_1090	-	Uncharacterized protein TM_0929;
cds_wt_1091	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1092	-	Inner membrane protein yccF;

cds_wt_1093	-	putative membrane protein
cds_wt_1094	-	hypothetical protein
cds_wt_1095	X	Uncharacterized protein X;
cds_wt_1096	-	membrane protein, putative
		Transcriptional regulatory protein <i>srrA</i> ;
cds_wt_1097	phoB	Staphylococcal respiratory response protein A;
cds_wt_1098	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1099	trpE	anthranilate synthase
cds_wt_1100	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1101	-	Uncharacterized protein Rv2286c/MT2344;
cds_wt_1102	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1103	-	Uncharacterized protein YMR196W;
cds_wt_1104	malQ	glycogen debranching enzyme
cds_wt_1105	pleD	Cellulose synthesis regulatory protein;
cds_wt_1106	-	RNA pyrophosphohydrolase;
cds_wt_1107	-	Response regulator <i>uvrY</i> ;
cds_wt_1108	-	Sensor histidine kinase <i>yvfT</i> ;
cds_wt_1109	-	putative integral membrane protein
cds_wt_1110	mtrR	HTH-type transcriptional regulator <i>mtrR</i> ;
cds_wt_1111	-	hypothetical protein
cds_wt_1112	idnK	putative gluconokinase
		5-methyltetrahydrofolate--homocysteine
cds_wt_1113	methH	methyltransferase
cds_wt_1114	polA	DNA polymerase I
		sn-glycerol-3-phosphate transport system permease
cds_wt_1115	malG	protein <i>ugpE</i> ;
cds_wt_1116	msmF	Probable ABC transporter permease protein <i>yurN</i> ;
		Uncharacterized ABC transporter extracellular-
cds_wt_1117	-	binding protein <i>yurO</i> ;
cds_wt_1118	malG	Probable ABC transporter permease protein <i>yurM</i> ;
cds_wt_1119	palF	Maltose transport system permease protein <i>malF</i> ;
		Uncharacterized ABC transporter extracellular-
cds_wt_1120	malE	binding protein <i>yurO</i> ;
		Glucosamine--fructose-6-phosphate
cds_wt_1121	rpiR	aminotransferase
cds_wt_1122	murD	UDP-N-acetylmuramoylalanine-D-glutamate ligase
cds_wt_1123	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1124	-	hypothetical protein
cds_wt_1125	fhbA	putative flavohemoprotein
cds_wt_1126	spoU	putative rRNA methylase
cds_wt_1127	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1128	-	Uncharacterized protein MTH_692;
cds_wt_1129	-	hypothetical protein
cds_wt_1130	pbp	FmtA-like protein
cds_wt_1131	-	Uncharacterized transporter <i>yyaM</i> ;
cds_wt_1132	-	putative GntR-family transcriptional regulator
cds_wt_1133	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1134	-	hypothetical protein
cds_wt_1135	-	Uncharacterized protein ML1804;
cds_wt_1136	-	NADH pyrophosphatase;

cds_wt_1137	-	putative MutT family protein
cds_wt_1138	-	RNA pyrophosphohydrolase;
		Signal peptidase complex catalytic subunit SEC11C; SEC11 homolog C; SEC11-like protein 3; Microsomal signal peptidase 21 kDa subunit; SPase 21 kDa subunit; SPC21;
cds_wt_1139	-	Uncharacterized 45.4 kDa protein in thiaminase I 5' region;
cds_wt_1140	nagD	ferrochelata
cds_wt_1141	hemH	putative enoyl-ACP reductase
cds_wt_1142	inhA	3-oxoacyl-
cds_wt_1143	fabG	Sensor protein vraS;
cds_wt_1144	-	Transcriptional regulatory protein liaR;
cds_wt_1145	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1146	-	UPF0353 protein MAP_3434;
cds_wt_1147	-	Uncharacterized protein Mb1516;
cds_wt_1148	-	Holliday junction ATP-dependent DNA helicase ruvB;
cds_wt_1149	moxR	hypothetical protein
cds_wt_1150	-	UPF0699 transmembrane protein ydbS;
cds_wt_1151	ydbS	UPF0699 transmembrane protein ydbT;
cds_wt_1152	-	hypothetical protein
cds_wt_1153	-	fructokinase
cds_wt_1154	-	Superoxide dismutase
cds_wt_1155	-	Xaa-Pro aminopeptidase
cds_wt_1156	pepP	hypothetical protein predicted by Glimmer/Critica
cds_wt_1157	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1158	-	aconitate hydratase 1
cds_wt_1159	acnA	Uncharacterized protein Mb0922c;
cds_wt_1160	-	RIO1/ZK632.3/MJ0444 family protein
cds_wt_1161	-	3-oxoacyl-
cds_wt_1162	-	Uncharacterized HAD-hydrolase PH1655;
cds_wt_1163	-	HTH-type transcriptional repressor acnR;
cds_wt_1164	acnR	hypothetical protein
cds_wt_1165	-	Putative HTH-type transcriptional regulatory protein Memar_2347;
cds_wt_1166	-	3-oxoacyl-(acyl carrier protein) reductase
cds_wt_1167	-	G/U mismatch-specific DNA glycosylase
cds_wt_1168	ygjF	Lipid A export ATP-binding/permease protein msbA;
cds_wt_1169	novA	3-hydroxybutyryl-CoA dehydratase
cds_wt_1170	ech4	putative transcriptional regulator
cds_wt_1171	-	Putative ABC transporter ATP-binding protein MA_1747;
cds_wt_1172	ybiT	Uncharacterized protein ypfJ;
cds_wt_1173	ypfJ	hypothetical protein predicted by Glimmer/Critica
cds_wt_1174	-	hypothetical protein
cds_wt_1175	alkD	Uncharacterized protein Mb1288c;
cds_wt_1176	-	hypothetical protein
cds_wt_1177	-	Putative amino-acid transporter yisU;
cds_wt_1178	-	putative hydrolase
cds_wt_1179	pip	hypothetical protein
cds_wt_1180	-	

cds_wt_1181	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1182	-	hypothetical protein
cds_wt_1183	-	UPF0195 protein yitW; Iron sulfur cluster assembly protein 1, mitochondrial;
cds_wt_1184	nifU	Iron sulfur cluster scaffold protein 1;
cds_wt_1185	csd	putative cysteine desulfurase
cds_wt_1186	sufC	Methionine import ATP-binding protein metN;
cds_wt_1187	sufD	UPF0051 protein ML0594;
cds_wt_1188	sufB	UPF0051 protein slr0074; Heme A synthase; HAS; Cytochrome aa3-controlling protein;
cds_wt_1189	ctaA	hypothetical protein
cds_wt_1190	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1191	-	protoheme IX farnesyltransferase
cds_wt_1192	ctaB	transketolase
cds_wt_1193	tkt	putative transaldolase
cds_wt_1194	tal	glucose-6-phosphate 1-dehydrogenase
cds_wt_1195	zwf2	Putative OxPP cycle protein opcA;
cds_wt_1196	opcA	6-phosphogluconolactonase
cds_wt_1197	devB	Bifunctional protein NCOAT; Nuclear cytoplasmic O-GlcNAcase and acetyltransferase; Meningioma-expressed antigen 5; Includes: Beta-hexosaminidase; N-acetyl-beta-glucosaminidase; Beta-N-acetylhexosaminidase; Hexosaminidase C; N-acetyl-beta-D-glucosaminidase; O-GlcNAcase; Includes:
cds_wt_1198	-	Histone acetyltransferase; HAT;
cds_wt_1199	-	putative electron transport protein
cds_wt_1200	secG	Protein-export membrane protein secG;
cds_wt_1201	tpi	triosephosphate isomerase
cds_wt_1202	pgk	phosphoglycerate kinase
cds_wt_1203	gap	glyceraldehyde 3-phosphate dehydrogenase
cds_wt_1204	whiA	hypothetical protein
cds_wt_1205	-	UPF0052 protein sll0154;
cds_wt_1206	-	UPF0042 protein RBAM_031990; UvrABC system protein C; Protein uvrC; Excinuclease ABC subunit C;
cds_wt_1207	uvrC	Cytochrome b6-f complex iron-sulfur subunit; Rieske iron-sulfur protein; Plastohydroquinone:plastocyanin oxidoreductase iron-sulfur protein; ISP; RISP;
cds_wt_1208	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1209	-	UvrABC system protein A; UvrA protein; Excinuclease ABC subunit A;
cds_wt_1210	uvrA	putative glycosyl transferase
cds_wt_1211	-	conserved hypothetical protein TIGR00157
cds_wt_1212	-	hypothetical protein
cds_wt_1213	-	Hydroxyacylglutathione hydrolase; Glyoxalase II; Glx II;
cds_wt_1214	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1215	-	RNA polymerase sigma-E factor;
cds_wt_1216	sigE	hypothetical protein predicted by Glimmer/Critica
cds_wt_1217	-	

cds_wt_1218	clpP	ATP-dependent Clp protease proteolytic subunit;
cds_wt_1219	rplK	Endopeptidase Clp;
		50S ribosomal protein L11;
cds_wt_1220	-	Membrane-bound lytic murein transglycosylase F;
cds_wt_1221	typA	EC=4.2.2.n1; Murein lyase F;
cds_wt_1222	terC	Elongation factor G; EF-G;
cds_wt_1223	-	Uncharacterized membrane protein RF_1252;
cds_wt_1224	-	Uncharacterized protein yczJ;
		Putative golgin subfamily A member 6-like protein 6;
		UvrABC system protein B; Protein uvrB;
cds_wt_1225	uvrB	Excinuclease ABC subunit B;
cds_wt_1226	coaE	dephospho-CoA kinase
cds_wt_1227	rpsA	30S ribosomal protein S1;
		Ubiquinone/menaquinone biosynthesis
cds_wt_1228	-	methyltransferase ubiE;
cds_wt_1229	-	hypothetical protein
cds_wt_1230	-	possible DNA-binding protein
		Cadmium efflux system accessory protein; Cadmium
cds_wt_1231	arsR	resistance regulatory protein;
cds_wt_1232	polA	DNA polymerase I
cds_wt_1233	atrC	putative ABC transporter ATP-binding protein
cds_wt_1234	occM	Octopine transport system permease protein occM;
		Membrane-bound lytic murein transglycosylase F;
cds_wt_1235	aotJ	EC=4.2.2.n1; Murein lyase F;
		Phosphate import ATP-binding protein pstB;
cds_wt_1236	livF	Phosphate-transporting ATPase; ABC phosphate
		transporter;
		branched-chain amino acid ABC transporter ATP-
cds_wt_1237	livG	binding protein
		High-affinity branched-chain amino acid transport
cds_wt_1238	livM	system permease protein livM; LIV-I protein M;
		Galactoside transport system permease protein mgIC
cds_wt_1239	braD	homolog;
cds_wt_1240	livA	Leu/Ile/Val-binding protein; LIV-BP;
		Probable transcriptional regulator ycf27; OmpR-like
cds_wt_1241	-	protein;
cds_wt_1242	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1243	tesB	acyl-CoA thioesterase II
cds_wt_1244	pykA	pyruvate kinase
cds_wt_1245	gltD	glutamate synthase (NADPH) small chain
cds_wt_1246	gltB	glutamate synthase, large subunit
cds_wt_1247	-	putative acetyltransferase
cds_wt_1248	nahG	Salicylate hydroxylase; Salicylate 1-monooxygenase;
cds_wt_1249	-	Squalene monooxygenase; Squalene epoxidase; SE;
cds_wt_1250	lgt	prolipoprotein diacylglycerol transferase
cds_wt_1251	pdxH	pyridoxamine 5'-phosphate oxidase
cds_wt_1252	trpA	tryptophan synthase alpha chain
cds_wt_1253	trpB	tryptophan synthase beta chain
cds_wt_1254	trpC	indole-3-glycerol phosphate synthase
cds_wt_1255	-	hypothetical protein predicted by Glimmer/Critica

cds_wt_1256	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1257	trpE	anthranilate synthase component I
cds_wt_1258	hisI	phosphoribosyl-AMP cyclohydrolase
cds_wt_1259	-	Collagen alpha-5
cds_wt_1260	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1261	-	Collagen alpha-4
cds_wt_1262	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1263	rpsD	30S ribosomal protein S4;
cds_wt_1264	yknV	Lipid A export ATP-binding/permease protein msbA;
cds_wt_1265	ywjA	Lipid A export ATP-binding/permease protein msbA;
		Large neutral amino acids transporter small subunit 2; L-type amino acid transporter 2; hLAT2; Solute carrier family 7 member 8;
cds_wt_1266	-	transcriptional regulator, GntR family
cds_wt_1267	mocR	long-chain fatty-acid-CoA ligase
cds_wt_1268	-	Uncharacterized protein HI0522;
cds_wt_1269	-	Serine hydroxymethyltransferase; Serine methylase; SHMT;
cds_wt_1270	aro8	hypothetical protein
cds_wt_1271	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1272	-	imidazoleglycerol-phosphate synthase cyclase
cds_wt_1273	hisF	phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase
cds_wt_1274	hisA	hypothetical protein predicted by Glimmer/Critica
cds_wt_1275	-	amidotransferase hisH
cds_wt_1276	hisH	imidazoleglycerol-phosphate dehydratase
cds_wt_1277	hisB	histidinol-phosphate aminotransferase
cds_wt_1278	hisC	histidinol dehydrogenase
cds_wt_1279	hisD	hypothetical protein
cds_wt_1280	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1281	-	DNA polymerase III alpha chain
cds_wt_1282	dnaE	hypothetical protein
cds_wt_1283	-	Transcription elongation factor SPT5; hSPT5; DRB sensitivity-inducing factor large subunit; DSIF large subunit; DSIF p160; Tat-cotransactivator 1 protein; Tat-CT1 protein;
cds_wt_1284	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1285	-	putative ribosomal large subunit pseudouridine synthase
cds_wt_1286	rluD	lipoprotein signal peptidase
cds_wt_1287	lspA	UPF0235 protein SbaI_3028;
cds_wt_1288	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1289	-	Antigen 84;
cds_wt_1290	ag84	hypothetical protein
cds_wt_1291	-	Cell division protein sepF;
cds_wt_1292	-	UPF0001 protein PM0112;
cds_wt_1293	-	Cell division protein ftsZ;
cds_wt_1294	ftsZ	Cell division protein ftsQ homolog;
cds_wt_1295	ftsQ	UDP-N-acetylmuramate--alanine ligase
cds_wt_1296	murC	

		UDP-N-acetylglucosamine--N-acetylmuramyl-(pentapeptide) pyrophosphoryl-undecaprenol N-acetylglucosamine transferase
cds_wt_1297	murG	
cds_wt_1298	ftsW	Cell division protein ftsW homolog;
cds_wt_1299	mraY	phospho-N-acetylmuramoyl-pentapeptide-transferase
		UDP-N-acetylmuramoylalanyl-D-glutamyl-2,6-diaminopimelate--D-alanyl-D-alanine ligase
cds_wt_1300	murF	
		putative UDP-N-acetylmuramoylalanyl-D-glutamate-2,6-diaminopimelate ligase
cds_wt_1301	murE	
cds_wt_1302	pbpB	penicillin-binding protein
cds_wt_1303	mraW	S-adenosyl-methyltransferase
cds_wt_1304	mraZ	Protein mraZ;
cds_wt_1305	iap	Endopeptidase ykfC;
cds_wt_1306	-	putative ligase
cds_wt_1307	cobQ	Cobyrinic acid synthase;
cds_wt_1308	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1309	-	TVP38/TMEM64 family membrane protein slr0305;
cds_wt_1310	leuS	leucyl-tRNA synthetase
cds_wt_1311	-	Collagen alpha-4
cds_wt_1312	-	Peptide-N
cds_wt_1313	-	putative membrane protein
cds_wt_1314	-	hypothetical protein
cds_wt_1315	-	putative methyltransferase
		3-demethylubiquinone-9 3-methyltransferase; 3,4-dihydroxy-5-hexaprenylbenzoate methyltransferase;
cds_wt_1316	smtA	DHMB methyltransferase;
cds_wt_1317	sti1	Protease inhibitor SIL-V3;
cds_wt_1318	dnaE	DNA polymerase III, alpha subunit
cds_wt_1319	-	DNA polymerase IV 1; Pol IV 1;
cds_wt_1320	-	Uncharacterized protein Rv3395c/MT3502;
cds_wt_1321	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1322	-	putative transcriptional regulator
cds_wt_1323	-	hypothetical protein
cds_wt_1324	-	hypothetical protein
cds_wt_1325	fabG	Retinol dehydrogenase 13;
cds_wt_1326	crtA	Spheroidene monooxygenase;
cds_wt_1327	-	hypothetical protein
		Probable mannan synthase 15; Cellulose synthase-like protein A15; AtCslA15;
cds_wt_1328	-	
cds_wt_1329	carB	putative phytoene dehydrogenase related protein
cds_wt_1330	-	Uncharacterized protein Rv1836c/MT1884;
cds_wt_1331	-	hypothetical protein
cds_wt_1332	cynR	Probable RuBisCO transcriptional regulator;
cds_wt_1333	sdhC	putative cytochrome B subunit
cds_wt_1334	frdA	succinate dehydrogenase flavoprotein subunit
cds_wt_1335	sdhB	fumarate reductase, iron-sulfur protein
cds_wt_1336	-	Uncharacterized phzA/B-like protein PA3332;
cds_wt_1337	-	HTH-type transcriptional regulator betI;
cds_wt_1338	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1339	spcT	hypothetical protein

cds_wt_1340	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1341	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1342	tetR	Tetracycline repressor protein class A from transposon 1721;
cds_wt_1343	-	membrane protein, putative
cds_wt_1344	cmcT	Cephamycin export protein cmcT;
cds_wt_1345	manR	mandelate racemase/muconate lactonizing enzyme family protein
cds_wt_1346	-	UPF0214 protein yfeW;
cds_wt_1347	-	hypothetical protein
cds_wt_1348	metF	putative 5,10-methylenetetrahydrofolate reductase
cds_wt_1349	gds	geranylgeranyl pyrophosphate synthase
cds_wt_1350	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1351	-	hypothetical protein
cds_wt_1352	-	hypothetical protein
cds_wt_1353	pknL	putative eukaryotic-type serine/threonine protein kinase
cds_wt_1354	nfo	endonuclease IV
cds_wt_1355	-	Fibrocystin-L; Polycystic kidney and hepatic disease 1-like protein 1; PKHD1-like protein 1; Protein D86;
cds_wt_1356	MET	Hepatocyte growth factor receptor; HGF receptor; Scatter factor receptor; SF receptor; HGF/SF receptor; Met proto-oncogene tyrosine kinase; c-Met;
cds_wt_1357	gly1	L-allo-threonine aldolase
cds_wt_1358	aroG	phospho-2-dehydro-3-deoxyheptonate aldolase
cds_wt_1359	chiD	chitinase
cds_wt_1360	gpo	glutathione peroxidase
cds_wt_1361	-	hypothetical protein
cds_wt_1362	-	hypothetical protein
cds_wt_1363	-	Nucleotide-binding protein 2; NBP 2;
cds_wt_1364	-	hypothetical protein
cds_wt_1365	-	putative membrane protein
cds_wt_1366	-	hypothetical protein
cds_wt_1367	aao	D-amino acid oxidase
cds_wt_1368	-	hypothetical protein
cds_wt_1369	proC	pyrroline-5-carboxylate reductase
cds_wt_1370	pfkA	6-phosphofructokinase
cds_wt_1371	pur8	Puromycin resistance protein pur8;
cds_wt_1372	-	HTH-type transcriptional regulator uidR; Uid operon repressor;
cds_wt_1373	-	hypothetical protein
cds_wt_1374	-	Homoserine kinase; HSK; HK;
cds_wt_1375	-	Anaerobic regulatory protein;
cds_wt_1376	plsC	1-acylglycerol-3-phosphate O-acyltransferase
cds_wt_1377	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1378	otsA	alpha,alpha-trehalose-phosphate synthase
cds_wt_1379	-	hypothetical protein
cds_wt_1380	pedG	flavin-binding monooxygenase-like protein
cds_wt_1381	-	hypothetical protein
cds_wt_1382	glk	putative sugar kinase

cds_wt_1383	-	Collagen alpha-5
cds_wt_1384	-	hypothetical protein
		Uncharacterized sensor-like histidine kinase
cds_wt_1385	narQ	Caur_0899;
cds_wt_1386	degU	Transcriptional regulatory protein degU;
cds_wt_1387	-	hypothetical protein
cds_wt_1388	hosA	Transcriptional regulator hosA;
cds_wt_1389	tetV	Uncharacterized MFS-type transporter yfiS;
cds_wt_1390	thiX	Thioredoxin; Trx;
cds_wt_1391	msbA	Lipid A export ATP-binding/permease protein msbA;
cds_wt_1392	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1393	-	Glycogen synthase; Starch
cds_wt_1394	yhfN	peptidase, M48 family
cds_wt_1395	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1396	-	Uncharacterized protein yacP;
cds_wt_1397	polC	DNA polymerase III, epsilon subunit
cds_wt_1398	relA	GTP pyrophosphokinase
cds_wt_1399	-	RNA pyrophosphohydrolase;
		Mannose-1-phosphate guanylttransferase; GTP-mannose-1-phosphate guanylyltransferase; GDP-mannose pyrophosphorylase;
cds_wt_1400	galF	
cds_wt_1401	-	Leucine-responsive regulatory protein;
cds_wt_1402	-	Esterase frsA;
cds_wt_1403	mobC	Diamine acetyltransferase 1; Spermidine/spermine N
cds_wt_1404	phaN	repressor in the phenylacetic acid catabolic pathway
cds_wt_1405	qcrB	cytochrome b subunit of the bc complex
		Probable menaquinol-cytochrome c reductase iron-sulfur subunit; Rieske iron-sulfur protein; Cytochrome bc1 complex Rieske iron-sulfur protein;
cds_wt_1406	qcrA	
		Menaquinol-cytochrome c reductase cytochrome c subunit; Cytochrome bc1 complex cytochrome c subunit; Cytochrome cc;
cds_wt_1407	qcrC	
cds_wt_1408	ctaE	cytochrome c oxidase subunit III
cds_wt_1409	-	Uncharacterized protein ML1998;
cds_wt_1410	-	hypothetical protein
cds_wt_1411	trpD	anthranilate phosphoribosyltransferase
cds_wt_1412	-	hypothetical protein predicted by Glimmer/Critica
		Probable cytochrome c oxidase polypeptide 4; Cytochrome c oxidase polypeptide IV; Cytochrome aa3 subunit 4;
cds_wt_1413	-	
cds_wt_1414	ctaC	putative cytochrome c oxidase chain II
cds_wt_1415	nifS	putative aminotransferase
		Sulfurtransferase tusA; tRNA 2-thiouridine synthesizing protein A;
cds_wt_1416	-	
		Adenylyl-sulfate kinase; APS kinase; Adenosine-5'-phosphosulfate kinase; ATP adenosine-5'-phosphosulfate 3'-phosphotransferase;
cds_wt_1417	-	
cds_wt_1418	cbhK	putative carbohydrate kinase
cds_wt_1419	-	Putative iron-sulfur cluster insertion protein erpA;
cds_wt_1420	glxK	glycerate kinase

cds_wt_1421	nadA	Quinolinate synthetase A;
cds_wt_1422	murA	UDP-N-acetylglucosamine 1-carboxyvinyltransferase
cds_wt_1423	-	Uncharacterized protein Mb2229;
cds_wt_1424	lamA	Endo-1,3-1,4-beta-glycanase eglC; Succinoglycan
cds_wt_1425	-	biosynthesis protein eglC;
cds_wt_1426	-	Methionine import ATP-binding protein metN 1;
cds_wt_1427	-	putative ABC-2 type transport system permease
cds_wt_1428	-	protein
cds_wt_1429	-	Aggrecan core protein; Cartilage-specific
cds_wt_1430	-	proteoglycan core protein; CSPCP;
cds_wt_1431	cobU	K ⁺ channel beta subunit
cds_wt_1432	cobT	Putative zinc metalloprotease ywhC;
cds_wt_1433	gcvT	hypothetical protein predicted by Glimmer/Critica
cds_wt_1434	-	putative cobinamide kinase/cobinamide phosphate
cds_wt_1435	pepB	guanylyltransferase
cds_wt_1436	-	Nicotinate-nucleotide--dimethylbenzimidazole
cds_wt_1437	acoL	phosphoribosyltransferase; NN:DBI PRT; N
cds_wt_1438	sucB	aminomethyltransferase
cds_wt_1439	sucB	Probable cytosol aminopeptidase; Leucine
cds_wt_1440	-	aminopeptidase; LAP; Leucyl aminopeptidase;
cds_wt_1441	-	putative aminopeptidase
cds_wt_1442	lipB	hypothetical protein
cds_wt_1443	-	dihydrolipoamide dehydrogenase
cds_wt_1444	aspS	putative dihydrolipoamide succinyltransferase
cds_wt_1445	lipA	dihydrolipoamide acyltransferase
cds_wt_1446	-	UPF0105 protein SH2119;
cds_wt_1447	-	putative glycosyl transferase
cds_wt_1448	-	lipoate-protein ligase B
cds_wt_1449	-	Lipoprotein yfgL;
cds_wt_1450	cfxQ	aspartyl-tRNA synthetase
cds_wt_1451	-	putative lipoic acid synthetase
cds_wt_1452	iga	hypothetical protein predicted by Glimmer/Critica
cds_wt_1453	-	Uncharacterized protein R02095;
cds_wt_1454	-	Uncharacterized protein Rv2219/MT2276;
cds_wt_1455	-	Translation initiation factor IF-2;
cds_wt_1456	-	Protein cfxQ homolog;
cds_wt_1457	-	hypothetical protein
cds_wt_1458	-	Immunoglobulin A1 protease; IgA1 protease; IgA-
cds_wt_1459	-	specific zinc metalloproteinase;
cds_wt_1460	-	hypothetical protein
cds_wt_1461	-	Protein essC;
cds_wt_1462	-	hypothetical protein
cds_wt_1463	-	hypothetical protein
cds_wt_1464	-	Proprotein convertase subtilisin/kexin type 6; Paired
cds_wt_1465	-	basic amino acid cleaving enzyme 4; Subtilisin/kexin-
cds_wt_1466	-	like protease PACE4; Subtilisin-like proprotein
cds_wt_1467	-	convertase 4; SPC4;
cds_wt_1468	-	hypothetical protein
cds_wt_1469	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1470	-	hypothetical protein predicted by Glimmer/Critica

		DNA-directed RNA polymerase subunit beta'; RNAP subunit beta'; Transcriptase subunit beta'; RNA polymerase subunit beta';
cds_wt_1461	-	
cds_wt_1462	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1463	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1464	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1465	-	hypothetical protein
cds_wt_1466	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1467	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1468	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1469	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1470	-	UPF0133 protein ESA_02800;
cds_wt_1471	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1472	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1473	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1474	-	Collagen alpha-4
cds_wt_1475	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1476	-	hypothetical protein
cds_wt_1477	glnA	glutamine synthetase
cds_wt_1478	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1479	-	Regulatory protein afsR;
		Spermidine/putrescine import ATP-binding protein
cds_wt_1480	-	potA;
cds_wt_1481	-	hypothetical protein
cds_wt_1482	-	hypothetical protein
cds_wt_1483	-	hypothetical protein predicted by Glimmer/Critica
		Organic hydroperoxide resistance transcriptional
cds_wt_1484	marR	regulator;
cds_wt_1485	glnE	glutamate-ammonia-ligase adenylyltransferase
cds_wt_1486	guaA	GMP synthase
cds_wt_1487	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1488	ltrA	Uncharacterized protein RA0937;
cds_wt_1489	-	UPF0719 transmembrane protein MAP_1032c;
cds_wt_1490	glnA	glutamine synthetase
cds_wt_1491	nadE	glutamine-dependent NAD(+) synthetase
cds_wt_1492	panB	3-methyl-2-oxobutanoate hydroxymethyltransferase
cds_wt_1493	rnr	putative ribonuclease R
		Polycystic kidney disease protein 1-like 3; Polycystin-
cds_wt_1494	-	1L3; PC1-like 3 protein;
		Mucin-4; MUC-4; Pancreatic adenocarcinoma mucin;
		Testis mucin; Ascites sialoglycoprotein; ASGP;
		Tracheobronchial mucin; Contains: Mucin-4 alpha
		chain; Ascites sialoglycoprotein 1; ASGP-1; Contains:
		Mucin-4 beta chain; Ascites sialoglycoprotein 2;
cds_wt_1495	MUC4	ASGP-2;
cds_wt_1496	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1497	asd	aspartate-semialdehyde dehydrogenase
cds_wt_1498	-	hypothetical protein
		D-alanyl-D-alanine carboxypeptidase; DD-peptidase;
cds_wt_1499	vanY	DD-carboxypeptidase;

cds_wt_1500	-	putative integral membrane protein
cds_wt_1501	iluA	threonine dehydratase
cds_wt_1502	gapA	glyceraldehyde-3-phosphate dehydrogenase
cds_wt_1503	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1504	-	UPF0721 transmembrane protein HI0198;
cds_wt_1505	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1506	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1507	-	Sodium/glucose cotransporter 1; Na
cds_wt_1508	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1509	yvbX	chitinase
		6PF-2-K/Fru-2,6-P2ASE liver/muscle isozymes;
		Includes: 6-phosphofructo-2-kinase; Includes:
cds_wt_1510	-	Fructose-2,6-bisphosphatase;
		Epidermal growth factor receptor substrate 15-like 1;
		Eps15-related protein; Eps15R; Epidermal growth
		factor receptor pathway substrate 15-related
cds_wt_1511	-	sequence; Eps15-rs;
cds_wt_1512	-	UPF0135 protein CPE2004;
cds_wt_1513	-	UPF0135 protein yqfO;
cds_wt_1514	dfp	hypothetical protein
cds_wt_1515	-	HTH-type transcriptional regulator immR;
cds_wt_1516	-	conserved hypothetical protein
cds_wt_1517	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1518	-	UPF0374 protein lwe1705;
cds_wt_1519	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1520	ahpE	putative thiol-specific antioxidant protein
cds_wt_1521	-	Uncharacterized protein Mb2263c;
cds_wt_1522	phdB	pyruvate dehydrogenase E1 component beta subunit
cds_wt_1523	-	2-oxoisovalerate dehydrogenase
cds_wt_1524	-	UPF0047 protein Mb2586c;
cds_wt_1525	aceE	pyruvate dehydrogenase E1 component
cds_wt_1526	gltX	glutamyl-tRNA synthetase
cds_wt_1527	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1528	-	HTH-type transcriptional repressor fabR;
cds_wt_1529	-	Uncharacterized protein Mb2266;
cds_wt_1530	fabD	malonyl CoA-acyl carrier protein transacylase
cds_wt_1531	fabH	3-oxoacyl-
cds_wt_1532	acpM	Acyl carrier protein; ACP;
cds_wt_1533	fabF	3-oxoacyl-
cds_wt_1534	pccB	propionyl-CoA carboxylase beta chain
		beta-N-acetylglucosaminidase (putative secreted
cds_wt_1535	ybbD	protein)
cds_wt_1536	-	hypothetical protein
cds_wt_1537	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1538	ecaB	carbonic anhydrase
		Homoserine O-acetyltransferase; Homoserine O-
cds_wt_1539	-	trans-acetylase; Homoserine transacetylase; HTA;
cds_wt_1540	-	Helicase IV;

		Bifunctional protein hldE; Includes: D-beta-D-heptose 7-phosphate kinase; D-beta-D-heptose 7-phosphotransferase; Includes: D-beta-D-heptose 1-phosphate adenosyltransferase;
cds_wt_1541	pfkB	
cds_wt_1542	surE	acid phosphatase
cds_wt_1543	-	Anti-sigma F factor antagonist; Stage II sporulation protein AA;
cds_wt_1544	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1545	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1546	pknA	putative serine/threonine protein kinase
cds_wt_1547	merR	Multidrug-efflux transporter 1 regulator;
cds_wt_1548	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1549	cpdB	2',3'-cyclic-nucleotide 2'-phosphodiesterase
cds_wt_1550	argS	arginyl-tRNA synthetase
cds_wt_1551	-	Receptor-type tyrosine-protein phosphatase S; R-PTP-S; Receptor-type tyrosine-protein phosphatase sigma; R-PTP-sigma;
cds_wt_1552	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1553	-	Probable ABC transporter-binding protein DR_1438;
cds_wt_1554	-	hypothetical protein
cds_wt_1555	-	Nephrocystin-3;
cds_wt_1556	-	Anaerobic sulfatase-maturing enzyme homolog aslB; AnSME homolog;
cds_wt_1557	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1558	-	Nephrocystin-3;
cds_wt_1559	-	hypothetical protein
cds_wt_1560	ydeM	Anaerobic sulfatase-maturing enzyme homolog aslB; AnSME homolog;
cds_wt_1561	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1562	yokD	aminoglycoside N3-acetyltransferase
cds_wt_1563	-	Uncharacterized MFS-type transporter ykuC;
cds_wt_1564	PLB1	Phospholipase B1, membrane-associated; Phospholipase B; Phospholipase B/lipase; PLB/LIP; Phospholipase AdRab-B; Includes: Phospholipase A2; Includes: Lysophospholipase;
cds_wt_1565	-	E3 ubiquitin-protein ligase UHRF1; Ubiquitin-like PHD and RING finger domain-containing protein 1; Ubiquitin-like-containing PHD and RING finger domains protein 1; Inverted CCAAT box-binding protein of 90 kDa; Transcription factor ICBP90; Nuclear zinc finger protein Np95; Nuclear protein 95; HuNp95; RING finger protein 106;
cds_wt_1566	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1567	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1568	mcpA	Biofilm dispersion protein bdlA; Chemotaxis regulator bdlA;
cds_wt_1569	-	Chemotaxis protein cheW;
cds_wt_1570	cpo	hypothetical protein
cds_wt_1571	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1572	-	hypothetical protein predicted by Glimmer/Critica

cds_wt_1573	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1574	lacZ	beta-galactosidase
		Carboxylesterase 7; Carboxylesterase-like urinary excreted protein homolog; Cauxin; Epididymis-specific gene 615 protein;
cds_wt_1575	Ces7	
cds_wt_1576	chiC	putative secreted sugar hydrolase
cds_wt_1577	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1578	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1579	-	Uncharacterized protein Rv1290c/MT1328;
		HTH-type transcriptional regulator hmrR; Copper efflux regulator; Copper export regulator;
cds_wt_1580	-	
cds_wt_1581	sitS	putative dehydrogenase
cds_wt_1582	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1583	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1584	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1585	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1586	yefM	Uncharacterized protein SCO2235; ORFU1E;
cds_wt_1587	yoeB	Toxin yoeB;
cds_wt_1588	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1589	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1590	pcrA	putative DNA helicase
cds_wt_1591	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1592	POX2	putative oxidoreductase
cds_wt_1593	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1594	-	hypothetical protein
cds_wt_1595	-	ribonuclease BN
cds_wt_1596	nodJ	Nodulation protein J;
cds_wt_1597	nodJ	Nodulation protein J;
cds_wt_1598	nodI	nodulation ABC transporter NodI
cds_wt_1599	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1600	dnaG	DNA primase
cds_wt_1601	dgt	deoxyguanosinetriphosphate triphosphohydrolase
cds_wt_1602	-	hypothetical protein
cds_wt_1603	-	hypothetical protein
		ADAM 12; A disintegrin and metalloproteinase domain 12; Meltrin-alpha;
cds_wt_1604	-	
cds_wt_1605	-	hypothetical protein
cds_wt_1606	-	hypothetical protein
cds_wt_1607	77	Gene 77 protein; Gp77;
cds_wt_1608	dus	Probable tRNA-dihydrouridine synthase;
cds_wt_1609	-	Uncharacterized protein yqeB;
cds_wt_1610	-	putative secreted protein
cds_wt_1611	glyS	glycyl-tRNA synthetase
cds_wt_1612	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1613	-	hypothetical protein
cds_wt_1614	scbA	Metal ABC transporter substrate-binding lipoprotein;
cds_wt_1615	-	hypothetical protein predicted by Glimmer/Critica
		Sulfate/thiosulfate import ATP-binding protein cysA;
cds_wt_1616	zurA	Sulfate-transporting ATPase;

cds_wt_1617	yceA	Chelated iron transport system membrane protein yfeD;
cds_wt_1618	-	Uncharacterized HTH-type transcriptional regulator MJ1325;
cds_wt_1619	fur	Ferric uptake regulation protein; Ferric uptake regulator;
cds_wt_1620	-	hypothetical protein
cds_wt_1621	-	hypothetical protein
cds_wt_1622	yfhM	hydrolase, alpha/beta fold family
cds_wt_1623	ykoD	Ribose import ATP-binding protein rbsA;
cds_wt_1624	ykoC	Putative permease ybaF;
cds_wt_1625	-	hypothetical protein
cds_wt_1626	-	hypothetical protein
cds_wt_1627	-	UPF0045 protein sll0230;
cds_wt_1628	-	hydrolase, haloacid dehalogenase-like family
cds_wt_1629	-	Phosphoglycerate mutase family member 5;
cds_wt_1630	uppS	putative undecaprenyl pyrophosphate synthetase
cds_wt_1631	recO	DNA repair protein recO; Recombination protein O;
cds_wt_1632	-	Protein liaG;
cds_wt_1633	-	Putative O-acetyltransferase SAV0974;
cds_wt_1634	era	GTP-binding protein era homolog;
cds_wt_1635	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1636	-	hypothetical protein
cds_wt_1637	-	UPF0053 protein Mb2387c;
cds_wt_1638	phoH	PhoH-like protein;
cds_wt_1639	adp	hypothetical protein
cds_wt_1640	-	beta-glucosidase
cds_wt_1641	matE	Multidrug resistance protein mdtK; Multidrug-efflux transporter;
cds_wt_1642	-	Uncharacterized protein yqjI;
cds_wt_1643	sdrD	Ribosomal RNA small subunit methyltransferase E;
cds_wt_1644	dnaJ	16S rRNA m3U1498 methyltransferase;
cds_wt_1645	hrcA	Chaperone protein dnaJ;
cds_wt_1646	-	Heat-inducible transcription repressor hrcA;
cds_wt_1647	hemN	putative inner membrane protein
cds_wt_1648	-	putative oxygen-independent coproporphyrinogen III oxidase
cds_wt_1649	-	enoyl-CoA hydratase
cds_wt_1650	-	putative secreted protein
cds_wt_1651	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1652	lepA	UPF0410 protein yeaQ;
cds_wt_1653	-	GTP-binding elongation factor
cds_wt_1654	-	hypothetical protein
cds_wt_1655	-	hypothetical protein
cds_wt_1656	-	hypothetical protein
cds_wt_1657	rpsT	hypothetical protein
cds_wt_1658	-	30S ribosomal protein S20;
cds_wt_1659	holA	Collagen alpha-5
cds_wt_1660	-	putative DNA polymerase III, delta subunit
		ComE operon protein 3;

cds_wt_1661	-	ComE operon protein 1;
cds_wt_1662	hemK	putative methyltransferase
cds_wt_1663	-	hypothetical protein
cds_wt_1664	degV	UPF0230 protein lin2658;
cds_wt_1665	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1666	gpm2	putative phosphoglycerate mutase
cds_wt_1667	-	Uncharacterized protein C7orf30 homolog;
cds_wt_1668	nadD	putative nicotinate-nucleotide adenyltransferase
cds_wt_1669	tcsA	Two-component system protein A;
cds_wt_1670	pepN	putative aminopeptidase
cds_wt_1671	trpS	tryptophanyl-tRNA synthetase
cds_wt_1672	-	Uncharacterized N-acetyltransferase ysnE;
cds_wt_1673	obg	Uncharacterized GTP-binding protein yhbZ;
cds_wt_1674	rpmA	50S ribosomal protein L27, chloroplastic; CL27;
cds_wt_1675	rplU	50S ribosomal protein L21;
cds_wt_1676	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1677	rne	possible ribonuclease
cds_wt_1678	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1679	-	hypothetical protein
cds_wt_1680	-	hypothetical protein
cds_wt_1681	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1682	rsbU	Uncharacterized protein Rv1364c/MT1410;
cds_wt_1683	yvfQ	putative hydrolase
cds_wt_1684	-	Putative DNA helicase ino80;
cds_wt_1685	plsC	1-acylglycerol-3-phosphate O-acyltransferase
cds_wt_1686	ileS	isoleucyl-tRNA synthetase
cds_wt_1687	ndk	nucleoside diphosphate kinase
cds_wt_1688	-	Collagen alpha-4
cds_wt_1689	Ttn	Titin; Connectin;
cds_wt_1690	-	hypothetical protein
cds_wt_1691	folC	folylpolyglutamate synthase / dihydrofolate synthase
cds_wt_1692	valS	valyl-tRNA synthetase
cds_wt_1693	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1694	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1695	Nit1	nitrilase 1
cds_wt_1696	-	hypothetical protein
cds_wt_1697	clpX	ATP-dependent clp protease ATP-binding subunit clpX
cds_wt_1698	-	ATP dependent Clp protease proteolytic subunit 2
cds_wt_1699	clpP	ATP-dependent Clp protease proteolytic subunit 1
cds_wt_1700	tig	Trigger factor; TF;
cds_wt_1701	-	RNA pyrophosphohydrolase;
cds_wt_1702	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1703	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1704	pfpl	Intracellular protease 1; Intracellular protease I;
cds_wt_1705	pfpl	Pfpl
cds_wt_1706	adhC	putative alcohol dehydrogenase
cds_wt_1707	fdh	zinc-containing alcohol dehydrogenase superfamily
cds_wt_1708	-	Uncharacterized 17.2 kDa protein in melC2-rnhH intergenic region; ORF3;

cds_wt_1709	-	Uncharacterized protein HI0828;
cds_wt_1710	vpr	Furin-like protease 2; Furin-2;
cds_wt_1711	yceJ	Uncharacterized MFS-type transporter yceJ;
cds_wt_1712	sigK	RNA polymerase sigma factor sigK; Sigma-K factor;
cds_wt_1713	-	Anti-sigma-K factor rskA; Regulator of sigK;
		Transforming growth factor-beta-induced protein ig-h3; Beta ig-h3; Kerato-epithelin; RGD-containing collagen-associated protein; RGD-CAP;
cds_wt_1714	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1715	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1716	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1717	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1718	cadC	Cadmium efflux system accessory protein;
cds_wt_1719	-	hypothetical protein
cds_wt_1720	-	hypothetical protein predicted by Glimmer/Critica
		Probable mannan synthase 9; Cellulose synthase-like protein A9; OsCslA9;
cds_wt_1721	-	DNA-directed RNA polymerase II subunit RPB1; RNA polymerase II subunit B1; DNA-directed RNA polymerase II subunit A; DNA-directed RNA polymerase III largest subunit;
cds_wt_1722	-	UPF0256 protein SAV_4024;
cds_wt_1723	eis	hypothetical protein predicted by Glimmer/Critica
cds_wt_1724	-	ribose 5-phosphate isomerase A
cds_wt_1725	rpiA	esterase/lipase/thioesterase
cds_wt_1726	estA	hypothetical protein
cds_wt_1727	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1728	-	aminopeptidase N
cds_wt_1729	pepN	hypothetical protein predicted by Glimmer/Critica
cds_wt_1730	-	hypothetical protein
cds_wt_1731	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1732	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1733	-	putative secreted protein
cds_wt_1734	-	hypothetical protein
cds_wt_1735	-	Small-conductance mechanosensitive channel;
cds_wt_1736	mscS	Uncharacterized MFS-type transporter yuxJ; ORF1;
cds_wt_1737	-	Hemoglobin-like protein HbO; Truncated hemoglobin; trHbO;
cds_wt_1738	glbO	hypothetical protein predicted by Glimmer/Critica
cds_wt_1739	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1740	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1741	-	Putative acyl-CoA thioester hydrolase ybaW;
cds_wt_1742	-	probable macrolide-transport ATP-binding protein ABC transporter
cds_wt_1743	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1744	-	alpha,alpha-trehalose-phosphate synthase
cds_wt_1745	otsA	uroporphyrin-III C-methyltransferase / precorrin-2 oxidase / ferrochelatase
cds_wt_1746	cysG	nicotinate-nucleotide--dimethylbenzimidazole phosphoribosyltransferase
cds_wt_1747	cobT	putative aminotransferase
cds_wt_1748	cobC	

cds_wt_1749	ponA	putative penicillin-binding protein
cds_wt_1750	-	hypothetical protein
cds_wt_1751	cobB	cobyrinic acid a,c-diamide synthase
cds_wt_1752	-	hypothetical protein
cds_wt_1753	ligB	DNA ligase
cds_wt_1754	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1755	pcpB	monooxygenase, FAD-binding
		Cytosolic non-specific dipeptidase; CNDP
cds_wt_1756	-	dipeptidase 2; Glutamate carboxypeptidase-like
cds_wt_1757	-	protein 1; Peptidase A;
cds_wt_1758	cobQ	Probable protease htpX homolog;
cds_wt_1759	cobD	cobyrinic acid synthase
cds_wt_1760	-	cobalamin biosynthetic protein
		hypothetical protein predicted by Glimmer/Critica
cds_wt_1761	ssb1	Single-stranded DNA-binding protein; SSB; Helix-
cds_wt_1762	-	destabilizing protein;
cds_wt_1763	-	Probable serine hydrolase C5E4.05c;
cds_wt_1764	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1765	-	hypothetical protein
cds_wt_1766	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1767	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1768	serA	hypothetical protein predicted by Glimmer/Critica
		D-3-phosphoglycerate dehydrogenase
		A disintegrin and metalloproteinase with
cds_wt_1769	-	thrombospondin motifs 7; ADAMTS-7; ADAM-TS 7;
		ADAM-TS7; COMPase;
cds_wt_1770	yhcZ	Chemotaxis response regulator protein-glutamate
cds_wt_1771	-	methylesterase 1;
cds_wt_1772	-	hypothetical protein predicted by Glimmer/Critica
		hypothetical protein
cds_wt_1773	-	Uncharacterized HTH-type transcriptional regulator
cds_wt_1774	-	ysaD;
		Uncharacterized MFS-type transporter C16A3.17c;
cds_wt_1775	-	Heme-degrading monooxygenase isdG; Iron-
cds_wt_1776	-	regulated surface determinant isdG; Iron-responsive
cds_wt_1777	-	surface determinant isdG; Heme oxygenase;
cds_wt_1778	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1779	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1780	-	UPF0713 protein yngL;
cds_wt_1781	ydzA	hypothetical protein predicted by Glimmer/Critica
cds_wt_1782	-	Uncharacterized protein ML1177;
cds_wt_1783	hrdB	Uncharacterized protein Rv1342c/MT1383;
cds_wt_1784	-	Uncharacterized protein Mb2213c;
cds_wt_1785	ywfD	RNA polymerase principal sigma factor hrdB;
cds_wt_1786	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1787	-	short-chain dehydrogenase/reductase SDR
cds_wt_1788	-	Thymidylate kinase; dTMP kinase;
cds_wt_1789	-	hypothetical protein
		hypothetical protein predicted by Glimmer/Critica
		hypothetical protein

cds_wt_1790	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1791	-	Signaling protein ykoW;
		Probable GTP pyrophosphokinase; ATP:GTP 3'-
cds_wt_1792	-	pyrophosphotransferase; ppGpp synthetase I;
cds_wt_1793	aglA	putative alpha-glucosidase
cds_wt_1794	proP	Protein spinster homolog 1;
cds_wt_1795	xylB	xylulose kinase
cds_wt_1796	xylA	xylose isomerase
cds_wt_1797	xylR	Putative xylose repressor;
cds_wt_1798	xylR	transcriptional repressor of the xylose operon
cds_wt_1799	-	Uncharacterized protein Rv1836c/MT1884;
cds_wt_1800	-	6-phosphogluconolactonase; 6-P-gluconolactonase;
		HTH-type transcriptional repressor purR; Purine
		nucleotide synthesis repressor; Pur regulon
cds_wt_1801	-	repressor;
cds_wt_1802	-	Translation initiation factor IF-2;
cds_wt_1803	-	hypothetical protein
cds_wt_1804	-	hypothetical protein
cds_wt_1805	PHY1	Phytochrome 1;
cds_wt_1806	-	putative secreted protein
cds_wt_1807	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1808	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1809	-	Zinc metalloprotease zmpB;
cds_wt_1810	nahB	beta-N-acetylhexosaminidase
cds_wt_1811	paiA	Uncharacterized N-acetyltransferase Mb2688;
		Uncharacterized HTH-type transcriptional regulator
cds_wt_1812	-	yobV;
cds_wt_1813	corA	Zinc transport protein zntB;
cds_wt_1814	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1815	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1816	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1817	-	Uncharacterized signaling protein PA3311;
		Chemotaxis response regulator protein-glutamate
cds_wt_1818	phoB	methylesterase;
cds_wt_1819	-	probable oxidoreductase
cds_wt_1820	-	hypothetical protein predicted by Glimmer/Critica
		RE1-silencing transcription factor; Neural-restrictive
cds_wt_1821	-	silencer factor;
cds_wt_1822	ftrA	transcriptional regulator, AraC family
cds_wt_1823	-	UPF0176 protein sll0765;
cds_wt_1824	-	putative secreted ATP/GTP binding protein
cds_wt_1825	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1826	-	Leucine efflux protein;
cds_wt_1827	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1828	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1829	pac	Puromycin N-acetyltransferase;
cds_wt_1830	-	Putrescine importer;
cds_wt_1831	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1832	-	putative DNA-binding protein
cds_wt_1833	-	hypothetical protein

cds_wt_1834	-	hypothetical protein
cds_wt_1835	-	Nucleoporin NUP159; Nuclear pore protein NUP159;
cds_wt_1836	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1837	-	Uncharacterized protein y4lL;
cds_wt_1838	-	conserved hypothetical protein
cds_wt_1839	yqiK	Inner membrane protein yqiK;
cds_wt_1840	-	hypothetical protein
cds_wt_1841	-	hypothetical protein
cds_wt_1842	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1843	cypA	putative cytochrome P450
cds_wt_1844	-	Putative cytochrome P450 141;
cds_wt_1845	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1846	-	Sensor protein vraS;
cds_wt_1847	-	Response regulator protein vraR;
cds_wt_1848	azr	NADPH azoreductase;
cds_wt_1849	-	Endoglucanase 6; Endo-1,4-beta glucanase 6;
cds_wt_1850	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1851	lppS	Uncharacterized protein Mb0493;
cds_wt_1852	lppS	Uncharacterized protein Mb0493;
cds_wt_1853	-	Amino-acid acetyltransferase; N-acetylglutamate synthase; AGS; NAGS;
cds_wt_1854	ymcC	hypothetical protein
cds_wt_1855	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1856	-	hypothetical protein
cds_wt_1857	rpoD	RNA polymerase sigma factor sigZ;
cds_wt_1858	celB	putative endo-1,4-beta-glucanase
cds_wt_1859	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1860	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1861	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1862	istA	Probable transposase for insertion sequence element IS701;
cds_wt_1863	orn	putative oligoribonuclease
cds_wt_1864	-	Polycystic kidney disease protein 1-like 3; Polycystin-1L3; PC1-like 3 protein;
cds_wt_1865	copC	Inner membrane protein yebZ;
cds_wt_1866	sigC	RNA polymerase sigma-E factor; Sigma-24;
cds_wt_1867	-	hypothetical protein
cds_wt_1868	pknE	Na
cds_wt_1869	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1870	-	DNA replication and repair protein recF;
cds_wt_1871	-	hypothetical protein
cds_wt_1872	-	Alkaline shock protein 23; S-adenosylmethionine decarboxylase proenzyme; AdoMetDC; SAMDC; Contains: S-adenosylmethionine decarboxylase beta chain; Contains: S-adenosylmethionine decarboxylase alpha chain;
cds_wt_1873	-	
cds_wt_1874	bcp	Probable peroxiredoxin;
cds_wt_1875	yoaJ	Expansin-A8; AtEXPA8; Alpha-expansin-8; At-EXP8; AtEx8; Ath-ExpAlpha-1.11;

cds_wt_1876	-	Molybdenum cofactor sulfurase; MoCo sulfurase; MOS;
cds_wt_1877	rpiR	Glucosamine--fructose-6-phosphate aminotransferase
cds_wt_1878	hutU	urocanate hydratase
cds_wt_1879	allC	allantoate amidohydrolase
cds_wt_1880	hutF	putative chlorohydrolase
cds_wt_1881	hutI	imidazolonepropionase
cds_wt_1882	hutH	histidine ammonia-lyase
cds_wt_1883	-	HAM1 protein
cds_wt_1884	rphA	ribonuclease PH
cds_wt_1885	-	Glycogen synthase; Starch
cds_wt_1886	-	Ribonuclease Z; RNase Z; tRNase Z; tRNA 3 endonuclease;
cds_wt_1887	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1888	cysM	putative cysteine synthase
cds_wt_1889	-	UPF0084 protein slr0821;
cds_wt_1890	-	Uncharacterized protein Mb1369;
cds_wt_1891	-	Uncharacterized protein Mb1367;
cds_wt_1892	pncB	hypothetical protein
cds_wt_1893	pncA	pyrazinamidase / nicotinamidase
cds_wt_1894	-	L-azetidine-2-carboxylic acid acetyltransferase;
cds_wt_1895	ssuD	Alkanesulfonate monooxygenase; FMNH2-dependent aliphatic sulfonate monooxygenase;
cds_wt_1896	-	Hippocampus abundant transcript 1 protein;
cds_wt_1897	JNA2	Polygalacturonase; PG; Pectinase; Major pollen allergen Jun a 2; AltName: Allergen=Jun a 2;
cds_wt_1898	ctaD	cytochrome-c oxidase
cds_wt_1899	ABA2	Zeaxanthin epoxidase, chloroplastic;
cds_wt_1900	lig3	hypothetical protein
cds_wt_1901	ygjK	Uncharacterized protein ygjK;
cds_wt_1902	-	NAD/factor-dependent formaldehyde dehydrogenase
cds_wt_1903	marR	Uncharacterized HTH-type transcriptional regulator yetL;
cds_wt_1904	-	Uncharacterized protein y4IL;
cds_wt_1905	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1906	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1907	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1908	-	DNA2-like helicase; DNA replication ATP-dependent helicase-like homolog;
cds_wt_1909	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1910	-	Phosphoserine phosphatase rsbP;
cds_wt_1911	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1912	-	hypothetical protein
cds_wt_1913	-	hypothetical protein
cds_wt_1914	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1915	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1916	-	hypothetical protein 2SC7G11.36
cds_wt_1917	-	Uncharacterized signaling protein PA3311;
cds_wt_1918	-	Nephrocystin-3;

cds_wt_1919	-	Anti-sigma F factor antagonist; Stage II sporulation protein AA;
cds_wt_1920	-	Monocarboxylate transporter 2; MCT 2; Solute carrier family 16 member 7;
cds_wt_1921	-	HTH-type transcriptional regulator glxA;
cds_wt_1922	tapB	Type IV pilus assembly protein tapB;
cds_wt_1923	pilT	Twitching motility protein;
cds_wt_1924	tapC	Type IV pilus assembly protein tapC;
cds_wt_1925	fimA	Fimbrial protein; Pilin; Serogroup B1/AC293;
cds_wt_1926	pilD	leader peptidase (prepilin peptidase) / N-methyltransferase
cds_wt_1927	pilM	Chaperone protein dnaK; Heat shock protein 70;
cds_wt_1928	-	Heat shock 70 kDa protein; HSP70;
cds_wt_1929	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1930	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1931	mtaP	Alkanesulfonate monooxygenase; FMNH2-dependent aliphatic sulfonate monooxygenase;
cds_wt_1932	-	5'-methylthioadenosine phosphorylase
cds_wt_1933	-	UPF0301 protein VC_0467;
cds_wt_1934	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1935	pntB	putative membrane protein
cds_wt_1936	pntA	pyridine nucleotide transhydrogenase, beta subunit
cds_wt_1937	-	NAD(P) transhydrogenase subunit alpha
cds_wt_1938	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1939	rpoE	hypothetical protein predicted by Glimmer/Critica
cds_wt_1940	-	RNA polymerase sigma factor sigW; Sigma-W factor;
cds_wt_1941	-	HTH-type transcriptional regulator immR;
cds_wt_1942	-	putative regulatory protein
cds_wt_1943	-	Thermolysin; Thermostable neutral proteinase;
cds_wt_1944	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1945	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1946	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1947	-	Uncharacterized protein Rv2079/MT2140;
cds_wt_1948	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1949	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1950	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1951	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1952	-	hypothetical protein
cds_wt_1953	-	2',3'-cyclic-nucleotide 2'-phosphodiesterase;
cds_wt_1954	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1955	-	putative MutT-like protein
cds_wt_1956	-	hypothetical protein
cds_wt_1957	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1958	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1959	ftsK	DNA translocase ftsK;
cds_wt_1960	-	Uncharacterized protein y4bA/y4pH;
cds_wt_1961	cenB	Endoglucanase B; Endo-1,4-beta-glucanase B;
cds_wt_1962	smpB	Cellulase B;
		SsrA-binding protein;

cds_wt_1963	-	hypothetical protein
cds_wt_1964	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1965	ftsX	Macrolide export ATP-binding/permease protein
cds_wt_1966	ftsE	macB;
cds_wt_1967	prfB	Methionine import ATP-binding protein metN;
cds_wt_1968	padR	Peptide chain release factor 2; RF-2;
		Negative transcription regulator padR;
		Zinc finger and BTB domain-containing protein 17;
		Zinc finger protein 151; Zinc finger protein Z13;
cds_wt_1969	-	Flags: Fragment;
cds_wt_1970	-	hypothetical protein
		Voltage-dependent P/Q-type calcium channel subunit
		alpha-1A; Voltage-gated calcium channel subunit
		alpha Cav2.1; Calcium channel, L type, alpha-1
cds_wt_1971	-	polypeptide isoform 4; Brain calcium channel I; BI;
cds_wt_1972	secA	Protein translocase subunit secA;
cds_wt_1973	hat2	Probable GMP synthase
cds_wt_1974	-	Uncharacterized protein SH2139;
cds_wt_1975	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1976	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_1977	-	Lipoprotein lpqB;
cds_wt_1978	mtrB	putative two-component system sensor kinase
cds_wt_1979	mtrA	Transcriptional regulatory protein yycF;
cds_wt_1980	-	hypothetical protein
cds_wt_1981	-	putative DNA-binding protein
cds_wt_1982	manA	putative mannose-6-phosphate isomerase
		Zinc transporter 9; ZnT-9; Solute carrier family 30
cds_wt_1983	tp37	member 9;
cds_wt_1984	-	hypothetical protein
cds_wt_1985	-	Tetraacyldisaccharide 4'-kinase; Lipid A 4'-kinase;
cds_wt_1986	pmmA	phosphomannomutase
cds_wt_1987	nfi	endonuclease V
		Uncharacterized 47.3 kDa protein in thcA 5'region;
cds_wt_1988	-	ORF3;
cds_wt_1989	aldA	aldehyde dehydrogenase
cds_wt_1990	-	hypothetical protein
cds_wt_1991	nodB	putative deacetylase
cds_wt_1992	-	hypothetical protein
cds_wt_1993	-	hypothetical protein
		probable transcriptional regulatory protein WhiB-like
cds_wt_1994	whiB	WhiB2
cds_wt_1995	fbiC	hypothetical protein
cds_wt_1996	-	Protein piccolo; Aczonin;
cds_wt_1997	fbiA	LPPG:FO 2-phospho-L-lactate transferase
		Uncharacterized 45.4 kDa protein in thiaminase I
cds_wt_1998	-	5'region;
cds_wt_1999	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2000	manC	mannose-1-phosphate guanylyltransferase
cds_wt_2001	rfbW	probable glycosyltransferase
cds_wt_2002	-	hypothetical protein

cds_wt_2003	-	putative acyl-CoA hydrolase
cds_wt_2004	Trio	Triple functional domain protein;
cds_wt_2005	-	Pathogen-related protein;
cds_wt_2006	megL	methionine gamma-lyase
		Glutamate-1-semialdehyde 2,1-aminomutase; GSA;
		Glutamate-1-semialdehyde aminotransferase; GSA-
cds_wt_2007	aro8	AT;
cds_wt_2008	srfJ	glycosyl hydrolase
cds_wt_2009	-	putative secreted hydrolase
		HTH-type transcriptional repressor purR; Purine
		nucleotide synthesis repressor; Pur regulon
cds_wt_2010	lacI	repressor;
cds_wt_2011	-	Uncharacterized protein Rv2079/MT2140;
cds_wt_2012	-	putative DNA-binding protein
cds_wt_2013	AMID	NADH dehydrogenase-like protein SAS0811;
cds_wt_2014	leuA	2-isopropylmalate synthase
		Anaerobic sulfatase-maturing enzyme; AnSME;
		Ser-type sulfatase-activating enzyme; Chondroitin
		sulfate/heparin utilization regulation protein;
cds_wt_2015	-	Protein tolB;
cds_wt_2016	-	Protein tolB;
cds_wt_2017	-	RNA polymerase sigma-E factor;
cds_wt_2018	-	Protein tolB;
		Plipastatin synthetase subunit D; Peptide synthetase
		4; Includes: ATP-dependent proline adenylation; ProA
		1; Proline activase 1; Includes: ATP-dependent
		glutamine adenylation; GlnA; Glutamine activase;
		Includes: ATP-dependent tyrosine adenylation 2; TyrA
cds_wt_2019	dhbF	2; Tyrosine activase 2;
cds_wt_2020	-	putative secreted protein
		Uncharacterized HTH-type transcriptional regulator
cds_wt_2021	-	MJ0229;
		Linear gramicidin synthetase subunit C; Includes:
		ATP-dependent valine adenylation; ValA; Valine
		activase; Includes: ATP-dependent D-valine
		adenylation; D-ValA; D-valine activase; Includes:
cds_wt_2022	lgrC	Valine racemase
		Gramicidin S synthetase 2; Gramicidin S synthetase
		II; Includes: ATP-dependent proline adenylation; ProA;
		Proline activase; Includes: ATP-dependent valine
		adenylation; ValA; Valine activase; Includes: ATP-
		dependent ornithine adenylation; OrnA; Ornithine
		activase; Includes: ATP-dependent leucine
cds_wt_2023	-	adenylation; LeuA; Leucine activase;
cds_wt_2024	mbtH	Protein mbtH;
		S-acyl fatty acid synthase thioesterase, medium
		chain; Oleoyl-ACP hydrolase; Thioesterase II;
cds_wt_2025	olmC	Thioesterase domain-containing protein 1;
cds_wt_2026	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2027	-	Putative membrane protein mmpL11;
cds_wt_2028	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2029	spcT	Uncharacterized MFS-type transporter yfiS;

cds_wt_2030	pbp	penicillin-binding protein, putative
cds_wt_2031	tycC	Tyrosidine synthetase 3; Tyrosidine synthetase III; Includes: ATP-dependent asparagine adenylation; AsnA; Asparagine activase; Includes: ATP-dependent glutamine adenylation; GlnA; Glutamine activase; Includes: ATP-dependent tyrosine adenylation; TyrA; Tyrosine activase; Includes: ATP-dependent valine adenylation; ValA; Valine activase; Includes: ATP-dependent ornithine adenylation; OrnA; Ornithine activase; Includes: ATP-dependent leucine adenylation; LeuA; Leucine activase;
cds_wt_2032	tycC	Tyrosidine synthetase 3; Tyrosidine synthetase III; Includes: ATP-dependent asparagine adenylation; AsnA; Asparagine activase; Includes: ATP-dependent glutamine adenylation; GlnA; Glutamine activase; Includes: ATP-dependent tyrosine adenylation; TyrA; Tyrosine activase; Includes: ATP-dependent valine adenylation; ValA; Valine activase; Includes: ATP-dependent ornithine adenylation; OrnA; Ornithine activase; Includes: ATP-dependent leucine adenylation; LeuA; Leucine activase;
cds_wt_2033	tycC	Tyrosidine synthetase 3; Tyrosidine synthetase III; Includes: ATP-dependent asparagine adenylation; AsnA; Asparagine activase; Includes: ATP-dependent glutamine adenylation; GlnA; Glutamine activase; Includes: ATP-dependent tyrosine adenylation; TyrA; Tyrosine activase; Includes: ATP-dependent valine adenylation; ValA; Valine activase; Includes: ATP-dependent ornithine adenylation; OrnA; Ornithine activase; Includes: ATP-dependent leucine adenylation; LeuA; Leucine activase;
cds_wt_2034	-	Protein mbtH;
cds_wt_2035	-	putative SyrP-like protein
cds_wt_2036	-	Regulatory protein afsR;
cds_wt_2037	abcA	Lipid A export ATP-binding/permease protein msbA;
cds_wt_2038	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2039	-	Multidrug resistance protein 2; P-glycoprotein 2;
cds_wt_2040	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2041	-	putative asparagine synthetase
cds_wt_2042	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2043	-	conserved hypothetical protein
cds_wt_2044	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2045	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2046	ocd	putative ornithine cyclodeaminase
cds_wt_2047	-	pyridoxal-phosphate dependent enzyme
cds_wt_2048	argF	family/ornithine cyclodeaminase family protein
cds_wt_2049	-	ornithine carbamoyltransferase
cds_wt_2050	-	hypothetical protein predicted by Glimmer/Critica
		4'-phosphopantetheinyl transferase entD;
		Enterobactin synthetase component D; Enterochelin

synthase D;

cds_wt_2051	aveR	HTH-type transcriptional regulator maltT; ATP-dependent transcriptional activator maltT;
cds_wt_2052	leuA	2-isopropylmalate synthase
cds_wt_2053	urah	5-hydroxyisourate hydrolase; HIU hydrolase; HIUase; Transthyretin-related protein;
cds_wt_2054	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2055	-	Regulatory protein afsR;
cds_wt_2056	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2057	lolD	Spermidine/putrescine import ATP-binding protein potA;
cds_wt_2058	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2059	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2060	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2061	-	Phytochrome-like protein cph2; Bacteriophytochrome cph2;
cds_wt_2062	-	hypothetical protein
cds_wt_2063	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2064	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2065	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2066	-	Tripartite motif-containing protein 71; Lin-41 homolog;
cds_wt_2067	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2068	-	acyl-CoA dehydrogenase
cds_wt_2069	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2070	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2071	purE	phosphoribosylaminoimidazole carboxylase catalytic subunit
cds_wt_2072	purK	putative phosphoribosylaminoimidazole carboxylase ATPase subunit
cds_wt_2073	yyaL	Spermatogenesis-associated protein 20; Sperm-specific protein 411; Ssp411;
cds_wt_2074	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2075	-	Uncharacterized protein y4IL;
cds_wt_2076	mca	Probable N-acetylglucosaminyl-phosphatidylinositol de-N-acetylase;
cds_wt_2077	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2078	greA	Transcription elongation factor greA; Transcript cleavage factor greA;
cds_wt_2079	-	Probable protease htpX homolog;
cds_wt_2080	ilvA	threonine dehydratase
cds_wt_2081	nylA	amidase
cds_wt_2082	metB	cystathionine gamma-synthase
cds_wt_2083	msrA	methionine sulfoxide reductase A
cds_wt_2084	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2085	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2086	-	Uncharacterized protein Rv2226/MT2285;
cds_wt_2087	ppk2	Uncharacterized protein in chlN 3'region; URF2;
cds_wt_2088	elaC	Flags: Fragment; ribonuclease Z

cds_wt_2089	-	Uncharacterized N-acetyltransferase yuaI;
cds_wt_2090	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2091	htrA	serine protease
cds_wt_2092	cbs	cystathionine beta-synthase
cds_wt_2093	-	hypothetical protein
cds_wt_2094	-	hypothetical protein
cds_wt_2095	-	hypothetical protein
cds_wt_2096	-	putative thiolase
cds_wt_2097	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2098	-	hypothetical protein
cds_wt_2099	ndh3	putative oxidoreductase
cds_wt_2100	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2101	-	Uncharacterized protein yeaD;
cds_wt_2102	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2103	-	Uncharacterized protein yeaC;
cds_wt_2104	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2105	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2106	-	putative transmembrane protein
cds_wt_2107	-	Uncharacterized protein ML1105;
		Transcription elongation factor SPT5; hSPT5; DRB
		sensitivity-inducing factor large subunit; DSIF large
		subunit; DSIF p160; Tat-cotransactivator 1 protein;
cds_wt_2108	-	Tat-CT1 protein;
cds_wt_2109	gppA	hypothetical protein
cds_wt_2110	-	putative acetyltransferase
cds_wt_2111	-	hypothetical protein
cds_wt_2112	-	putative membrane protein
cds_wt_2113	eno	enolase
cds_wt_2114	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2115	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2116	-	hypothetical protein
cds_wt_2117	-	Protein mazG homolog;
cds_wt_2118	-	hypothetical protein predicted by Glimmer/Critica
		Transcription-repair-coupling factor; TRCF; ATP-
cds_wt_2119	mfd	dependent helicase mfd;
cds_wt_2120	hoxX	probable sensor protein
cds_wt_2121	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2122	ppc	phosphoenolpyruvate carboxylase
cds_wt_2123	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2124	qor	quinone oxidoreductase
cds_wt_2125	arsR	Arsenical resistance operon repressor;
cds_wt_2126	-	possible integral membrane protein
cds_wt_2127	-	ABC transporter, ATP-binding protein
cds_wt_2128	-	possible integral membrane protein
		Spermidine/putrescine import ATP-binding protein
cds_wt_2129	bcrA	potA;
		Endoglucanase H; Endo-1,4-beta-glucanase H; EgH;
cds_wt_2130	-	Cellulase H;
cds_wt_2131	cysD	sulfate adenylyltransferase
cds_wt_2132	etk	Tyrosine-protein kinase etk;

cds_wt_2133	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2134	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2135	-	similar to N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 4
cds_wt_2136	tp56	Uncharacterized membrane protein MJ1068;
cds_wt_2137	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2138	-	Endoglucanase H; Endo-1,4-beta-glucanase H; EgH;
cds_wt_2139	-	Cellulase H;
cds_wt_2140	-	hypothetical protein
cds_wt_2141	tagA	hypothetical protein predicted by Glimmer/Critica
		glycosyl transferase WecB/TagA/CpsF
		Carbohydrate sulfotransferase 4; N-
		acetylglucosamine 6-O-sulfotransferase 2;
		GlcNAc6ST-2; High endothelial cells N-
		acetylglucosamine 6-O-sulfotransferase; HEC-
		GlcNAc6ST; L-selectin ligand sulfotransferase; LSST;
cds_wt_2142	-	Galactose/N-acetylglucosamine/N-acetylglucosamine
		6-O-sulfotransferase 3; GST-3;
		Polypeptide N-acetylgalactosaminyltransferase 10;
		Polypeptide GalNAc transferase 10; pp-GaNTase 10;
		GalNAc-T10; Protein-UDP
		acetylgalactosaminyltransferase 10; UDP-
		GalNAc:polypeptide N-
cds_wt_2143	-	acetylgalactosaminyltransferase 10;
cds_wt_2144	ygbI	Putative aga operon transcriptional repressor;
cds_wt_2145	galT	galactose-1-phosphate uridylyltransferase
cds_wt_2146	icd1	isocitrate dehydrogenase
cds_wt_2147	hglK	BTB/POZ domain-containing protein KCTD9;
cds_wt_2148	-	hypothetical protein predicted by Glimmer/Critica
		phosphoribosylaminoimidazolecarboxamide
cds_wt_2149	purH	formyltransferase / IMP cyclohydrolase
cds_wt_2150	purN	phosphoribosylglycinamide formyltransferase
cds_wt_2151	-	Uncharacterized protein Mb0980;
cds_wt_2152	sucD	putative succinyl-CoA synthetase alpha subunit
cds_wt_2153	sucC	succinyl-CoA synthetase beta chain
cds_wt_2154	icmB	methylmalonyl-CoA mutase, alpha subunit, chain B
cds_wt_2155	nlpD	Uncharacterized lipoprotein ygeR;
		SPBc2 prophage-derived uncharacterized
cds_wt_2156	nlpD	transglycosylase yomI;
cds_wt_2157	uvrD	DNA helicase II
cds_wt_2158	-	5'-nucleotidase
		3-dehydroquinate dehydratase; 3-dehydroquinase;
cds_wt_2159	-	Type I DHQase;
cds_wt_2160	appF	Methionine import ATP-binding protein metN;
cds_wt_2161	dppD	Dipeptide transport ATP-binding protein dppD;
		Oligopeptide transport system permease protein
cds_wt_2162	dppC	oppC;
cds_wt_2163	dppB	Nickel transport system permease protein nikB;
cds_wt_2164	dppA	Periplasmic oligopeptide-binding protein;
cds_wt_2165	narL	Nitrate/nitrite response regulator protein narP;

cds_wt_2166	-	Uncharacterized sensor-like histidine kinase Caur_0899;
cds_wt_2167	Pclo	Protein piccolo; Aczonin; Multidomain presynaptic cytomatrix protein;
cds_wt_2168	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2169	psd	phosphatidylserine decarboxylase
cds_wt_2170	pssA	CDP-diacylglycerol--serine O-phosphatidyltransferase; Phosphatidylserine synthase;
cds_wt_2171	-	RNA pyrophosphohydrolase;
cds_wt_2172	-	RNA pyrophosphohydrolase;
cds_wt_2173	guaA	GMP synthase
cds_wt_2174	lytR	Membrane-bound protein lytR;
cds_wt_2175	-	Leukotriene A-4 hydrolase; Leukotriene A
cds_wt_2176	guaB	putative inosine-5'-monophosphate dehydrogenase
cds_wt_2177	guaB	inosine-5'-monophosphate dehydrogenase
cds_wt_2178	-	Uncharacterized protein ML0386;
cds_wt_2179	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2180	-	Uncharacterized transcriptional regulatory protein yxjL;
cds_wt_2181	wblB	transcriptional regulatory protein WhiB-like WhiB3
cds_wt_2182	soxC	probable sulfite oxidase
cds_wt_2183	-	Uncharacterized zinc protease Rv2782c/MT2852;
cds_wt_2184	-	hypothetical protein
cds_wt_2185	xylR	Xylose repressor;
cds_wt_2186	lsrC	Autoinducer 2 import system permease protein lsrC;
cds_wt_2187	-	AI-2 import system permease protein lsrC;
cds_wt_2188	xylF	putative ABC transporter ATP-binding protein
cds_wt_2189	ybaK	HTH-type transcriptional repressor purR; Purine nucleotide synthesis repressor; Pur regulon repressor;
cds_wt_2190	-	Prolyl-tRNA synthetase; Proline--tRNA ligase; ProRS;
cds_wt_2191	-	23S rRNA
cds_wt_2192	-	10 kDa chaperonin; Protein Cpn10; groES protein;
cds_wt_2193	yfiC	60 kDa chaperonin; Protein Cpn60; groEL protein;
cds_wt_2194	yhel	Lipid A export ATP-binding/permease protein msbA;
cds_wt_2195	gcp	Lipid A export ATP-binding/permease protein msbA;
cds_wt_2196	rimI	putative glycoprotease
cds_wt_2197	-	putative acetyltransferase
cds_wt_2198	ung	Probable O-sialoglycoprotein endopeptidase;
cds_wt_2199	-	Glycoprotease;
cds_wt_2200	hpx	uracil-DNA glycosylase
cds_wt_2201	alr	UPF0079 ATP-binding protein RF_0017;
cds_wt_2202	-	putative hydrolase
cds_wt_2203	acpS	alanine racemase
cds_wt_2204	-	Uncharacterized protein yjeF;
cds_wt_2205	-	Holo-
cds_wt_2206	-	hypothetical protein predicted by Glimmer/Critica
		hypothetical protein predicted by Glimmer/Critica
		Uncharacterized protein Rv2079/MT2140;

cds_wt_2207	glmS	putative L-glutamine-D-fructose-6-phosphate amidotransferase
cds_wt_2208	-	Putative membrane protein mmpS4; PGB14T-X;
cds_wt_2209	dapC	N-succinylidiaminopimelate aminotransferase
cds_wt_2210	mrsA	putative phosphoglucomutase/phosphomannomutase
cds_wt_2211	rpsI	30S ribosomal protein S9;
cds_wt_2212	rplM	50S ribosomal protein L13;
		Putative uroporphyrinogen-III synthase; UROS;
cds_wt_2213	yjjA	Hydroxymethylbilane hydrolyase
cds_wt_2214	-	Translation initiation factor IF-2;
cds_wt_2215	-	hypothetical protein
cds_wt_2216	-	hypothetical protein
cds_wt_2217	virA	Wide host range virA protein; WHR virA;
cds_wt_2218	-	Collagen alpha-4
cds_wt_2219	-	Ribonuclease; Barnase; RNase Ba;
cds_wt_2220	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2221	Zan	Zonadhesin;
cds_wt_2222	thiC	Thiamine biosynthesis protein thiC;
cds_wt_2223	thiD	phosphomethylpyrimidine kinase
		Thiamine-phosphate pyrophosphorylase; TMP pyrophosphorylase; TMP-PPase; Thiamine- phosphate synthase;
cds_wt_2224	-	
cds_wt_2225	thiG	Thiazole biosynthesis protein thiG;
cds_wt_2226	thiO	D-amino acid dehydrogenase small subunit;
cds_wt_2227	thiE	thiamine-phosphate pyrophosphorylase
		Putative ABC transporter ATP-binding protein MA_1747;
cds_wt_2228	-	
cds_wt_2229	-	Ribosomal protein L11 methyltransferase; L11 Mtase;
cds_wt_2230	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2231	truA	tRNA pseudouridine synthase A
cds_wt_2232	rplQ	50S ribosomal protein L17;
cds_wt_2233	rpoA	DNA-directed RNA polymerase alpha chain
cds_wt_2234	rpsD	30S ribosomal protein S4;
cds_wt_2235	rpsK	30S ribosomal protein S11;
cds_wt_2236	rpsM	30S ribosomal protein S13;
cds_wt_2237	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2238	infA	Translation initiation factor IF-1;
cds_wt_2239	-	Uncharacterized protein Rv0966c/MT0994;
cds_wt_2240	map	methionine aminopeptidase
cds_wt_2241	adk	adenylate kinase
cds_wt_2242	secY	Preprotein translocase subunit secY;
cds_wt_2243	rplO	50S ribosomal protein L15;
cds_wt_2244	rpmD	50S ribosomal protein L30;
cds_wt_2245	rpsE	30S ribosomal protein S5;
cds_wt_2246	rplR	50S ribosomal protein L18; BL22;
cds_wt_2247	rplF	50S ribosomal protein L6; BL10;
cds_wt_2248	rpsH	30S ribosomal protein S8;
cds_wt_2249	rpsN	30S ribosomal protein S14, chloroplastic;
cds_wt_2250	rplE	50S ribosomal protein L5;
cds_wt_2251	rplX	50S ribosomal protein L24;

cds_wt_2252	rplN	50S ribosomal protein L14;
cds_wt_2253	rpsQ	30S ribosomal protein S17;
cds_wt_2254	rpmC	50S ribosomal protein L29;
cds_wt_2255	rplP	50S ribosomal protein L16;
cds_wt_2256	rpsC	30S ribosomal protein S3;
cds_wt_2257	rplV	50S ribosomal protein L22, chloroplastic;
cds_wt_2258	rpsS	30S ribosomal protein S19;
cds_wt_2259	rplB	50S ribosomal protein L2;
cds_wt_2260	rplW	50S ribosomal protein L23;
cds_wt_2261	rplD	50S ribosomal protein L4; BL4;
cds_wt_2262	rplC	50S ribosomal protein L3;
cds_wt_2263	rpsJ	30S ribosomal protein S10;
cds_wt_2264	tuf	elongation factor EF-Tu
cds_wt_2265	fusA	elongation factor G
cds_wt_2266	rpsG	30S ribosomal protein S7;
cds_wt_2267	rpsL	30S ribosomal protein S12;
cds_wt_2268	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2269	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2270	rpoC	DNA-directed RNA polymerase beta' chain
cds_wt_2271	rpoB	DNA-directed RNA polymerase beta chain
cds_wt_2272	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2273	rplL	50S ribosomal protein L7/L12;
cds_wt_2274	rplJ	50S ribosomal protein L10;
cds_wt_2275	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2276	nosF	Spermidine/putrescine import ATP-binding protein potA;
cds_wt_2277	rplA	50S ribosomal protein L1;
cds_wt_2278	nusG	Transcription antitermination protein nusG;
cds_wt_2279	secE	Probable preprotein translocase subunit secE;
cds_wt_2280	-	UPF0336 protein SACE_6876;
cds_wt_2281	-	UPF0336 protein Mb0656;
cds_wt_2282	-	50S ribosomal protein L33;
cds_wt_2283	-	Uncharacterized signaling protein CC_0091;
cds_wt_2284	-	hypothetical protein
cds_wt_2285	sseB	3-mercaptopyruvate sulfurtransferase
cds_wt_2286	rhtB	Leucine efflux protein;
cds_wt_2287	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2288	-	UPF0234 protein Sde_0533;
cds_wt_2289	-	hypothetical protein
cds_wt_2290	-	hypothetical protein
cds_wt_2291	-	Uncharacterized protein yjdJ;
cds_wt_2292	-	Uncharacterized protein yfIK;
cds_wt_2293	-	acetyltransferase, GNAT family
cds_wt_2294	yvbT	bacterial luciferase family protein
cds_wt_2295	-	Uncharacterized protein Rv0048c/MT0054;
cds_wt_2296	htpX	putative peptidase
cds_wt_2297	nuoN	NADH dehydrogenase I, N subunit
cds_wt_2298	nuoM	NADH dehydrogenase I chain M
cds_wt_2299	nuoL	NADH-ubiquinone oxidoreductase, chain L
cds_wt_2300	ndhE	NAD

cds_wt_2301	ndhG	NAD
cds_wt_2302	nuoI	NADH dehydrogenase I, I subunit
cds_wt_2303	nuoH	NADH dehydrogenase I, H subunit
cds_wt_2304	fpoC	F(420)H(2) dehydrogenase, subunit FpoC
cds_wt_2305	sigV	RNA polymerase sigma factor sigW; Sigma-W factor;
cds_wt_2306	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2307	-	hypothetical protein
cds_wt_2308	ndhH	NADH dehydrogenase (ubiquinone), 20 kDa subunit
cds_wt_2309	-	FIC domain-containing protein;
cds_wt_2310	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2311	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2312	ggt	gamma-glutamyltranspeptidase
cds_wt_2313	-	hypothetical protein
cds_wt_2314	-	Uncharacterized HTH-type transcriptional regulator Mb1846;
cds_wt_2315	-	Putative S-adenosyl-L-methionine-dependent
cds_wt_2316	-	methyltransferase MAV_4444;
cds_wt_2317	proB	Uncharacterized protein ybaZ;
cds_wt_2318	proA	glutamate 5-kinase
cds_wt_2319	-	gamma-glutamyl phosphate reductase
cds_wt_2320	moeZ	hypothetical protein predicted by Glimmer/Critica
cds_wt_2321	-	Probable molybdopterin biosynthesis protein moeB;
cds_wt_2322	-	Cortactin-binding protein 2; CortBP2;
cds_wt_2323	-	hypothetical protein
cds_wt_2324	-	2-hydroxy-6-oxononadienedioate/2-hydroxy-6-oxonatrienedioate hydrolase; EC=3.7.1.n1; 2-hydroxy-6-oxonona-2,4-diene-1,9-dioic acid 5,6-hydrolase; 2-hydroxy-6-ketonona-2,4-diene-1,9-dioic acid 5,6-hydrolase; 2-hydroxy-6-oxonona-2,4,7-triene-1,9-dioic acid 5,6-hydrolase;
cds_wt_2325	-	Protein Daple; Dvl-associating protein with a high frequency of leucine residues; hDaple; Coiled-coil domain-containing protein 88C; Hook-related protein 2; HkRP2;
cds_wt_2326	-	HTH-type protein slmA;
cds_wt_2327	rhIE	hypothetical protein
cds_wt_2328	pbsA	ATP-dependent RNA helicase DBP2;
cds_wt_2329	hmuO	Heme oxygenase;
cds_wt_2330	-	Heme oxygenase 1; HO-1;
cds_wt_2331	-	Glutathione S-transferase C-terminal domain-containing protein;
cds_wt_2332	-	hypothetical protein
cds_wt_2333	-	Cation-transporting ATPase pacS;
cds_wt_2334	-	Copper-sensing transcriptional repressor csoR;
cds_wt_2335	-	Copper-sensitive operon repressor;
cds_wt_2336	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2337	-	acetyltransferase, GNAT family
cds_wt_2338	fabG	putative ATP-dependent DNA helicase
		hypothetical protein predicted by Glimmer/Critica
		3-oxoacyl-

cds_wt_2339	prkC	serine/threonine protein kinase
cds_wt_2340	-	conserved hypothetical protein
cds_wt_2341	gno	gluconate 5-dehydrogenase
cds_wt_2342	cbbF	putative inositol monophosphatase
cds_wt_2343	-	Probable transcriptional regulator ycf27; OmpR-like protein;
cds_wt_2344	PHYB	Phytochrome B;
cds_wt_2345	-	Chemotaxis response regulator protein-glutamate methylesterase;
cds_wt_2346	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2347	Fxna	Endoplasmic reticulum metalloproteinase 1; Felix-ina;
cds_wt_2348	-	hypothetical protein
cds_wt_2349	Ogt	UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase 110 kDa subunit; O-linked N-acetylglucosamine transferase 110 kDa subunit; O-GlcNAc transferase subunit p110;
cds_wt_2350	trcR	Alkaline phosphatase synthesis transcriptional regulatory protein sphR;
cds_wt_2351	-	putative two-component system sensor kinase
cds_wt_2352	aroG	phospho-2-dehydro-3-deoxyheptonate aldolase, Phe-sensitive
cds_wt_2353	yycA	Undecaprenyl phosphate-alpha-4-amino-4-deoxy-L-arabinose arabinosyl transferase; Undecaprenyl phosphate-alpha-L-Ara4N transferase; 4-amino-4-deoxy-L-arabinose lipid A transferase; Polymyxin resistance protein pmrK;
cds_wt_2354	DPM1	Dolichol-phosphate mannosyltransferase; Dolichol-phosphate mannose synthase; DPM synthase;
cds_wt_2355	-	Dolichyl-phosphate beta-D-mannosyltransferase; Mannose-P-dolichol synthase; MPD synthase;
cds_wt_2356	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2357	-	hypothetical protein
cds_wt_2358	-	hypothetical protein
cds_wt_2359	-	Alanyl-tRNA synthetase; Alanine--tRNA ligase; AlaRS;
cds_wt_2360	-	3-demethylubiquinone-9 3-methyltransferase; 3,4-dihydroxy-5-hexaprenylbenzoate methyltransferase;
cds_wt_2361	rpfE	DHBB methyltransferase;
cds_wt_2362	-	Trans-acting enoyl reductase;
cds_wt_2363	-	putative secreted protein
cds_wt_2364	nuc2	hypothetical protein
cds_wt_2365	-	Probable RuBisCO transcriptional regulator;
cds_wt_2366	yheB	hypothetical protein
cds_wt_2367	-	Collagen alpha-5
cds_wt_2368	toxB	chitinase
cds_wt_2369	ribG	Phytochrome-like protein cph2; Bacteriophytochrome cph2;
cds_wt_2370	-	GTP cyclohydrolase II
		5-amino-6-(5-phosphoribosylamino)uracil reductase
		Transcriptional repressor mprA; Protein emrR;

cds_wt_2371	-	putative secreted protein Cholinesterase; Acylcholine acylhydrolase; Choline esterase II; Butyrylcholine esterase;
cds_wt_2372	BCHE	Pseudocholinesterase;
cds_wt_2373	-	HTH-type transcriptional regulator betI;
cds_wt_2374	ydfJ	Membrane protein ydfJ;
cds_wt_2375	pip	Phage infection protein;
cds_wt_2376	-	hypothetical protein predicted by Glimmer/Critica Teneurin-3; Ten-3; Tenascin-M3; Ten-m3; Protein Odd Oz/ten-m homolog 3;
cds_wt_2377	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2378	-	RNA polymerase sigma-H factor; Sigma-30;
cds_wt_2379	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2380	-	Cellulose synthesis regulatory protein;
cds_wt_2381	-	Bacillolysin; Neutral protease;
cds_wt_2382	-	Uncharacterized signaling protein PA1727;
cds_wt_2383	pleD	hypothetical protein predicted by Glimmer/Critica
cds_wt_2384	-	ADIPOR-like receptor CG5315;
cds_wt_2385	-	GPI mannosyltransferase 2; GPI mannosyltransferase II; GPI-MT-II; Glycosylphosphatidylinositol-anchor biosynthesis protein 18;
cds_wt_2386	-	RNA polymerase sigma factor sigW; Sigma-W factor;
cds_wt_2387	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2388	-	HTH-type transcriptional repressor yvoA;
cds_wt_2389	gntR	deoxyribose-phosphate aldolase
cds_wt_2390	deoC	Inter-alpha-trypsin inhibitor heavy chain H5; Inter-alpha-inhibitor heavy chain 5; ITI heavy chain H5;
cds_wt_2391	ywmD	hypothetical protein
cds_wt_2392	-	ribonucleoside-diphosphate reductase, beta subunit
cds_wt_2393	nrdB	ribonucleoside-diphosphate reductase alpha chain
cds_wt_2394	nrdA	hypothetical protein predicted by Glimmer/Critica
cds_wt_2395	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2396	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2397	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2398	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2399	-	putative hydrolase (putative secreted protein)
cds_wt_2400	-	UPF0309 protein GTNG_1302; Glucosamine--fructose-6-phosphate aminotransferase
cds_wt_2401	rpiR	hypothetical protein predicted by Glimmer/Critica
cds_wt_2402	-	Regulatory protein afsR;
cds_wt_2403	-	putative ABC transporter ATP-binding protein
cds_wt_2404	modC	Probable sulfate transport system permease protein cysT;
cds_wt_2405	cysT	Molybdate/tungstate-binding protein wtpA;
cds_wt_2406	modA	Molybdenum import ATP-binding protein modC;
cds_wt_2407	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2408	-	Hexose transporter 2;
cds_wt_2409	KHT2	UDP-glucose 4-epimerase
cds_wt_2410	rfaD	Poly
cds_wt_2411	-	

cds_wt_2412	tlpB	Putative sensory transducer protein;
cds_wt_2413	-	Uncharacterized protein R00370;
cds_wt_2414	celR	HTH-type transcriptional regulator celR;
cds_wt_2415	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2416	sahH	putative S-adenosyl-L-homocysteine hydrolase
cds_wt_2417	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2418	-	Sodium/hydrogen exchanger 2; Na
		putative ABC-2 type transport system permease
cds_wt_2419	yjjD	protein
		Spermidine/putrescine import ATP-binding protein
cds_wt_2420	-	potA;
cds_wt_2421	mtrR	HTH-type transcriptional regulator mtrR;
		Membrane-bound lytic murein transglycosylase F;
cds_wt_2422	aotJ	EC=4.2.2.n1; Murein lyase F;
cds_wt_2423	-	hypothetical protein
cds_wt_2424	-	hypothetical protein
cds_wt_2425	frcA	putative ATP-binding ABC transporter protein
		Autoinducer 2 import system permease protein lsrC;
cds_wt_2426	lsrC	AI-2 import system permease protein lsrC;
		HTH-type transcriptional repressor purR; Purine
		nucleotide synthesis repressor; Pur regulon
		repressor;
cds_wt_2427	rbsB	
cds_wt_2428	nedA	Sialidase; Neuraminidase;
cds_wt_2429	glyA	serine hydroxymethyltransferase
cds_wt_2430	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2431	sigF	RNA polymerase sigma factor rpoD; Sigma-70;
cds_wt_2432	-	Uncharacterized membrane protein Mb2670;
cds_wt_2433	-	probable short-chain type dehydrogenase/reductase
cds_wt_2434	-	putative membrane protein
cds_wt_2435	chiD	chitinase
		Voltage-dependent N-type calcium channel subunit
		alpha-1B; Voltage-gated calcium channel subunit
cds_wt_2436	-	alpha Cav2.2; Calcium channel, L type, alpha-1
		polypeptide isoform 5; Brain calcium channel III; BIII;
		Uncharacterized HTH-type transcriptional regulator
cds_wt_2437	-	ML2140;
cds_wt_2438	-	Uncharacterized MFS-type transporter yusP;
		Transmembrane and TPR repeat-containing protein
cds_wt_2439	-	4;
		UDP-N-acetylglucosamine--peptide N-
		acetylglucosaminyltransferase 110 kDa subunit; O-
cds_wt_2440	Ogt	linked N-acetylglucosamine transferase 110 kDa
cds_wt_2441	-	subunit; O-GlcNAc transferase subunit p110;
		hypothetical protein
		Transmembrane protein 165; Transmembrane
cds_wt_2442	-	protein TPAL; Transmembrane protein PT27;
cds_wt_2443	slpD	putative secreted peptidase
cds_wt_2444	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2445	-	Multidrug resistance protein mdtL;
cds_wt_2446	mcbR	HTH-type transcriptional regulator betI;

cds_wt_2447	-	UPF0104 membrane protein MJ1078;
cds_wt_2448	ndh3	putative dehydrogenase
cds_wt_2449	-	High-affinity glutamine permease;
cds_wt_2450	-	hypothetical protein
cds_wt_2451	yhdV	Protein crcB homolog;
cds_wt_2452	crcB	Protein crcB homolog;
cds_wt_2453	-	Membrane protein ydfJ;
cds_wt_2454	-	Response regulator gacA; Global activator;
cds_wt_2455	-	Sensor protein kdpD;
cds_wt_2456	-	quinone oxidoreductase
cds_wt_2457	ETR1	Ethylene receptor;
cds_wt_2458	-	Putative multidrug resistance protein mdtD;
cds_wt_2459	mccF	Microcin C7 self-immunity protein mccF;
cds_wt_2460	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2461	sigL	RNA polymerase sigma factor sigX;
		Liprin-alpha-3; Protein tyrosine phosphatase receptor
		type f polypeptide-interacting protein alpha-3;
cds_wt_2462	-	PTPRF-interacting protein alpha-3;
		Cysteine dioxygenase type 1; Cysteine dioxygenase
cds_wt_2463	CDO1	type I; CDO-I; CDO;
cds_wt_2464	-	UPF0176 protein Ava_2825;
cds_wt_2465	tetR	Tetracycline repressor protein class H;
cds_wt_2466	-	Probable actinorhodin transporter;
cds_wt_2467	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2468	nadR	transcriptional regulator NadR
cds_wt_2469	-	hypothetical protein predicted by Glimmer/Critica
		Uncharacterized HTH-type transcriptional regulator
cds_wt_2470	ydeS	ydeS;
cds_wt_2471	rfbA	O-antigen export system permease protein rfbA;
cds_wt_2472	tagH	putative ABC transporter ATP-binding protein
cds_wt_2473	-	conserved hypothetical protein
cds_wt_2474	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2475	-	putative trehalose/maltose hydrolase
cds_wt_2476	-	probable hydrolase
cds_wt_2477	-	hypothetical protein
		Spermidine/putrescine import ATP-binding protein
cds_wt_2478	msmK	potA;
cds_wt_2479	-	hypothetical protein
cds_wt_2480	-	putative secreted protein
cds_wt_2481	-	glutaryl-CoA dehydrogenase
cds_wt_2482	-	hypothetical protein
cds_wt_2483	-	NADPH-dependent oxidoreductase;
cds_wt_2484	yihR	putative aldose-1-epimerase
cds_wt_2485	-	Enterobactin exporter entS;
cds_wt_2486	pdxH	pyridoxamine 5'-phosphate oxidase
cds_wt_2487	citA	citrate synthase
cds_wt_2488	serC	phosphoserine aminotransferase
cds_wt_2489	-	Uncharacterized protein Mb0907c;
cds_wt_2490	-	UPF0477 protein BT9727_1129;
cds_wt_2491	-	hypothetical protein predicted by Glimmer/Critica

cds_wt_2492	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2493	pimH	Uncharacterized MFS-type transporter yfiS;
cds_wt_2494	marR	Multiple antibiotic resistance protein marR;
cds_wt_2495	pbuG	Putative xanthine/uracil permease C887.17;
cds_wt_2496	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2497	tetV	Probable glucose transporter HXT5;
cds_wt_2498	-	Uncharacterized protein Mb0901;
cds_wt_2499	-	Uncharacterized protein ML2143;
		Purine nucleoside phosphorylase deoD-type 2; PNP
cds_wt_2500	-	2;
cds_wt_2501	mosC	Membrane protein mosC;
cds_wt_2502	-	HTH-type transcriptional regulator betI;
cds_wt_2503	bglA	putative beta-glucosidase
cds_wt_2504	-	hypothetical protein
cds_wt_2505	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2506	-	hypothetical protein
		Y-box-binding protein 2; Germ cell-specific Y-box-
		binding protein; Contrin; MSY2 homolog; DNA-
cds_wt_2507	cspB	binding protein C; Dbpc;
cds_wt_2508	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2509	-	hypothetical protein
cds_wt_2510	-	hypothetical protein predicted by Glimmer/Critica
		DNA repair helicase RAD25; General transcription
		and DNA repair factor IIH subunit RAD25; TFIIH
cds_wt_2511	xpbC	subunit RAD25;
cds_wt_2512	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2513	X	Uncharacterized protein X;
cds_wt_2514	-	Uncharacterized MFS-type transporter yfiS;
cds_wt_2515	mutT	RNA pyrophosphohydrolase;
cds_wt_2516	ku2	Accumulation-associated protein;
cds_wt_2517	ligD	hypothetical protein
cds_wt_2518	-	putative DNA-binding protein
cds_wt_2519	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2520	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2521	-	putative DNA-binding protein
cds_wt_2522	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2523	-	hypothetical protein predicted by Glimmer/Critica
		Digeranylgeranylglycerophospholipid reductase 2;
		DGGGPL reductase 2; 2,3-di-O-
		geranylgeranylglyceryl phosphate reductase 2;
cds_wt_2524	-	Geranylgeranyl reductase 2; GGR 2;
cds_wt_2525	-	hypothetical protein predicted by Glimmer/Critica
		Indian hedgehog protein; IHH; HHG-2; Contains:
		Indian hedgehog protein N-product; Contains: Indian
cds_wt_2526	lhh	hedgehog protein C-product;
cds_wt_2527	-	Laminin subunit beta-1; Laminin B1 chain;
cds_wt_2528	aprX	alkaline serine protease
cds_wt_2529	-	hypothetical protein
cds_wt_2530	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2531	-	hypothetical protein predicted by Glimmer/Critica

cds_wt_2532	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2533	-	Stage 0 sporulation protein yaaT;
cds_wt_2534	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2535	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2536	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2537	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2538	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2539	holB	DNA polymerase III, delta' subunit
cds_wt_2540	xynA	putative glycosyl hydrolase
cds_wt_2541	tmk	thymidylate kinase
cds_wt_2542	-	Uncharacterized protein YGL196W;
cds_wt_2543	-	HTH-type transcriptional regulator betI;
cds_wt_2544	GULO	probable oxidoreductase
cds_wt_2545	topA	DNA topoisomerase I
cds_wt_2546	-	hypothetical protein
cds_wt_2547	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2548	ppa	inorganic H ⁺ pyrophosphatase
cds_wt_2549	-	putative anti-sigma factor
cds_wt_2550	rsbV	Anti-sigma-B factor antagonist; Anti-anti-sigma-B factor;
cds_wt_2551	-	Putative ATP-dependent helicase HRQ1;
cds_wt_2552	-	Homologous to recQ protein 1;
cds_wt_2553	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2554	-	hypothetical protein
cds_wt_2555	-	putative membrane protein
cds_wt_2556	cpaF	Chaperone protein clpB 1;
cds_wt_2557	-	Anti-sigma F factor antagonist; Stage II sporulation protein AA;
cds_wt_2558	ssgB	hypothetical protein
cds_wt_2559	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2560	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2561	-	hypothetical protein
cds_wt_2562	acoE	acetyl-coenzyme A synthetase
cds_wt_2563	ina	immune inhibitor A metalloprotease
cds_wt_2564	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2565	ephE	putative hydrolase
cds_wt_2566	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2567	-	Collagen alpha-2
cds_wt_2568	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2569	-	Cortactin-binding protein 2; CortBP2;
cds_wt_2570	-	Uncharacterized protein SCO3922;
cds_wt_2571	rarD	Protein rarD;
cds_wt_2572	-	hypothetical protein
cds_wt_2573	yagl	Acetate operon repressor;
cds_wt_2574	grcC	geranylgeranyl pyrophosphate synthase
cds_wt_2575	nuoN	NADH dehydrogenase I chain N
cds_wt_2576	nuoL	NADH dehydrogenase I chain L
cds_wt_2577	nuoK	NADH dehydrogenase I chain K
cds_wt_2578	nuoJ	NADH dehydrogenase I chain J
cds_wt_2579	nuoI	NADH dehydrogenase I chain I

cds_wt_2579	nuoH	NADH dehydrogenase I chain H
cds_wt_2580	nuoG	NADH dehydrogenase I chain G
cds_wt_2581	nuoF	NADH dehydrogenase I chain F
cds_wt_2582	nuoE	NADH dehydrogenase I chain E
cds_wt_2583	nuoD	NADH dehydrogenase I chain D
cds_wt_2584	nuoC	NADH dehydrogenase I chain C
cds_wt_2585	nuoB	NADH dehydrogenase I chain B
cds_wt_2586	nuoA	NADH dehydrogenase I chain A
cds_wt_2587	-	putative electron transfer oxidoreductase
cds_wt_2588	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2589	ubiE	putative ubiquinone/menaquinone methyltransferase
cds_wt_2590	-	FO synthase subunit 2 1; 7,8-didemethyl-8-hydroxy-5-deazariboflavin synthase subunit 2 1;
cds_wt_2591	tetR	Tetracycline repressor protein class E;
cds_wt_2592	-	hypothetical protein
cds_wt_2593	helZ	DEAD/DEAH box helicase-like
cds_wt_2594	-	hypothetical protein
cds_wt_2595	mocA	oxidoreductase
cds_wt_2596	-	hypothetical protein
cds_wt_2597	mef	Multidrug resistance protein mdtG;
cds_wt_2598	-	putative ArsR-family transcriptional regulator
cds_wt_2599	mer	F420-dependent N5,N10-methylene-tetrahydromethanopterin reductase
cds_wt_2600	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2601	dnrV	27 kDa antigen Cfp30B;
cds_wt_2602	-	Acetyltransferase ECA0875;
cds_wt_2603	fliQ	Flagellar biosynthetic protein fliQ;
cds_wt_2604	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2605	fhuC	ATP-binding protein of iron(III) ABC transporter
cds_wt_2606	fecD	Vitamin B12 import system permease protein btuC;
cds_wt_2607	yvrC	Vitamin B12-binding protein;
cds_wt_2608	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2609	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2610	-	FO synthase subunit 2 1; 7,8-didemethyl-8-hydroxy-5-deazariboflavin synthase subunit 2 1;
cds_wt_2611	-	DNA ligase; Polydeoxyribonucleotide synthase
cds_wt_2612	-	Vascular endothelial zinc finger 1; Zinc finger protein 161; Putative transcription factor DB1;
cds_wt_2613	DDX5	Probable ATP-dependent RNA helicase DDX5;
cds_wt_2614	-	DEAD box protein 5;
cds_wt_2615	-	hypothetical protein
cds_wt_2616	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2617	lrp	Leucine-responsive regulatory protein;
cds_wt_2618	-	Chromosome-anchoring protein racA;
cds_wt_2619	ubiX	3-octaprenyl-4-hydroxybenzoate carboxy-lyase
cds_wt_2620	ubiA	4-hydroxybenzoate octaprenyltransferase
cds_wt_2621	yigC	3-octaprenyl-4-hydroxybenzoate carboxy-lyase
cds_wt_2622	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2623	ccsA	Cytochrome c biogenesis protein ccsA;
	ccsB	cytochrome c biogenesis protein

cds_wt_2624	ccdA	Thiol:disulfide interchange protein dsbD; Protein-
cds_wt_2625	-	disulfide reductase; Disulfide reductase;
		hypothetical protein
		2,3-bisphosphoglycerate-dependent
cds_wt_2626	-	phosphoglycerate mutase; Phosphoglyceromutase;
cds_wt_2627	hemL	PGAM; BPG-dependent PGAM; dPGM;
		glutamate-1-semialdehyde 2,1-aminomutase
cds_wt_2628	-	Anti-sigma F factor antagonist; Stage II sporulation
cds_wt_2629	-	protein AA;
cds_wt_2630	sigE	hypothetical protein
		RNA polymerase sigma factor sigW; Sigma-W factor;
		Alpha-N-arabinofuranosidase 1; Alpha-N-
cds_wt_2631	yvpA	arabinofuranosidase I; Arabinosidase I; Alpha-N-
		AFase I;
cds_wt_2632	-	Chemotaxis response regulator protein-glutamate
cds_wt_2633	dhkJ	methylesterase;
		GAF sensor hybrid histidine kinase
cds_wt_2634	prpK	Phosphoserine phosphatase rsbU; Sigma factor sigB
cds_wt_2635	yudH	regulation protein rsbU;
cds_wt_2636	-	Uncharacterized protein ywjB;
		Uncharacterized protein ywjB;
cds_wt_2637	-	Alkyldihydroxyacetonephosphate synthase; Alkyl-
cds_wt_2638	ptrB	DHAP synthase; Alkylglycerone-phosphate synthase;
cds_wt_2639	-	protease II
cds_wt_2640	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2641	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2642	-	Uncharacterized protein Rv0093c/MT0102;
cds_wt_2643	mscL	hypothetical protein predicted by Glimmer/Critica
		Large-conductance mechanosensitive channel;
cds_wt_2644	rsbV	Anti-sigma F factor antagonist; Stage II sporulation
cds_wt_2645	rsbR	protein AA;
cds_wt_2646	rsbS	positive regulator of sigma-B
cds_wt_2647	rsbT	negative regulator of sigma-B
		Anti-sigma F factor; Stage II sporulation protein AB;
cds_wt_2648	-	Phosphoserine phosphatase rsbU; Sigma factor sigB
cds_wt_2649	-	regulation protein rsbU;
		Sensor histidine kinase mtrB;
		Acetoacetate metabolism regulatory protein atoC;
cds_wt_2650	prpD	Ornithine/arginine decarboxylase inhibitor; Ornithine
		decarboxylase antizyme;
		Integrin alpha-V; Vitronectin receptor subunit alpha;
cds_wt_2651	-	AltName: CD_antigen=CD51; Contains: Integrin
cds_wt_2652	-	alpha-V heavy chain; Contains: Integrin alpha-V light
cds_wt_2653	-	chain;
		hypothetical protein predicted by Glimmer/Critica
		hypothetical protein
cds_wt_2654	lolD	Spermidine/putrescine import ATP-binding protein
cds_wt_2655	-	potA;
cds_wt_2656	-	hypothetical protein
		hypothetical protein predicted by Glimmer/Critica

cds_wt_2657	thrS	threonyl-tRNA synthetase
cds_wt_2658	tetA	Tetracycline resistance protein, class B; TetA
		Gamma-butyrobetaine dioxygenase; Gamma-butyrobetaine,2-oxoglutarate dioxygenase; Gamma-butyrobetaine hydroxylase; Gamma-BBH;
cds_wt_2659	-	
cds_wt_2660	mocD	Omega-3 fatty acid desaturase, chloroplastic;
cds_wt_2661	Prr6	hypothetical protein
cds_wt_2662	-	hypothetical protein
cds_wt_2663	-	hypothetical protein
cds_wt_2664	-	Carboxylate-amine ligase Mmcs_0573;
cds_wt_2665	-	RNA polymerase sigma factor rpoD; Sigma-42;
cds_wt_2666	rsbU	Uncharacterized protein Rv1364c/MT1410;
cds_wt_2667	-	Carboxylate-amine ligase RoseRS_2615;
cds_wt_2668	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2669	-	Uncharacterized protein DR_0705;
cds_wt_2670	rmd	putative NDP-hexose 4-ketoreductase
cds_wt_2671	mpg2	nucleotidyltransferase family protein
cds_wt_2672	-	putative UDP-glucose 4-epimerase
cds_wt_2673	-	hypothetical protein
cds_wt_2674	icsA	Glycogen synthase; Starch
cds_wt_2675	-	hypothetical protein
cds_wt_2676	-	hypothetical protein 2SCK36.03c
cds_wt_2677	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2678	-	hypothetical protein predicted by Glimmer/Critica
		Abrin-b; Contains: Abrin-b A chain; rRNA N-glycosidase; Contains: Linker peptide; Contains: Abrin-b B chain;
cds_wt_2679	-	
cds_wt_2680	int7	ICEBs1 integrase;
cds_wt_2681	int7	Tyrosine recombinase xerC;
cds_wt_2682	copB	Copper resistance protein B;
cds_wt_2683	-	Uncharacterized protein L153;
cds_wt_2684	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2685	Cbs	cysteine synthase
cds_wt_2686	yceL	Multidrug resistance protein mdtH;
cds_wt_2687	-	Uncharacterized protein Rv2715/MT2788;
		Glycyl-glycine endopeptidase ALE-1; Staphylolytic enzyme ALE-1;
cds_wt_2688	-	
cds_wt_2689	-	Uncharacterized lipoprotein yafL;
cds_wt_2690	-	hypothetical protein predicted by Glimmer/Critica
		Ubiquinone/menaquinone biosynthesis
cds_wt_2691	-	methyltransferase ubiE;
		HTH-type transcriptional regulator hmrR; Copper efflux regulator; Copper export regulator;
cds_wt_2692	merR	
cds_wt_2693	-	sensor histidine kinase
		Response regulator mprA; Mycobacterial persistence regulator A;
cds_wt_2694	tcrA	
cds_wt_2695	bcrC	Uncharacterized protein ywoA;
cds_wt_2696	yhch	Ribose import ATP-binding protein rbsA;
cds_wt_2697	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2698	-	hypothetical protein predicted by Glimmer/Critica

cds_wt_2699	tnp	Transposase for insertion sequence element ISRM3;
cds_wt_2700	-	membrane protein, putative
cds_wt_2701	-	hypothetical protein
cds_wt_2702	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2703	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2704	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2705	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2706	-	hypothetical protein
		Phytochrome-like protein cph2; Bacteriophytochrome
cds_wt_2707	-	cph2;
cds_wt_2708	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2709	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2710	-	hypothetical protein
cds_wt_2711	-	NADH-dependent flavin oxidoreductase, Oye family
cds_wt_2712	-	HTH-type transcriptional regulator betI;
cds_wt_2713	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2714	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2715	-	hypothetical protein predicted by Glimmer/Critica
		Serine-protein kinase rsbW; Anti-sigma-B factor;
cds_wt_2716	prsR	Sigma-B negative effector rsbW;
cds_wt_2717	PHYB	two-component hybrid sensor and regulator
cds_wt_2718	-	hypothetical protein predicted by Glimmer/Critica

		Replicase polyprotein 1ab; pp1ab; ORF1ab
		polyprotein; Contains: Non-structural protein 1; nsp1;
		p28; Contains: Non-structural protein 2; nsp2; p65;
		Contains: Non-structural protein 3; nsp3; Papain-like
		proteinases 1/2; PL1-PRO/PL2-PRO; p210;
		Contains: Non-structural protein 4; nsp4; Peptide
		HD2; p44; Contains: 3C-like proteinase; 3CL-PRO;
		3CLp; M-PRO; p27; nsp5; Contains: Non-structural
		protein 6; nsp6; Contains: Non-structural protein 7;
		nsp7; p10; Contains: Non-structural protein 8; nsp8;
		p22; Contains: Non-structural protein 9; nsp9; p12;
		Contains: Non-structural protein 10; nsp10; Growth
		factor-like peptide; GFL; p15; Contains: RNA-directed
		RNA polymerase; RdRp; Pol; p100; nsp12; Contains:
		Helicase; Hel; p67; nsp13; Contains:
		Exoribonuclease; ExoN; nsp14; Contains: Uridylate-
		specific endoribonuclease; NendoU; nsp15; p35;
cds_wt_2719	cbp	Contains: Putative 2'-O-methyl transferase; nsp16;
cds_wt_2720	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2721	-	hypothetical protein
cds_wt_2722	-	UPF0059 membrane protein ECA2389;
cds_wt_2723	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2724	-	Transposase B from transposon Tn554;
cds_wt_2725	-	Uncharacterized protein F42H10.9;
cds_wt_2726	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2727	-	Uncharacterized protein y4kF;
cds_wt_2728	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2729	-	hypothetical protein predicted by Glimmer/Critica

cds_wt_2730	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2731	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2732	-	Transposase for insertion sequence element IS1106;
cds_wt_2733	-	ORF 1;
cds_wt_2734	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2735	xerC	hypothetical protein predicted by Glimmer/Critica
cds_wt_2736	-	Tyrosine recombinase xerC;
cds_wt_2737	-	site-specific recombinase, phage integrase family
cds_wt_2738	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2739	-	Tyrosine recombinase xerC;
cds_wt_2740	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2741	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2742	sodA	hypothetical protein predicted by Glimmer/Critica
cds_wt_2743	-	superoxide dismutase
cds_wt_2744	-	D-alanyl-D-alanine carboxypeptidase; DD-peptidase;
cds_wt_2745	-	DD-carboxypeptidase;
cds_wt_2746	-	putative membrane protein
cds_wt_2747	NAS3	hypothetical protein predicted by Glimmer/Critica
cds_wt_2748	-	hypothetical protein
cds_wt_2749	-	hypothetical protein
cds_wt_2750	-	Urease subunit alpha; Urea amidohydrolase subunit
cds_wt_2751	ycgR	alpha;
cds_wt_2752	cadC	hypothetical protein predicted by Glimmer/Critica
cds_wt_2753	mtsB	UPF0703 protein ycgQ;
cds_wt_2754	mntD	UPF0718 protein ycgR;
cds_wt_2755	mntB	Cadmium efflux system accessory protein;
cds_wt_2756	psaA	Chelated iron transport system membrane protein
cds_wt_2757	-	yfeD;
cds_wt_2758	int7	Chelated iron transport system membrane protein
cds_wt_2759	sigY	yfeD;
cds_wt_2760	pknB	Sulfate/thiosulfate import ATP-binding protein cysA;
cds_wt_2761	-	Sulfate-transporting ATPase;
cds_wt_2762	phy	Manganese ABC transporter substrate-binding
cds_wt_2763	phrB	lipoprotein; Pneumococcal surface adhesin A;
cds_wt_2764	crtB	hypothetical protein predicted by Glimmer/Critica
cds_wt_2765	-	Tyrosine recombinase xerD;
cds_wt_2766	crtl	RNA polymerase sigma-E factor; Sigma-24;
cds_wt_2767	mvaD	serine/threonine protein kinase
cds_wt_2768	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2769	-	probable phytase
cds_wt_2770	-	deoxyribodipyrimidine photolyase
cds_wt_2771	-	phytoene synthase
cds_wt_2772	-	putative polyprenyl synthase
		putative phytoene desaturase
		putative isopentenyl-diphosphate delta-isomerase
		Histone deacetylase 1; HD1;
		putative transcriptional regulator
		hypothetical protein predicted by Glimmer/Critica
		hypothetical protein predicted by Glimmer/Critica
		UPF0152 protein PM0788;

cds_wt_2773	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2774	-	putative integral membrane protein
cds_wt_2775	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2776	kptA	probable RNA 2'-phosphotransferase
		3-demethylubiquinone-9 3-methyltransferase; 3,4-dihydroxy-5-hexaprenylbenzoate methyltransferase; DHHB methyltransferase;
cds_wt_2777	-	
cds_wt_2778	-	Uncharacterized protein MJ0014;
cds_wt_2779	-	Uncharacterized protein SCO4090;
cds_wt_2780	dhIE	leucine dehydrogenase
cds_wt_2781	-	hypothetical protein
cds_wt_2782	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2783	aslB	Uncharacterized protein slI1766;
cds_wt_2784	purM	phosphoribosylformylglycinamide cyclo-ligase
cds_wt_2785	purF	amidophosphoribosyltransferase
cds_wt_2786	-	hypothetical protein
cds_wt_2787	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2788	-	Glutamate
cds_wt_2789	purL	phosphoribosylformylglycinamide synthase II
cds_wt_2790	purQ	phosphoribosylformylglycinamide synthase I
cds_wt_2791	purS	hypothetical protein
cds_wt_2792	purB	adenylosuccinate lyase
cds_wt_2793	-	Arsenical resistance operon repressor;
cds_wt_2794	-	Hydroxysteroid dehydrogenase-like protein 2;
cds_wt_2795	purD	phosphoribosylamine-glycine ligase
cds_wt_2796	purA	adenylosuccinate synthetase
cds_wt_2797	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2798	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2799	-	hypothetical protein
cds_wt_2800	yegU	putative ADP-ribosylglycohydrolase
cds_wt_2801	-	hypothetical protein
cds_wt_2802	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2803	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2804	fba	fructose-bisphosphate aldolase
cds_wt_2805	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2806	-	UPF0486 protein C1orf59;
cds_wt_2807	prpA	putative phosphatase
cds_wt_2808	-	Uncharacterized membrane protein Rv0364/MT0380;
cds_wt_2809	fucA	fucose-1-phosphate aldolase
		Cadmium efflux system accessory protein; Cadmium resistance regulatory protein;
cds_wt_2810	arsR	
cds_wt_2811	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2812	-	Collagen alpha-4
cds_wt_2813	-	Cortactin-binding protein 2; CortBP2;
cds_wt_2814	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2815	clpB	ATPase
cds_wt_2816	setA	Sugar efflux transporter B;
cds_wt_2817	-	K(+)/H(+) antiporter subunit khtT;
		Glutathione-regulated potassium-efflux system protein kefB; K
cds_wt_2818	-	

cds_wt_2819	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2820	hspR	Probable heavy metal-dependent transcriptional regulator HI0293;
cds_wt_2821	dnaJ	Chaperone protein dnaJ;
cds_wt_2822	grpE	Protein grpE; HSP-70 cofactor;
cds_wt_2823	dnaK	Chaperone protein dnaK; Heat shock protein 70;
cds_wt_2824	-	Heat shock 70 kDa protein; HSP70;
cds_wt_2825	-	putative ABC transporter
cds_wt_2826	-	putative ATP-binding membrane protein
cds_wt_2827	-	putative ABC transporter
cds_wt_2828	-	hypothetical protein
cds_wt_2829	-	Putative surface-exposed virulence protein bigA;
cds_wt_2830	pdhA	FERM, RhoGEF and pleckstrin domain-containing protein 1;
cds_wt_2831	pdhB	pyruvate dehydrogenase E1 component, alpha subunit
cds_wt_2832	pdhC	putative branched-chain alpha keto acid dehydrogenase E1 beta subunit
cds_wt_2833	-	putative dihydrolipoamide acyltransferase component
cds_wt_2834	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2835	-	Collagen alpha-2
cds_wt_2836	brpL	NHL repeat-containing protein 2;
cds_wt_2837	-	RNA polymerase sigma-E factor; Sigma-24;
cds_wt_2838	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2839	-	UPF0271 protein PYRAB09930;
cds_wt_2840	sixA	ADIPOR-like receptor CG5315;
cds_wt_2841	-	Phosphoglycerate mutase family member 5 homolog;
cds_wt_2842	-	putative acyl-CoA dehydrogenase
cds_wt_2843	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2844	-	Phosphoserine phosphatase rsbU; Sigma factor sigB
cds_wt_2845	-	regulation protein rsbU;
cds_wt_2846	-	Adenine phosphoribosyltransferase; APRT;
cds_wt_2847	dcd	uncharacterized conserved protein, YCII family
cds_wt_2848	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2849	-	deoxycytidine triphosphate deaminase
cds_wt_2850	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2851	-	UPF0053 protein yugS;
cds_wt_2852	whiP	UPF0053 protein yugS;
cds_wt_2853	-	putative iron-sulphur-binding reductase
cds_wt_2854	-	UPF0233 membrane protein whiP;
cds_wt_2855	Zan	Uncharacterized protein ylxX;
cds_wt_2856	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2857	pabA	para-aminobenzoate synthetase component II
cds_wt_2858	pknB	putative serine/threonine protein kinase
cds_wt_2859	pknA	putative serine/threonine protein kinase
cds_wt_2860	pbpA	putative penicillin-binding protein
cds_wt_2861	rodA	Probable cell division protein ftsW;
cds_wt_2862	ppp	possible serine/threonine phosphatase ppp

cds_wt_2863	-	Oxoglutarate dehydrogenase inhibitor;
cds_wt_2864	-	Oxoglutarate dehydrogenase inhibitor;
cds_wt_2865	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2866	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2867	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2868	-	hypothetical protein
cds_wt_2869	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2870	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2871	-	Hansenula MRAKII killer toxin-resistant protein 1;
cds_wt_2872	-	Protein ycel;
cds_wt_2873	marR	Uncharacterized HTH-type transcriptional regulator ykoM;
cds_wt_2874	luxR	Uncharacterized protein Mb0918;
cds_wt_2875	-	acyl-CoA dehydrogenase
cds_wt_2876	yngE	carboxyl transferase domain protein
cds_wt_2877	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2878	-	Polycystic kidney disease protein 1-like 3; Polycystin-1L3; PC1-like 3 protein;
cds_wt_2879	yngG	hydroxymethylglutaryl-CoA lyase
cds_wt_2880	pcc	pyruvate carboxylase, subunit A
cds_wt_2881	-	HTH-type transcriptional regulator betI;
cds_wt_2882	-	hypothetical protein
cds_wt_2883	htpG	Chaperone protein htpG; Heat shock protein htpG;
cds_wt_2884	sseA	High temperature protein G;
cds_wt_2885	-	thiosulfate sulfurtransferase
cds_wt_2886	-	Arylesterase; Aryl-ester hydrolase;
cds_wt_2887	sufE	Probable phosphosugar isomerase HI1678;
cds_wt_2888	frnE	Cysteine desulfuration protein sufE;
cds_wt_2889	-	polyketide synthase
cds_wt_2890	-	hypothetical protein
cds_wt_2891	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2892	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2893	-	RNA pyrophosphohydrolase;
cds_wt_2894	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2895	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2896	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2897	-	Sensor histidine kinase comP;
cds_wt_2898	-	Transcriptional regulatory protein degU; Protease production enhancer protein;
cds_wt_2899	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2900	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2901	-	Uncharacterized protein Rv0007/MT0007;
cds_wt_2902	gyrA	hypothetical protein predicted by Glimmer/Critica
cds_wt_2903	gyrB	DNA gyrase subunit A
cds_wt_2904	-	DNA gyrase subunit B
cds_wt_2905	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2906	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2907	recF	UPF0232 protein ML0004;
cds_wt_2908	gnd	DNA replication and repair protein recF;
		6-phosphogluconate dehydrogenase

cds_wt_2909	dnaN	DNA polymerase III, beta chain
cds_wt_2910	dnaA	Chromosomal replication initiator protein dnaA;
cds_wt_2911	rpmH	50S ribosomal protein L34;
cds_wt_2912	rnpA	ribonuclease P protein component
cds_wt_2913	-	Inner membrane protein oxaA;
cds_wt_2914	jag	Protein jag;
cds_wt_2915	gidB	glucose-inhibited division protein B
cds_wt_2916	parA	Sporulation initiation inhibitor protein soj;
cds_wt_2917	parB	Probable chromosome-partitioning protein parB;
cds_wt_2918	-	putative membrane protein
cds_wt_2919	-	Serine/threonine-protein kinase hal4; Halotolerance protein 4; Serine/threonine-protein kinase ppk10;
cds_wt_2920	ddlB	D-alanine--D-alanine ligase
cds_wt_2921	avtA	valine-pyruvate aminotransferase
cds_wt_2922	-	hypothetical protein
cds_wt_2923	cwlM	putative hydrolase
cds_wt_2924	trxA	Thioredoxin-1; Trx-1; Thioredoxin-M;
cds_wt_2925	trxB	thioredoxin reductase
cds_wt_2926	sigM	RNA polymerase sigma-H factor; Sigma-30;
cds_wt_2927	pkaF	hypothetical protein
cds_wt_2928	-	Virulence factor mviN;
cds_wt_2929	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2930	pcnA	putative tRNA nucleotidyltransferase
cds_wt_2931	-	Uncharacterized WD repeat-containing protein alr3466;
cds_wt_2932	sigE	RNA polymerase sigma-E factor;
cds_wt_2933	-	hypothetical protein
cds_wt_2934	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2935	ogt	methylated-DNA--protein-cysteine methyltransferase
cds_wt_2936	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2937	-	putative secreted protein
cds_wt_2938	-	Capsule biosynthesis protein capC;
cds_wt_2939	capB	PGA synthase capB; Gamma-polyglutamic acid synthase;
cds_wt_2940	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2941	capA	PGA biosynthesis protein capA;
cds_wt_2942	ino1	myo-inositol-1-phosphate synthase
cds_wt_2943	-	Negative transcription regulator padR;
cds_wt_2944	-	Uncharacterized protein Mb0050;
cds_wt_2945	mrcB	penicillin-binding protein
cds_wt_2946	-	GPI mannosyltransferase 1; GPI mannosyltransferase I; GPI-MT-I;
cds_wt_2947	-	Glycosylphosphatidylinositol-anchor biosynthesis protein 14;
cds_wt_2948	end	Collagen alpha-4 endonuclease IV
cds_wt_2949	-	Myosin light chain kinase 2, skeletal/cardiac muscle; MLCK2;
cds_wt_2950	rpsF	30S ribosomal protein S6;

cds_wt_2951	ssb	Single-stranded DNA-binding protein; SSB; Helix-destabilizing protein;
cds_wt_2952	rpsR	30S ribosomal protein S18;
cds_wt_2953	rplI	50S ribosomal protein L9;
cds_wt_2954	-	Polycystic kidney disease protein 1-like 3; Polycystin-1L3; PC1-like 3 protein;
cds_wt_2955	-	Eukaryotic translation initiation factor 3 subunit A; eIF3a; Eukaryotic translation initiation factor 3 subunit 10; eIF-3-theta; eIF3 p167; eIF3 p180; eIF3 p185; p162; Centrosomin;
cds_wt_2956	dnaB	putative replicative DNA helicase
cds_wt_2957	-	UPF0133 protein VF_1686;
cds_wt_2958	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2959	-	putative integral membrane protein
cds_wt_2960	-	Uncharacterized signaling protein PA3311;
cds_wt_2961	moaC	Molybdenum cofactor biosynthesis protein C;
cds_wt_2962	mog	Putative competence-damage inducible protein;
cds_wt_2963	moeA	Molybdopterin biosynthesis protein moeA;
cds_wt_2964	moaE	Molybdenum cofactor synthesis protein 2 large subunit; MPT synthase large subunit; Molybdopterin synthase large subunit; MOCS2B; MOCO1-B;
cds_wt_2965	-	probable conserved integral membrane protein
cds_wt_2966	-	hypothetical protein
cds_wt_2967	-	hypothetical protein
cds_wt_2968	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2969	pilD	Type 4 prepilin-like proteins leader peptide-processing enzyme; Includes: Leader peptidase;
cds_wt_2970	pcrA	Prepilin peptidase; Includes: N-methyltransferase; ATP-dependent DNA helicase, UvrD/REP family
cds_wt_2971	-	Putative metallophosphoesterase FLJ45032
cds_wt_2972	-	homolog;
cds_wt_2973	moaA	hypothetical protein predicted by Glimmer/Critica
cds_wt_2974	-	Probable molybdopterin cofactor synthesis protein A;
cds_wt_2975	-	Uncharacterized protein VV1_2562;
cds_wt_2976	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2977	fdhD	hypothetical protein
		Protein fdhD homolog;
cds_wt_2978	mobA	Bifunctional protein glmU; Includes: UDP-N-acetylglucosamine pyrophosphorylase; N-acetylglucosamine-1-phosphate uridyltransferase; Includes: Glucosamine-1-phosphate N-acetyltransferase;
cds_wt_2979	-	putative molybdopterin-guanine dinucleotide biosynthesis protein
cds_wt_2980	-	hypothetical protein
cds_wt_2981	-	Uncharacterized HTH-type transcriptional regulator PH1519;
cds_wt_2982	-	Arginine deiminase; ADI; Arginine dihydrolase; AD;
cds_wt_2983	-	Uncharacterized protein Mb3809;
cds_wt_2984	-	HMP-PP phosphatase;

cds_wt_2985	-	HMP-PP phosphatase;
cds_wt_2986	serS	seryl-tRNA synthetase
cds_wt_2987	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2988	osmC	Peroxiredoxin osmC; Osmotically-inducible protein C;
cds_wt_2989	-	hypothetical protein
cds_wt_2990	pheA	prephenate dehydratase
		Probable global transcription activator SNF2L2; ATP-dependent helicase SMARCA2; SNF2-alpha; SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 2; hBRM;
cds_wt_2991	-	hypothetical protein
cds_wt_2992	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2993	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2994	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_2995	arcA	arginine deiminase
cds_wt_2996	-	hypothetical protein
cds_wt_2997	PHY1	Phytochrome 1;
cds_wt_2998	glpQ	glycerophosphoryl diester phosphodiesterase
cds_wt_2999	-	Membrane-bound protein lytR;
cds_wt_3000	-	Uncharacterized symporter ywCA;
cds_wt_3001	-	hypothetical protein
cds_wt_3002	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3003	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3004	-	putative integral membrane transport protein
cds_wt_3005	-	putative integral membrane transport protein
		Spermidine/putrescine import ATP-binding protein
cds_wt_3006	natA	potA;
		Uncharacterized 23.9 kDa protein in glnII region;
cds_wt_3007	-	ORF2;
cds_wt_3008	-	hypothetical protein
cds_wt_3009	-	hypothetical protein
cds_wt_3010	resE	putative two-component system sensor kinase
		Probable transcriptional regulator ycf27; OmpR-like protein;
cds_wt_3011	mtrA	Uncharacterized response regulatory protein
		VC_0693;
cds_wt_3012	algR	two-component sensor histidine kinase
cds_wt_3013	lytS	Sensor protein lytS; Autolysin sensor kinase;
cds_wt_3014	lytS	
cds_wt_3015	-	Vegetative incompatibility protein HET-E-1;
cds_wt_3016	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3017	cpsD	probable glycosyltransferase
cds_wt_3018	-	putative formamidopyrimidine-DNA glycosylase
cds_wt_3019	assT	conserved hypothetical protein
		Cholinephosphotransferase 1; Diacylglycerol
cds_wt_3020	-	cholinephosphotransferase 1;
cds_wt_3021	gldA	putative glycerol 1-phosphate dehydrogenase
cds_wt_3022	rfbF	putative nucleotide sugar-1-phosphate transferase
cds_wt_3023	-	multiple substrate aminotransferase
cds_wt_3024	corA	Magnesium transport protein corA;
cds_wt_3025	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3026	-	hypothetical protein predicted by Glimmer/Critica

cds_wt_3027	ppiA	peptidyl-prolyl cis-trans isomerase
cds_wt_3028	yggP	Rhomboid family member 1;
cds_wt_3029	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3030	-	C-terminal region of transketolase
cds_wt_3031	tktB	transketolase, N-terminal subunit
cds_wt_3032	soxR	Redox-sensitive transcriptional activator soxR;
cds_wt_3033	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3034	qor	putative quinone oxidoreductase
cds_wt_3035	-	conserved hypothetical protein
cds_wt_3036	iap	Uncharacterized protein ydhO;
cds_wt_3037	ybcL	UPF0098 protein ybcL;
		3-demethylubiquinone-9 3-methyltransferase; 3,4-dihydroxy-5-hexaprenylbenzoate methyltransferase; DHHB methyltransferase;
cds_wt_3038	-	
cds_wt_3039	-	putative glycosyl transferase
cds_wt_3040	-	hypothetical protein
cds_wt_3041	def	Peptide deformylase; PDF; Polypeptide deformylase;
cds_wt_3042	fhbA	putative flavohemoprotein
cds_wt_3043	-	hypothetical protein
		Polycystic kidney disease protein 1-like 3; Polycystin-1L3; PC1-like 3 protein;
cds_wt_3044	-	
cds_wt_3045	-	Nuclease sbcCD subunit C;
cds_wt_3046	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3047	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3048	-	NFX1-type zinc finger-containing protein 1;
cds_wt_3049	-	hypothetical protein predicted by Glimmer/Critica
		Ubiquinone/menaquinone biosynthesis
cds_wt_3050	pcm	methyltransferase ubiE;
		Probable DHNTP pyrophosphohydrolase;
		Dihydroneopterin triphosphate
cds_wt_3051	-	pyrophosphohydrolase;
cds_wt_3052	-	conserved hypothetical protein
cds_wt_3053	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3054	-	Uncharacterized protein Rv2079/MT2140;
cds_wt_3055	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3056	-	Transposase insF for insertion sequence IS3fB;
cds_wt_3057	orfB	Transposase for insertion sequence element IS629;
cds_wt_3058	-	hypothetical protein predicted by Glimmer/Critica
		Anti-sigma F factor antagonist; Stage II sporulation protein AA;
cds_wt_3059	rsbV	
cds_wt_3060	-	hypothetical protein predicted by Glimmer/Critica
		Signal transduction histidine-protein
		kinase/phosphatase mprB; Mycobacterial persistence regulator B;
cds_wt_3061	cckA	
		Cell surface glycoprotein 1; Outer layer protein B; S-layer protein 1;
cds_wt_3062	-	
cds_wt_3063	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3064	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3065	thcR	Probable thc operon regulatory protein;
cds_wt_3066	-	hypothetical protein predicted by Glimmer/Critica

cds_wt_3067	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3068	bcpB	Putative peroxiredoxin Q, chloroplastic; Thioredoxin reductase;
cds_wt_3069	eno	enolase
cds_wt_3070	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3071	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3072	-	hypothetical protein
cds_wt_3073	-	Mixed-linked glucan synthase 2; 1,3;1,4-beta-D-glucan synthase 2; Cellulose synthase-like protein F2; OsCsIF2;
cds_wt_3074	yheB	chitinase
cds_wt_3075	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3076	-	hypothetical protein
cds_wt_3077	-	Flotillin-2a; Reggie-1a; REG-1;
cds_wt_3078	PLG	putative secreted protein
cds_wt_3079	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3080	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3081	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3082	-	hypothetical protein
cds_wt_3083	-	Receptor-type tyrosine-protein phosphatase delta; Protein-tyrosine phosphatase delta; R-PTP-delta; Chaperone protein dnaK; Heat shock protein 70; Heat shock 70 kDa protein; HSP70;
cds_wt_3084	dnaK	
cds_wt_3085	tdk	Thymidine kinase;
cds_wt_3086	adp	alkaline D-peptidase
cds_wt_3087	katG	catalase/peroxidase HPI
cds_wt_3088	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3089	fdhF	nitrate reductase
cds_wt_3090	-	Trans-1,2-dihydrobenzene-1,2-diol dehydrogenase; Dimeric dihydrodiol dehydrogenase; D-xylose-NADP dehydrogenase; D-xylose 1-dehydrogenase; JMO2DD;
cds_wt_3091	-	Putative hexulose-6-phosphate isomerase; HUMPI;
cds_wt_3092	-	hypothetical protein
cds_wt_3093	sigE	RNA polymerase sigma-E factor; Sigma-24;
cds_wt_3094	-	putative integral membrane protein
cds_wt_3095	-	Phosphate import ATP-binding protein pstB; Phosphate-transporting ATPase; ABC phosphate transporter;
cds_wt_3096	-	hypothetical protein
cds_wt_3097	-	hypothetical protein
cds_wt_3098	PGFS	Aldo-keto reductase family 1 member C23-like protein; Putative prostaglandin F synthase;
cds_wt_3099	arsR	Biofilm growth-associated repressor;
cds_wt_3100	-	hypothetical protein
cds_wt_3101	p20	ribosomal-protein-serine acetyltransferase
cds_wt_3102	-	hypothetical protein
cds_wt_3103	bioY	Probable biotin transporter bioY;
cds_wt_3104	-	putative neutral zinc metalloprotease
cds_wt_3105	-	DNA mismatch repair protein mutL;

cds_wt_3106	phoP	Probable transcriptional regulator ycf27; OmpR-like protein;
cds_wt_3107	cpxA	two component sensor kinase
cds_wt_3108	chb	GlcNAc-binding protein A;
cds_wt_3109	-	hypothetical protein
cds_wt_3110	-	Uncharacterized protein MJECL23;
		phosphoribosylaminoimidazole-succinocarboxamide synthase
cds_wt_3111	purC	hypothetical protein predicted by Glimmer/Critica
cds_wt_3112	-	nitroreductase
cds_wt_3113	-	Uncharacterized HTH-type transcriptional regulator ydeP;
cds_wt_3114	yodB	hypothetical protein predicted by Glimmer/Critica
cds_wt_3115	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3116	-	putative DNA-binding protein
cds_wt_3117	-	putative regulator
cds_wt_3118	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3119	-	hypothetical protein
cds_wt_3120	-	Diguanylate cyclase yddV; DGC;
cds_wt_3121	pleD	Uncharacterized transporter C3H1.06c;
cds_wt_3122	-	HTH-type transcriptional regulator tcmR;
		Tetracenomycin C transcriptional repressor;
cds_wt_3123	tcmR	putative sugar hydrolase
cds_wt_3124	chiC	HTH-type transcriptional regulator betI;
cds_wt_3125	-	putative hydrolase
cds_wt_3126	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3127	-	Uncharacterized protein ydaL;
cds_wt_3128	-	UDP-GlcNAc 2-epimerase
cds_wt_3129	mnaA	hypothetical protein predicted by Glimmer/Critica
cds_wt_3130	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3131	-	Translation initiation factor IF-2;
cds_wt_3132	-	hypothetical protein
cds_wt_3133	-	Sensor histidine kinase resE;
cds_wt_3134	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3135	-	hypothetical protein
cds_wt_3136	-	Putative hydrolase Shewmr7_2686;
cds_wt_3137	-	Probable protease htpX homolog;
cds_wt_3138	-	initiation factor eIF-2B
cds_wt_3139	gcn3	Mini-circle uncharacterized 19.1 kDa protein;
cds_wt_3140	-	prephenate dehydrogenase
cds_wt_3141	tyrA	L-Ala--D-Glu endopeptidase; Peptidoglycan hydrolase; Sporulation-specific endopeptidase;
cds_wt_3142	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3143	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3144	-	conserved hypothetical protein
cds_wt_3145	-	hypothetical protein
cds_wt_3146	cdd3	purine nucleoside phosphorylase
cds_wt_3147	deoD	hypothetical protein predicted by Glimmer/Critica
cds_wt_3148	-	Anti-sigma F factor antagonist; Stage II sporulation protein AA;
cds_wt_3149	-	

cds_wt_3150	dnaX	DNA polymerase III gamma and tau subunit
cds_wt_3151	-	UPF0133 protein ESA_02800;
cds_wt_3152	recR	Recombination protein recR;
cds_wt_3153	dppC	Dipeptide transport system permease protein dppC;
cds_wt_3154	-	Periplasmic oligopeptide-binding protein;
cds_wt_3155	dppB	Putative peptide permease protein BOV_A0351;
		Phosphate import ATP-binding protein pstB;
		Phosphate-transporting ATPase; ABC phosphate transporter;
cds_wt_3156	dppD	
cds_wt_3157	appF	Oligopeptide transport ATP-binding protein appF;
cds_wt_3158	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3159	-	putative secreted protein
cds_wt_3160	leuA	2-isopropylmalate synthase
cds_wt_3161	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3162	ask	aspartate kinase
cds_wt_3163	asd	aspartate-semialdehyde dehydrogenase
cds_wt_3164	pyrE	orotate phosphoribosyltransferase
cds_wt_3165	-	hypothetical protein predicted by Glimmer/Critica
		Uncharacterized metallophosphoesterase
cds_wt_3166	-	CPn_0578/CP_0170/CPj0578/CpB0602;
cds_wt_3167	-	Aspartyl/glutamyl-tRNA
cds_wt_3168	ponA	penicillin-binding protein
cds_wt_3169	wblA	putative regulatory protein
cds_wt_3170	-	putative ion-transporting ATPase
cds_wt_3171	-	putative ion-transporting ATPase
cds_wt_3172	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3173	-	UPF0076 protein PH0854;
cds_wt_3174	-	putative hydrolase
		adenylyl cyclase class-3/4/guanylyl
cds_wt_3175	-	cyclase:tetratricopeptide TPR_4
cds_wt_3176	pknK	serine/threonine protein kinase
cds_wt_3177	MCCA	propionyl-CoA carboxylase alpha chain
		putative acetyl/propionyl CoA carboxylase, beta subunit
cds_wt_3178	-	
cds_wt_3179	hlyX	Regulatory protein hlyX;
cds_wt_3180	capA	Capsule biosynthesis protein capA;
cds_wt_3181	nth	putative endonuclease III
		Thiol:disulfide interchange protein dsbE; Cytochrome c biogenesis protein ccmG;
cds_wt_3182	resA	
		Peroxisomal coenzyme A diphosphatase NUDT7;
		Nucleoside diphosphate-linked moiety X motif 7;
cds_wt_3183	-	Nudix motif 7;
cds_wt_3184	-	putative membrane-associated serine protease
cds_wt_3185	-	serine protease
cds_wt_3186	-	Protein essC;
cds_wt_3187	-	hypothetical protein
cds_wt_3188	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3189	ppa	putative inorganic pyrophosphatase
cds_wt_3190	dacE	D-alanyl-D-alanine carboxypeptidase
cds_wt_3191	-	hypothetical protein

cds_wt_3192	mesJ	cell cycle protein MesJ
cds_wt_3193	-	tRNA
cds_wt_3194	hpt	putative hypoxanthine phosphoribosyltransferase
cds_wt_3195	ftsH	cell division protein
cds_wt_3196	folE	GTP cyclohydrolase I
cds_wt_3197	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3198	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3199	-	DNA translocase ftsK 2;
cds_wt_3200	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3201	-	hypothetical protein
cds_wt_3202	-	Obscurin; Obscurin-myosin light chain kinase;
cds_wt_3203	-	Obscurin-MLCK; Obscurin-RhoGEF;
cds_wt_3204	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3205	folP	hypothetical protein predicted by Glimmer/Critica
cds_wt_3206	folB	dihydropteroate synthase
cds_wt_3207	folK	dihydroneopterin aldolase
cds_wt_3208	-	putative 7,8-dihydro-6-hydroxymethylpterin-
cds_wt_3209	-	pyrophosphokinase
cds_wt_3210	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3211	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3212	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3213	proW	putative ABC transporter ATP-binding protein
cds_wt_3214	proZ	Putative osmoprotectant uptake system permease
cds_wt_3215	proX	protein yehY;
cds_wt_3216	-	Nitrate transport permease protein nrtB;
cds_wt_3217	-	Glycine betaine/carnitine/choline-binding protein;
cds_wt_3218	nuoD	Osmoprotectant-binding protein;
cds_wt_3219	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3220	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3221	panC	NADH dehydrogenase I, D subunit
cds_wt_3222	panD	hypothetical protein
cds_wt_3223	-	hypothetical protein
cds_wt_3224	nadB	pantoate--beta-alanine ligase
cds_wt_3225	nadC	aspartate 1-decarboxylase
cds_wt_3226	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3227	lysS	L-aspartate oxidase
cds_wt_3228	lsr2	nicotinate-mononucleotide pyrophosphorylase
cds_wt_3229	clpB	Type III pantothenate kinase; Pantothenic acid
cds_wt_3230	-	kinase; PanK-III;
cds_wt_3231	-	putative lysyl-tRNA synthetase
cds_wt_3232	-	Protein Lsr2; 15 kDa antigen; A15;
cds_wt_3233	-	Chaperone protein clpB;
cds_wt_3234	mutY	hypothetical protein predicted by Glimmer/Critica
cds_wt_3235	-	hypothetical protein
cds_wt_3236	-	hypothetical protein predicted by Glimmer/Critica
		RNA polymerase sigma-E factor;
		putative A/G-specific adenine glycosylase
		hypothetical protein predicted by Glimmer/Critica
		Aggregation substance;

cds_wt_3237	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3238	-	Probable hemoglobin and hemoglobin-haptoglobin-binding protein 3;
cds_wt_3239	-	DNA integrity scanning protein disA;
cds_wt_3240	radA	DNA repair protein
cds_wt_3241	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3242	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3243	menA	Protoheme IX farnesyltransferase; Heme O synthase;
cds_wt_3244	chsA	Heme B farnesyltransferase;
cds_wt_3245	-	hypothetical protein
cds_wt_3246	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3247	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3248	ispD	putative transcription factor
cds_wt_3249	ispF	4-diphosphocytidyl-2C-methyl-D-erythritol synthase
cds_wt_3250	-	putative 2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase
cds_wt_3251	-	Transmembrane and TPR repeat-containing protein 4;
cds_wt_3252	-	hypothetical protein
cds_wt_3253	xylR	Serine/threonine-protein kinase afsK;
cds_wt_3254	ydeA	NagC/XylR-type transcriptional regulator
cds_wt_3255	-	Probable sugar efflux transporter;
cds_wt_3256	-	putative histidinol-phosphate aminotransferase
cds_wt_3257	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3258	hppD	hypothetical protein predicted by Glimmer/Critica
cds_wt_3259	asnC	4-hydroxyphenylpyruvate dioxygenase
cds_wt_3260	-	Uncharacterized HTH-type transcriptional regulator PH1519;
cds_wt_3261	fumB	hypothetical protein predicted by Glimmer/Critica
cds_wt_3262	-	fumarate hydratase, class I
cds_wt_3263	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3264	fum	Regulatory protein afsR;
cds_wt_3265	ssp	fumarate hydratase C
cds_wt_3266	cysS	putative subtilisin-like protease
cds_wt_3267	-	putative cysteinyl-tRNA synthetase
cds_wt_3268	-	putative tRNA/rRNA methyltransferase
cds_wt_3269	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3270	-	Laminin subunit beta-2; S-laminin; Laminin B1s chain;
cds_wt_3271	-	putative large secreted protein
cds_wt_3272	-	hypothetical protein
cds_wt_3273	msiK	N-terminal domain intergin-like repeats and C-terminal-cell wall-associated hydrolase domain
cds_wt_3274	-	Spermidine/putrescine import ATP-binding protein potA;
cds_wt_3275	-	Synaptojanin-2; Synaptic inositol-1,4,5-trisphosphate 5-phosphatase 2;
cds_wt_3276	Gak	hypothetical protein
		Cyclin G-associated kinase;

cds_wt_3277	-	Glutathione-regulated potassium-efflux system protein kefC; K
cds_wt_3278	-	hypothetical protein
cds_wt_3279	-	Glutamyl endopeptidase; Staphylococcal serine proteinase; V8 protease; V8 proteinase; Endoproteinase Glu-C;
cds_wt_3280	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3281	-	UPF0173 metal-dependent hydrolase Smar_0891;
cds_wt_3282	nreC	Oxygen regulatory protein nreC; Nitrogen regulation protein C;
cds_wt_3283	moxY	Methanol utilization control sensor protein moxY;
cds_wt_3284	-	putative ABC transporter integral membrane protein
cds_wt_3285	-	Spermidine/putrescine import ATP-binding protein potA;
cds_wt_3286	nagA	N-acetylglucosamine-6-phosphate deacetylase
cds_wt_3287	glcK	glucokinase, putative
cds_wt_3288	glmS	hypothetical protein
cds_wt_3289	agaR	Glycerol-3-phosphate regulon repressor;
cds_wt_3290	yhch	Methionine import ATP-binding protein metN 2;
cds_wt_3291	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3292	-	hypothetical protein
cds_wt_3293	-	putative conserved ATPase
cds_wt_3294	bcrA	Spermidine/putrescine import ATP-binding protein potA;
cds_wt_3295	-	putative ABC transporter membrane protein
cds_wt_3296	thrC	threonine synthase
cds_wt_3297	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3298	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3299	-	60 kDa chaperonin; Protein Cpn60; groEL protein;
cds_wt_3300	bcpB	Peroxiredoxin-1;
cds_wt_3301	glpD	glycerol-3-phosphate dehydrogenase
cds_wt_3302	-	hypothetical protein
cds_wt_3303	-	Putative permease perM homolog;
cds_wt_3304	-	10 kDa chaperonin 5; Protein Cpn10 5; groES protein 5;
cds_wt_3305	-	Protease prsW; Protease responsible for activating sigma-W;
cds_wt_3306	-	Uncharacterized protein Cgl2769/cg3067;
cds_wt_3307	-	hypothetical protein
cds_wt_3308	sseC	hypothetical protein
cds_wt_3309	-	thiosulfate sulfurtransferase
cds_wt_3310	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3311	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3312	glnR	Transcriptional regulatory protein glnR;
cds_wt_3313	mshD	Uncharacterized N-acetyltransferase MJ1207;
cds_wt_3314	pstS	Phosphate-binding protein pstS; PBP;
cds_wt_3315	pstC	Phosphate transport system permease protein pstC;
cds_wt_3316	pstA	Phosphate transport system permease protein pstA;
cds_wt_3317	pstB	ABC transporter, ATP-binding protein
cds_wt_3318	dhdh	putative oxidoreductase

cds_wt_3319	-	Probable low-affinity inorganic phosphate transporter;
cds_wt_3320	-	Putative pit accessory protein;
cds_wt_3321	-	RNA polymerase sigma factor sigW; Sigma-W factor;
cds_wt_3322	-	UPF0374 protein SMU_1781;
cds_wt_3323	dinG	putative ATP-dependent helicase
cds_wt_3324	mutT	RNA pyrophosphohydrolase;
cds_wt_3325	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3326	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3327	-	THAP domain-containing protein 4;
cds_wt_3328	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3329	pabC	putative aminotransferase
cds_wt_3330	fur	Ferric uptake regulation protein; Ferric uptake regulator;
cds_wt_3331	-	Aminomethyltransferase; Glycine cleavage system T protein;
cds_wt_3332	-	hypothetical protein
cds_wt_3333	-	hypothetical protein
cds_wt_3334	-	Uncharacterized HTH-type transcriptional regulator ydcN;
cds_wt_3335	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3336	-	Uncharacterized protein ML2453;
cds_wt_3337	-	2-hydroxy-6-oxononadienedioate/2-hydroxy-6-oxononatrienedioate hydrolase; EC=3.7.1.n1; 2-hydroxy-6-oxonona-2,4-diene-1,9-dioic acid 5,6-hydrolase; 2-hydroxy-6-ketonona-2,4-diene-1,9-dioic acid 5,6-hydrolase; 2-hydroxy-6-oxonona-2,4,7-triene-1,9-dioic acid 5,6-hydrolase;
cds_wt_3338	-	Putative DNA helicase INO80;
cds_wt_3339	cysZ	Protein cysZ homolog;
cds_wt_3340	-	UPF0189 protein XAC3343; HTH-type transcriptional repressor purR; Purine nucleotide synthesis repressor; Pur regulon repressor;
cds_wt_3341	lacI	
cds_wt_3342	bglA	beta-glucosidase
cds_wt_3343	-	hypothetical protein
cds_wt_3344	murB	UDP-N-acetylmuramate dehydrogenase
cds_wt_3345	-	hypothetical protein
cds_wt_3346	phoP	Transcriptional regulatory protein yycF;
cds_wt_3347	cheA	Chemotaxis protein cheA;
cds_wt_3348	cheA	chemotaxis protein CheA
cds_wt_3349	cheW	Chemotaxis protein cheW;
cds_wt_3350	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3351	cheB	glutamate methylesterase
cds_wt_3352	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3353	cheB	glutamate methylesterase
cds_wt_3354	cheR	chemotaxis protein methyltransferase CheR
cds_wt_3355	cheY	response regulator
cds_wt_3356	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3357	-	Probable transcriptional regulator ycf27; OmpR-like protein;

cds_wt_3358	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3359	flgD	Basal-body rod modification protein flgD;
cds_wt_3360	flgE	Flagellar hook protein flgE;
cds_wt_3361	fliO	motility protein
cds_wt_3362	motA	Chemotaxis protein motA; Motility protein A;
cds_wt_3363	motB	Chemotaxis protein motB; Motility protein B;
cds_wt_3364	fliL	Flagellar fliL protein;
cds_wt_3365	fliM	Flagellar motor switch protein fliM;
cds_wt_3366	fliY	Flagellar motor switch protein fliM;
cds_wt_3367	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3368	fliP	Flagellar biosynthetic protein fliP;
cds_wt_3369	fliR	Flagellar biosynthetic protein fliR;
cds_wt_3370	flhB	Flagellar biosynthetic protein flhB;
cds_wt_3371	flhA	Flagellar biosynthesis protein flhA;
cds_wt_3372	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3373	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3374	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3375	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3376	yjbJ	Membrane-bound lytic murein transglycosylase F; EC=4.2.2.n1; Murein lyase F;
cds_wt_3377	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3378	fliI	flagellar-specific ATP synthase
cds_wt_3379	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3380	fliG	Flagellar motor switch protein fliG;
cds_wt_3381	fliF	Flagellar M-ring protein;
cds_wt_3382	-	Flagellar hook-basal body complex protein fliE;
cds_wt_3383	flgC	Flagellar basal-body rod protein flgC;
cds_wt_3384	-	Flagellar basal-body rod protein flgB; Putative proximal rod protein;
cds_wt_3385	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3386	fliS	Flagellar protein fliS;
cds_wt_3387	fliD	Flagellar hook-associated protein 2; HAP2; Filament cap protein; Flagellar cap protein;
cds_wt_3388	flaD	Flagellin A; Flagellin core protein;
cds_wt_3389	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3390	flgK	Flagellar hook-associated protein 1; HAP1;
cds_wt_3391	flgL	Flagellar filament 33 kDa core protein; Class B;
cds_wt_3392	yviF	Flagellar assembly factor fliW;
cds_wt_3393	csrA	Carbon storage regulator homolog;
cds_wt_3394	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3395	-	Uncharacterized 17.2 kDa protein in melC2-rnhH intergenic region; ORF3;
cds_wt_3396	-	Sensor histidine kinase yycG;
cds_wt_3397	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3398	PRB1	putative subtilase-type peptidase
cds_wt_3399	cheY	Probable transcriptional regulator ycf27; OmpR-like protein;
cds_wt_3400	-	hypothetical protein
cds_wt_3401	-	putative short-chain type oxidoreductase
cds_wt_3402	-	putative glycosyltransferase

cds_wt_3403	-	Uncharacterized protein ML2442;
cds_wt_3404	-	Uncharacterized MFS-type transporter yhjO;
cds_wt_3405	-	Multidrug resistance protein mdtH;
cds_wt_3406	gpm1	phosphoglycerate mutase
cds_wt_3407	phoU	Phosphate transport system protein phoU homolog 2;
cds_wt_3408	phoR	putative two-component system sensor kinase
cds_wt_3409	phoP	Sensory transduction protein regX3;
cds_wt_3410	-	Uncharacterized protein Mb0506c;
cds_wt_3411	-	Uncharacterized protein Mb0509;
cds_wt_3412	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3413	-	hypothetical protein
cds_wt_3414	ycgM	proline dehydrogenase
cds_wt_3415	-	Uncharacterized protein yvgK;
cds_wt_3416	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3417	-	Uncharacterized protein ML2427;
cds_wt_3418	-	Nipped-B-like protein; Delangin homolog; SCC2 homolog;
cds_wt_3419	sigX	RNA polymerase sigma-H factor; Sigma-30;
cds_wt_3420	yhfL	AMP-dependent synthetase and ligase
cds_wt_3421	-	Uncharacterized protein Mb0520;
cds_wt_3422	-	putative phosphatase
cds_wt_3423	-	Redox-sensing transcriptional repressor rex;
cds_wt_3424	hemA	glutamyl-tRNA reductase
cds_wt_3425	hemC	prophobilinogen deaminase
cds_wt_3426	hemD	uroporphyrin-III C-methyltransferase /
cds_wt_3427	hemB	uroporphyrinogen-III synthase
cds_wt_3428	-	prophobilinogen synthase
cds_wt_3429	-	Mini-circle putative transposase for IS117;
cds_wt_3430	-	Mini-circle putative transposase for IS117;
cds_wt_3431	lpqU	hypothetical protein
cds_wt_3432	-	Nucleoporin NUP159; Nuclear pore protein NUP159;
cds_wt_3433	-	hypothetical protein
cds_wt_3434	-	Disease resistance protein RPS5; Resistance to Pseudomonas syringae protein 5; pNd3/pNd10;
cds_wt_3435	korB	Potassium channel subfamily T member 2; Sequence like an intermediate conductance potassium channel subunit; Sodium and chloride-activated ATP-sensitive potassium channel Slo2.1;
cds_wt_3436	korA	2-oxoglutarate ferredoxin oxidoreductase, beta subunit
cds_wt_3437	ndhC	2-oxoglutarate ferredoxin oxidoreductase, alpha subunit
cds_wt_3438	-	NADH dehydrogenase subunit 3
cds_wt_3439	tagA	hypothetical protein predicted by Glimmer/Critica
cds_wt_3440	-	DNA-3-methyladenine glycosidase I
cds_wt_3441	paaB	hypothetical protein predicted by Glimmer/Critica
cds_wt_3442	paaX	enoyl-CoA hydratase
cds_wt_3443	-	Phenylacetic acid degradation operon negative regulatory protein paaX;
		hypothetical protein

cds_wt_3444	pepA	leucyl aminopeptidase
cds_wt_3445	-	probable methyltransferase
cds_wt_3446	-	trypsin-like serine proteases typically periplasmic contain C-terminal PDZ domain
cds_wt_3447	-	Sec-independent protein translocase protein tatB homolog;
cds_wt_3448	mrp	Protein mrp homolog;
cds_wt_3449	-	hypothetical protein
cds_wt_3450	-	hypothetical protein
cds_wt_3451	phzF	Diaminopimelate epimerase; DAP epimerase;
cds_wt_3452	-	hypothetical protein
cds_wt_3453	-	Uncharacterized HAD-hydrolase MJ1437;
cds_wt_3454	yxxF	Uncharacterized transporter AF_0510;
cds_wt_3455	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3456	fabG	3-oxoacyl-
cds_wt_3457	-	hypothetical protein
cds_wt_3458	-	Uncharacterized protein Mb2609c;
cds_wt_3459	trxA	thioredoxin
cds_wt_3460	spoU	23S rRNA
cds_wt_3461	-	hypothetical protein
cds_wt_3462	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3463	-	hypothetical protein
cds_wt_3464	-	Protein trpH;
cds_wt_3465	yche	UPF0056 membrane protein BUsg_257;
cds_wt_3466	recB	putative RecB family exonuclease
cds_wt_3467	-	hypothetical protein
cds_wt_3468	fur	Ferric uptake regulation protein; Ferric uptake regulator;
cds_wt_3469	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3470	-	Protein FAM75A2;
cds_wt_3471	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3472	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3473	-	hypothetical protein
cds_wt_3474	-	hypothetical protein
cds_wt_3475	pleD	hypothetical protein
cds_wt_3476	galF	UTP-glucose-1-phosphate uridylyltransferase
cds_wt_3477	moeA	Gephyrin;
cds_wt_3478	rimJ	ribosomal-protein-alanine acetyltransferase
cds_wt_3479	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3480	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3481	-	Tyrosine recombinase xerD;
cds_wt_3482	-	hypothetical protein
cds_wt_3483	-	two-component hybrid sensor and regulator
cds_wt_3484	-	Probable xyloglucan glycosyltransferase 8; Cellulose synthase-like protein C8; AtCsIC8;
cds_wt_3485	-	Uncharacterized protein Rv1002c/MT1031;
cds_wt_3486	-	UPF0011 protein yral;
cds_wt_3487	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3488	metG	methionyl-tRNA synthetase
cds_wt_3489	-	hypothetical protein predicted by Glimmer/Critica

cds_wt_3490	tatD	putative deoxyribonuclease
cds_wt_3491	ksgA	putative dimethyladenosine transferase
		Putative ABC transporter ATP-binding protein
cds_wt_3492	-	VV2_1533;
cds_wt_3493	-	hypothetical protein
cds_wt_3494	-	HTH-type transcriptional regulator betI;
cds_wt_3495	-	hypothetical protein predicted by Glimmer/Critica
		glucosamine-1-phosphate N-acetyltransferase / UDP-
cds_wt_3496	glmU	N-acetylglucosamine pyrophosphorylase
cds_wt_3497	prsA	ribose-phosphate pyrophosphokinase
		50S ribosomal protein L25; General stress protein
cds_wt_3498	rpIY	CTC;
cds_wt_3499	pth	peptidyl-tRNA hydrolase
cds_wt_3500	cpsD	sugar transferase
cds_wt_3501	IMP3	Inositol monophosphatase 3; Inositol-1
cds_wt_3502	cysD	sulfate adenylyltransferase subunit 2
cds_wt_3503	cysN	sulfate adenylyltransferase subunit 1
		putative magnesium or manganese-dependent
cds_wt_3504	-	protein phosphatase
cds_wt_3505	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3506	galE	UDP-glucose 4-epimerase
cds_wt_3507	trpS	tryptophanyl-tRNA synthetase
cds_wt_3508	-	UPF0477 protein yjcG;
		Uncharacterized 36.0 kDa protein in kdgK 5'region;
cds_wt_3509	yhjD	K1 ORF;
cds_wt_3510	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3511	-	hypothetical protein predicted by Glimmer/Critica
		Basic membrane protein A2; Immunodominant
cds_wt_3512	tmpC	antigen P39;
cds_wt_3513	rbsA	putative sugar ABC transporter (ATP-binding protein)
		Uncharacterized ABC transporter permease protein
cds_wt_3514	-	yufP;
cds_wt_3515	rbsC	Uncharacterized protein MG121;
cds_wt_3516	cdd	cytidine deaminase
cds_wt_3517	deoA	thymidine phosphorylase
cds_wt_3518	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3519	rrmA	putative ribosomal RNA methyltransferase
cds_wt_3520	add	putative adenosine deaminase
cds_wt_3521	-	Sensor protein torS;
cds_wt_3522	-	hypothetical protein
cds_wt_3523	-	hypothetical protein
cds_wt_3524	-	Elongation factor G; EF-G;
		Voltage-dependent N-type calcium channel subunit
		alpha-1B; Voltage-gated calcium channel subunit
		alpha Cav2.2; Calcium channel, L type, alpha-1
cds_wt_3525	-	polypeptide isoform 5; Brain calcium channel III; BIII;
cds_wt_3526	-	Putative transposase y4uE;
cds_wt_3527	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3528	dhaS	aldehyde dehydrogenase
cds_wt_3529	dhaS	aldehyde dehydrogenase

cds_wt_3530	deoC	putative deoxyribose-phosphate aldolase
cds_wt_3531	upp	uracil phosphoribosyltransferase
cds_wt_3532	mutT	7,8-dihydro-8-oxoguanine-triphosphatase
cds_wt_3533	degT	UDP-4-amino-4-deoxy-L-arabinose--oxoglutarate aminotransferase; EC=2.6.1.n1; UDP-
cds_wt_3534	-	myo-inositol 2-dehydrogenase
cds_wt_3535	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3536	rfaG	Glycogen synthase; Starch
cds_wt_3537	-	glycosyl transferase, group 1 family protein
cds_wt_3538	-	Uncharacterized glycosyltransferase MJ1607;
cds_wt_3539	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3540	-	Ubiquinone/menaquinone biosynthesis methyltransferase ubiE;
cds_wt_3541	-	UDP-N-acetyl-D-mannosaminuronic acid dehydrogenase
cds_wt_3542	wbpD	putative acetyltransferase
cds_wt_3543	-	Uncharacterized protein C5D6.13;
cds_wt_3544	yhxB	phosphomannomutase
cds_wt_3545	-	putative serine/threonine protein kinase
cds_wt_3546	sbm5	Methylmalonyl-CoA mutase, N-terminal domain/subunit
cds_wt_3547	amiA	metal-dependent amidase/aminoacylase/carboxypeptidase
cds_wt_3548	-	hypothetical protein
cds_wt_3549	-	UPF0173 metal-dependent hydrolase CHY_0920;
cds_wt_3550	-	Kinesin heavy chain isoform 5A;
cds_wt_3551	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3552	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3553	Ggct	Gamma-glutamylcyclotransferase;
cds_wt_3554	lpdA	dihydrolipoamide dehydrogenase
cds_wt_3555	-	Protein dedA; Protein DSG-1;
cds_wt_3556	-	HTH-type transcriptional regulator betI;
cds_wt_3557	-	biotin carboxylase
cds_wt_3558	maf	Maf-like protein Pfl01_0841;
cds_wt_3559	-	Polycystic kidney disease protein 1-like 3; Polycystin-1L3; PC1-like 3 protein;
cds_wt_3560	-	Duffy receptor gamma form; Erythrocyte-binding protein;
cds_wt_3561	-	putative serine/threonine protein kinase
cds_wt_3562	-	Cortactin-binding protein 2; CortBP2;
cds_wt_3563	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3564	-	putative integral membrane protein
cds_wt_3565	pccB	propionyl-CoA carboxylase beta chain
cds_wt_3566	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3567	-	Halomucin;
cds_wt_3568	birA	biotin acetyl-CoA carboxylase ligase
cds_wt_3569	-	Separin; Separase; Caspase-like protein ESPL1;
cds_wt_3570	-	Extra spindle poles-like 1 protein;
cds_wt_3571	-	conserved hypothetical protein
		Uncharacterized protein ML0110;

cds_wt_3572	-	RNA polymerase sigma factor ylaC;
cds_wt_3573	pckA	phosphoenolpyruvate carboxykinase
cds_wt_3574	-	putative undecaprenyl pyrophosphate synthetase
cds_wt_3575	otsB	Trehalose-phosphatase; Trehalose-6-phosphate phosphatase; TPP;
cds_wt_3576	phoH	Chaperone protein clpB;
cds_wt_3577	-	hypothetical protein
cds_wt_3578	-	transmembrane serine protease 9
cds_wt_3579	-	Rhomboid protease glpP; Intramembrane serine protease;
cds_wt_3580	glpX	glpX protein
cds_wt_3581	-	Polycystic kidney disease protein 1-like 3; Polycystin-1L3; PC1-like 3 protein;
cds_wt_3582	xseB	Exodeoxyribonuclease 7 small subunit;
cds_wt_3583	xseA	Exodeoxyribonuclease VII small subunit;
cds_wt_3584	lytB	Exonuclease VII small subunit;
cds_wt_3585	-	exonuclease VII, large subunit
cds_wt_3586	-	lytB protein
cds_wt_3587	yteT	DNA recombination protein rmuC homolog;
cds_wt_3588	valS	hypothetical protein predicted by Glimmer/Critica
cds_wt_3589	-	Glycosyl hydrolase family 109 protein 1;
cds_wt_3590	-	valyl-tRNA synthetase
cds_wt_3591	ogt	hypothetical protein predicted by Glimmer/Critica
cds_wt_3592	alkA	LIM and UIM domain-containing At1g19270;
cds_wt_3593	-	O-6-alkylguanine-DNA/cysteine-protein methyltransferase
cds_wt_3594	yehF	putative ADA-like regulatory protein
cds_wt_3595	-	Tropinesterase; Atropinesterase; Atropine acylhydrolase;
cds_wt_3596	-	Putative GTP-binding protein tag-210;
cds_wt_3597	-	hypothetical protein
cds_wt_3598	-	hypothetical protein
cds_wt_3599	-	Uncharacterized protein MJ0611.1;
cds_wt_3600	-	putative acetyltransferase
cds_wt_3601	-	Uncharacterized HTH-type transcriptional regulator yetL;
cds_wt_3602	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3603	ygaJ	hypothetical protein predicted by Glimmer/Critica
cds_wt_3604	-	hypothetical protein
cds_wt_3605	-	Peptidase E; Alpha-aspartyl dipeptidase; Asp-specific dipeptidase; Dipeptidase E;
cds_wt_3606	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3607	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3608	-	hypothetical protein
cds_wt_3609	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3610	tetR	RNA pyrophosphohydrolase;
		putative acyl-CoA synthetase, long-chain fatty acid:CoA ligase
		Tetracycline repressor protein class B from transposon Tn10;

cds_wt_3611	aldA	aldehyde dehydrogenase
cds_wt_3612	adhC	putative alcohol dehydrogenase (zinc-binding)
cds_wt_3613	pteR	HTH-type transcriptional regulator maltT; ATP-dependent transcriptional activator maltT;
cds_wt_3614	-	Uncharacterized HTH-type transcriptional regulator Mb2936c;
cds_wt_3615	-	putative acyl-CoA dehydrogenase
cds_wt_3616	-	putative phosphotransferase
cds_wt_3617	ptlF	3-oxoacyl-
cds_wt_3618	-	putative short chain dehydrogenase
cds_wt_3619	ilvJ	Leu/Ile/Val-binding protein homolog 1;
cds_wt_3620	livC	High-affinity branched-chain amino acid transport system permease protein livM; LIV-I protein M;
cds_wt_3621	-	High-affinity branched-chain amino acid transport system permease protein livH; LIV-I protein H;
cds_wt_3622	livF	putative high-affinity branched-chain amino acid transporter ATP-binding protein
cds_wt_3623	livG	Spermidine/putrescine import ATP-binding protein potA;
cds_wt_3624	-	Myosin-1; Class I unconventional myosin; Type I myosin;
cds_wt_3625	-	Alpha-ketoglutarate-dependent dioxygenase alkB homolog 3; Alkylated DNA repair protein alkB homolog 3;
cds_wt_3626	-	putative acetyltransferase
cds_wt_3627	sdhb	putative succinate dehydrogenase iron-sulfur subunit
cds_wt_3628	sdhA	succinate dehydrogenase flavoprotein subunit
cds_wt_3629	-	hypothetical protein
cds_wt_3630	tldD	Protein pmbA;
cds_wt_3631	-	Uncharacterized protein MJ0996;
cds_wt_3632	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3633	pepX	putative peptidase
cds_wt_3634	mshB	N-acetylglucosaminyl-phosphatidylinositol de-N-acetylase; Phosphatidylinositol-glycan biosynthesis class L protein; PIG-L;
cds_wt_3635	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3636	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3637	-	Uncharacterized N-acetyltransferase yobR;
cds_wt_3638	dapC	putative aminotransferase
cds_wt_3639	-	hypothetical protein
cds_wt_3640	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3641	yxnA	short-chain dehydrogenase/reductase SDR
cds_wt_3642	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3643	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3644	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3645	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3646	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3647	-	hypothetical protein
cds_wt_3648	prpH	DNA polymerase III subunit beta;
cds_wt_3649	yggA	Arginine exporter protein argO;

cds_wt_3650	-	Chromosome initiation inhibitor; OriC replication inhibitor;
cds_wt_3651	dapD	2,3,4,5-tetrahydropyridine-2-carboxylate N-succinyltransferase
cds_wt_3652	dapE	succinyl-diaminopimelate desuccinylase
cds_wt_3653	-	UPF0717 protein yvdD;
cds_wt_3654	-	UPF0717 protein At5g11950;
cds_wt_3655	-	putative ATP-dependent DNA helicase
cds_wt_3656	-	putative ATP-dependent DNA helicase
cds_wt_3657	-	probable ATP-dependent DNA helicase
cds_wt_3658	-	hypothetical protein
cds_wt_3659	cspG	Cold shock-like protein cspG; CPS-G;
cds_wt_3660	-	hypothetical protein
cds_wt_3661	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3662	ssuC	Nitrate transport permease protein nrtB;
cds_wt_3663	ssuB	Spermidine/putrescine import ATP-binding protein potA;
cds_wt_3664	ssuA	Nitrate transport protein nrtA;
cds_wt_3665	iscR	HTH-type transcriptional regulator iscR;
cds_wt_3666	pqqL	Mitochondrial-processing peptidase subunit beta; Beta-MPP;
cds_wt_3667	pqqL	Uncharacterized zinc protease Rv2782c/MT2852;
cds_wt_3668	nudC	MutT/nudix family protein
cds_wt_3669	-	Ectoine hydroxylase;
cds_wt_3670	glrX	Glutaredoxin-C6; Glutaredoxin-C2 homolog 1;
cds_wt_3671	-	putative ATP-dependent DNA helicase
cds_wt_3672	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3673	-	putative DNA-binding protein
cds_wt_3674	-	Probable ubiquinone biosynthesis protein ubiB;
cds_wt_3675	-	Aminoglycoside acetyltransferase regulator;
cds_wt_3676	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3677	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3678	-	hypothetical protein
cds_wt_3679	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3680	-	hypothetical protein
cds_wt_3681	-	ATP-dependent protease La 1;
cds_wt_3682	-	UPF0182 protein Strop_3729;
cds_wt_3683	-	lectin repeat domain protein
cds_wt_3684	-	Uncharacterized HTH-type transcriptional regulator ydcN;
cds_wt_3685	-	Putative multidrug resistance protein mdtD;
cds_wt_3686	-	Multidrug resistance protein B;
cds_wt_3687	-	Uncharacterized WD repeat-containing protein alr3466;
cds_wt_3688	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3689	yrfE	Membrane-bound protein lytR;
cds_wt_3690	-	putative lipase
cds_wt_3691	-	Putative peptidoglycan O-acetyltransferase yrhL;
cds_wt_3692	yybG	Uncharacterized protein yybG;

cds_wt_3693	terC	Uncharacterized membrane protein Rv2723/MT2795;
cds_wt_3694	-	Translation initiation factor IF-2;
cds_wt_3695	-	Spermidine synthase; Putrescine
cds_wt_3696	-	aminopropyltransferase; PAPT; SPDSY;
cds_wt_3697	-	hypothetical protein
cds_wt_3698	-	hypothetical protein
cds_wt_3699	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3700	malQ	hypothetical protein predicted by Glimmer/Critica
cds_wt_3701	-	putative 4-alpha-glucanotransferase
cds_wt_3702	csn	hypothetical protein predicted by Glimmer/Critica
cds_wt_3703	bglA	putative secreted protein
cds_wt_3704	-	putative secreted hydrolase
cds_wt_3705	-	Xyloglucan endotransglucosylase/hydrolase protein
cds_wt_3706	-	2; At-XTH2; XTH-2;
cds_wt_3707	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3708	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3709	aroA	Inositol-1-monophosphatase; IMPase; Inositol-1-
cds_wt_3710	-	phosphatase; I-1-Pase;
cds_wt_3711	sigH	hypothetical protein
cds_wt_3712	-	3-phosphoshikimate 1-carboxyvinyltransferase
cds_wt_3713	-	hypothetical protein
cds_wt_3714	accB	RNA polymerase sigma-E factor; Sigma-24;
cds_wt_3715	-	putative anti-sigma factor
cds_wt_3716	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3717	PHYB	hypothetical protein predicted by Glimmer/Critica
cds_wt_3718	nirA	Inositol-1-monophosphatase; IMPase; Inositol-1-
cds_wt_3719	cysH	phosphatase; I-1-Pase;
cds_wt_3720	-	hypothetical protein
cds_wt_3721	-	3-phosphoshikimate 1-carboxyvinyltransferase
cds_wt_3722	-	hypothetical protein
cds_wt_3723	-	RNA polymerase sigma-E factor; Sigma-24;
cds_wt_3724	gntR	putative anti-sigma factor
cds_wt_3725	rsbW	hypothetical protein predicted by Glimmer/Critica
cds_wt_3726	sodN	hypothetical protein predicted by Glimmer/Critica
cds_wt_3727	-	Uxu operon regulator;
cds_wt_3728	me	Serine-protein kinase rsbW; Anti-sigma-B factor;
cds_wt_3729	badC	Sigma-B negative effector rsbW;
cds_wt_3730	ackA	putative nickel-containing superoxide dismutase
cds_wt_3731	pta	precursor (NISOD)
cds_wt_3732	-	Mitochondrial inner membrane protease subunit 1;
cds_wt_3733	sucA	IMP1-like protein;
cds_wt_3734	invS	malic enzyme
cds_wt_3735	-	putative dehydrogenase
		acetate kinase
		phosphate acetyltransferase
		hypothetical protein
		2-oxoglutarate dehydrogenase E1 component
		Inversin;
		hypothetical protein

cds_wt_3736	plsC	hypothetical protein
cds_wt_3737	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3738	phoP	Transcriptional regulatory protein yycF;
cds_wt_3739	phoR	sensor histidine kinase
cds_wt_3740	pepD	trypsin-like serine proteases typically periplasmic contain C-terminal PDZ domain
cds_wt_3741	-	Putative zinc metalloprotease sll0528;
cds_wt_3742	-	Adenomatous polyposis coli protein; Protein APC; Deleted in polyposis 2.5;
cds_wt_3743	-	Patatin-like phospholipase domain-containing protein ACLA_029670;
cds_wt_3744	-	1-acyl-sn-glycerol-3-phosphate acyltransferase delta;
cds_wt_3745	-	1-AGP acyltransferase 4; 1-AGPAT 4;
cds_wt_3746	-	Lysophosphatidic acid acyltransferase delta; LPAAT-delta;
cds_wt_3747	rocD	1-acylglycerol-3-phosphate O-acyltransferase 4;
cds_wt_3748	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3749	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3750	clpP	ornithine aminotransferase
cds_wt_3751	nei2	Arginine deiminase 1; ADI 1; Arginine dihydrolase 1; AD 1;
cds_wt_3752	nodB	hypothetical protein predicted by Glimmer/Critica
cds_wt_3753	-	ATP-dependent Clp protease proteolytic subunit 1
cds_wt_3754	-	formamidopyrimidine-DNA glycosylase
cds_wt_3755	-	polysaccharide deacetylase, putative
cds_wt_3756	bglA	Carboxylate-amine ligase Arth_2891;
cds_wt_3757	chiA	Inner membrane protein oxaA;
cds_wt_3758	chiC	hypothetical protein predicted by Glimmer/Critica
cds_wt_3759	X	Beta-glucanase; Endo-beta-1,3-1,4 glucanase; 1,3-1,4-beta-D-glucan 4-glucanohydrolase; Lichenase;
cds_wt_3760	-	extracellular exochitinase Chi36
cds_wt_3761	treS	chitinase
cds_wt_3762	-	Uncharacterized protein X;
cds_wt_3763	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3764	ygiC	Trehalose synthase; Maltose alpha-D-glucosyltransferase;
cds_wt_3765	-	putative short chain dehydrogenase
cds_wt_3766	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3767	-	Uncharacterized protein yjfC;
cds_wt_3768	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3769	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3770	-	putative integral membrane protein
cds_wt_3771	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3772	-	putative oxidoreductase
cds_wt_3773	ycjY	hypothetical protein predicted by Glimmer/Critica
		XylIDLEGF operon transcriptional activator 3;
		Anti-sigma F factor antagonist; Stage II sporulation protein AA;
		Uncharacterized protein ycjY;

cds_wt_3774	-	Uncharacterized HTH-type transcriptional regulator ydeP;
cds_wt_3775	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3776	-	hypothetical protein
cds_wt_3777	cocE	similar to acylase and diesterase
cds_wt_3778	prkC	protein kinase
cds_wt_3779	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3780	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3781	-	putative transcriptional regulator
cds_wt_3782	-	hypothetical protein
cds_wt_3783	-	hypothetical protein
cds_wt_3784	sipY	putative signal peptidase
cds_wt_3785	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3786	-	Carbamoyl-phosphate synthase large chain, N-terminal section; Carbamoyl-phosphate synthetase ammonia chain;
cds_wt_3787	rimK	Ribosomal protein S6 modification protein 1;
cds_wt_3788	degT	Serine hydroxymethyltransferase; Serine methylase; SHMT;
cds_wt_3789	argC	N-acetyl-gamma-glutamyl-phosphate reductase
cds_wt_3790	argE	acetyl-lysine deacetylase
cds_wt_3791	tktC	transketolase
cds_wt_3792	hpbA	Periplasmic oligopeptide-binding protein;
cds_wt_3793	-	Multidrug resistance protein mdtH;
cds_wt_3794	-	hypothetical protein
cds_wt_3795	pepN	aminopeptidase N
cds_wt_3796	ywqN	Putative NAD
cds_wt_3797	-	hypothetical protein
cds_wt_3798	argS	arginyl-tRNA synthetase
cds_wt_3799	lysA	diaminopimelate decarboxylase
cds_wt_3800	thrA	homoserine dehydrogenase
cds_wt_3801	gloA	hypothetical protein
cds_wt_3802	thrC	threonine synthase
cds_wt_3803	marR	HTH-type transcriptional regulator hpr; Protease production regulatory protein hpr;
cds_wt_3804	yerP	Multidrug resistance protein mdtC; Multidrug transporter mdtC;
cds_wt_3805	bacE	Putative bacilysin exporter bacE;
cds_wt_3806	thrB	homoserine kinase
cds_wt_3807	-	Transcription termination factor rho; ATP-dependent helicase rho;
cds_wt_3808	rho	ATP synthase subunit beta; F-ATPase subunit beta;
cds_wt_3809	nos	ATP synthase F1 sector subunit beta;
cds_wt_3810	-	nitric oxide synthase
cds_wt_3811	pseT	hypothetical protein
cds_wt_3812	-	Polynucleotide kinase; PNK; Polynucleotide 5'-hydroxyl-kinase;
		Putative bifunctional polynucleotide kinase/RNA ligase; Includes: Polynucleotide kinase; PNK;
		Polynucleotide 5'-hydroxy-kinase; Includes: RNA

ligase;

cds_wt_3813	rpmE	50S ribosomal protein L31;
cds_wt_3814	prfA	Peptide chain release factor 1; RF-1;
cds_wt_3815	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3816	-	Uncharacterized signaling protein PA3311;
		Carbamoyltransferase hypF; Carbamoyl phosphate-converting enzyme hypF;
cds_wt_3817	sua5	hypothetical protein predicted by Glimmer/Critica
cds_wt_3818	-	UPF0076 protein PH0854;
cds_wt_3819	tdcF	Uncharacterized protein ybjT;
cds_wt_3820	-	serine hydroxymethyltransferase
cds_wt_3821	glyA	hypothetical protein predicted by Glimmer/Critica
cds_wt_3822	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3823	-	ATP synthase A chain
cds_wt_3824	atpB	ATP synthase lipid-binding protein, mitochondrial;
		ATP synthase proteolipid P2; ATPase protein 9;
cds_wt_3825	atpE	ATPase subunit c;
cds_wt_3826	atpF	ATP synthase B chain
cds_wt_3827	atpH	F-type H ⁺ -transporting ATPase delta / B chain
cds_wt_3828	atpA	ATP synthase alpha chain
cds_wt_3829	atpG	ATP synthase gamma chain
cds_wt_3830	atpD	ATP synthase F1, beta subunit
cds_wt_3831	-	Membrane-bound protein lytR;
		ATP synthase epsilon chain; ATP synthase F1 sector
cds_wt_3832	atpC	epsilon subunit; F-ATPase epsilon subunit;
cds_wt_3833	-	Uncharacterized protein ML1147;
cds_wt_3834	phzF	Diaminopimelate epimerase; DAP epimerase;
cds_wt_3835	pduO	hypothetical protein
cds_wt_3836	murA	UDP-N-acetylglucosamine 1-carboxyvinyltransferase
cds_wt_3837	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3838	hbd2	3-hydroxyacyl-CoA dehydrogenase
cds_wt_3839	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3840	-	DNA translocase ftsK;
cds_wt_3841	-	Collagen alpha-4
cds_wt_3842	-	UPF0286 protein Mvan_4308;
cds_wt_3843	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3844	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3845	-	Uncharacterized protein RP471;
cds_wt_3846	-	Uncharacterized protein Mb1356;
cds_wt_3847	gabD	putative aldehyde dehydrogenase
cds_wt_3848	-	ABC transporter, ATP-binding protein
cds_wt_3849	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3850	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3851	phr2	Cryptochrome DASH;
cds_wt_3852	-	Laminin subunit beta-1; Laminin B1 chain;
		Laminin subunit alpha-3; Epiligrin 170 kDa subunit;
cds_wt_3853	-	E170; Nicein subunit alpha;

cds_wt_3854	MCEE	Methylmalonyl-CoA epimerase, mitochondrial; DL-methylmalonyl-CoA racemase;
cds_wt_3855	phbA	acetyl-CoA acetyltransferase
cds_wt_3856	-	Negative transcription regulator padR;
cds_wt_3857	-	hypothetical protein
cds_wt_3858	icmA	methylmalonyl-CoA mutase, N-terminus of large subunit
cds_wt_3859	trxA	putative thioredoxin
cds_wt_3860	arc	arginase
cds_wt_3861	pbp	putative penicillin-binding protein
cds_wt_3862	gdh	hypothetical protein
cds_wt_3863	-	Xylose repressor;
cds_wt_3864	-	putative iron transport system ATP-binding protein
cds_wt_3865	pfkB	ribokinase
cds_wt_3866	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3867	crt2	putative enoyl-coA hydratase
cds_wt_3868	ilvG	acetolactate synthase large subunit
cds_wt_3869	-	RNA polymerase sigma-E factor;
cds_wt_3870	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3871	-	membrane protein
cds_wt_3872	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3873	yidH	Inner membrane protein yidH;
cds_wt_3874	fixA	Protein fixA;
cds_wt_3875	fixB	Protein fixB;
cds_wt_3876	iscS	putative pyridoxal-phosphate-dependent aminotransferase
cds_wt_3877	trmU	tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase
cds_wt_3878	-	hypothetical protein
cds_wt_3879	ligA	DNA ligase
cds_wt_3880	-	putative phosphodiesterase
cds_wt_3881	gatC	Glutamyl-tRNA
cds_wt_3882	gatA	glutamyl-tRNA(Gln) amidotransferase, subunit A
cds_wt_3883	-	Aminopeptidase 2, mitochondrial; Aminopeptidase II; AP-II; YscII;
cds_wt_3884	gatB	glutamyl-tRNA(Gln) amidotransferase subunit B
cds_wt_3885	-	Uncharacterized metallophosphoesterase aq_1054;
cds_wt_3886	-	putative oxidoreductase
cds_wt_3887	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3888	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3889	rtn	Uncharacterized protein AZC_3085;
cds_wt_3890	lacI	HTH-type transcriptional repressor purR; Purine nucleotide synthesis repressor; Pur regulon repressor;
cds_wt_3891	-	Uncharacterized MFS-type transporter C16A3.17c;
cds_wt_3892	-	hypothetical protein
cds_wt_3893	SFI1	Protein SFI1 homolog;
cds_wt_3894	cotA	spore coat protein (outer)
cds_wt_3895	-	hypothetical protein predicted by Glimmer/Critica

cds_wt_3896	mpx	secreted hemolysin-type calcium-binding bacteriocin, putative
cds_wt_3897	ilvD	dihydroxy-acid dehydratase
cds_wt_3898	-	Signaling protein ykoW;
cds_wt_3899	ilvB	acetolactate synthase large subunit
cds_wt_3900	ilvN	acetolactate synthase small subunit
cds_wt_3901	ilvC	ketol-acid reductoisomerase
cds_wt_3902	serA	D-3-phosphoglycerate dehydrogenase
cds_wt_3903	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3904	leuB	3-isopropylmalate dehydrogenase
cds_wt_3905	ilvE	branched-chain amino acid aminotransferase
cds_wt_3906	-	hypothetical protein
cds_wt_3907	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3908	prfB	Peptide chain release factor 1; RF-1;
cds_wt_3909	pqqL	Mitochondrial-processing peptidase subunit beta; Beta-MPP; P-52;
cds_wt_3910	pqqL	Uncharacterized zinc protease ML0855;
cds_wt_3911	-	hypothetical protein
cds_wt_3912	rimJ	ribosomal protein alanine acetyltransferase
cds_wt_3913	thrS	threonyl-tRNA synthetase
cds_wt_3914	leuA	2-isopropylmalate synthase
cds_wt_3915	-	hypothetical protein
cds_wt_3916	-	putative membrane protein
cds_wt_3917	-	hypothetical protein
cds_wt_3918	-	Spermidine/putrescine import ATP-binding protein potA;
cds_wt_3919	-	putative transporter
cds_wt_3920	-	Uncharacterized HTH-type transcriptional regulator MJ0272;
cds_wt_3921	-	possible 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase (HhdD isomerase)
cds_wt_3922	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3923	iclR	HTH-type transcriptional repressor allR; Negative regulator of allantoin and glyoxylate utilization operons;
cds_wt_3924	leuC	3-isopropylmalate dehydratase large subunit
cds_wt_3925	leuD	3-isopropylmalate dehydratase small subunit
cds_wt_3926	hupB	Integration host factor subunit beta; IHF-beta;
cds_wt_3927	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3928	-	hypothetical protein
cds_wt_3929	ppk	polyphosphate kinase
cds_wt_3930	plsC	putative acyltransferase
cds_wt_3931	gpsA	glycerol-3-phosphate dehydrogenase (NAD(P)+)
cds_wt_3932	cthI	cystathionine gamma-lyase
cds_wt_3933	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3934	ddlA	D-alanine-D-alanine ligase
cds_wt_3935	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3936	-	Uncharacterized HTH-type transcriptional regulator PH1916;
cds_wt_3937	thiL	thiamine monophosphate kinase

cds_wt_3938	-	IAA acetyltransferase;
cds_wt_3939	rpmB	50S ribosomal protein L28;
cds_wt_3940	degV	Uncharacterized protein SAS1160;
cds_wt_3941	recG	ATP-dependent DNA helicase RecG
cds_wt_3942	-	hypothetical protein
cds_wt_3943	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3944	-	hypothetical protein
cds_wt_3945	kdtB	pantetheine-phosphate adenylyltransferase
cds_wt_3946	ntpF	Uncharacterized protein ML1661;
cds_wt_3947	-	Uncharacterized protein ML1660;
cds_wt_3948	rpmF	50S ribosomal protein L32;
cds_wt_3949	plsX	Fatty acid/phospholipid synthesis protein plsX;
cds_wt_3950	rnc	ribonuclease III
		GPI mannosyltransferase 2; GPI
		mannosyltransferase II; GPI-MT-II;
		Phosphatidylinositol-glycan biosynthesis class V
cds_wt_3951	Pigv	protein; PIG-V;
cds_wt_3952	fpg	formamidopyrimidine-DNA glycosylase
cds_wt_3953	-	Spherulin-4;
		Histone-lysine N-methyltransferase MLL3;
		Myeloid/lymphoid or mixed-lineage leukemia protein
		3; Homologous to ALR protein; Lysine N-
		methyltransferase 2C;
cds_wt_3954	-	
cds_wt_3955	icsA	Glycogen synthase; Starch
cds_wt_3956	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3957	smc	Chromosome partition protein smc;
cds_wt_3958	smc	Chromosome partition protein smc;
cds_wt_3959	-	Phosphoglycolate phosphatase; PGPase; PGP;
cds_wt_3960	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3961	-	Mini-circle uncharacterized 19.1 kDa protein;
cds_wt_3962	-	hypothetical protein
cds_wt_3963	ftsY	Cell division protein ftsY homolog;
cds_wt_3964	tfxG	Trifolitoxin immunity protein;
cds_wt_3965	amt	Ammonium transporter 1 member 2; LeAMT1;2;
cds_wt_3966	glnB	Nitrogen regulatory protein P-II;
cds_wt_3967	glnD	PII uridylyl-transferase
cds_wt_3968	pglA	putative glycosyl transferase
		Protein-L-isoaspartate O-methyltransferase; Protein-
		beta-aspartate methyltransferase; PIMT; Protein L-
		isoaspartyl methyltransferase; L-isoaspartyl protein
		carboxyl methyltransferase;
cds_wt_3969	-	
cds_wt_3970	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3971	-	hypothetical protein
cds_wt_3972	pglA	putative glycosyl transferase
cds_wt_3973	-	UDP-N-acetylglucosamine--N-acetylmuramyl-
cds_wt_3974	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3975	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3976	wbpC	Putative peptidoglycan O-acetyltransferase yrhL;
cds_wt_3977	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3978	-	putative glycosyl transferase

cds_wt_3979	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3980	wbpA	putative UDP-glucose/GDP-mannose dehydrogenase
cds_wt_3981	cpsY	hypothetical protein
cds_wt_3982	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3983	ffh	Signal recognition 54 kDa protein; SRP54;
cds_wt_3984	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3985	-	Uncharacterized protein Rv2915c/MT2982.1;
cds_wt_3986	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_3987	-	RNA polymerase sigma factor sigW; Sigma-W factor;
cds_wt_3988	proS	prolyl-tRNA synthetase
cds_wt_3989	-	hypothetical protein
cds_wt_3990	rpsP	30S ribosomal protein S16;
cds_wt_3991	-	UPF0109 protein Mb2932c;
cds_wt_3992	rimM	Ribosome maturation factor rimM;
cds_wt_3993	trmD	tRNA (guanine-N1)-methyltransferase
cds_wt_3994	rplS	50S ribosomal protein L19;
cds_wt_3995	lepB	signal peptidase I
cds_wt_3996	lepB	signal peptidase I
cds_wt_3997	-	RNA pyrophosphohydrolase;
cds_wt_3998	rnhB	ribonuclease HII
cds_wt_3999	-	Uncharacterized protein Mb2925c;
cds_wt_4000	-	Uncharacterized protein Rv2891/MT2958.2;
cds_wt_4001	cefD	isopenicillin N epimerase
cds_wt_4002	xerC	Tyrosine recombinase xerC;
cds_wt_4003	-	Putative transcriptional regulator of 2-aminoethylphosphonate degradation operons;
cds_wt_4004	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4005	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4006	smf	Uncharacterized protein Rv2896c/MT2964;
cds_wt_4007	-	Uncharacterized protein Mb2921c;
cds_wt_4008	-	UPF0102 protein Gmet_2864;
cds_wt_4009	rpsB	30S ribosomal protein S2;
cds_wt_4010	tsf	Elongation factor Ts; EF-Ts;
cds_wt_4011	pyrH	uridylate kinase
cds_wt_4012	frr	Ribosome-recycling factor; RRF; Ribosome-releasing factor;
cds_wt_4013	cdsA	phosphatidate cytidyltransferase
cds_wt_4014	-	Ribosomal RNA large subunit methyltransferase N;
cds_wt_4015	-	23S rRNA m2A2503 methyltransferase;
cds_wt_4016	-	Protein piccolo; Aczonin; Flags: Fragment;
		hypothetical protein predicted by Glimmer/Critica
		Cytidine monophosphate-N-acetylneuraminic acid hydroxylase; CMP-N-acetylneuraminic acid hydroxylase; CMP-Neu5Ac hydroxylase; CMP-NeuAc hydroxylase; CMP-N-acetylneuraminate monooxygenase; Flags: Fragment;
cds_wt_4017	CMAH	Probable oxidoreductase C10orf33;
cds_wt_4018	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4019	-	1-deoxy-D-xylulose 5-phosphate reductoisomerase
cds_wt_4020	dxr	hypothetical zinc metalloprotease
cds_wt_4021	-	

cds_wt_4022	ispG	putative 1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate synthase
cds_wt_4023	-	Serotonin N-acetyltransferase; Serotonin acetylase;
cds_wt_4024	-	Aralkylamine N-acetyltransferase; AA-NAT;
cds_wt_4025	ydfF	Uncharacterized protein yqjI;
cds_wt_4026	mer2	Uncharacterized HTH-type transcriptional regulator ydfF;
cds_wt_4027	bag	5,10-methylenetetrahydromethanopterin reductase;
cds_wt_4028	pip	Coenzyme F420-dependent N
cds_wt_4029	acrR	Spermidine/putrescine import ATP-binding protein potA;
cds_wt_4030	-	Phage infection protein;
cds_wt_4031	-	HTH-type transcriptional regulator acrR; Potential
cds_wt_4032	PHY1	acrAB operon repressor;
cds_wt_4033	-	putative DNA-binding protein
cds_wt_4034	yhaQ	Probable heavy metal-dependent transcriptional
cds_wt_4035	-	regulator HI0293;
cds_wt_4036	-	Phytochrome 1;
cds_wt_4037	-	Transcriptional regulatory protein ydfI;
cds_wt_4038	-	Spermidine/putrescine import ATP-binding protein
cds_wt_4039	aldC	potA;
cds_wt_4040	-	Uncharacterized protein yhaP;
cds_wt_4041	-	Integrin alpha-8; Contains: Integrin alpha-8 heavy
cds_wt_4042	-	chain; Contains: Integrin alpha-8 light chain;
cds_wt_4043	cckA	Uncharacterized amino-acid permease C1039.01;
cds_wt_4044	-	putative glutamine synthetase
cds_wt_4045	-	aldehyde dehydrogenase
cds_wt_4046	mapB	probable short chain dehydrogenase
cds_wt_4047	-	hypothetical protein
cds_wt_4048	-	hypothetical protein
cds_wt_4049	-	two-component hybrid sensor and regulator
cds_wt_4050	-	Uncharacterized protein Rv1364c/MT1410;
cds_wt_4051	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4052	nusA	methionine aminopeptidase
cds_wt_4053	-	Fe
cds_wt_4054	infB	hypothetical protein predicted by Glimmer/Critica
cds_wt_4055	infB	hypothetical protein
cds_wt_4056	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4057	-	UPF0090 protein VP2458;
cds_wt_4058	rbfA	Transcription elongation protein nusA;
cds_wt_4059	mgpA	hypothetical protein
		Translation initiation factor IF-2;
		Translation initiation factor IF-2;
		hypothetical protein
		Uncharacterized protein ylxP; ORF5;
		Ribosome-binding factor A;
		Probable manganese-dependent inorganic
		pyrophosphatase; Pyrophosphate phospho-
		hydrolase; PPase;

cds_wt_4060	dinF	Multidrug resistance protein mdtK; Multidrug-efflux transporter;
cds_wt_4061	truB	tRNA pseudouridine synthase B
cds_wt_4062	kdpE	Transcriptional regulatory protein resD;
cds_wt_4063	-	Aerobic respiration control sensor protein arcB;
cds_wt_4064	ribF	riboflavin kinase / FMN adenylyltransferase
cds_wt_4065	rpsO	30S ribosomal protein S15;
cds_wt_4066	gpsI	polyribonucleotide nucleotidyltransferase
cds_wt_4067	pepR	putative zinc protease
cds_wt_4068	dapB	dihydrodipicolinate reductase
cds_wt_4069	-	HTH-type transcriptional regulator hmrR; Copper efflux regulator; Copper export regulator;
cds_wt_4070	-	Cold shock protein cspA; CSP-A; 7.4 kDa cold shock protein; CS7.4;
cds_wt_4071	-	Uncharacterized N-acetyltransferase yuaI;
cds_wt_4072	yfbM	Uncharacterized N-acetyltransferase yuaI;
cds_wt_4073	-	Uncharacterized protein ycaQ;
cds_wt_4074	-	hypothetical protein
cds_wt_4075	dapA	dihydrodipicolinate synthase
cds_wt_4076	-	Ribonuclease J 2; RNase J2;
cds_wt_4077	sprB	Serine protease 1; Serine protease I; RPI;
cds_wt_4078	-	hypothetical protein
cds_wt_4079	ftsK	DNA translocase ftsK;
cds_wt_4080	-	hypothetical protein
cds_wt_4081	-	hypothetical protein
cds_wt_4082	-	
cds_wt_4083	pgsA	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase
cds_wt_4084	-	Putative competence-damage inducible protein;
cds_wt_4085	-	hypothetical protein
cds_wt_4086	-	Laminin subunit beta-1; Laminin B1 chain;
cds_wt_4087	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4088	nei	putative endonuclease VIII
cds_wt_4089	-	Alkanesulfonate monooxygenase; FMNH2-dependent aliphatic sulfonate monooxygenase;
cds_wt_4090	lhr	member of ATP-dependent helicase superfamily II
cds_wt_4091	-	putative serine/threonine protein kinase
cds_wt_4092	-	Leucine efflux protein;
cds_wt_4093	-	Uncharacterized protein YIR042C;
cds_wt_4094	ptsJ	Serine hydroxymethyltransferase; Serine methylase; SHMT;
cds_wt_4095	dpoL	putative DNA polymerase related protein
cds_wt_4096	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4097	recA	putative RecA protein
cds_wt_4098	recX	Regulatory protein recX;
cds_wt_4099	-	2',3'-cyclic-nucleotide 2'-phosphodiesterase;
cds_wt_4100	gluD	Arginine transport system permease protein artQ;
cds_wt_4101	occM	Octopine transport system permease protein occM;
cds_wt_4102	gluB	Membrane-bound lytic murein transglycosylase F; EC=4.2.2.n1; Murein lyase F;

cds_wt_4103	gluA	ABC-type polar amino acid transport system ATPase component
cds_wt_4104	miaB	
cds_wt_4105	-	RNA polymerase sigma-E factor;
cds_wt_4106	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4107	-	Probable RuBisCO transcriptional regulator;
cds_wt_4108	thd	threonine dehydratase
cds_wt_4109	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4110	-	conserved hypothetical protein
cds_wt_4111	-	hypothetical protein
cds_wt_4112	miaA	tRNA delta(2)-isopentenylpyrophosphate transferase
cds_wt_4113	dapF	diaminopimelate epimerase
cds_wt_4114	me	malic enzyme
cds_wt_4115	hflX	GTP-binding protein
cds_wt_4116	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4117	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4118	lexA	SOS regulatory protein
cds_wt_4119	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4120	-	Transcriptional repressor nrdR;
cds_wt_4121	nrdA	ribonucleoside-diphosphate reductase alpha chain
cds_wt_4122	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4123	ybjJ	Inner membrane protein ybjJ;
cds_wt_4124	-	Abhydrolase domain-containing protein 7; Epoxide hydrolase-related protein;
cds_wt_4125	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4126	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4127	ideR	Iron-dependent repressor ideR;
cds_wt_4128	acuC	putative acetoin dehydrogenase
cds_wt_4129	-	hypothetical protein
cds_wt_4130	-	conserved hypothetical protein
cds_wt_4131	sigA	RNA polymerase principal sigma factor hrdB;
cds_wt_4132	-	Sporulation-control protein spo0M; Stage 0 sporulation protein M;
cds_wt_4133	dtd	D-tyrosyl-tRNA(Tyr) deacylase
cds_wt_4134	-	Polycystic kidney disease protein 1-like 3; Polycystin-1L3; PC1-like 3 protein;
cds_wt_4135	mcpA	Laminin subunit alpha-3; Nicein subunit alpha;
cds_wt_4136	-	Chemotaxis protein cheW;
cds_wt_4137	cheB	protein-glutamate methylesterase CheB
cds_wt_4138	-	hypothetical protein
cds_wt_4139	cheR	chemotaxis protein methyltransferase CheR
cds_wt_4140	cheY	Probable transcriptional regulator ycf27; OmpR-like protein;
cds_wt_4141	cheA	Chemotaxis protein cheA;
cds_wt_4142	cheA	histidine kinase
cds_wt_4143	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4144	cheY	Transcriptional regulatory protein resD;
cds_wt_4145	mcpB	Methyl-accepting chemotaxis protein tlpB;
cds_wt_4146	-	GAF domain/GGDEF domain/EAL domain protein
cds_wt_4147	-	hypothetical protein

cds_wt_4148	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4149	suk	putative sugar kinase
cds_wt_4150	indA	UPF0724 protein yeiN;
cds_wt_4151	-	hypothetical protein
cds_wt_4152	-	UPF0126 membrane protein HI1240;
cds_wt_4153	sdrA	Uncharacterized protein Rv2917/MT2985;
cds_wt_4154	-	Uncharacterized signaling protein PA3311;
cds_wt_4155	-	Uncharacterized signaling protein PA1727;
cds_wt_4156	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4157	sigA	RNA polymerase sigma factor rpoD; Sigma-A;
cds_wt_4158	suhB	putative extragenic suppressor protein homolog
cds_wt_4159	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4160	-	hypothetical protein
cds_wt_4161	-	hypothetical protein
cds_wt_4162	dut	deoxyuridine 5'-triphosphate nucleotidohydrolase
cds_wt_4163	-	hypothetical protein
cds_wt_4164	-	hypothetical protein
cds_wt_4165	-	hypothetical protein
cds_wt_4166	trkB	Trk system potassium uptake protein trkA homolog; K
cds_wt_4167	ceoB	Trk system potassium uptake protein trkA; K
cds_wt_4168	-	Aromatic amino acid transport protein aroP; General aromatic amino acid permease;
cds_wt_4169	-	putative RNA methyltransferase
cds_wt_4170	folD	methylenetetrahydrofolate dehydrogenase (NADP+) / methenyltetrahydrofolate cyclohydrolase
cds_wt_4171	dctA	C4-dicarboxylate transport protein;
cds_wt_4172	dxs	putative 1-deoxy-D-xylulose 5-phosphate synthase
cds_wt_4173	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4174	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4175	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4176	cutR	Alkaline phosphatase synthesis transcriptional regulatory protein phoP;
cds_wt_4177	cutS	sensor histidine kinase
cds_wt_4178	-	Polycystic kidney disease protein 1-like 3; Polycystin-1L3; PC1-like 3 protein;
cds_wt_4179	fadJ	fatty acid oxidation complex alpha-subunit
cds_wt_4180	atoB	acetyl-CoA acetyltransferase
cds_wt_4181	rnd	ribonuclease D, putative
cds_wt_4182	htrB	Protease Do-like 4, mitochondrial;
cds_wt_4183	hemE	uroporphyrinogen decarboxylase
cds_wt_4184	hemY	protoporphyrinogen oxidase
cds_wt_4185	-	UPF0447 protein BLi03998/BL03956;
cds_wt_4186	wrbA	Flavoprotein wrbA;
cds_wt_4187	thyA	thymidylate synthase
cds_wt_4188	folA	dihydrofolate reductase
cds_wt_4189	-	peptide methionine sulfoxide reductase
cds_wt_4190	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4191	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4192	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4193	-	hypothetical protein predicted by Glimmer/Critica

cds_wt_4194	-	hypothetical protein
cds_wt_4195	-	Uncharacterized N-acetyltransferase MJ1207;
cds_wt_4196	slpE	Uncharacterized protein Mb2247c;
cds_wt_4197	ligC	putative DNA ligase
cds_wt_4198	-	hypothetical protein
cds_wt_4199	-	hypothetical protein
cds_wt_4200	-	Uncharacterized protein Mb1296;
cds_wt_4201	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4202	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4203	-	HTH-type transcriptional regulator betI;
cds_wt_4204	dgt	deoxyguanosinetriphosphate triphosphohydrolase
cds_wt_4205	-	hypothetical protein predicted by Glimmer/Critica
		N-acyl-phosphatidylethanolamine-hydrolyzing phospholipase D; N-acyl phosphatidylethanolamine phospholipase D; NAPE-hydrolyzing phospholipase D; NAPE-PLD;
cds_wt_4206	romA	
cds_wt_4207	linA	Lincosamide resistance protein;
cds_wt_4208	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4209	-	Probable lipid kinase yegS-like;
		DNA-3-methyladenine glycosylase; 3-methyladenine-DNA glycosidase;
cds_wt_4210	-	
		Ribosome-binding protein 1; Ribosome receptor protein; 180 kDa ribosome receptor homolog; ES/130-related protein;
cds_wt_4211	-	
cds_wt_4212	-	putative secreted protein
cds_wt_4213	-	putative lipoprotein
cds_wt_4214	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4215	-	putative membrane protein
cds_wt_4216	sigL	RNA polymerase sigma factor sigK; Sigma-K factor;
cds_wt_4217	-	hypothetical protein
		Spermidine/putrescine import ATP-binding protein potA;
cds_wt_4218	sbcC	
cds_wt_4219	sbcC	DNA replication and repair protein recF;
cds_wt_4220	sbcD	Nuclease sbcCD subunit D;
cds_wt_4221	-	hypothetical protein
cds_wt_4222	ribD	5-amino-6-(5-phosphoribosylamino)uracil reductase
cds_wt_4223	-	
cds_wt_4224	-	hypothetical protein
cds_wt_4225	-	Uncharacterized protein Mb1616;
cds_wt_4226	bioB	biotin synthase
cds_wt_4227	bioF	8-amino-7-oxononanoate synthase
cds_wt_4228	bioD	dethiobiotin synthetase
cds_wt_4229	ppgK	polyphosphate glucokinase
		Haloacid dehalogenase-like hydrolase domain-containing protein 3;
cds_wt_4230	-	
cds_wt_4231	-	hypothetical protein
cds_wt_4232	-	Signaling protein ykoW;
		UDP-glucose 4-epimerase; UDP-galactose 4-epimerase; Galactowaldenase;
cds_wt_4233	galE	
cds_wt_4234	lsr2	Protein lsr2; 15 kDa antigen; A15;

cds_wt_4235	choD	putative cholesterol oxidase
cds_wt_4236	-	Dolichyl-phosphate-mannose--protein
cds_wt_4237	acsA	mannosyltransferase 1;
cds_wt_4238	-	putative acetyl-coenzyme A synthetase
cds_wt_4239	-	conserved hypothetical protein
cds_wt_4240	wcbT	Putative membrane protein mmpL11;
cds_wt_4241	-	putative polyketide synthase
cds_wt_4242	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4243	-	Fatty acid desaturase 2-like protein;
		Sensor histidine kinase liaS;
cds_wt_4244	nreC	Oxygen regulatory protein nreC; Nitrogen regulation
cds_wt_4245	-	protein C;
cds_wt_4246	-	Ycf48-like protein;
cds_wt_4247	-	hypothetical protein
cds_wt_4248	-	acyl-CoA dehydrogenase family protein
cds_wt_4249	-	hypothetical protein
		hypothetical protein predicted by Glimmer/Critica
		HTH-type transcriptional repressor purR; Purine
		nucleotide synthesis repressor; Pur regulon
cds_wt_4250	purR	repressor;
cds_wt_4251	abfA	alpha-L-arabinofuranosidase
		Endoglucanase C; Endo-1,4-beta-glucanase C; EGC;
cds_wt_4252	celC	Cellulase C; Cellodextrinase C;
cds_wt_4253	glcI	Glucan endo-1,3-beta-glucosidase;
cds_wt_4254	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4255	bga7	beta-galactosidase
cds_wt_4256	-	Uncharacterized protein ybiU;
cds_wt_4257	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4258	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4259	-	HTH-type transcriptional regulator betI;
cds_wt_4260	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4261	ftrA	HTH-type transcriptional regulator glxA;
cds_wt_4262	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4263	slpD	probable exported protease
cds_wt_4264	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4265	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4266	alcB	Putative lysine N-acyltransferase C17G9.06c;
cds_wt_4267	-	penicillin amidase
cds_wt_4268	alcC	Rhizobactin siderophore biosynthesis protein rhbF;
cds_wt_4269	alcA	Alcaligin biosynthesis enzyme;
cds_wt_4270	ysuJ	putative decarboxylase
cds_wt_4271	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4272	-	Uncharacterized signaling protein PA3311;
cds_wt_4273	cobK	precorrin-6x reductase
		precorrin-6Y C5,15-methyltransferase
cds_wt_4274	cobL	(decarboxylating)
cds_wt_4275	-	putative oxidoreductase
		Phosphoinositide phospholipase C 6;
		Phosphoinositide phospholipase PLC6; PI-PLC6;
cds_wt_4276	-	AtPLC6; AtPLC8;

cds_wt_4277	nosX	Thiamine biosynthesis lipoprotein apbE;
cds_wt_4278	-	UPF0256 protein SAV_4024;
cds_wt_4279	tnpR	Transposon Tn552 DNA-invertase binR;
cds_wt_4280	tnpR	DNA-invertase from lambdoid prophage e14;
cds_wt_4281	X	Uncharacterized protein X;
cds_wt_4282	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4283	-	Kinesin light chain; KLC;
cds_wt_4284	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4285	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4286	-	hypothetical protein
cds_wt_4287	-	Seed lectin; LECSJASG;
cds_wt_4288	-	Uncharacterized HTH-type transcriptional regulator yobV;
cds_wt_4289	lipH	hypothetical protein
cds_wt_4290	Klc2	Kinesin light chain 2; KLC 2;
cds_wt_4291	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4292	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4293	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4294	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4295	-	hypothetical protein
cds_wt_4296	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4297	ydjl	hypothetical protein
cds_wt_4298	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4299	-	RNA polymerase sigma factor ylaC;
cds_wt_4300	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4301	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4302	msbA	ABC transporter ATP-binding protein
cds_wt_4303	-	Signal peptidase I T; SPase I; Leader peptidase I;
cds_wt_4304	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4305	-	Adaptive-response sensory-kinase sasA;
cds_wt_4306	-	Synechococcus adaptive sensor protein A;
cds_wt_4307	-	hypothetical protein
cds_wt_4308	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4309	-	GTP-binding protein lepA;
cds_wt_4310	-	D-amino acid dehydrogenase small subunit;
cds_wt_4311	-	UPF0353 protein Mvan_2751;
cds_wt_4312	-	UPF0353 protein Mvan_2751;
cds_wt_4313	-	Uncharacterized protein Mb1516;
cds_wt_4314	-	ATP-dependent Clp protease ATP-binding subunit clpX;
cds_wt_4315	moxR	clpX;
cds_wt_4316	degP	peptidase S1 and S6, chymotrypsin/Hap
cds_wt_4317	-	Collagen alpha-5
cds_wt_4318	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4319	-	Tolloid-like protein 1;
cds_wt_4320	-	putative IS630 family transposase
cds_wt_4321	-	fibronectin type III domain protein
cds_wt_4322	-	putative secreted protein
cds_wt_4323	-	Teneurin-1; Ten-1; Tenascin-M1; Ten-m1; Protein
cds_wt_4324	-	Odd Oz/ten-m homolog 1;
cds_wt_4325	-	hypothetical protein predicted by Glimmer/Critica

cds_wt_4323	-	Uncharacterized protein y4sN;
cds_wt_4324	-	hypothetical protein predicted by Glimmer/Critica
		Uncharacterized ATP-dependent helicase
cds_wt_4325	-	C29A10.10c;
cds_wt_4326	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4327	-	RNA polymerase sigma-E factor; Sigma-24;
cds_wt_4328	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4329	-	Uncharacterized protein yfaP;
cds_wt_4330	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4331	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4332	-	glutaryl-CoA dehydrogenase
cds_wt_4333	-	hypothetical protein
		Mucin-6; MUC-6; Gastric mucin-6; Secreted gel-forming mucin-6;
cds_wt_4334	Muc6	
cds_wt_4335	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4336	-	hypothetical protein predicted by Glimmer/Critica
		UvrABC system protein A; UvrA protein;
cds_wt_4337	drnC	Excinuclease ABC subunit A;
cds_wt_4338	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4339	-	RNA polymerase sigma factor sigZ;
		MANSC domain-containing protein 1; Loss of heterozygosity 12 chromosomal region 3 protein;
cds_wt_4340	-	
cds_wt_4341	malP	glycogen phosphorylase
		Glutamine amidotransferase subunit pdxT; Glutamine amidotransferase glutaminase subunit pdxT;
cds_wt_4342	-	
cds_wt_4343	-	Phosphoglycolate phosphatase 1; PGPase 1; PGP 1; 4'-phosphopantetheinyl transferase entD; Enterobactin synthetase component D; Enterochelin synthase D;
cds_wt_4344	-	
		Uncharacterized WD repeat-containing protein
cds_wt_4345	-	alr3466;
		Uncharacterized WD repeat-containing protein
cds_wt_4346	-	all2124;
cds_wt_4347	-	hypothetical protein
		5,10-methylenetetrahydromethanopterin reductase;
cds_wt_4348	-	Coenzyme F420-dependent N
cds_wt_4349	-	Uncharacterized transporter yycB;
cds_wt_4350	viuB	Vibriobactin utilization protein viuB;
cds_wt_4351	14	Glycoprotein GPV;
cds_wt_4352	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4353	-	Seed lectin; LECSJASG;
		Dolichol-phosphate mannosyltransferase; Dolichol-phosphate mannose synthase; DPM synthase; Dolichyl-phosphate beta-D-mannosyltransferase; Mannose-P-dolichol synthase; MPD synthase;
cds_wt_4354	Dpm1	
cds_wt_4355	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4356	-	Translation initiation factor IF-2;
cds_wt_4357	-	Glycogen synthase; Starch
cds_wt_4358	-	glycosyl transferase

cds_wt_4359	-	Endoglucanase; Endo-1,4-beta-glucanase; Carboxymethyl-cellulase; CMCase; Cellulase; precorrin-2 C20-methyltransferase / precorrin-3B C17-methyltransferase
cds_wt_4360	cobI	precorrin-8X methylmutase
cds_wt_4361	cobH	possible cobalamin biosynthesis protein CobG
cds_wt_4362	cobG	cobalamin biosynthesis protein
cds_wt_4363	cobN	Uncharacterized protein ydfG;
cds_wt_4364	ydfG	putative sigma factor
cds_wt_4365	-	tetrapyrrole methylase family protein
cds_wt_4366	cobF	hypothetical protein predicted by Glimmer/Critica
cds_wt_4367	-	RNA polymerase sigma factor sigW; Sigma-W factor;
cds_wt_4368	sigW	Cold shock protein cspA; CSP-A; 7.4 kDa cold shock protein; CS7.4;
cds_wt_4369	-	DNA polymerase IV
cds_wt_4370	dinP	17.5 kDa class I heat shock protein; HSP 17.5-M;
cds_wt_4371	hspX	Arabinoxylan arabinofuranohydrolase; AXH; AXH-m2,3; AXH-m23; Alpha-L-arabinofuranosidase; AF;
cds_wt_4372	-	Alkanal monooxygenase alpha chain; Bacterial luciferase alpha chain;
cds_wt_4373	luxA	Signaling protein ykoW;
cds_wt_4374	-	Nitrate/nitrite response regulator protein narP;
cds_wt_4375	-	Sensor protein vraS;
cds_wt_4376	-	expressed protein
cds_wt_4377	-	hypothetical protein
cds_wt_4378	ykoU	hypothetical protein predicted by Glimmer/Critica
cds_wt_4379	-	hypothetical protein
cds_wt_4380	-	Uncharacterized protein R02095;
cds_wt_4381	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4382	-	Fimbriae Z protein;
cds_wt_4383	-	Nuclear receptor interaction protein; NRIP; IQ motif and WD repeat-containing protein 1;
cds_wt_4384	-	hypothetical protein
cds_wt_4385	-	hypothetical protein
cds_wt_4386	-	Putative transcriptional regulatory protein for hcr operon;
cds_wt_4387	-	ribonuclease H
cds_wt_4388	rnhA	Spermidine/putrescine import ATP-binding protein potA;
cds_wt_4389	-	putative integral membrane transport protein
cds_wt_4390	-	Spermidine/putrescine import ATP-binding protein potA;
cds_wt_4391	-	Pleiotropic drug resistance protein 3; OsPDR9;
cds_wt_4392	-	Sensor protein vraS;
cds_wt_4393	-	Transcriptional regulatory protein degU; Protease production enhancer protein;
cds_wt_4394	yvqC	alkaline phosphatase
cds_wt_4395	phoA	hemagglutinin
cds_wt_4396	-	Lipid A export ATP-binding/permease protein msbA;
cds_wt_4397	pimB	Lipid A export ATP-binding/permease protein msbA;
cds_wt_4398	pimA	

cds_wt_4399	-	putative membrane protein
cds_wt_4400	-	hypothetical protein
cds_wt_4401	-	hypothetical protein
cds_wt_4402	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4403	ubiE	Menaquinone biosynthesis methyltransferase ubiE;
cds_wt_4404	-	HMP-PP phosphatase;
cds_wt_4405	ppnK	probable inorganic polyphosphate/ATP-NAD kinase
cds_wt_4406	trxB	putative thioredoxin reductase
cds_wt_4407	ETR1	similar to two-component sensor histidine kinase
cds_wt_4408	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4409	-	Putative S-adenosyl-L-methionine-dependent methyltransferase MAV_4444;
cds_wt_4410	-	hypothetical protein
cds_wt_4411	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4412	-	Probable glucarate transporter; D-glucarate permease;
cds_wt_4413	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4414	pop	acylamino-acid-releasing enzyme
cds_wt_4415	asnB	asparagine synthase, glutamine-hydrolyzing
cds_wt_4416	-	Carboxylate-amine ligase Francci3_2911;
cds_wt_4417	rfbE	CDP-tyvelose-2-epimerase
cds_wt_4418	-	Polycystic kidney disease protein 1-like 3; Polycystin-1L3; PC1-like 3 protein;
cds_wt_4419	ST2	carbonic anhydrase
cds_wt_4420	lacI	HTH-type transcriptional repressor purR; Purine nucleotide synthesis repressor; Pur regulon repressor;
cds_wt_4421	-	sn-glycerol-3-phosphate-binding periplasmic protein ugpB;
cds_wt_4422	araP	L-arabinose transport system permease protein araP;
cds_wt_4423	lacG	sn-glycerol-3-phosphate transport system permease protein ugpE;
cds_wt_4424	aglA	putative alpha-glucosidase
cds_wt_4425	-	putative secreted glycosyl hydrolase
cds_wt_4426	chb	Tenascin; TN; Tenascin-C; TN-C; Hexabrachion; Cytotactin; Neuronectin; GMEM; JI; Myotendinous antigen; Glioma-associated-extracellular matrix antigen; GP 150-225; P230;
cds_wt_4427	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4428	mcpK	Methyl-accepting chemotaxis protein II; MCP-II; Aspartate chemoreceptor protein;
cds_wt_4429	-	UPF0225 protein CV_3559;
cds_wt_4430	-	tryptophan 2,3-dioxygenase
cds_wt_4431	kynU	kynureninase
cds_wt_4432	-	Myosin-XVIIIb;
cds_wt_4433	yvaA	Uncharacterized oxidoreductase yvaA;
cds_wt_4434	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4435	-	hypothetical protein
cds_wt_4436	-	hypothetical protein
cds_wt_4437	-	hypothetical protein

cds_wt_4438	rfaG	Glycogen synthase; Starch
cds_wt_4439	-	putative glycosyltransferase
cds_wt_4440	malL	oligo-1,6-glucosidase
cds_wt_4441	-	putative regulator
cds_wt_4442	psp5	Peptidoglycan-recognition protein-LF; PGRP-like protein;
cds_wt_4443	-	Uncharacterized protein Rv1260/MT1298;
cds_wt_4444	-	Fatty acid metabolism regulator protein;
cds_wt_4445	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4446	kdgA	2-dehydro-3-deoxyphosphogluconate aldolase / 4-hydroxy-2-oxoglutarate aldolase
cds_wt_4447	kdgK	2-keto-3-deoxygluconate kinase
cds_wt_4448	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4449	-	hypothetical protein
cds_wt_4450	-	HTH-type transcriptional regulator cueR; Copper efflux regulator; Copper export regulator;
cds_wt_4451	-	hypothetical protein
cds_wt_4452	-	hypothetical protein
cds_wt_4453	-	HTH-type transcriptional regulator glxA;
cds_wt_4454	-	hypothetical protein
cds_wt_4455	-	hypothetical protein
cds_wt_4456	-	hypothetical protein
cds_wt_4457	-	Oxygen sensor histidine kinase nreB; Nitrogen regulation protein B;
cds_wt_4458	-	Nitrate/nitrite response regulator protein narP;
cds_wt_4459	-	Uncharacterized protein yehI;
cds_wt_4460	-	hypothetical protein
cds_wt_4461	isp6	putative subtilase-type peptidase
cds_wt_4462	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4463	-	FMN-dependent NADH-azoreductase; FMN-dependent NADH-azo compound oxidoreductase; Azo-dye reductase;
cds_wt_4464	mtrA	Transcriptional regulatory protein yycF;
cds_wt_4465	sprD	Streptogrisin-D; Serine protease D; SGPD;
cds_wt_4466	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4467	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4468	-	Putative lipoprotein lppW;
cds_wt_4469	-	Protein dedA; Protein DSG-1;
cds_wt_4470	-	UPF0173 metal-dependent hydrolase MTH_1902;
cds_wt_4471	bmrU	Probable lipid kinase yegS;
cds_wt_4472	yodM	Lipid phosphate phosphohydrolase 1; Phosphatidic acid phosphatase 2a; PAP2-alpha; PAP-2a; PAP2a;
cds_wt_4473	-	Phosphatidate phosphohydrolase type 2a;
cds_wt_4474	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4475	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4476	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4477	amt	Ammonium transporter 1 member 1; AtAMT1;1;
cds_wt_4478	-	Mini-circle uncharacterized 19.1 kDa protein;
cds_wt_4479	pleD	Cellulose synthesis regulatory protein;

cds_wt_4480	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4481	-	Calnexin homolog 1;
cds_wt_4482	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4483	-	hypothetical protein
cds_wt_4484	-	HTH-type transcriptional regulator iscR;
		HTH-type transcriptional activator rhaR; L-rhamnose
cds_wt_4485	araC	operon transcriptional activator rhaR;
cds_wt_4486	-	putative cell division protein, regulatory protein
cds_wt_4487	-	hypothetical protein
cds_wt_4488	xerD	Tyrosine recombinase xerD;
cds_wt_4489	-	hypothetical protein
cds_wt_4490	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4491	-	putative transposase
cds_wt_4492	-	putative transposase
cds_wt_4493	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4494	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4495	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4496	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4497	-	Uncharacterized protein Cgl0967/cg1104; ORF2;
		Probable lysylphosphatidylglycerol synthetase; LPG
cds_wt_4498	lysX	synthetase; Multiple peptide resistance factor;
		Macrolide export ATP-binding/permease protein
cds_wt_4499	-	macB;
		Spermidine/putrescine import ATP-binding protein
cds_wt_4500	-	potA;
cds_wt_4501	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4502	-	Uncharacterized protein ypmR;
cds_wt_4503	phbZ	putative polyhydroxyalkanoate depolymerase
cds_wt_4504	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4505	tetR	HTH-type transcriptional regulator betI;
cds_wt_4506	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4507	ydCH	Transcriptional regulator slyA;
cds_wt_4508	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4509	-	unknown protein
cds_wt_4510	-	hypothetical protein predicted by Glimmer/Critica
		Sonic hedgehog protein; SHH; HHG-1; Contains:
		Sonic hedgehog protein N-product; Contains: Sonic
cds_wt_4511	-	hedgehog protein C-product;
		Laminin subunit beta-2; S-laminin; Laminin B1s
cds_wt_4512	-	chain;
cds_wt_4513	yfbQ	putative aminotransferase
cds_wt_4514	sigG	RNA polymerase sigma factor rpoD; Sigma-42;
cds_wt_4515	-	hypothetical protein
cds_wt_4516	tetR	Tetracycline repressor protein class C;
cds_wt_4517	-	Putative multidrug resistance protein mdtD;
cds_wt_4518	benE	Benzoate membrane transport protein;
cds_wt_4519	pnuC	nicotinamide mononucleotide transporter
cds_wt_4520	corA	Zinc transport protein zntB;
		Spermidine/putrescine import ATP-binding protein
cds_wt_4521	ytrE	potA;

cds_wt_4522	-	putative secreted protein
cds_wt_4523	-	Methionine import ATP-binding protein metN 1;
cds_wt_4524	prs	ribose-phosphate pyrophosphokinase
cds_wt_4525	cckA	two-component hybrid sensor and regulator
cds_wt_4526	pknA	serine/threonine protein kinase
cds_wt_4527	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4528	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4529	-	putative membrane protein
cds_wt_4530	-	Lipase; Extracellular lipase; SRL; GDSL-like lipase;
cds_wt_4531	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4532	-	Spermidine/putrescine import ATP-binding protein potA;
cds_wt_4533	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4534	-	Bacitracin export permease protein bceB;
cds_wt_4535	-	Sensor histidine kinase yfiJ;
cds_wt_4536	nreC	Oxygen regulatory protein nreC; Nitrogen regulation protein C;
cds_wt_4537	lacI	HTH-type transcriptional repressor purR; Purine nucleotide synthesis repressor; Pur regulon repressor;
cds_wt_4538	bga6	putative beta-galactosidase
cds_wt_4539	-	sn-glycerol-3-phosphate transport system permease protein ugpA;
cds_wt_4540	-	Probable ABC transporter permease protein yesQ;
cds_wt_4541	rafA	alpha-galactosidase
cds_wt_4542	PRB1	vacuolar protease B
cds_wt_4543	phal	putative oxidoreductase
cds_wt_4544	-	UPF0190 protein yedY;
cds_wt_4545	-	alkaline serine protease, subtilase family
cds_wt_4546	-	Uncharacterized protein Mb1584;
cds_wt_4547	-	Cell division control protein 48 homolog D; AtCDC48d; Transitional endoplasmic reticulum ATPase D;
cds_wt_4548	-	Laccase-12; Benzenediol:oxygen oxidoreductase 12;
cds_wt_4549	-	Urishiol oxidase 12; Diphenol oxidase 12;
cds_wt_4550	purA	hypothetical protein predicted by Glimmer/Critica
cds_wt_4551	-	adenylosuccinate synthetase
cds_wt_4552	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4553	-	Serine/threonine-protein kinase Sgk3;
cds_wt_4554	-	Serum/glucocorticoid-regulated kinase 3;
cds_wt_4555	-	Serum/glucocorticoid-regulated kinase-like; Cytokine-independent survival kinase;
cds_wt_4556	-	putative DNA hydrolase
cds_wt_4557	-	hypothetical protein
cds_wt_4558	-	Fibrocystin-L; Polycystic kidney and hepatic disease 1-like protein 1; PKHD1-like protein 1; Protein D86;
cds_wt_4559	-	Fibrocystin-L; Polycystic kidney and hepatic disease 1-like protein 1; PKHD1-like protein 1;
cds_wt_4560	-	hypothetical protein predicted by Glimmer/Critica

		Hepatocyte growth factor receptor; HGF receptor; Scatter factor receptor; SF receptor; HGF/SF receptor; Met proto-oncogene tyrosine kinase; c-Met;
cds_wt_4558	MET	
cds_wt_4559	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4560	-	alkaline serine protease, subtilase family
cds_wt_4561	-	Neuronal acetylcholine receptor subunit alpha-4;
cds_wt_4562	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4563	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4564	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4565	yehP	Uncharacterized protein yehP;
cds_wt_4566	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4567	-	Uncharacterized protein yehM;
		ATP-dependent Clp protease ATP-binding subunit clpX;
cds_wt_4568	yehL	
cds_wt_4569	-	hypothetical protein
cds_wt_4570	-	conserved hypothetical protein
cds_wt_4571	pecM	Protein pecM;
cds_wt_4572	pecS	HTH-type transcriptional regulator pecS;
cds_wt_4573	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4574	cho	DNA polymerase III, epsilon subunit
		Response regulator mprA; Mycobacterial persistence regulator A;
cds_wt_4575	yycF	
cds_wt_4576	baeS	sensor protein for BaeR
cds_wt_4577	-	hypothetical protein
		HTH-type transcriptional regulator malT; ATP-dependent transcriptional activator malT;
cds_wt_4578	-	
cds_wt_4579	gyrB	DNA gyrase subunit B
cds_wt_4580	gyrA	DNA gyrase subunit A
cds_wt_4581	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4582	marR	Multiple antibiotic resistance protein marR;
cds_wt_4583	-	hypothetical protein
		Aldo-keto reductase family 1 member C1 homolog; 20-alpha-hydroxysteroid dehydrogenase; 20-alpha-HSD; Dihydrodiol dehydrogenase 1; DD-1; DD1;
cds_wt_4584	-	
cds_wt_4585	-	hypothetical protein
		3-demethylubiquinone-9 3-methyltransferase; 3,4-dihydroxy-5-hexaprenylbenzoate methyltransferase; DHHB methyltransferase;
cds_wt_4586	-	
cds_wt_4587	bglA	putative beta-glucosidase
cds_wt_4588	-	Methionine import ATP-binding protein metN 1;
cds_wt_4589	-	Dipeptide transport system permease protein dppC;
		Oligopeptide transport system permease protein oppB; Stage 0 sporulation protein KB;
cds_wt_4590	dppB	
cds_wt_4591	appF	Methionine import ATP-binding protein metN;
cds_wt_4592	dppA	Periplasmic oligopeptide-binding protein;
		HTH-type transcriptional repressor purR; Purine nucleotide synthesis repressor; Pur regulon repressor;
cds_wt_4593	cytR	
		NAD-dependent deacetylase; Regulatory protein SIR2 homolog;
cds_wt_4594	-	

cds_wt_4595	-	Spartin; Trans-activated by hepatitis C virus core protein 1;
cds_wt_4596	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4597	-	Actin patch protein 1;
cds_wt_4598	-	hypothetical protein
cds_wt_4599	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4600	rhIE	DEAD-box ATP-dependent RNA helicase 42;
cds_wt_4601	fliA	RNA polymerase sigma factor rpoD; Sigma-70;
cds_wt_4602	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4603	-	Helicase IV;
		3-demethylubiquinone-9 3-methyltransferase; 3,4-dihydroxy-5-hexaprenylbenzoate methyltransferase; DHHB methyltransferase;
cds_wt_4604	-	
cds_wt_4605	fliA	RNA polymerase sigma factor rpoD; Sigma-42;
cds_wt_4606	-	hypothetical protein
cds_wt_4607	dacF	putative D-alanyl-D-alanine carboxypeptidase
cds_wt_4608	-	hypothetical protein
cds_wt_4609	lsr2	Protein Lsr2; 15 kDa antigen; A15;
cds_wt_4610	mer	hypothetical protein
		Uncharacterized HTH-type transcriptional regulator ysmB;
cds_wt_4611	-	
		Phosphoserine phosphatase rsbU; Sigma factor sigB regulation protein rsbU;
cds_wt_4612	rsbU	
		Serine-protein kinase rsbW; Anti-sigma-B factor;
cds_wt_4613	rsbW	Sigma-B negative effector rsbW;
cds_wt_4614	-	RNA polymerase sigma factor rpoD;
		F420-dependent glucose-6-phosphate dehydrogenase
cds_wt_4615	fgd1	
		Undecaprenyl-phosphate 4-deoxy-4-formamido-L-arabinose transferase; EC=2.7.8.n1; Undecaprenyl-phosphate Ara4FN transferase; Ara4FN transferase;
cds_wt_4616	-	
cds_wt_4617	-	hypothetical protein
cds_wt_4618	-	Phosphoglycolate phosphatase 1; PGPase 1; PGP 1;
cds_wt_4619	-	putative monooxygenase
cds_wt_4620	tetR	Tetracycline repressor protein class H;
cds_wt_4621	-	Sodium/glucose cotransporter 1; Na
cds_wt_4622	-	hypothetical protein
cds_wt_4623	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4624	slpE	Uncharacterized protein Mb2247c;
cds_wt_4625	ggt	gamma-glutamyltranspeptidase
cds_wt_4626	-	Vegetative incompatibility protein HET-E-1;
cds_wt_4627	trmB	hypothetical protein
cds_wt_4628	-	Filamentous hemagglutinin;
cds_wt_4629	PHYB	two-component sensor histidine kinase
cds_wt_4630	-	Selenium-binding protein 1;
cds_wt_4631	-	hypothetical protein
cds_wt_4632	ywfM	Uncharacterized inner membrane transporter yicL;
cds_wt_4633	estA	tributylin esterase
cds_wt_4634	-	Cortactin-binding protein 2; CortBP2;
cds_wt_4635	nha	Sodium/hydrogen exchanger 2; Na

cds_wt_4636	-	hypothetical protein
cds_wt_4637	apbA	2-dehydropantoate 2-reductase
cds_wt_4638	-	hypothetical protein
cds_wt_4639	malQ	glycogen debranching enzyme
cds_wt_4640	glgX	glycogen debranching enzyme
cds_wt_4641	treY	maltooligosyl trehalose synthase
cds_wt_4642	treZ	maltooligosyl trehalose trehalohydrolase
cds_wt_4643	-	UPF0161 protein Atu1747; Membrane-bound lytic murein transglycosylase F; EC=4.2.2.n1; Murein lyase F;
cds_wt_4644	glnH	
cds_wt_4645	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4646	ppp	possible serine/threonine phosphatase ppp
cds_wt_4647	rtn5	Uncharacterized signaling protein PA1727; 3-demethylubiquinone-9 3-methyltransferase; 3,4-dihydroxy-5-hexaprenylbenzoate methyltransferase; DHHB methyltransferase;
cds_wt_4648	smtA	
cds_wt_4649	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4650	hrpB	ATP-dependent helicase HrpB Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15; DEAH box protein 15;
cds_wt_4651	hrpB	
cds_wt_4652	TTR	Transthyretin; Prealbumin; TBPA;
cds_wt_4653	aceB	malate synthase A
cds_wt_4654	-	Translation initiation factor IF-2;
cds_wt_4655	-	putative O-methyltransferase
cds_wt_4656	-	hypothetical protein predicted by Glimmer/Critica Oxygen regulatory protein nreC; Nitrogen regulation protein C;
cds_wt_4657	nreC	
cds_wt_4658	-	Sensor protein vraS;
cds_wt_4659	pldA	phospholipase D, putative
cds_wt_4660	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4661	ampS	aminopeptidase
cds_wt_4662	-	hypothetical protein ATP-dependent Clp protease ATP-binding subunit clpA homolog;
cds_wt_4663	clpC	
cds_wt_4664	-	Pirin-like protein At1g50590;
cds_wt_4665	suhB	inositol-1(or 4)-monophosphatase
cds_wt_4666	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4667	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4668	RPGR	X-linked retinitis pigmentosa GTPase regulator; Uncharacterized HTH-type transcriptional regulator ykoM;
cds_wt_4669	-	
cds_wt_4670	-	27 kDa antigen Cfp30B;
cds_wt_4671	-	Phosphoserine phosphatase rsbP; Endoglucanase E-4; Endo-1,4-beta-glucanase E-4;
cds_wt_4672	celD	Cellulase E-4; Cellulase E4;
cds_wt_4673	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4674	-	hypothetical protein
cds_wt_4675	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4676	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4677	-	hypothetical protein predicted by Glimmer/Critica

cds_wt_4678	-	Uncharacterized 17.2 kDa protein in melC2-rnhH intergenic region; ORF3;
cds_wt_4679	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4680	-	Dehydrosqualene desaturase; Diapophytoene desaturase; 4,4'-diapophytoene desaturase;
cds_wt_4681	-	hypothetical protein
cds_wt_4682	-	putative transferase
cds_wt_4683	-	Spermidine/putrescine import ATP-binding protein potA;
cds_wt_4684	-	Putative pleiotropic drug resistance protein 7;
cds_wt_4685	-	two-component sensor histidine kinase
cds_wt_4686	chrA	Uncharacterized transcriptional regulatory protein yhcZ;
cds_wt_4687	-	hypothetical protein
cds_wt_4688	-	Uncharacterized protein Mb0911c;
cds_wt_4689	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4690	-	hydrolase, putative
cds_wt_4691	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4692	recQ	ATP-dependent DNA helicase RecQ
cds_wt_4693	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4694	nagA	Beta-glucosidase-related glycosidases
cds_wt_4695	-	Uncharacterized protein yjdJ;
cds_wt_4696	-	Uncharacterized protein yxxB;
cds_wt_4697	-	Uncharacterized mscS family protein HP_0415;
cds_wt_4698	-	putative integral membrane protein
cds_wt_4699	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4700	-	hypothetical protein
cds_wt_4701	cspA	Cold shock protein cspA; CSP-A; 7.4 kDa cold shock protein; CS7.4;
cds_wt_4702	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4703	gsp	probable oxidoreductase
cds_wt_4704	tam	trans-aconitate methyltransferase
cds_wt_4705	add	adenosine deaminase
cds_wt_4706	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4707	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4708	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4709	envZ	sensor histidine kinase
cds_wt_4710	srrB	Alkaline phosphatase synthesis transcriptional regulatory protein sphR;
cds_wt_4711	thrS	threonyl-tRNA synthetase
cds_wt_4712	-	Uncharacterized HIT-like protein MG132;
cds_wt_4713	mtrR	HTH-type transcriptional regulator mtrR;
cds_wt_4714	-	3-
cds_wt_4715	-	elongation factor EF-G
cds_wt_4716	pgsA	phosphatidylglycerophosphate synthase
cds_wt_4717	-	lipid A biosynthesis lauroyl acyltransferase
cds_wt_4718	pimA	putative glycosyltransferase
cds_wt_4719	-	putative secreted protein
cds_wt_4720	-	Pyridoxal biosynthesis lyase pdxS;

cds_wt_4721	-	Glutamine amidotransferase subunit pdxT; Glutamine amidotransferase glutaminase subunit pdxT;
cds_wt_4722	-	UPF0082 protein Sare_1779;
cds_wt_4723	ccrB	Transposon Tn552 DNA-invertase binR;
cds_wt_4724	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4725	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4726	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4727	ruvC	crossover junction endodeoxyribonuclease
cds_wt_4728	ruvA	Holliday junction ATP-dependent DNA helicase ruvA;
cds_wt_4729	ruvB	Holliday junction DNA helicase RuvB
cds_wt_4730	yrbF	UPF0092 membrane protein BB_0651;
cds_wt_4731	secD	Protein-export membrane protein secD;
cds_wt_4732	secD	Protein-export membrane protein secD;
cds_wt_4733	secF	Protein-export membrane protein secF;
cds_wt_4734	apt	adenine phosphoribosyltransferase
cds_wt_4735	rel	GTP pyrophosphokinase
cds_wt_4736	ppiB	peptidyl-prolyl cis-trans isomerase
cds_wt_4737	ppiB	putative peptidyl-prolyl cis-trans isomerase
cds_wt_4738	-	putative hydrolase
cds_wt_4739	hisS	histidyl-tRNA synthetase
cds_wt_4740	-	UPF0152 protein SSO2140;
cds_wt_4741	-	Uncharacterized HTH-type transcriptional regulator Rv3095/MT3179;
cds_wt_4742	cphB	cyanophycinase
cds_wt_4743	cphA	cyanophycin synthetase
cds_wt_4744	pknB	putative serine/threonine protein kinase
cds_wt_4745	-	Polycystic kidney disease protein 1-like 3; Polycystin-1L3; PC1-like 3 protein;
cds_wt_4746	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4747	fliA	RNA polymerase sigma factor rpoD;
cds_wt_4748	adh	alcohol dehydrogenase
cds_wt_4749	ureC	urease alpha subunit
cds_wt_4750	ureB	urease beta subunit
cds_wt_4751	ureA	urease gamma subunit
cds_wt_4752	pknA	putative serine/threonine protein kinase
cds_wt_4753	yjgF	UPF0076 protein PH0854;
cds_wt_4754	-	Urease subunit alpha; Urea amidohydrolase subunit alpha;
cds_wt_4755	-	hypothetical protein
cds_wt_4756	nahA	beta-hexosaminidase precursor
cds_wt_4757	strB	Streptomycin 6-kinase; Streptidine kinase;
cds_wt_4758	dsd	Streptomycin 6-phosphotransferase; APH
cds_wt_4759	-	hypothetical protein
cds_wt_4760	-	Homoserine kinase; HSK; HK;
cds_wt_4761	-	hypothetical protein
cds_wt_4762	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4763	aspS	aspartyl-tRNA synthetase
cds_wt_4764	-	hypothetical protein predicted by Glimmer/Critica

cds_wt_4765	-	Dihydroorotate dehydrogenase; Dihydroorotate oxidase; DHODEHase; DHODase; DHOD;
cds_wt_4766	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4767	-	Replication-associated recombination protein A;
cds_wt_4768	-	Collagen alpha-5
cds_wt_4769	-	Collagen alpha-2
cds_wt_4770	-	Collagen alpha-5
cds_wt_4771	-	putative secreted protein
cds_wt_4772	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4773	alaS	alanyl-tRNA synthetase
cds_wt_4774	yqgF	putative Holliday junction resolvase
cds_wt_4775	-	Uncharacterized protein yceG;
cds_wt_4776	-	Uncharacterized protein HI0457;
cds_wt_4777	aroE	shikimate 5-dehydrogenase
cds_wt_4778	aroC	chorismate synthase
cds_wt_4779	aroK	shikimate kinase
cds_wt_4780	aroB	3-dehydroquinate synthase
cds_wt_4781	aroD	3-dehydroquinate dehydratase
cds_wt_4782	efp	Elongation factor P; EF-P;
cds_wt_4783	nusB	N utilization substance protein B homolog; Protein nusB;
cds_wt_4784	-	putative DNA-binding protein
cds_wt_4785	pyrR	putative pyrimidine operon regulatory protein
cds_wt_4786	pyrB	aspartate carbamoyltransferase
cds_wt_4787	pyrC	dihydroorotase
cds_wt_4788	carA	carbamoyl-phosphate synthase small chain
cds_wt_4789	carB	carbamoyl-phosphate synthase large chain
cds_wt_4790	pyrD	dihydroorotate dehydrogenase
cds_wt_4791	bioA	adenosylmethionine-8-amino-7-oxononanoate aminotransferase
cds_wt_4792	pyrF	orotidine-5'-phosphate decarboxylase
cds_wt_4793	mihF	hypothetical protein
cds_wt_4794	gmK	guanylate kinase
cds_wt_4795	rpoZ	DNA-directed RNA polymerase subunit omega
cds_wt_4796	dfp	putative pantothenate metabolism flavoprotein
cds_wt_4797	metK	S-adenosylmethionine synthetase
cds_wt_4798	priA	Primosomal protein N'; ATP-dependent helicase priA;
cds_wt_4799	def2	Replication factor Y;
cds_wt_4800	fnt	putative polypeptide deformylase
cds_wt_4801	fmu	methionyl-tRNA formyltransferase
cds_wt_4802	rpe	Sun protein
cds_wt_4803	-	ribulose-phosphate 3-epimerase
cds_wt_4804	plsC	Chemotaxis response regulator protein-glutamate methylesterase 1;
cds_wt_4805	-	1-acylglycerol-3-phosphate O-acyltransferase
cds_wt_4806	-	putative TetR-family transcriptional regulator
cds_wt_4807	ribD	probable class-V aminotransferase
		diaminohydroxyphosphoribosylaminopyrimidine deaminase / 5-amino-6-(5-phosphoribosylamino)uracil reductase

cds_wt_4808	ribA	GTP cyclohydrolase II / 3,4-dihydroxy-2-butanone 4-phosphate synthase (dhbp synthase)
cds_wt_4809	ribH	riboflavin synthase beta chain
cds_wt_4810	glnQ	putative ABC transporter ATP-binding protein
cds_wt_4811	-	Inner membrane amino-acid ABC transporter permease protein yecS;
cds_wt_4812	hisE	phosphoribosyl-ATP pyrophosphatase
cds_wt_4813	hisG	ATP phosphoribosyltransferase
cds_wt_4814	-	Uncharacterized protein Mb1452;
cds_wt_4815	infC	Translation initiation factor IF-3;
cds_wt_4816	rpml	50S ribosomal protein L35;
cds_wt_4817	rpIT	50S ribosomal protein L20;
cds_wt_4818	tsnR	putative rRNA methylase
cds_wt_4819	pheS	phenylalanyl-tRNA synthetase alpha chain
cds_wt_4820	pheT	phenylalanyl-tRNA synthetase beta chain
cds_wt_4821	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4822	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4823	-	Uncharacterized protein L662;
cds_wt_4824	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4825	apAC	aminopeptidase
cds_wt_4826	-	hypothetical protein
cds_wt_4827	yhjG	putative rifampin monooxygenase
cds_wt_4828	-	Uncharacterized protein ygjQ;
cds_wt_4829	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4830	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4831	-	hypothetical protein
cds_wt_4832	-	Laminin subunit beta-2; S-laminin; S-LAM;
cds_wt_4833	bglX	periplasmic beta-glucosidase precursor
cds_wt_4834	gshA	gamma-glutamylcysteine synthetase
cds_wt_4835	-	Sulfatase-modifying factor 1; C-alpha-formylglycine-generating enzyme 1;
cds_wt_4836	cbiN	Glucosamine--fructose-6-phosphate aminotransferase
cds_wt_4837	-	Meiotically up-regulated gene 158 protein;
cds_wt_4838	-	hypothetical protein
cds_wt_4839	-	hypothetical lipoprotein SCF55.31
cds_wt_4840	-	Inversin; Inversion of embryo turning homolog; Nephrocystin-2;
cds_wt_4841	argG	argininosuccinate synthase
cds_wt_4842	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4843	argR	Arginine repressor;
cds_wt_4844	argF	ornithine carbamoyltransferase
cds_wt_4845	argD	acetylornithine aminotransferase
cds_wt_4846	argJ	glutamate N-acetyltransferase / amino-acid N-acetyltransferase
cds_wt_4847	argC	N-acetyl-gamma-glutamyl-phosphate reductase
cds_wt_4848	-	Platelet-activating factor acetylhydrolase; PAF acetylhydrolase; PAF 2-acylhydrolase; LDL-associated phospholipase A2; LDL-PLA
cds_wt_4849	-	Fatty acid metabolism regulator protein;

cds_wt_4850	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4851	-	Putative membrane protein mmpL3;
cds_wt_4852	-	putative integral membrane protein
cds_wt_4853	argH	argininosuccinate lyase
cds_wt_4854	dapE	succinyl-diaminopimelate desuccinylase
cds_wt_4855	lacI	HTH-type transcriptional regulator malR; Maltose operon transcriptional repressor;
cds_wt_4856	-	Maltotriose-binding protein; MMBP; Maltodextrin-binding protein;
cds_wt_4857	malF	Maltose transport system permease protein malF;
cds_wt_4858	malD	Maltose transport system permease protein malG;
cds_wt_4859	pulA	putative pullulanase precursor
cds_wt_4860	morA	Uncharacterized signaling protein PA3311;
cds_wt_4861	yjnA	UPF0721 transmembrane protein HI0198;
cds_wt_4862	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4863	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4864	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4865	phoD	phosphodiesterase/alkaline phosphatase D
cds_wt_4866	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4867	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4868	-	UPF0173 metal-dependent hydrolase PF1764;
cds_wt_4869	-	Helicase IV;
cds_wt_4870	mag	putative 3-methylpurine DNA glycosylase
cds_wt_4871	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4872	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4873	-	putative DNA-binding protein
cds_wt_4874	-	hypothetical protein
cds_wt_4875	ykwD	allergen V5/TPX-1 related
cds_wt_4876	-	HTH-type transcriptional regulator betI;
cds_wt_4877	speB	agmatinase
cds_wt_4878	-	hypothetical protein
cds_wt_4879	adk	adenylate kinase
cds_wt_4880	-	Putative multidrug resistance protein mdtD;
cds_wt_4881	lysR	Nodulation protein D 1;
cds_wt_4882	-	Lactose phosphotransferase system repressor;
cds_wt_4883	fruB	1-phosphofructokinase
cds_wt_4884	mtlA	PTS system, mannitol-specific IIBC component
cds_wt_4885	cmtA	PTS system mannitol-specific EIICB component;
cds_wt_4886	fruB	EIICB-Mtl; EII-Mtl; Includes: Mannitol permease IIC component; PTS system mannitol-specific EIIC component; Includes: Mannitol-specific phosphotransferase enzyme IIB component; PTS system mannitol-specific EIIB component;
cds_wt_4887	-	PTS system, fructose-specific IIA/fpr component
cds_wt_4888	ptsH	sorbitol dehydrogenase
cds_wt_4889	ptsI	Phosphocarrier protein HPr; Histidine-containing protein;
cds_wt_4890	-	phosphoenolpyruvate-protein phosphotransferase
		hypothetical protein predicted by Glimmer/Critica

cds_wt_4891	-	Uncharacterized protein in chlN 3'region; URF2;
cds_wt_4892	tyrS	Flags: Fragment; tyrosyl-tRNA synthetase
Replicase polyprotein 1ab; pp1ab; ORF1ab polyprotein; Contains: Non-structural protein 1; nsp1; p28; Contains: Non-structural protein 2; nsp2; p65; Contains: Non-structural protein 3; nsp3; Papain-like proteinases 1/2; PL1-PRO/PL2-PRO; p210; Contains: Non-structural protein 4; nsp4; Peptide HD2; p44; Contains: 3C-like proteinase; 3CL-PRO; 3CLp; M-PRO; p27; nsp5; Contains: Non-structural protein 6; nsp6; Contains: Non-structural protein 7; nsp7; p10; Contains: Non-structural protein 8; nsp8; p22; Contains: Non-structural protein 9; nsp9; p12; Contains: Non-structural protein 10; nsp10; Growth factor-like peptide; GFL; p15; Contains: RNA-directed RNA polymerase; RdRp; Pol; p100; nsp12; Contains: Helicase; Hel; p67; nsp13; Contains: Exoribonuclease; ExoN; nsp14; Contains: Uridylate- specific endoribonuclease; NendoU; nsp15; p35; Contains: Putative 2'-O-methyl transferase; nsp16;		
cds_wt_4893	-	Contains: Putative 2'-O-methyl transferase; nsp16;
cds_wt_4894	-	Protein nagD homolog;
cds_wt_4895	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4896	htr8	Methyl-accepting chemotaxis protein 4;
cds_wt_4897	-	hypothetical protein
cds_wt_4898	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4899	-	UPF0182 protein Mjls_1469;
cds_wt_4900	tlyA	Uncharacterized protein yqxC;
cds_wt_4901	ppnK	probable inorganic polyphosphate/ATP-NAD kinase
cds_wt_4902	recN	DNA repair protein recN; Recombination protein N;
cds_wt_4903	-	Uncharacterized protein MTH_1600;
cds_wt_4904	-	conserved hypothetical protein
cds_wt_4905	-	hypothetical protein
cds_wt_4906	mviN	Virulence factor mviN;
cds_wt_4907	-	putative glycosyl transferase
cds_wt_4908	-	hypothetical protein
cds_wt_4909	pyrG	CTP synthetase
cds_wt_4910	mutT	GDP-mannose pyrophosphatase nudK;
cds_wt_4911	slpE	probable exported protease
cds_wt_4912	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4913	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4914	-	hypothetical protein
cds_wt_4915	ydeP	Uncharacterized HTH-type transcriptional regulator ydeP;
cds_wt_4916	-	Uncharacterized oxidoreductase yesF;
cds_wt_4917	-	hypothetical protein
cds_wt_4918	celA	putative endo-1,4-beta-glucanase
cds_wt_4919	-	hypothetical protein
cds_wt_4920	ald	alanine dehydrogenase
cds_wt_4921	xerD	Tyrosine recombinase xerD;

cds_wt_4922	parA	Sporulation initiation inhibitor protein soj;
cds_wt_4923	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4924	-	3-oxoacyl-
cds_wt_4925	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4926	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4927	-	HTH-type transcriptional regulator hpr; Protease production regulatory protein hpr;
cds_wt_4928	thiJ	ThiJ/Pfpl family protein
cds_wt_4929	darR	HTH-type transcriptional regulator glxA;
cds_wt_4930	-	Protein split ends;
cds_wt_4931	scpA	Segregation and condensation protein A;
cds_wt_4932	scpB	Segregation and condensation protein B;
cds_wt_4933	rluB	pseudouridylate synthase
cds_wt_4934	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4935	pcaD	putative hydrolase
cds_wt_4936	PAPL	Iron/zinc purple acid phosphatase-like protein;
cds_wt_4937	xclC	acyl-CoA synthase
cds_wt_4938	ykfJ	UPF0027 protein MMP1392;
cds_wt_4939	prfH	Peptide chain release factor 1; RF-1;
cds_wt_4940	relA	GTP pyrophosphokinase; ATP:GTP 3'-pyrophosphotransferase; ppGpp synthetase I;
cds_wt_4941	LIP4	Lipase 4;
cds_wt_4942	cmk	cytidylate kinase
cds_wt_4943	engA	GTP-binding protein engA;
cds_wt_4944	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4945	ftsK	DNA translocase ftsK;
cds_wt_4946	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4947	-	hypothetical protein
cds_wt_4948	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4949	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4950	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4951	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4952	-	Replication initiator protein;
cds_wt_4953	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4954	int	Integrase;
cds_wt_4955	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4956	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4957	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4958	sap	55.5 kDa and 49.5 kDa sporulation proteins; ORF1590 and ORF1422;
cds_wt_4959	-	hypothetical protein
cds_wt_4960	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4961	int7	Tyrosine recombinase xerD;
cds_wt_4962	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4963	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4964	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4965	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4966	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4967	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4968	-	hypothetical protein predicted by Glimmer/Critica

cds_wt_4969	-	Insertion element IS6110 uncharacterized 12.0 kDa protein;
cds_wt_4970	tnp	Transposase for insertion sequence element IS1086;
cds_wt_4971	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4972	-	hypothetical protein
cds_wt_4973	-	Teneurin-2; Ten-2; Tenascin-M2; Ten-m2; Protein Odd Oz/ten-m homolog 2; Neurestin;
cds_wt_4974	rhsA	Teneurin-1; Ten-1; Tenascin-M1; Ten-m1; Protein Odd Oz/ten-m homolog 1;
cds_wt_4975	-	Teneurin-3; Ten-3; Tenascin-M3; Ten-m3; Protein Odd Oz/ten-m homolog 3;
cds_wt_4976	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4977	-	Putative transposase for insertion sequence element IS402;
cds_wt_4978	466aa (51,3kD)	hypothetical protein predicted by Glimmer/Critica
cds_wt_4979	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4980	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4981	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4982	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4983	-	transposase
cds_wt_4984	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4985	-	hypothetical protein
cds_wt_4986	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4987	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4988	-	hypothetical protein
cds_wt_4989	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4990	-	hypothetical protein
cds_wt_4991	-	hypothetical protein
cds_wt_4992	-	hypothetical protein
cds_wt_4993	iap	Lipoprotein spr;
cds_wt_4994	-	L-threonine 3-dehydrogenase;
cds_wt_4995	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4996	aroB	3-dehydroquinate synthase
cds_wt_4997	-	N-acetyl-D-glucosamine kinase; GlcNAc kinase;
cds_wt_4998	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_4999	-	Uncharacterized WD repeat-containing protein alr3466;
		L-glutamine:2-deoxy-scylo-inosose aminotransferase; L-glutamine:DOI aminotransferase; L-glutamine:3-amino-2,3-dideoxy-scylo-inosose aminotransferase; L-glutamine:amino-DOI aminotransferase;
cds_wt_5000	parS	Diflavin flavoprotein A 1; NADH:oxygen oxidoreductase; SsATF573;
cds_wt_5001	-	AMP-dependent synthetase and ligase
cds_wt_5002	fadD	Orn/DAP/Arg decarboxylase 2
cds_wt_5003	lysA	hypothetical protein predicted by Glimmer/Critica
cds_wt_5004	-	acyl-CoA dehydrogenase
cds_wt_5005	acd	hypothetical protein predicted by Glimmer/Critica
cds_wt_5006	-	hypothetical protein predicted by Glimmer/Critica

cds_wt_5007	-	hypothetical protein predicted by Glimmer/Critica Plipastatin synthetase subunit D; Peptide synthetase 4; Includes: ATP-dependent proline adenylation; ProA 1; Proline activase 1; Includes: ATP-dependent glutamine adenylation; GlnA; Glutamine activase; Includes: ATP-dependent tyrosine adenylation 2; TyrA 2; Tyrosine activase 2;
cds_wt_5008	-	hypothetical protein
cds_wt_5009	-	hypothetical protein
cds_wt_5010	tetV	Enterobactin exporter entS;
cds_wt_5011	asnB	asparagine synthetase
cds_wt_5012	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5013	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5014	-	Uncharacterized protein yxbA;
cds_wt_5015	-	hypothetical protein
cds_wt_5016	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5017	-	hypothetical protein
cds_wt_5018	-	hypothetical protein Probable arylformamidase; Kynurenine formamidase; KF;
cds_wt_5019	-	Methionyl-tRNA formyltransferase;
cds_wt_5020	-	Nucleoside diphosphate kinase; NDK; NDP kinase; Nucleoside-2-P kinase;
cds_wt_5021	-	4-aminobutyrate aminotransferase
cds_wt_5022	rhbA	hypothetical protein predicted by Glimmer/Critica
cds_wt_5023	-	hypothetical protein
cds_wt_5024	-	hypothetical protein
cds_wt_5025	manA	mannose-6-phosphate isomerase
cds_wt_5026	tetV	Uncharacterized MFS-type transporter yfiS;
cds_wt_5027	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5028	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5029	-	RNA polymerase sigma-E factor; Sigma-24;
cds_wt_5030	-	Poly
cds_wt_5031	-	Uncharacterized protein ywoF;
cds_wt_5032	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5033	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5034	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5035	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5036	adp	D-alanyl-D-alanine carboxypeptidase
cds_wt_5037	-	Response regulator gacA; Global activator; Oxygen sensor histidine kinase nreB; Nitrogen regulation protein B;
cds_wt_5038	-	Uncharacterized signaling protein PA3311;
cds_wt_5039	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5040	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5041	-	Signaling protein ykoW;
cds_wt_5042	-	Uncharacterized transcriptional regulatory protein yclJ;
cds_wt_5043	lcoR	conserved hypothetical protein TIGR00157
cds_wt_5044	yloQ	Uncharacterized N-acetyltransferase p20;
cds_wt_5045	p20	Uncharacterized MFS-type transporter yhjO;
cds_wt_5046	-	histidinol-phosphate aminotransferase
cds_wt_5047	hisC	

cds_wt_5048	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5049	-	hypothetical protein
cds_wt_5050	lgrD	Linear gramicidin synthetase subunit D; Includes: ATP-dependent tryptophan adenylase; TrpA; Tryptophan activase; Includes: ATP-dependent D-leucine adenylase; D-LeuA; D-Leucine activase; Includes: Leucine racemase
cds_wt_5051	bacC	Bacitracin synthetase 3; BA3; Includes: ATP-dependent isoleucine adenylase; IleA; Isoleucine activase; Includes: ATP-dependent D-phenylalanine adenylase; D-PheA; D-phenylalanine activase; Includes: ATP-dependent histidine adenylase; HisA; Histidine activase; Includes: ATP-dependent D-aspartate adenylase; D-AspA; D-aspartate activase; Includes: ATP-dependent asparagine adenylase; AsnA; Asparagine activase; Includes: Aspartate racemase; Includes: Phenylalanine racemase
cds_wt_5052	-	Gramicidin S synthetase 2; Gramicidin S synthetase II; Includes: ATP-dependent proline adenylase; ProA; Proline activase; Includes: ATP-dependent valine adenylase; ValA; Valine activase; Includes: ATP-dependent ornithine adenylase; OrnA; Ornithine activase; Includes: ATP-dependent leucine adenylase; LeuA; Leucine activase;
cds_wt_5053	dhbF	amino acid adenylation
cds_wt_5054	olmC	putative thioesterase
cds_wt_5055	-	Carbamoyl-phosphate synthase large chain, N-terminal section; Carbamoyl-phosphate synthetase ammonia chain;
cds_wt_5056	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5057	-	Tryptophan 2,3-dioxygenase; TDO; Tryptophan pyrrolase; Tryptophanase; Tryptophan oxygenase; TRPO; TO; Tryptamin 2,3-dioxygenase;
cds_wt_5058	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5059	brpA	Bialaphos biosynthetic pathway regulatory protein;
cds_wt_5060	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5061	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5062	-	Uncharacterized membrane protein SSP1970;
cds_wt_5063	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5064	-	Uncharacterized membrane protein in Ilm 5'region; ORF1;
cds_wt_5065	-	Diamine acetyltransferase 2; Spermidine/spermine N
cds_wt_5066	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5067	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5068	-	Mannose receptor-like protein;
cds_wt_5069	bglC	hypothetical protein
cds_wt_5070	GALC	similar to Galactocerebrosidase precursor (GALCERase) (Galactosylceramidase) (Galactosylceramide beta-galactosidase) (Galactocerebroside beta-galactosidase)

cds_wt_5071	abfB	putative secreted alpha-galactosidase
cds_wt_5072	sigF	RNA polymerase sigma factor rpoD; Sigma-70;
cds_wt_5073	-	hypothetical protein
cds_wt_5074	-	hypothetical protein
cds_wt_5075	rsbV	Anti-sigma F factor antagonist; Stage II sporulation protein AA;
cds_wt_5076	orfY	oxidoreductase
cds_wt_5077	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5078	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5079	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5080	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5081	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5082	-	hypothetical protein
cds_wt_5083	tetR	Tetracycline repressor protein class B from transposon Tn10;
cds_wt_5084	-	Multidrug resistance protein B homolog;
cds_wt_5085	-	Lipid A export ATP-binding/permease protein msbA;
cds_wt_5086	ybtQ	Lipid A export ATP-binding/permease protein msbA;
cds_wt_5087	pchE	yersiniabactin non-ribosomal peptide synthetase
cds_wt_5088	irp2	yersiniabactin biosynthetic protein
cds_wt_5089	pchC	putative thioesterase
cds_wt_5090	dhbE	2,3-dihydroxybenzoate-AMP ligase
cds_wt_5091	trpE	Anthranilate synthase component 1; Anthranilate synthase component I;
cds_wt_5092	-	Regulatory protein afsR;
cds_wt_5093	-	Ribosomal RNA large subunit methyltransferase N;
cds_wt_5094	pltA	23S rRNA m2A2503 methyltransferase;
cds_wt_5095	-	oxidoreductase, FAD-binding, putative
cds_wt_5096	prnC	Sodium/hydrogen exchanger 2; Na
cds_wt_5097	pks5	putative halogenase
cds_wt_5098	-	mycocerosic acid synthase
cds_wt_5099	-	polyketide synthase
cds_wt_5100	pks5	modular polyketide synthase
cds_wt_5101	-	similar to polyketide synthase
cds_wt_5102	-	polyketide synthase
cds_wt_5103	pteH	Putative polyketide synthase pksM;
cds_wt_5104	ntaB	S-acyl fatty acid synthase thioesterase, medium chain; Oleoyl-ACP hydrolase; Thioesterase II;
cds_wt_5105	-	Thioesterase domain-containing protein 1;
cds_wt_5106	-	4-hydroxyphenylacetate 3-monooxygenase reductase component; 4-HPA 3-monooxygenase small component; Flavin:NADH reductase;
cds_wt_5107	ephA	Protein fixC;
cds_wt_5108	cypA	putative monooxygenase
cds_wt_5109	tetR	epoxide hydrolase
cds_wt_5110	-	cytochrome P450
		Tetracycline repressor protein class A from transposon 1721;
		Trans-acting enoyl reductase;

		Tyrocidine synthetase 3; Tyrocidine synthetase III; Includes: ATP-dependent asparagine adenylase; AsnA; Asparagine activase; Includes: ATP- dependent glutamine adenylase; GlnA; Glutamine activase; Includes: ATP-dependent tyrosine adenylase; TyrA; Tyrosine activase; Includes: ATP- dependent valine adenylase; ValA; Valine activase; Includes: ATP-dependent ornithine adenylase; OrnA; Ornithine activase; Includes: ATP-dependent leucine adenylase; LeuA; Leucine activase;
cds_wt_5111	tycC	
cds_wt_5112	-	putative two-component system sensor kinase
cds_wt_5113	-	Cytospin-A; SPECC1-like protein;
cds_wt_5114	resD	Transcriptional regulatory protein yycF;
cds_wt_5115	-	Thermolysin; Thermostable neutral proteinase;
cds_wt_5116	-	hypothetical protein predicted by Glimmer/Critica Kinesin-like protein KIF13B; Kinesin-like protein GAKIN;
cds_wt_5117	-	
cds_wt_5118	-	Cellulose synthesis regulatory protein;
cds_wt_5119	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5120	-	hypothetical protein
cds_wt_5121	celC	endoglucanase family 5
cds_wt_5122	-	Uncharacterized WD repeat-containing protein alr3466; Uncharacterized WD repeat-containing protein alr3466;
cds_wt_5123	-	
cds_wt_5124	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5125	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5126	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5127	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5128	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5129	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5130	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5131	gdhB	Quinoprotein glucose dehydrogenase B; Glucose dehydrogenase B
cds_wt_5132	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5133	-	Galactose oxidase; GAO; GOase; GO;
cds_wt_5134	-	hypothetical protein
cds_wt_5135	-	glycosyl transferase, group 2 family protein
cds_wt_5136	amtR	HTH-type transcriptional regulator betI;
cds_wt_5137	-	Uncharacterized amino-acid permease C74.04;
cds_wt_5138	-	hypothetical protein
cds_wt_5139	-	Uncharacterized protein ycgI;
cds_wt_5140	DUR1	allophanate hydrolase subunit 2
cds_wt_5141	-	amidase
cds_wt_5142	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5143	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5144	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5145	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5146	-	Uncharacterized HTH-type transcriptional regulator ykoM;

cds_wt_5147	-	Putative multidrug resistance protein mdtD;
cds_wt_5148	-	DNA translocase ftsK;
cds_wt_5149	-	hypothetical protein
cds_wt_5150	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5151	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5152	-	Nucleoporin NUP159; Nuclear pore protein NUP159;
cds_wt_5153	yurO	Uncharacterized ABC transporter extracellular-binding protein yurO;
cds_wt_5154	-	sn-glycerol-3-phosphate transport system permease protein ugpA;
cds_wt_5155	-	Probable ABC transporter permease protein yurM;
cds_wt_5156	-	Uncharacterized protein ywoF;
cds_wt_5157	-	putative integral membrane protein
cds_wt_5158	-	Signaling protein ykoW;
cds_wt_5159	linC	3-oxoacyl-
cds_wt_5160	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5161	lldA	putative dehydrogenase
cds_wt_5162	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5163	grsT	Gramicidin S biosynthesis protein grsT;
cds_wt_5164	-	Uncharacterized kamA family protein aq_1632;
cds_wt_5165	aatA	aspartate aminotransferase A
cds_wt_5166	fabD	Malonyl CoA-acyl carrier protein transacylase; MCT;
cds_wt_5167	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5168	-	amino acid adenylation
cds_wt_5169	dhbF	Acetyl-coenzyme A synthetase; Acetate--CoA ligase; Acyl-activating enzyme;
cds_wt_5170	eryA	Erythronolide synthase, modules 3 and 4; ORF 2; 6-deoxyerythronolide B synthase II; DEBS 2;
cds_wt_5171	Fasn	Fatty acid synthase; Includes:
cds_wt_5172	-	Phenolphthiocerol synthesis polyketide synthase ppsA;
cds_wt_5173	eryA	Erythronolide synthase, modules 3 and 4; ORF 2; 6-deoxyerythronolide B synthase II; DEBS 2;
cds_wt_5174	pip2	proline imino-peptidase
cds_wt_5175	-	oxidoreductase, putative
cds_wt_5176	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5177	tcmR	HTH-type transcriptional regulator tcmR;
cds_wt_5178	-	Tetracenomycin C transcriptional repressor;
cds_wt_5179	dnrl	hypothetical protein
cds_wt_5180	-	Regulatory protein dnrl;
cds_wt_5181	-	hypothetical protein
cds_wt_5182	-	Zeaxanthin epoxidase, chloroplastic; Xanthophyll epoxidase; Beta-cyclohexenyl epoxidase;
cds_wt_5183	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5184	-	Probable transposase for insertion sequence element ISRM3-like;
cds_wt_5185	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5186	-	hypothetical protein
cds_wt_5187	-	hypothetical protein predicted by Glimmer/Critica

cds_wt_5188	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5189	-	Uncharacterized protein MJ0432;
cds_wt_5190	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5191	ttgR	HTH-type transcriptional regulator ttgR; Toluene
cds_wt_5192	qacA	efflux pump ttgABC operon repressor;
		Antiseptic resistance protein;
cds_wt_5193	aveR	HTH-type transcriptional regulator malT; ATP-
cds_wt_5194	-	dependent transcriptional activator malT;
cds_wt_5195	-	hypothetical protein predicted by Glimmer/Critica
		hypothetical protein
cds_wt_5196	eryA	Erythronolide synthase, modules 3 and 4; ORF 2; 6-
		deoxyerythronolide B synthase II; DEBS 2;
cds_wt_5197	eryA	Erythronolide synthase, modules 3 and 4; ORF 2; 6-
		deoxyerythronolide B synthase II; DEBS 2;
		Bacitracin synthetase 3; BA3; Includes: ATP-
		dependent isoleucine adenylation; IleA; Isoleucine
		activase; Includes: ATP-dependent D-phenylalanine
		adenylation; D-PheA; D-phenylalanine activase;
		Includes: ATP-dependent histidine adenylation; HisA;
		Histidine activase; Includes: ATP-dependent D-
		aspartate adenylation; D-AspA; D-aspartate activase;
		Includes: ATP-dependent asparagine adenylation;
		AsnA; Asparagine activase; Includes: Aspartate
cds_wt_5198	bacC	racemase; Includes: Phenylalanine racemase
cds_wt_5199	orfB	Oleandomycin polyketide synthase, modules 5 and 6;
cds_wt_5200	eryA	Erythronolide synthase, modules 5 and 6; ORF 3; 6-
		deoxyerythronolide B synthase III; DEBS 3;
cds_wt_5201	eryA	Erythronolide synthase, modules 5 and 6; ORF 3; 6-
cds_wt_5202	-	deoxyerythronolide B synthase III; DEBS 3;
cds_wt_5203	Fasn	Putative polyketide synthase pksJ; PKS;
cds_wt_5204	-	Fatty acid synthase; Includes:
		Putative polyketide synthase pksJ; PKS;
		Phenolphthiocerol synthesis polyketide synthase
cds_wt_5205	pks8	ppsA;
cds_wt_5206	Fasn	Fatty acid synthase; Includes:
		Erythronolide synthase, modules 5 and 6; ORF 3; 6-
cds_wt_5207	eryA	deoxyerythronolide B synthase III; DEBS 3;
cds_wt_5208	orfB	Oleandomycin polyketide synthase, modules 5 and 6;
cds_wt_5209	eryA	Erythronolide synthase, modules 3 and 4; ORF 2; 6-
cds_wt_5210	orfB	deoxyerythronolide B synthase II; DEBS 2;
cds_wt_5211	orfB	Oleandomycin polyketide synthase, modules 5 and 6;
		Oleandomycin polyketide synthase, modules 5 and 6;
cds_wt_5212	eryA	Erythronolide synthase, modules 3 and 4; ORF 2; 6-
		deoxyerythronolide B synthase II; DEBS 2;
cds_wt_5213	eryA	Erythronolide synthase, modules 3 and 4; ORF 2; 6-
cds_wt_5214	luxA	deoxyerythronolide B synthase II; DEBS 2;
cds_wt_5215	-	luciferase-like
		hypothetical protein
cds_wt_5216	aveR	HTH-type transcriptional regulator malT; ATP-
		dependent transcriptional activator malT;

cds_wt_5217	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5218	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5219	-	hypothetical protein
cds_wt_5220	pqqE	Coenzyme PQQ synthesis protein E; Pyrroloquinoline
cds_wt_5221	-	quinone biosynthesis protein E;
cds_wt_5222	-	putative glycosyltransferase
cds_wt_5223	-	hypothetical protein
		hypothetical protein predicted by Glimmer/Critica
		HTH-type transcriptional repressor purR; Purine
		nucleotide synthesis repressor; Pur regulon
cds_wt_5224	rbsR	repressor;
cds_wt_5225	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5226	MEL	hypothetical protein
cds_wt_5227	pstI	Aqualysin-1; Aqualysin I;
cds_wt_5228	lieB	Leupeptin-inactivating enzyme 2; LIE2;
cds_wt_5229	DPOL	DNA polymerase beta;
cds_wt_5230	aac	aminoglycoside 2'-N-acetyltransferase
cds_wt_5231	-	Probable amino-acid metabolite efflux pump;
cds_wt_5232	-	Peptide transporter PTR2; Peptide permease PTR2;
cds_wt_5233	-	hypothetical protein
cds_wt_5234	-	RNA polymerase sigma-E factor;
		Insertion element IS110 uncharacterized 43.6 kDa
cds_wt_5235	-	protein;
cds_wt_5236	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5237	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5238	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5239	-	hypothetical protein predicted by Glimmer/Critica
		Transposase for insertion sequence element IS1106;
cds_wt_5240	-	ORF 1;
cds_wt_5241	-	putative two-component system sensor kinase
cds_wt_5242	-	31 kDa immunogenic protein;
cds_wt_5243	-	putative dehydrogenase
		Aspartate carbamoyltransferase; Aspartate
cds_wt_5244	-	transcarbamylase; ATCase;
cds_wt_5245	-	Sporulation-delaying protein sdpB;
cds_wt_5246	-	hypothetical protein predicted by Glimmer/Critica
		Tripeptidyl-peptidase 1; TPP-1; Tripeptidyl-peptidase
		I; TPP-I; Tripeptidyl aminopeptidase; Lysosomal
cds_wt_5247	-	pepstatin-insensitive protease; LPIC;
cds_wt_5248	-	hypothetical protein predicted by Glimmer/Critica
		Transposase insH for insertion sequence element
cds_wt_5249	-	IS5Y;
cds_wt_5250	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5251	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5252	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5253	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5254	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5255	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5256	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5257	-	hypothetical protein predicted by Glimmer/Critica

cds_wt_5258	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5259	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5260	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5261	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5262	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5263	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5264	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5265	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5266	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5267	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5268	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5269	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5270	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5271	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5272	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5273	-	putative DNA-binding protein
cds_wt_5274	-	hypothetical protein
cds_wt_5275	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5276	-	Uncharacterized protein yqjL;
cds_wt_5277	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5278	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5279	-	putative membrane protein
cds_wt_5280	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5281	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5282	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5283	-	Transposase for insertion sequence element ISRM3;
cds_wt_5284	iga	Immunoglobulin A1 protease; IGA1 protease;
cds_wt_5285	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5286	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5287	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5288	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5289	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5290	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5291	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5292	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5293	-	hypothetical protein predicted by Glimmer/Critica
		Putative transposase for insertion sequence element
cds_wt_5294	-	IS6501;
cds_wt_5295	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5296	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5297	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5298	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5299	Son	SON protein;
cds_wt_5300	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5301	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5302	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5303	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5304	-	hypothetical protein
cds_wt_5305	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5306	-	hypothetical protein predicted by Glimmer/Critica

cds_wt_5307	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5308	dnaG	DNA primase
cds_wt_5309	traG	Conjugal transfer protein traG;
cds_wt_5310	dnaB	hypothetical protein
cds_wt_5311	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5312	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5313	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5314	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5315	-	putative lipoprotein
cds_wt_5316	-	hypothetical protein
cds_wt_5317	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5318	-	conserved hypothetical protein
cds_wt_5319	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5320	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5321	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5322	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5323	Cml2	Probable N-acetyltransferase CML2; Camello-like protein 2;
cds_wt_5324	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5325	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5326	ligC	putative DNA ligase
cds_wt_5327	yjhQ	Amino-acid acetyltransferase; N-acetylglutamate synthase; AGS; NAGS;
cds_wt_5328	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5329	-	transposase
cds_wt_5330	-	putative IS6 family transposase
cds_wt_5331	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5332	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5333	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5334	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5335	-	hypothetical protein
cds_wt_5336	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5337	-	hypothetical protein
cds_wt_5338	-	morphinone reductase
cds_wt_5339	-	HTH-type transcriptional regulator betI;
cds_wt_5340	tlpB	Methyl-accepting chemotaxis protein II; MCP-II;
cds_wt_5341	-	Aspartate chemoreceptor protein;
cds_wt_5342	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5343	-	sensory histidine protein kinase
cds_wt_5344	-	putative transposase
cds_wt_5345	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5346	-	hypothetical protein
cds_wt_5347	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5348	-	Type 4 prepilin-like proteins leader peptide-processing enzyme; Late competence protein comC; Includes: Leader peptidase; Prepilin peptidase;
cds_wt_5349	-	Includes: N-methyltransferase;
cds_wt_5350	-	hypothetical protein predicted by Glimmer/Critica
		hypothetical protein

cds_wt_5351	-	hypothetical protein
cds_wt_5352	cpaF	Uncharacterized protein MJ0900;
cds_wt_5353	-	putative integral membrane protein
cds_wt_5354	-	putative integral membrane protein
cds_wt_5355	-	Translation initiation factor IF-2;
cds_wt_5356	-	putative membrane protein
cds_wt_5357	-	Otogelin;
cds_wt_5358	-	hypothetical protein
cds_wt_5359	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5360	-	Translation initiation factor IF-2;
cds_wt_5361	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5362	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5363	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5364	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5365	-	Homoserine kinase; HSK; HK;
cds_wt_5366	tfxG	Trifolitoxin immunity protein;
cds_wt_5367	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5368	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5369	-	hypothetical protein
cds_wt_5370	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5371	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5372	-	UPF0133 protein Bcen_6253;
cds_wt_5373	-	hypothetical protein
cds_wt_5374	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5375	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5376	-	Collagen alpha-4
cds_wt_5377	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5378	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5379	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5380	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5381	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5382	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5383	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5384	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5385	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5386	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5387	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5388	-	Probable protease htpX homolog;
cds_wt_5389	-	hypothetical protein
cds_wt_5390	lysM	putative lysozyme precursor
cds_wt_5391	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5392	ycdB	Peroxidase ycdB;
cds_wt_5393	rhs	Teneurin-4; Ten-4; Tenascin-M4; Ten-m4; Protein Odd Oz/ten-m homolog 4;
cds_wt_5394	cgt	Cyclomaltodextrin glucanotransferase; Cyclodextrin- glycosyltransferase; CGTase; Raw-starch-digesting amylase;
cds_wt_5395	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5396	-	Transcription activator gutR;

cds_wt_5397	-	Anti-sigma F factor antagonist; Stage II sporulation protein AA;
cds_wt_5398	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5399	-	Methyl-accepting chemotaxis protein mcpA; H1;
cds_wt_5400	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5401	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5402	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5403	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5404	dnaB	replicative DNA helicase
cds_wt_5405	dnaB	Replicative DNA helicase;
cds_wt_5406	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5407	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5408	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5409	-	hypothetical protein predicted by Glimmer/Critica Uncharacterized transcriptional regulatory protein
cds_wt_5410	-	yxjL;
cds_wt_5411	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5412	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5413	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5414	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5415	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5416	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5417	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5418	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5419	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5420	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5421	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5422	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5423	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5424	-	LexA repressor;
cds_wt_5425	-	hypothetical protein predicted by Glimmer/Critica Single-stranded DNA-binding protein; SSB; Helix-destabilizing protein;
cds_wt_5426	ssb	
cds_wt_5427	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5428	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5429	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5430	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5431	-	hypothetical protein
cds_wt_5432	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5433	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5434	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5435	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5436	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5437	-	hypothetical protein predicted by Glimmer/Critica Modification methylase Rho11sl; M.Rho11sl; Cytosine-specific methyltransferase Rho11sl; Bsu P11s;
cds_wt_5438	-	
cds_wt_5439	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5440	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5441	-	hypothetical protein predicted by Glimmer/Critica

cds_wt_5442	-	Putative HTH-type transcriptional regulatory protein MTH_967;
cds_wt_5443	-	hypothetical protein
cds_wt_5444	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5445	-	hypothetical protein
cds_wt_5446	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5447	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5448	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5449	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5450	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5451	-	hypothetical protein
cds_wt_5452	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5453	-	hypothetical protein
cds_wt_5454	-	Uncharacterized protein y4bA/y4pH;
cds_wt_5455	yclF	Di-/tripeptide transporter;
cds_wt_5456	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5457	-	Chitodextrinase;
		Eukaryotic translation initiation factor 3 subunit A; eIF3a; Eukaryotic translation initiation factor 3 subunit 10; eIF-3-theta; eIF3 p167; eIF3 p180; eIF3 p185; p162; Centrosomin;
cds_wt_5458	-	
cds_wt_5459	repC	Uncharacterized protein YPL245W;
		Cold-shock DEAD box protein A; ATP-dependent RNA helicase deaD;
cds_wt_5460	deaD	
cds_wt_5461	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5462	-	probable hemagglutinin-related protein
cds_wt_5463	-	hypothetical protein
cds_wt_5464	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5465	-	hypothetical protein predicted by Glimmer/Critica
		Protein piccolo; Aczonin; Multidomain presynaptic cytomatrix protein;
cds_wt_5466	Pclo	
		formate dehydrogenase, alpha subunit, selenocysteine-containing
cds_wt_5467	fdnG	
cds_wt_5468	fdoG	formate dehydrogenase alpha subunit
cds_wt_5469	fdnH	formate dehydrogenase, iron-sulfur subunit
cds_wt_5470	-	hypothetical protein
cds_wt_5471	-	Glutamate
cds_wt_5472	selD	selenide, water dikinase
cds_wt_5473	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5474	-	Glucans biosynthesis protein C;
cds_wt_5475	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5476	selA	selenocysteine synthase
		DNA-directed RNA polymerase II subunit RPB1; RNA polymerase II subunit B1; DNA-directed RNA polymerase III largest subunit;
cds_wt_5477	RPII	
cds_wt_5478	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5479	selB	selenocysteine-specific translation elongation factor
		Selenocysteine-specific elongation factor; SelB translation factor;
cds_wt_5480	-	
cds_wt_5481	-	Alkaline shock protein 23;

cds_wt_5482	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5483	-	hypothetical protein
cds_wt_5484	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5485	-	acyl-CoA dehydrogenase
cds_wt_5486	mtrR	HTH-type transcriptional regulator mtrR;
cds_wt_5487	-	hypothetical protein
cds_wt_5488	-	putative acyl-CoA synthetase
cds_wt_5489	zwf	glucose-6-phosphate 1-dehydrogenase
cds_wt_5490	-	Uncharacterized protein Mb1584;
cds_wt_5491	-	3-oxoacyl-
cds_wt_5492	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5493	-	Putative peptidoglycan O-acetyltransferase yrhL;
cds_wt_5494	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5495	-	hypothetical protein
cds_wt_5496	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5497	wbpA	UDP-N-acetyl-D-mannosamine dehydrogenase; EC=1.1.1.n3; UDP-ManNAc 6-dehydrogenase;
cds_wt_5498	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5499	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5500	-	hypothetical protein
cds_wt_5501	-	putative secreted protein
cds_wt_5502	-	HTH-type transcriptional repressor Bm3R1;
cds_wt_5503	-	putative cholesterol esterase
cds_wt_5504	-	hypothetical protein
cds_wt_5505	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5506	-	putative pectinesterase
cds_wt_5507	Glb1	putative secreted beta-galactosidase
cds_wt_5508	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5509	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5510	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5511	-	Multidrug resistance protein mdtH;
cds_wt_5512	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5513	-	Probable protease htpX homolog;
cds_wt_5514	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5515	DPPV	Dipeptidyl-peptidase 5; Dipeptidyl-peptidase V; DPP V; DppV; AltName: Allergen=Tri s 4;
cds_wt_5516	pknA	putative serine/threonine protein kinase
cds_wt_5517	-	Protein PS1;
cds_wt_5518	-	hypothetical protein
cds_wt_5519	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5520	-	HTH-type transcriptional regulator betI;
cds_wt_5521	-	hypothetical protein
cds_wt_5522	yhjG	putative rifampin monooxygenase
cds_wt_5523	novA	Lipid A export ATP-binding/permease protein msbA;
cds_wt_5524	-	Sensor protein zraS;
cds_wt_5525	-	Response regulator gacA; Global activator;
cds_wt_5526	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5527	-	Uncharacterized protein yqjI;
cds_wt_5528	PHY1	putative two-component system sensor kinase

cds_wt_5529	-	Protease synthase and sporulation negative regulatory protein PAI 1;
cds_wt_5530	-	Lipid A export ATP-binding/permease protein msbA;
cds_wt_5531	-	Lipid A export ATP-binding/permease protein msbA;
cds_wt_5532	-	Lipid A export ATP-binding/permease protein msbA;
cds_wt_5533	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5534	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5535	-	hypothetical protein
cds_wt_5536	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5537	plcN	non-hemolytic phospholipase C precursor
cds_wt_5538	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5539	-	Uncharacterized protein Mb0918;
cds_wt_5540	PDR1	Pleiotropic drug resistance protein 1; NtPDR1;
		Spermidine/putrescine import ATP-binding protein potA;
cds_wt_5541	-	
cds_wt_5542	rtn	Uncharacterized signaling protein PA3311;
cds_wt_5543	erg3	hypothetical protein
cds_wt_5544	-	hypothetical protein
cds_wt_5545	-	HTH-type transcriptional regulator betI;
cds_wt_5546	-	Uncharacterized MFS-type transporter yhcA;
cds_wt_5547	-	hypothetical protein predicted by Glimmer/Critica HTH-type transcriptional repressor purR; Purine nucleotide synthesis repressor; Pur regulon repressor;
cds_wt_5548	lacI	
cds_wt_5549	cebE	Probable arabinose-binding protein;
cds_wt_5550	araP	Probable ABC transporter permease protein yurN;
		sn-glycerol-3-phosphate transport system permease protein ugpE;
cds_wt_5551	cebG	putative beta-glucosidase
cds_wt_5552	bglA	
cds_wt_5553	-	hypothetical protein predicted by Glimmer/Critica Uncharacterized transcriptional regulatory protein yxjL;
cds_wt_5554	-	
cds_wt_5555	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5556	fusA	translation elongation factor EF-G
cds_wt_5557	-	probable conserved integral membrane protein
cds_wt_5558	emrB	Uncharacterized MFS-type transporter yhcA;
cds_wt_5559	amfR	Nitrate/nitrite response regulator protein narP;
cds_wt_5560	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5561	-	putative glycosyl transferase
cds_wt_5562	capD	capsular polysaccharide biosynthesis UDP-N-acetyl-D-mannosaminuronate dehydrogenase
cds_wt_5563	wbpA	
cds_wt_5564	wcaJ	Uncharacterized sugar transferase HI0872;
cds_wt_5565	-	hypothetical protein
cds_wt_5566	-	putative membrane protein
cds_wt_5567	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5568	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5569	sta	Streptothricin acetyltransferase; STAT;
		Uncharacterized WD repeat-containing protein alr3466;
cds_wt_5570	-	

cds_wt_5571	-	hypothetical protein
cds_wt_5572	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5573	-	MOSC domain-containing protein 1, mitochondrial;
cds_wt_5574	-	Cellulose synthesis regulatory protein;
cds_wt_5575	-	hypothetical protein
cds_wt_5576	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5577	-	Putative lipopolysaccharide biosynthesis protein PA4999;
cds_wt_5578	ndhD	NAD
cds_wt_5579	yveL	protein-tyrosine kinase
cds_wt_5580	-	putative glycosyl transferase
cds_wt_5581	yvfE	UDP-4-amino-4-deoxy-L-arabinose--oxoglutarate aminotransferase; EC=2.6.1.n1; UDP-
cds_wt_5582	wcfH	Putative polysaccharide deacetylase yxkH;
cds_wt_5583	-	Aminoacyltransferase femX; Factor essential for expression of methicillin resistance X;
cds_wt_5584	-	Dynamin-3; Dynamin, testicular; T-dynamin;
cds_wt_5585	-	Ketol-acid reductoisomerase; Acetohydroxy-acid isomeroeductase; Alpha-keto-beta-hydroxylacil reductoisomerase;
cds_wt_5586	-	hypothetical protein
cds_wt_5587	-	hypothetical protein
cds_wt_5588	glpK	glycerol kinase
cds_wt_5589	kdgR	HTH-type transcriptional repressor allR; Negative regulator of allantoin and glyoxylate utilization operons;
cds_wt_5590	AQP4	Aquaporin-4; AQP-4;
cds_wt_5591	glpK	glycerol kinase
cds_wt_5592	glpD	glycerol-3-phosphate dehydrogenase
cds_wt_5593	yljG	Ubiquinone/menaquinone biosynthesis methyltransferase ubiE;
cds_wt_5594	betI	HTH-type transcriptional regulator betI;
cds_wt_5595	-	Lipase; Extracellular lipase; SRL; GDSL-like lipase;
cds_wt_5596	Amy2	amylase 2, pancreatic
cds_wt_5597	asfB	NADH-quinone oxidoreductase subunits H/I; NADH dehydrogenase I subunits H/I; NDH-1 subunit H/I;
cds_wt_5598	nadB	hypothetical protein
cds_wt_5599	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5600	-	Protein yobA;
cds_wt_5601	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5602	-	Endoglucanase H; Endo-1,4-beta-glucanase H; EgH;
cds_wt_5603	-	Cellulase H;
cds_wt_5604	-	hypothetical protein
cds_wt_5605	hpbA	hypothetical protein predicted by Glimmer/Critica
cds_wt_5606	appC	Periplasmic oligopeptide-binding protein; Oligopeptide transport system permease protein appC;
cds_wt_5607	dppB	Probable D,D-dipeptide transport system permease protein ddpB;
cds_wt_5608	dppD	Glutathione import ATP-binding protein gsiA;

cds_wt_5609	-	hypothetical protein
cds_wt_5610	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5611	-	hypothetical protein
cds_wt_5612	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5613	-	RNA polymerase sigma factor sigM;
cds_wt_5614	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5615	-	Signaling protein ykoW;
cds_wt_5616	tuf	elongation factor EF-Tu
cds_wt_5617	ctpA	putative cation-transporting P-type ATPase
cds_wt_5618	-	hypothetical protein
cds_wt_5619	-	HTH-type transcriptional regulator betI;
cds_wt_5620	dltE	putative dehydrogenase
cds_wt_5621	-	hydrolase
cds_wt_5622	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5623	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5624	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5625	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5626	sigE	RNA polymerase sigma-E factor;
cds_wt_5627	-	putative dioxygenase
cds_wt_5628	-	hypothetical protein
cds_wt_5629	-	Negative transcription regulator padR; HTH-type transcriptional repressor purR; Purine nucleotide synthesis repressor; Pur regulon repressor;
cds_wt_5630	lacI	
cds_wt_5631	araP	Probable ABC transporter permease protein yurN; L-arabinose transport system permease protein araQ;
cds_wt_5632	-	Probable arabinose-binding protein;
cds_wt_5633	-	putative beta-galactosidase
cds_wt_5634	bga6	Arabinofuranosidase/B-xylosidase; Includes: Alpha- N-arabinofuranosidase; Arabinosidase; Includes: Beta-xylosidase; 1,4-beta-D-xylan xylohydrolase; Xylan 1,4-beta-xylosidase;
cds_wt_5635	xylI	
cds_wt_5636	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5637	-	hypothetical protein predicted by Glimmer/Critica Putative phosphoethanolamine N-methyltransferase 3;
cds_wt_5638	nodS	
cds_wt_5639	rtn5	Uncharacterized protein AZC_3085;
cds_wt_5640	celA	putative endo-1,4-beta-glucanase
cds_wt_5641	-	Probable serine/threonine-protein kinase pknK;
cds_wt_5642	PDR1	Pleiotropic drug resistance protein 1; NtPDR1;
cds_wt_5643	-	Methionine import ATP-binding protein metN;
cds_wt_5644	-	hypothetical protein
cds_wt_5645	-	putative glycosyl transferase
cds_wt_5646	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5647	-	Transmembrane protein 175;
cds_wt_5648	acx	hypothetical protein

		DNA-directed RNA polymerase II subunit RPB1; RNA polymerase II subunit B1; DNA-directed RNA polymerase II subunit A; DNA-directed RNA polymerase III largest subunit; RNA-directed RNA polymerase II subunit RPB1;
cds_wt_5649	-	
cds_wt_5650	-	ADP-ribose 1"-phosphate phosphatase; EC=3.1.3.n2;
cds_wt_5651	yhjG	putative rifampin monooxygenase
cds_wt_5652	yqiQ	carboxyvinyl-carboxyphosphonate phosphorylmutase
cds_wt_5653	-	hypothetical protein predicted by Glimmer/Critica
		Sphingomyelin phosphodiesterase 2; Neutral sphingomyelinase; nSMase; N-SMase; Lyso-platelet-activating factor-phospholipase C; Lyso-PAF-PLC;
cds_wt_5654	-	
cds_wt_5655	-	hypothetical protein
cds_wt_5656	-	Lipid A export ATP-binding/permease protein msbA;
cds_wt_5657	yknU	Lipid A export ATP-binding/permease protein msbA;
cds_wt_5658	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5659	tdk	thymidine kinase
cds_wt_5660	ndh	NADH dehydrogenase
cds_wt_5661	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5662	tcbF	iron-containing alcohol dehydrogenase
cds_wt_5663	-	hypothetical protein
cds_wt_5664	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5665	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5666	-	hypothetical protein
cds_wt_5667	lexA	SOS regulatory protein
cds_wt_5668	-	UPF0189 protein in sno 5'region; ORF7;
cds_wt_5669	-	Uncharacterized MFS-type transporter y4rN;
cds_wt_5670	-	hypothetical protein predicted by Glimmer/Critica
		UDP-4-amino-4-deoxy-L-arabinose--oxoglutarate aminotransferase; EC=2.6.1.n1; UDP-
cds_wt_5671	yvfE	Undecaprenyl-phosphate galactose phosphotransferase; Galactosyl-P-P-undecaprenol synthetase;
cds_wt_5672	pglB	
cds_wt_5673	pglB	acetyltransferase
cds_wt_5674	-	glycosyl transferase, group 1
cds_wt_5675	ywqD	putative ATPase involved in chromosome partitioning
cds_wt_5676	capD	putative nucleoside-diphosphate sugar epimerase
		Probable helicase senataxin; SEN1 homolog;
cds_wt_5677	-	Amyotrophic lateral sclerosis 4 protein homolog;
cds_wt_5678	-	hypothetical protein
cds_wt_5679	ponA	putative penicillin-binding protein
cds_wt_5680	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5681	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5682	-	hypothetical protein predicted by Glimmer/Critica
		Uncharacterized HTH-type transcriptional regulator Mb1581;
cds_wt_5683	ydeS	
cds_wt_5684	-	Uncharacterized MFS-type transporter yhcA;
cds_wt_5685	-	Uncharacterized protein sl1895;
cds_wt_5686	-	
cds_wt_5687	-	transcriptional regulator, Sir2 family

cds_wt_5688	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5689	acoC	putative hydrolase
cds_wt_5690	choD	putative cholesterol oxidase
cds_wt_5691	hapE	flavin-binding monooxygenase-like protein
cds_wt_5692	add	adenosine deaminase
cds_wt_5693	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5694	-	Signaling protein ykoW;
cds_wt_5695	PHYA	Phytochrome A;
		Alpha-N-arabinofuranosidase 2; Alpha-N-arabinofuranosidase II; Arabinosidase II; Alpha-N-AFase II;
cds_wt_5696	abf2	Alpha-N-arabinofuranosidase 1; Alpha-N-arabinofuranosidase I; Arabinosidase I; Alpha-N-AFase I;
cds_wt_5697	-	3-hydroxybutyryl-CoA dehydratase
cds_wt_5698	crt2	Sensor protein kinase walk;
cds_wt_5699	smrB	D-isomer specific 2-hydroxyacid dehydrogenase family protein
cds_wt_5700	yugC	Uncharacterized HTH-type transcriptional regulator ydcN;
cds_wt_5701	-	Thioredoxin reductase; TRXR;
cds_wt_5702	-	hypothetical protein
cds_wt_5703	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5704	-	Uncharacterized protein Mb2934c;
cds_wt_5705	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5706	-	putative acyl-CoA dehydrogenase
cds_wt_5707	bcd1	acyl-CoA synthase
cds_wt_5708	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5709	-	phosphoesterase, PA-phosphatase related
cds_wt_5710	cpo	Probable transcriptional regulator ycf27; OmpR-like protein;
cds_wt_5711	-	Uncharacterized HTH-type transcriptional regulator yjgJ;
cds_wt_5712	-	quinone oxidoreductase
cds_wt_5713	qor	hypothetical protein predicted by Glimmer/Critica
cds_wt_5714	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5715	-	putative dehydratase
cds_wt_5716	-	thiolase family protein
cds_wt_5717	-	Inner membrane protein yiaA;
cds_wt_5718	yiaA	hypothetical protein predicted by Glimmer/Critica
cds_wt_5719	-	Endo-1,4-beta-xylanase A; Xylanase A; 1,4-beta-D-xylan xylanohydrolase A;
cds_wt_5720	xysA	hypothetical protein predicted by Glimmer/Critica
cds_wt_5721	-	Phosphocarrier protein HPr; Histidine-containing protein;
cds_wt_5722	ptsH	PTS-dependent dihydroxyacetone kinase, phosphotransferase subunit dhaM;
		Phosphotransferase enzyme IIA component; PTS system EIIA component;
cds_wt_5723	-	dihydroxyacetone kinase
cds_wt_5724	dak1	

cds_wt_5725	dak1	putative dihydroxyacetone kinase
cds_wt_5726	tse	Methyl-accepting chemotaxis serine transducer;
cds_wt_5727	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5728	-	hypothetical protein
cds_wt_5729	recD	helicase RecD/TraA
cds_wt_5730	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5731	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5732	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5733	xylC	benzaldehyde dehydrogenase II
cds_wt_5734	-	hypothetical protein
cds_wt_5735	menG	Regulator of ribonuclease activity A;
cds_wt_5736	yqaB	Phosphoglycolate phosphatase; PGPase; PGP;
cds_wt_5737	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5738	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5739	putA	proline dehydrogenase
cds_wt_5740	-	Probable RuBisCO transcriptional regulator;
cds_wt_5741	-	o-phthalyl amidase;
cds_wt_5742	-	autotransporter
cds_wt_5743	-	Uncharacterized protein Mb0912;
cds_wt_5744	-	hypothetical protein
cds_wt_5745	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5746	-	Phosphoenolpyruvate-protein phosphotransferase;
cds_wt_5747	-	Phosphotransferase system, enzyme I;
cds_wt_5748	-	hypothetical protein
cds_wt_5749	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5750	-	hypothetical protein
cds_wt_5751	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5752	-	hypothetical protein
cds_wt_5753	-	Spermidine/putrescine import ATP-binding protein
cds_wt_5754	PDR1	potA;
cds_wt_5755	-	Pleiotropic drug resistance protein 1; NtPDR1;
cds_wt_5756	tas	HTH-type transcriptional regulator betI;
cds_wt_5757	-	Methyl-accepting chemotaxis aspartate transducer;
cds_wt_5758	phy	hypothetical protein predicted by Glimmer/Critica
cds_wt_5759	-	Adaptive-response sensory-kinase sasA;
cds_wt_5760	DPOL	hypothetical protein predicted by Glimmer/Critica
cds_wt_5761	mmyQ	DNA polymerase beta;
cds_wt_5762	yfmJ	Glycerol-3-phosphate dehydrogenase
cds_wt_5763	-	putative oxidoreductase
cds_wt_5764	-	Transcription elongation factor spt5; Chromatin
cds_wt_5765	-	elongation factor spt5;
cds_wt_5766	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5767	sgaE	Regulator of nonsense transcripts 1; ATP-dependent
		helicase RENT1; Nonsense mRNA reducing factor 1;
		NORF1; Up-frameshift suppressor 1 homolog;
		mUpf1;
		Hydroxyacylglutathione hydrolase; Glyoxalase II; Glx
		II;
		putative epimerase/aldolase

cds_wt_5768	-	IQ motif and SEC7 domain-containing protein 3;
cds_wt_5769	lacI	HTH-type transcriptional repressor purR; Purine nucleotide synthesis repressor; Pur regulon repressor;
cds_wt_5770	ytfQ	HTH-type transcriptional repressor purR; Purine nucleotide synthesis repressor; Pur regulon repressor;
cds_wt_5771	ytfR	putative ATP-binding component of a transport system
cds_wt_5772	-	Autoinducer 2 import system permease protein lsrC; AI-2 import system permease protein lsrC;
cds_wt_5773	yjfF	Autoinducer 2 import system permease protein lsrC;
cds_wt_5774	araA	AI-2 import system permease protein lsrC;
cds_wt_5775	iga	L-arabinose isomerase
cds_wt_5776	-	IgA-specific serine endopeptidase; IgA protease;
cds_wt_5777	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5778	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5779	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5780	-	Putative amidohydrolase ytcJ;
cds_wt_5781	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5782	ydfJ	HTH-type protein slmA;
cds_wt_5783	X	Putative membrane protein mmpL3;
cds_wt_5784	-	Uncharacterized protein X;
cds_wt_5785	galA	hypothetical protein predicted by Glimmer/Critica
cds_wt_5786	yvfO	putative galactosidase
cds_wt_5787	lacI	putative galactosidase
cds_wt_5788	araQ	HTH-type transcriptional repressor purR; Purine nucleotide synthesis repressor; Pur regulon repressor;
cds_wt_5789	-	Probable ABC transporter permease protein yurM;
cds_wt_5790	-	sn-glycerol-3-phosphate transport system permease protein ugpA;
cds_wt_5791	GLB1	Probable arabinose-binding protein;
cds_wt_5792	galT	beta-galactosidase precursor
cds_wt_5793	-	galactose-1-phosphate uridylyltransferase
cds_wt_5794	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5795	-	putative integral membrane protein
		Uncharacterized protein in chlN 3' region; URF2;
		Flags: Fragment;
cds_wt_5796	-	Sialic acid TRAP transporter permease protein siaT;
cds_wt_5797	-	N-acetylneuraminic acid permease; Neu5Ac permease; N-acetylneuraminic acid transporter;
cds_wt_5798	-	31 kDa immunogenic protein;
cds_wt_5799	-	RNA polymerase sigma factor sigM;
cds_wt_5800	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5801	-	putative oxidoreductase
cds_wt_5802	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5803	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5804	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5805	-	hypothetical protein
		Hemolysin secretion protein;

cds_wt_5806	-	hypothetical protein
cds_wt_5807	-	hypothetical protein
cds_wt_5808	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5809	rbsK	putative carbohydrate kinase
cds_wt_5810	uspA	sn-glycerol-3-phosphate transport system permease protein ugpA;
cds_wt_5811	uspB	sn-glycerol-3-phosphate transport system permease protein ugpE;
cds_wt_5812	uspC	Maltose/maltodextrin-binding protein;
cds_wt_5813	celF	6-phospho-beta-glucosidase
cds_wt_5814	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5815	-	hypothetical protein
cds_wt_5816	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5817	-	hypothetical protein
cds_wt_5818	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5819	-	linoleoyl-CoA desaturase, putative
cds_wt_5820	vanB	putative oxidoreductase
cds_wt_5821	-	Uncharacterized protein Mb2266;
cds_wt_5822	ETR2	Ethylene receptor 2; PhETR2;
cds_wt_5823	-	Transcriptional regulatory protein degU; Protease production enhancer protein;
cds_wt_5824	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5825	-	Transmembrane protease, serine 13; Membrane-type mosaic serine protease; Mosaic serine protease;
cds_wt_5826	ald	alanine dehydrogenase
cds_wt_5827	putR	Leucine-responsive regulatory protein;
cds_wt_5828	Ttn	Titin; Connectin;
cds_wt_5829	-	Maltose transport system permease protein malG;
cds_wt_5830	yesP	Probable ABC transporter permease protein yesP;
cds_wt_5831	-	Probable arabinose-binding protein;
cds_wt_5832	yteT	Glycosyl hydrolase family 109 protein;
cds_wt_5833	uxaC	hexuronic acid isomerase
cds_wt_5834	uxuB	putative D-mannonate oxidoreductase
cds_wt_5835	-	Inositol 2-dehydrogenase; Myo-inositol 2-dehydrogenase; MI 2-dehydrogenase;
cds_wt_5836	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5837	pel	pectate lyase
cds_wt_5838	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5839	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5840	-	putative secreted protein
cds_wt_5841	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5842	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5843	-	Cell surface glycoprotein 1; Outer layer protein B; S-layer protein 1;
cds_wt_5844	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5845	galS	HTH-type transcriptional repressor purR; Purine nucleotide synthesis repressor; Pur regulon repressor;
cds_wt_5846	gap	glyceraldehyde-3-phosphate dehydrogenase
cds_wt_5847	-	HTH-type transcriptional regulator glxA;

		HTH-type transcriptional repressor purR; Purine nucleotide synthesis repressor; Pur regulon repressor;
cds_wt_5848	lacI	
cds_wt_5849	-	hypothetical protein predicted by Glimmer/Critica
		Transcription elongation factor SPT5; DRB
		sensitivity-inducing factor large subunit; DSIF large subunit;
cds_wt_5850	-	
cds_wt_5851	-	Uncharacterized protein yegE;
cds_wt_5852	-	Uncharacterized signaling protein PA3311;
cds_wt_5853	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5854	-	hypothetical protein
cds_wt_5855	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5856	pitA	Probable low-affinity inorganic phosphate transporter;
cds_wt_5857	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5858	glpQ	glycerophosphoryl diester phosphodiesterase
cds_wt_5859	-	Sensor histidine kinase liaS;
		Phosphate regulon transcriptional regulatory protein
cds_wt_5860	-	phoB;
cds_wt_5861	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5862	glyQ	aminoacyl-t-RNA synthetase, putative
cds_wt_5863	yhcW	Phosphoglycolate phosphatase; PGPase; PGP;
cds_wt_5864	-	Uncharacterized protein yegE;
cds_wt_5865	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5866	cbhA	1,4-beta-cellobiosidase
cds_wt_5867	pphA	Protein phosphatase prpC;
cds_wt_5868	-	hypothetical protein
cds_wt_5869	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5870	-	putative integral membrane protein
cds_wt_5871	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5872	nuoF	putative oxidoreductase
cds_wt_5873	dsbF	Thiol-disulfide oxidoreductase resA;
cds_wt_5874	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5875	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5876	pkn7	CBL-interacting protein kinase 32; OsCIPK32;
cds_wt_5877	-	hypothetical protein
cds_wt_5878	ppp	hypothetical protein
cds_wt_5879	ynaD	ribosomal-protein-serine acetyltransferase
cds_wt_5880	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5881	glgB	1,4-alpha-glucan branching enzyme
cds_wt_5882	pep2	hypothetical protein
cds_wt_5883	treS	putative trehalose synthase
cds_wt_5884	glgE	putative alpha-amylase
cds_wt_5885	-	hypothetical protein
cds_wt_5886	-	hypothetical protein
cds_wt_5887	ppgK	polyphosphate glucokinase
cds_wt_5888	rpoD	RNA polymerase sigma factor rpoD; Sigma-70;
cds_wt_5889	-	hypothetical protein
cds_wt_5890	-	possible pre-pilin peptidase
cds_wt_5891	resE	two-component sensor histidine kinase

cds_wt_5892	cheY	Probable transcriptional regulator ycf27; OmpR-like protein;
cds_wt_5893	-	Membrane-bound protein lytR;
cds_wt_5894	hrpA	ATP-dependent RNA helicase hrpA homolog;
cds_wt_5895	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5896	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5897	-	hypothetical protein predicted by Glimmer/Critica
		Methionine synthase; 5-methyltetrahydrofolate--homocysteine methyltransferase; Methionine synthase, vitamin-B12 dependent; MS;
cds_wt_5898	-	Phosphoserine phosphatase rsbU; Sigma factor sigB regulation protein rsbU;
cds_wt_5899	-	putative exonuclease
cds_wt_5900	xthA	hypothetical protein predicted by Glimmer/Critica
cds_wt_5901	-	Uncharacterized signaling protein PA3311;
cds_wt_5902	-	Uncharacterized protein Mb2028c;
cds_wt_5903	-	citrate synthase
cds_wt_5904	gltA	Arsenical resistance operon repressor;
cds_wt_5905	arsR	hypothetical protein
cds_wt_5906	-	Metallothiol transferase fosB; Fosfomycin resistance protein;
cds_wt_5907	-	magnesium-chelatase subunit
cds_wt_5908	chlI	hypothetical protein predicted by Glimmer/Critica
cds_wt_5909	-	cob(I)alamin adenosyltransferase
cds_wt_5910	cobO	cobyrinic acid a,c-diamide synthase
cds_wt_5911	cobB	hypothetical protein predicted by Glimmer/Critica
cds_wt_5912	-	hypothetical protein
cds_wt_5913	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5914	-	Collagen alpha-5
cds_wt_5915	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5916	-	Triple functional domain protein; PTPRF-interacting protein;
cds_wt_5917	TRIO	hypothetical protein
cds_wt_5918	-	Protein translocase subunit secA;
cds_wt_5919	secA	Uncharacterized transcriptional regulatory protein
cds_wt_5920	yclJ	yclJ;
cds_wt_5921	-	hypothetical protein
cds_wt_5922	-	DnaK suppressor protein homolog;
cds_wt_5923	yunF	hypothetical protein
cds_wt_5924	-	Uncharacterized protein yecE;
cds_wt_5925	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5926	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5927	-	DNA translocase ftsK;
cds_wt_5928	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5929	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5930	bag	IgA FC receptor; Beta antigen; B antigen;
		ATP-dependent Clp protease ATP-binding subunit
cds_wt_5931	clpB	clpC;
cds_wt_5932	-	hypothetical protein predicted by Glimmer/Critica

cds_wt_5933	-	Transcriptional regulatory protein degU; Protease production enhancer protein;
cds_wt_5934	-	Cell division control protein 48 homolog E;
cds_wt_5935	-	AtCDC48e; Transitional endoplasmic reticulum ATPase E;
cds_wt_5936	-	unknown protein
cds_wt_5937	-	Probable RuBisCO transcriptional regulator;
cds_wt_5938	-	Uncharacterized hemerythrin-like protein C869.06c;
cds_wt_5939	-	Probable carboxypeptidase PM20D1; Peptidase M20 domain-containing protein 1;
cds_wt_5940	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5941	-	hypothetical protein
cds_wt_5942	-	Uncharacterized transcriptional regulatory protein yfiK;
cds_wt_5943	-	Sensor protein vraS;
cds_wt_5944	-	Aldo-keto reductase family 1 member C1 homolog;
cds_wt_5945	-	20-alpha-hydroxysteroid dehydrogenase; 20-alpha-HSD; Dihydrodiol dehydrogenase 1; DD-1; DD1;
cds_wt_5946	-	hypothetical protein
cds_wt_5947	mshC	hypothetical protein
cds_wt_5948	-	hypothetical protein
cds_wt_5949	-	hypothetical protein
cds_wt_5950	-	hypothetical protein
cds_wt_5951	-	hypothetical protein
cds_wt_5952	-	cysteinyI-tRNA synthetase
cds_wt_5953	arsR	hypothetical protein predicted by Glimmer/Critica
cds_wt_5954	-	Transcriptional regulatory protein degU; Protease production enhancer protein;
cds_wt_5955	-	hydrolase, alpha/beta fold family, putative
cds_wt_5956	hisE	HTH-type transcriptional regulator frlR;
cds_wt_5957	-	Voltage-dependent N-type calcium channel subunit alpha-1B; Voltage-gated calcium channel subunit alpha Cav2.2; Calcium channel, L type, alpha-1 polypeptide isoform 5; Brain calcium channel III; BIII;
cds_wt_5958	-	Arsenical resistance operon repressor;
cds_wt_5959	-	hypothetical protein
cds_wt_5960	-	Macrolide export ATP-binding/permease protein
cds_wt_5961	-	macB;
cds_wt_5962	fdxG	putative hydrolase
cds_wt_5963	-	Uncharacterized transcriptional regulatory protein
cds_wt_5964	-	yxjL;
cds_wt_5965	-	Gene 69 protein; Gp69;
cds_wt_5966	-	hypothetical protein
cds_wt_5967	prcB	putative protein-L-isoaspartate methyltransferase
cds_wt_5968	prcA	hypothetical protein predicted by Glimmer/Critica
cds_wt_5969	-	putative ferredoxin
cds_wt_5970	-	putative AAA-family ATPase
		Putative peptidoglycan O-acetyltransferase yrhL;
		Uncharacterized protein ML1328;
		hypothetical protein
		proteasome, beta subunit
		20S proteasome alpha-subunit
		Uncharacterized protein Mb2124c;
		hypothetical protein predicted by Glimmer/Critica

cds_wt_5971	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5972	omt	O-methyltransferase
cds_wt_5973	-	Uncharacterized signaling protein PA3311;
cds_wt_5974	-	Helicase domino;
cds_wt_5975	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5976	-	hypothetical protein
cds_wt_5977	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5978	-	hypothetical protein
cds_wt_5979	catA	Zinc transporter 9; ZnT-9; Solute carrier family 30 member 9;
cds_wt_5980	-	Uncharacterized protein ML1329;
cds_wt_5981	-	Uncharacterized protein ML1330;
cds_wt_5982	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5983	tatA	Sec-independent protein translocase protein tatA/E homolog;
cds_wt_5984	tatC	Sec-independent protein translocase protein tatC homolog;
cds_wt_5985	bmrU	Lipid kinase yegS;
cds_wt_5986	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5987	helY	putative helicase
cds_wt_5988	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5989	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5990	glgB	1,4-alpha-glucan branching enzyme
cds_wt_5991	baiG	Bile acid transporter;
cds_wt_5992	-	Uncharacterized MFS-type transporter ydeG;
cds_wt_5993	-	hypothetical protein
cds_wt_5994	-	long-chain fatty-acid-CoA ligase
cds_wt_5995	-	putative transcriptional regulator
cds_wt_5996	-	putative monophosphatase
cds_wt_5997	-	hypothetical protein
cds_wt_5998	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_5999	-	Oxoglutarate dehydrogenase inhibitor;
cds_wt_6000	-	Collagen alpha-1
cds_wt_6001	prpC	hypothetical protein
cds_wt_6002	pknG	putative serine/threonine protein kinase
cds_wt_6003	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6004	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6005	-	hypothetical protein
cds_wt_6006	-	putative acyl-CoA synthetase, long-chain fatty acid:CoA ligase
cds_wt_6007	yuxH	Uncharacterized protein yuxH;
cds_wt_6008	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6009	fimA	hypothetical protein
cds_wt_6010	-	hypothetical protein
cds_wt_6011	tcmR	HTH-type transcriptional regulator tcmR; Tetracenomycin C transcriptional repressor; Hydroxyacylglutathione hydrolase; Glyoxalase II; Glx II;
cds_wt_6012	-	
cds_wt_6013	lytR	Membrane-bound protein lytR;
cds_wt_6014	fhbA	putative oxidoreductase

cds_wt_6015	-	Uncharacterized protein TP_0572;
cds_wt_6016	mprA	Transcriptional regulatory protein yycF;
cds_wt_6017	mprB	putative two-component system sensor kinase
cds_wt_6018	-	hypothetical protein
cds_wt_6019	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6020	fepC	ABC-type cobalamin/Fe ³⁺ -siderophores transport systems ATPase components
cds_wt_6021	fepG	Vitamin B12 import system permease protein btuC;
cds_wt_6022	fepD	Vitamin B12 import system permease protein btuC;
cds_wt_6023	sidF	iron-siderophore uptake ABC system substrate-binding component
cds_wt_6024	-	hypothetical protein
cds_wt_6025	ydeS	Uncharacterized HTH-type transcriptional regulator Mb1581;
cds_wt_6026	-	Protein rhsD;
cds_wt_6027	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6028	-	Uncharacterized protein yjbR;
cds_wt_6029	-	Uncharacterized protein yndB;
cds_wt_6030	-	Arsenical resistance operon repressor;
cds_wt_6031	bglC	endo-1,4-beta-glucanase
cds_wt_6032	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6033	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6034	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6035	-	hypothetical protein
cds_wt_6036	smtA	Ubiquinone/menaquinone biosynthesis methyltransferase ubiE;
cds_wt_6037	lpqL	probable aminopeptidase
cds_wt_6038	-	Cell division cycle protein 48 homolog AF_1297;
cds_wt_6039	aidB	putative acyl-CoA dehydrogenase
cds_wt_6040	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6041	-	Uncharacterized HTH-type transcriptional regulator ywaE;
cds_wt_6042	acpD	acyl carrier protein phosphodiesterase
cds_wt_6043	-	Sphingosine-1-phosphate phosphatase 1; SPPase1; Spp1; Sphingosine-1-phosphatase 1; hSPPase1;
cds_wt_6044	-	Putative lipid phosphate phosphatase 3, chloroplastic; AtLPP3; Phosphatidic acid phosphatase 3; Phosphatidate phosphohydrolase 3;
cds_wt_6045	aslA	arylsulphatase A
cds_wt_6046	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6047	-	Putative pterin-4-alpha-carbinolamine dehydratase; PHS; 4-alpha-hydroxy-tetrahydropterin dehydratase;
cds_wt_6048	-	Pterin carbinolamine dehydratase; PCD;
cds_wt_6049	-	Mini-circle putative transposase for IS117;
cds_wt_6050	aceA	malate synthase
cds_wt_6051	hipB	isocitrate lyase
cds_wt_6052	-	Immunity repressor protein;
cds_wt_6053	-	tRNA
		N-acetylglucosaminyltransferase; Nodulation protein C;

cds_wt_6054	capD	capsular polysaccharide biosynthesis
cds_wt_6055	chb	GlcNAc-binding protein A;
cds_wt_6056	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6057	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6058	-	Probable RuBisCO transcriptional regulator;
cds_wt_6059	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6060	-	Nitrate/nitrite response regulator protein narP;
cds_wt_6061	-	Sensor histidine kinase yxjM;
cds_wt_6062	-	Spermidine/putrescine import ATP-binding protein potA;
cds_wt_6063	-	Macrolide export ATP-binding/permease protein macB 1;
cds_wt_6064	ETR1	Ethylene receptor; MEETR1; Cm-ETR1;
cds_wt_6065	-	response regulator receiver (CheY-like) modulated
cds_wt_6066	sthK	CheB methylesterase
cds_wt_6067	pilJ	sensor histidine kinase/response regulator
cds_wt_6068	-	Methyl-accepting chemotaxis protein II; MCP-II;
cds_wt_6069	cheR	Aspartate chemoreceptor protein;
cds_wt_6070	-	Chemotaxis protein cheW;
cds_wt_6071	-	MCP methyltransferase, CheR-type
cds_wt_6072	-	Chemotaxis protein cheV;
cds_wt_6073	ykwD	hypothetical protein predicted by Glimmer/Critica
cds_wt_6074	-	putative integral membrane protein
cds_wt_6075	lktD	hypothetical protein
cds_wt_6076	-	Leukotoxin secretion protein D;
cds_wt_6077	salY	ABC-type antimicrobial peptide transport system,
cds_wt_6078	ybiF	ATPase component
cds_wt_6079	ycdT	Macrolide export ATP-binding/permease protein macB;
cds_wt_6080	-	Uncharacterized transporter ywfM;
cds_wt_6081	TRIO	Uncharacterized signaling protein PA3311;
cds_wt_6082	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6083	-	Triple functional domain protein; PTPRF-interacting protein;
cds_wt_6084	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6085	pimB	Eukaryotic translation initiation factor 3 subunit A;
cds_wt_6086	-	eIF3a; Eukaryotic translation initiation factor 3 subunit
cds_wt_6087	-	10; eIF-3-theta; eIF3 p167; eIF3 p180; eIF3 p185;
cds_wt_6088	lacI	p162; Centrosomin;
cds_wt_6089	araA	DNA damage-inducible protein 1; v-SNARE-master
cds_wt_6090	chvE	1;
		glycosyl transferase
		hypothetical protein
		hypothetical protein
		HTH-type transcriptional repressor purR; Purine
		nucleotide synthesis repressor; Pur regulon
		repressor;
		L-arabinose isomerase
		Multiple sugar-binding periplasmic receptor chvE;

cds_wt_6091	gguA	ribose ABC transporter ATP-binding protein
cds_wt_6092	gguB	Xylose transport system permease protein xylH;
cds_wt_6093	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6094	-	hypothetical protein
cds_wt_6095	-	hypothetical protein
cds_wt_6096	glk	glucose kinase
cds_wt_6097	-	Anti-sigma F factor antagonist; Stage II sporulation protein AA;
cds_wt_6098	zwf	glucose-6-phosphate 1-dehydrogenase
cds_wt_6099	-	hypothetical protein
cds_wt_6100	-	hypothetical protein
cds_wt_6101	yaaA	Uncharacterized protein yaaA;
cds_wt_6102	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6103	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6104	fkb	peptidyl-prolyl cis-trans isomerase
cds_wt_6105	cpbD	GlcNAc-binding protein A;
cds_wt_6106	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6107	-	hypothetical protein
cds_wt_6108	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6109	-	XylIDLEGF operon transcriptional activator 3;
cds_wt_6110	-	RNA pyrophosphohydrolase;
cds_wt_6111	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6112	chiA	chitinase B
cds_wt_6113	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6114	-	Uncharacterized signaling protein PA3311;
cds_wt_6115	glgC	glucose-1-phosphate adenylyltransferase
cds_wt_6116	rtn	Uncharacterized signaling protein PA3311;
cds_wt_6117	fenI	Uncharacterized lipoprotein yddW;
cds_wt_6118	cgt	Cyclomaltodextrin glucanotransferase; Cyclodextrin-glycosyltransferase; CGTase; Raw-starch-digesting amylase;
cds_wt_6119	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6120	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6121	-	putative ABC transporter ATP-binding protein
cds_wt_6122	-	Uncharacterized signaling protein PA3311;
cds_wt_6123	-	Diaminopimelate epimerase; DAP epimerase;
cds_wt_6124	chII	magnesium chelatase, putative
cds_wt_6125	-	Uncharacterized protein Rv0959/MT0986;
cds_wt_6126	arsR	Arsenical resistance operon repressor;
cds_wt_6127	-	hypothetical protein
cds_wt_6128	-	HTH-type transcriptional activator rhaR; L-rhamnose operon transcriptional activator rhaR;
cds_wt_6129	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6130	sigG	RNA polymerase sigma factor rpoD; Sigma-43;
cds_wt_6131	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6132	pgsA	putative CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyl-transferase
cds_wt_6133	-	Uncharacterized protein ylxX;
cds_wt_6134	sbp	Small basic protein;
cds_wt_6135	-	Uncharacterized protein Mb1856;

cds_wt_6136	gcvH	Glycine cleavage system H protein;
cds_wt_6137	garA	Oxoglutarate dehydrogenase inhibitor;
		Uncharacterized HTH-type transcriptional regulator
cds_wt_6138	-	Mb1859;
cds_wt_6139	-	Uncharacterized protein Rv1829/MT1877;
		Uncharacterized HTH-type transcriptional regulator
cds_wt_6140	-	Mb1861;
		UvrABC system protein A; UvrA protein;
cds_wt_6141	drrC	Excinuclease ABC subunit A;
cds_wt_6142	asnB	asparagine synthase
cds_wt_6143	-	TPR repeat
cds_wt_6144	-	hypothetical protein
cds_wt_6145	kka	putative phosphotransferase
cds_wt_6146	baeS	sensor protein (for BaeR)
		Probable transcriptional regulator ycf27; OmpR-like
cds_wt_6147	-	protein;
cds_wt_6148	-	hypothetical protein predicted by Glimmer/Critica
		Nucleoside diphosphate kinase; NDK; NDP kinase;
cds_wt_6149	-	Nucleoside-2-P kinase;
cds_wt_6150	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6151	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6152	ileS	isoleucyl-tRNA synthetase
cds_wt_6153	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6154	-	Collagen alpha-5
cds_wt_6155	-	Extracellular matrix protein FRAS1;
cds_wt_6156	nhoA	N-hydroxyarylamine O-acetyltransferase
cds_wt_6157	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6158	-	Uncharacterized zinc protease ML0855;
cds_wt_6159	-	hypothetical protein
cds_wt_6160	mhpA	3-(3-hydroxyphenyl)propionate hydroxylase
cds_wt_6161	-	hypothetical protein
cds_wt_6162	yehP	Uncharacterized protein yehP;
cds_wt_6163	-	Holliday junction ATP-dependent DNA helicase ruvB;
cds_wt_6164	-	Uncharacterized protein yegE;
cds_wt_6165	-	hypothetical protein
cds_wt_6166	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6167	-	hypothetical protein
cds_wt_6168	-	DNA translocase ftsK;
		Immunoglobulin G-binding protein A; IgG-binding
cds_wt_6169	-	protein A; Staphylococcal protein A;
cds_wt_6170	-	Holliday junction ATP-dependent DNA helicase ruvB;
cds_wt_6171	-	Uncharacterized protein TM_0929;
		transcriptional regulator, AraC family with parallel
cds_wt_6172	-	beta-helix repeat
cds_wt_6173	-	hypothetical protein
		Probable isochorismatase; 2,3 dihydro-2,3
cds_wt_6174	phzA	dihydroxybenzoate synthase;
cds_wt_6175	-	Haloalkane dehalogenase;
cds_wt_6176	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6177	-	hypothetical protein

cds_wt_6178	kasA	3-oxoacyl-
cds_wt_6179	-	transcriptional regulatory protein
cds_wt_6180	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6181	dac	putative D-alanyl-D-alanine carboxypeptidase
cds_wt_6182	dcsA	Uncharacterized transporter yoaV;
		Kynurenine/alpha-aminoadipate aminotransferase mitochondrial; KAT/AadAT; Kynurenine aminotransferase II; Kynurenine--oxoglutarate aminotransferase II; Kynurenine--oxoglutarate transaminase II; 2-aminoadipate transaminase; 2- aminoadipate aminotransferase; Alpha-aminoadipate aminotransferase; AadAT;
cds_wt_6183	gntR	
cds_wt_6184	pknA	putative serine/threonine protein kinase
cds_wt_6185	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6186	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6187	pelB	pectate lyase
cds_wt_6188	-	pectinesterase
cds_wt_6189	-	UPF0308 protein C9orf21 homolog;
cds_wt_6190	-	tyrosinase
cds_wt_6191	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6192	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6193	-	inosine-uridine preferring nucleoside hydrolase
cds_wt_6194	-	putative integral membrane transport protein
cds_wt_6195	-	conserved hypothetical protein
cds_wt_6196	-	Methionine import ATP-binding protein metN;
cds_wt_6197	-	Homoserine kinase; HSK; HK;
cds_wt_6198	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6199	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6200	-	Uncharacterized protein yfeS;
		Arabinofuranosidase/B-xylosidase; Includes: Alpha- N-arabinofuranosidase; Arabinosidase; Includes: Beta-xylosidase; 1,4-beta-D-xylan xylohydrolase; Xylan 1,4-beta-xylosidase;
cds_wt_6201	xylI	
cds_wt_6202	sndH	L-sorbose dehydrogenase
cds_wt_6203	-	Endoglucanase; Endo-1,4-beta-glucanase; Cellulase;
cds_wt_6204	-	hypothetical protein
cds_wt_6205	-	hypothetical protein
		HTH-type transcriptional activator rhaR; L-rhamnose operon transcriptional activator rhaR;
cds_wt_6206	-	
cds_wt_6207	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6208	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6209	-	Prestalk A differentiation protein A;
cds_wt_6210	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6211	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6212	-	Putative multidrug resistance protein mdtD;
cds_wt_6213	-	conserved hypothetical protein
cds_wt_6214	-	conserved hypothetical protein
cds_wt_6215	-	conserved hypothetical protein
cds_wt_6216	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6217	-	hypothetical protein predicted by Glimmer/Critica

cds_wt_6218	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6219	-	hypothetical protein
cds_wt_6220	nreC	Oxygen regulatory protein nreC; Nitrogen regulation protein C;
cds_wt_6221	mmvF	probable oxidoreductase
cds_wt_6222	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6223	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6224	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6225	-	Uncharacterized hemerythrin-like protein C869.06c;
cds_wt_6226	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6227	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6228	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6229	-	UPF0145 protein BVU_2335;
cds_wt_6230	-	UPF0145 protein ECA2666;
cds_wt_6231	cutM	oxidoreductase, medium chain
cds_wt_6232	-	Xanthine dehydrogenase; XD; Protein rosy locus;
cds_wt_6233	nahB	beta-N-acetylhexosaminidase
cds_wt_6234	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6235	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6236	-	putative secreted protein
cds_wt_6237	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6238	cbgA	putative secreted protein
cds_wt_6239	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6240	-	hypothetical protein
cds_wt_6241	-	hypothetical protein
cds_wt_6242	-	HTH-type protein slmA;
cds_wt_6243	-	Uncharacterized MFS-type transporter C16A3.17c;
cds_wt_6244	splB	spore photoproduct lyase
cds_wt_6245	-	hypothetical protein
cds_wt_6246	-	acetyltransferase, GNAT family
cds_wt_6247	alsR	HTH-type transcriptional regulator benM; Ben and cat operon transcriptional regulator;
cds_wt_6248	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6249	-	Amine oxidase
cds_wt_6250	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6251	csd	selenocysteine lyase
cds_wt_6252	mcpB	Methyl-accepting chemotaxis protein mcpA; H1;
cds_wt_6253	tcmR	HTH-type transcriptional regulator tcmR;
cds_wt_6254	-	Tetracenomycin C transcriptional repressor;
cds_wt_6255	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6256	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6257	-	possible transmembrane acyltransferase
cds_wt_6258	-	possible transmembrane acyltransferase
cds_wt_6259	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6260	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6261	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6262	xysA	endo-1,4-beta-xylanase
cds_wt_6263	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6264	-	hypothetical protein predicted by Glimmer/Critica

cds_wt_6265	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6266	galM	aldose 1-epimerase
cds_wt_6267	murX	phospho-N-acetylmuramoyl-pentapeptide-transferase
cds_wt_6268	-	hypothetical protein
cds_wt_6269	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6270	-	hypothetical protein
cds_wt_6271	-	hypothetical protein
cds_wt_6272	SCD	Acyl-CoA desaturase; Stearoyl-CoA desaturase;
cds_wt_6273	-	Fatty acid desaturase; Delta
cds_wt_6274	lacI	Transcription activator gutR; HTH-type transcriptional repressor purR; Purine nucleotide synthesis repressor; Pur regulon repressor;
cds_wt_6275	CPD	Carboxypeptidase D; Metalloprotease D;
cds_wt_6276	xynB	CPD-2; Flags: Fragment;
cds_wt_6277	-	putative endo-1,4-beta-glucanase
cds_wt_6278	tetR	Probable oxidoreductase ordL;
cds_wt_6279	-	Tetracycline repressor protein class G;
cds_wt_6280	-	hypothetical protein
cds_wt_6281	-	hypothetical protein
cds_wt_6282	prpH	sulfotransferase
cds_wt_6283	-	Multidrug-efflux transporter 1 regulator;
cds_wt_6284	-	hypothetical protein
cds_wt_6285	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6286	-	O-acetyltransferase oatA;
cds_wt_6287	lppS	hypothetical protein predicted by Glimmer/Critica
cds_wt_6288	npr	Uncharacterized protein Mb0493;
cds_wt_6289	-	Bacillolysin; Thermostable neutral protease;
cds_wt_6290	alkB	possible transcriptional regulatory protein (probably TetR-family)
cds_wt_6291	-	alkane-1 monooxygenase
cds_wt_6292	infA	Protein patched homolog 1; PTC1; PTC;
cds_wt_6293	-	Translation initiation factor IF-1;
cds_wt_6294	-	N-acetyltransferase 8-like protein; Camello-like protein 3;
cds_wt_6295	ydhT	Polycystic kidney disease protein 1-like 3; Polycystin- 1L3; PC1-like 3 protein;
cds_wt_6296	-	putative secreted hydrolase
cds_wt_6297	-	ATP-dependent Clp protease ATP-binding subunit clpX;
cds_wt_6298	-	Uncharacterized signaling protein CC_0091;
cds_wt_6299	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6300	-	hypothetical protein
cds_wt_6301	-	Uncharacterized protein yyaP;
cds_wt_6302	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6303	isp	RNA polymerase sigma-H factor; Sigma-30;
cds_wt_6304	-	Intracellular serine protease;
		Tetratricopeptide repeat protein 28; TPR repeat protein 28;

cds_wt_6305	-	Tetratricopeptide repeat protein 28; TPR repeat protein 28;
cds_wt_6306	tlpB	Putative sensory transducer protein;
cds_wt_6307	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6308	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6309	qacA	Putative multidrug resistance protein mdtD;
cds_wt_6310	tetR	Tetracycline repressor protein class B from transposon Tn10;
cds_wt_6311	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6312	-	Serotonin N-acetyltransferase; Serotonin acetylase;
cds_wt_6313	chrA	Aralkylamine N-acetyltransferase; AA-NAT;
cds_wt_6314	-	Probable chromate transport protein;
cds_wt_6315	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6316	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6317	-	Probable disease resistance protein RDL5/RF45;
cds_wt_6318	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6319	-	putative DNA-binding protein
cds_wt_6320	-	hypothetical protein
cds_wt_6321	-	Uncharacterized signaling protein PA1727;
cds_wt_6322	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6323	ltaE	threonine aldolase
cds_wt_6324	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6325	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6326	-	UPF0548 protein At2g17695;
cds_wt_6327	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6328	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6329	-	hypothetical protein
cds_wt_6330	-	hypothetical protein
cds_wt_6331	asnC	Uncharacterized HTH-type transcriptional regulator PH1519;
cds_wt_6332	pdhA	pyruvate dehydrogenase E1 component, alpha subunit
cds_wt_6333	pdhB	putative branched-chain alpha keto acid dehydrogenase E1 beta subunit
cds_wt_6334	-	hypothetical protein
cds_wt_6335	-	hypothetical protein
cds_wt_6336	-	Receptor-type tyrosine-protein phosphatase delta;
cds_wt_6337	pecS	Protein-tyrosine phosphatase delta; R-PTP-delta;
cds_wt_6338	Fmo3	HTH-type transcriptional regulator pecS;
cds_wt_6339	-	Dimethylaniline monooxygenase
cds_wt_6340	-	T-cell immunomodulatory protein; Protein TIP;
cds_wt_6341	-	Integrin-alpha FG-GAP repeat-containing protein 1;
cds_wt_6342	stuC	hypothetical protein predicted by Glimmer/Critica
cds_wt_6343	xlnB	UPF0421 protein SAR1980;
cds_wt_6344	nodB	sensor histidine kinase
		Endo-1,4-beta-xylanase B; Xylanase B; 1,4-beta-D-xylan xylanohydrolase B;
		Chitooligosaccharide deacetylase; Nodulation protein B;

cds_wt_6345	xlnB	endo-1,4-beta-xylanase
cds_wt_6346	-	hypothetical protein predicted by Glimmer/Critica
		Ubiquinone/menaquinone biosynthesis
cds_wt_6347	ubiE	methyltransferase ubiE;
cds_wt_6348	-	Chaperone protein clpB;
cds_wt_6349	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6350	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6351	smvA	Putative multidrug resistance protein mdtD;
cds_wt_6352	tetR	Tetracycline repressor protein class G;
cds_wt_6353	tlpB	Methyl-accepting chemotaxis protein mcpB; H3;
cds_wt_6354	prpD	Phosphoserine phosphatase rsbP;
cds_wt_6355	-	putative secreted protein
cds_wt_6356	frnE	FrnE protein
cds_wt_6357	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6358	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6359	-	UPF0272 protein SE_0371;
cds_wt_6360	-	Uncharacterized protein MJ0165;
cds_wt_6361	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6362	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6363	-	hypothetical protein predicted by Glimmer/Critica
		Teneurin-3; Ten-3; Tenascin-M3; Ten-m3; Protein
cds_wt_6364	-	Odd Oz/ten-m homolog 3;
cds_wt_6365	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6366	-	putative secreted protein
cds_wt_6367	-	hypothetical protein
cds_wt_6368	-	Vegetative incompatibility protein HET-E-1;
cds_wt_6369	nodB	polysaccharide deacetylase, putative
cds_wt_6370	-	hypothetical protein predicted by Glimmer/Critica
		Putative rhamnogalacturonase; Rhamnogalacturonan
cds_wt_6371	rhgB	lyase; RGase; Ascus development protein 1; Asd-I;
cds_wt_6372	yccK	putative oxidoreductase
cds_wt_6373	-	Uncharacterized signaling protein PA1727;
cds_wt_6374	yusZ	short chain dehydrogenase
cds_wt_6375	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6376	-	hypothetical protein
cds_wt_6377	-	hypothetical protein predicted by Glimmer/Critica
		Replicative DNA helicase; Contains: Endonuclease
cds_wt_6378	dnaB	PI-Rma43812IP; Rma dnaB intein;
cds_wt_6379	-	Agglutinin receptor; SSP-5;
cds_wt_6380	-	membrane protein, putative
cds_wt_6381	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6382	-	Uncharacterized signaling protein CC_0091;
cds_wt_6383	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6384	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6385	-	two-component system sensor protein
cds_wt_6386	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6387	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6388	-	hypothetical protein predicted by Glimmer/Critica
		Probable transcriptional regulator ycf27; OmpR-like
cds_wt_6389	-	protein;

cds_wt_6390	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6391	-	Glycogen synthase; Starch
cds_wt_6392	-	Neogenin; Fragment;
cds_wt_6393	aphA	sensory box histidine kinase
cds_wt_6394	-	two-component system sensor protein
cds_wt_6395	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6396	-	hypothetical protein predicted by Glimmer/Critica
		Tartrate-resistant acid phosphatase type 5; TR-AP;
		Tartrate-resistant acid ATPase; TrATPase; Acid
cds_wt_6397	phoA	phosphatase 5, tartrate resistant;
cds_wt_6398	PIGA	possible conserved protein
cds_wt_6399	-	conserved membrane protein
		Putative peroxiredoxin Q, chloroplastic; Thioredoxin
cds_wt_6400	bcpB	reductase;
cds_wt_6401	amo	luciferase-like monooxygenase
cds_wt_6402	salE	AB hydrolase superfamily protein yfhM;
cds_wt_6403	-	putative transcriptional regulator
cds_wt_6404	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6405	-	Uncharacterized transporter ywfM;
		GTP pyrophosphokinase; ATP:GTP 3'-
cds_wt_6406	ywaC	pyrophosphotransferase; ppGpp synthetase I;
cds_wt_6407	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6408	pkn4	Nephrocystin-3;
cds_wt_6409	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6410	marR	Uncharacterized protein MJ0432;
cds_wt_6411	-	hypothetical protein
cds_wt_6412	-	Beta-agarase AgaB34;
cds_wt_6413	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6414	-	Regulatory protein afsR;
cds_wt_6415	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6416	-	hypothetical protein predicted by Glimmer/Critica
		Putative HTH-type transcriptional regulatory protein
cds_wt_6417	-	UNCMA_15260;
cds_wt_6418	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6419	-	hypothetical protein
cds_wt_6420	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6421	-	hypothetical protein
cds_wt_6422	xylB	sugar kinase, possible xylulose kinase
cds_wt_6423	-	putative secreted esterase
cds_wt_6424	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6425	-	putative DNA-binding protein
cds_wt_6426	adhC	NADP-dependent alcohol dehydrogenase
cds_wt_6427	ydbM	acyl-CoA dehydrogenase
cds_wt_6428	cbs	cystathionine beta-synthase
		FMN-dependent NADH-azoreductase 2; FMN-
		dependent NADH-azo compound oxidoreductase 2;
cds_wt_6429	-	Azo-dye reductase 2;
		Peroxiredoxin Q, chloroplastic; Thioredoxin
cds_wt_6430	PRXQ	reductase; Fragment;
cds_wt_6431	-	hypothetical protein predicted by Glimmer/Critica

cds_wt_6432	-	Carboxylate-amine ligase NFA_52970;
cds_wt_6433	-	putative peptidase
cds_wt_6434	-	putative peptidase
cds_wt_6435	-	Diamine acetyltransferase 2; Spermidine/spermine N
cds_wt_6436	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6437	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6438	-	protein of unknown function DUF1330
cds_wt_6439	-	D-methionine-binding lipoprotein metQ;
cds_wt_6440	proV	Methionine import ATP-binding protein metN;
		Probable D-methionine transport system permease
cds_wt_6441	-	protein metI;
cds_wt_6442	tetV	Uncharacterized MFS-type transporter ykuC;
cds_wt_6443	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6444	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6445	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6446	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6447	dpm	dolichyl-phosphate mannan synthase-like
cds_wt_6448	lpqM	possible lipoprotein peptidase LpqM
		Alpha-N-arabinofuranosidase B; Arabinosidase B;
cds_wt_6449	abfB	ABF B;
		Alpha-N-arabinofuranosidase B; Arabinosidase B;
cds_wt_6450	abfB	ABF B;
cds_wt_6451	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6452	-	hypothetical protein
cds_wt_6453	pip	proline iminopeptidase
cds_wt_6454	-	hypothetical protein predicted by Glimmer/Critica
		26 kDa periplasmic immunogenic protein; 28 kDa
		outer membrane protein; 28 kDa cytosoluble protein;
cds_wt_6455	lpqG	CP28;
cds_wt_6456	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6457	-	nitroreductase family protein
cds_wt_6458	fabH	3-oxoacyl-
cds_wt_6459	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6460	-	hypothetical protein predicted by Glimmer/Critica
		Alpha-N-arabinofuranosidase B; Arabinosidase B;
cds_wt_6461	abfB	ABF B;
cds_wt_6462	cad	lysine decarboxylase
cds_wt_6463	-	Phytochrome B;
cds_wt_6464	aprX	alkaline serine protease
		Heme-regulated cyclic di-GMP, cyclic AMP
		phosphodiesterase,; Direct oxygen sensor protein; Ec
cds_wt_6465	-	DOS;
cds_wt_6466	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6467	-	hypothetical protein
cds_wt_6468	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6469	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6470	-	Uncharacterized protein ML1998;
cds_wt_6471	-	hypothetical protein
cds_wt_6472	xyIS	alpha-xylosidase
cds_wt_6473	-	putative DNA-binding protein

cds_wt_6474	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6475	-	hypothetical protein
cds_wt_6476	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6477	-	hypothetical protein
cds_wt_6478	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6479	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6480	-	hypothetical protein
cds_wt_6481	-	UDP-glucose 4-epimerase
cds_wt_6482	-	hypothetical protein
cds_wt_6483	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6484	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6485	NITA	Nitrate reductase
cds_wt_6486	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6487	phoP	Alkaline phosphatase synthesis transcriptional regulatory protein phoP;
cds_wt_6488	-	Transcriptional regulatory protein yvrH;
cds_wt_6489	phoR	sensory box histidine kinase PhoR
cds_wt_6490	-	Uncharacterized protein Mb1369;
cds_wt_6491	ttgR	HTH-type transcriptional regulator ttgR; Toluene efflux pump ttgABC operon repressor;
cds_wt_6492	cyp7	Cytochrome P450-SOY;
cds_wt_6493	-	Ferredoxin fas2;
cds_wt_6494	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6495	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6496	-	Carboxylate-amine ligase Mmcs_0573;
cds_wt_6497	hemK	hypothetical protein
cds_wt_6498	dltE	probable short-chain dehydrogenase
cds_wt_6499	ftrA	Protein DJ-1; Parkinson disease protein 7 homolog;
cds_wt_6500	-	hypothetical protein
cds_wt_6501	glgX	glycogen debranching enzyme
cds_wt_6502	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6503	-	Uncharacterized signaling protein PA3311;
cds_wt_6504	-	Purine catabolism regulatory protein;
cds_wt_6505	ousA	Osmoprotectant uptake system A;
cds_wt_6506	-	putative transmembrane efflux protein
cds_wt_6507	-	putative secreted protein
cds_wt_6508	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6509	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6510	-	acyl-CoA dehydrogenase
cds_wt_6511	-	hypothetical protein
cds_wt_6512	-	Uncharacterized protein ML0378;
cds_wt_6513	-	hypothetical protein 2SC10A7.04c
cds_wt_6514	gltC	Probable RuBisCO transcriptional regulator;
cds_wt_6515	-	Uncharacterized protein YLL056C;
cds_wt_6516	sir2	putative Sir2 family regulator
cds_wt_6517	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6518	ino1	myo-inositol-1-phosphate synthase
cds_wt_6519	tetR	Tetracycline repressor protein class H;
cds_wt_6520	LYS1	saccharopine dehydrogenase
cds_wt_6521	cfa	cyclopropane-fatty-acyl-phospholipid synthase

cds_wt_6522	-	hypothetical protein
cds_wt_6523	cspA	Cold shock protein cspA; CSP-A; 7.4 kDa cold shock protein; CS7.4;
cds_wt_6524	frp	putative ferredoxin/ferredoxin-NADP reductase
cds_wt_6525	-	Probable transcriptional regulator ycf27; OmpR-like protein;
cds_wt_6526	nudF	hypothetical protein
cds_wt_6527	-	Glycerol-3-phosphate regulon repressor; HTH-type transcriptional repressor purR; Purine nucleotide synthesis repressor; Pur regulon repressor;
cds_wt_6528	degA	
cds_wt_6529		14 Glycoprotein GPV;
cds_wt_6530	-	Uncharacterized protein Rv1002c/MT1031;
cds_wt_6531	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6532	garD	hydrolase, UxaA family
cds_wt_6533	-	unknown protein
cds_wt_6534	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6535	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6536	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6537	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6538	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6539	-	hypothetical protein
cds_wt_6540	cyaC	hypothetical protein
cds_wt_6541	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6542	abfB	putative secreted protein
cds_wt_6543	arsC	putative arsenate reductase
cds_wt_6544	-	Probable aquaporin PIP1-2; Plasma membrane intrinsic protein 1-2; OsPIP1;2;
cds_wt_6545	cadC	Cadmium efflux system accessory protein; Cadmium resistance regulatory protein;
cds_wt_6546	-	Monocarboxylate transporter 2; MCT 2; Solute carrier family 16 member 7;
cds_wt_6547	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6548	luxA	putative oxidoreductase protein
cds_wt_6549	-	Ubiquinone/menaquinone biosynthesis methyltransferase ubiE;
cds_wt_6550	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6551	-	hypothetical protein
cds_wt_6552	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6553	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6554	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6555	pcaD	Proline iminopeptidase; PIP; Prolyl aminopeptidase; PAP;
cds_wt_6556	yxjI	UPF0706 protein yxjI;
cds_wt_6557	-	Cellulose synthesis regulatory protein;
cds_wt_6558	-	Uncharacterized MFS-type transporter yqjV;
cds_wt_6559	-	putative transcriptional regulator
cds_wt_6560	-	Uncharacterized protein ML1329;
cds_wt_6561	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6562	-	hypothetical protein predicted by Glimmer/Critica

cds_wt_6563	-	HTH-type transcriptional activator tipA;
cds_wt_6564	malE	Uncharacterized ABC transporter extracellular-binding protein yurO;
cds_wt_6565	palF	sn-glycerol-3-phosphate transport system permease protein ugpA;
cds_wt_6566	malG	Probable ABC transporter permease protein yesQ;
cds_wt_6567	phoR	sensory box histidine kinase PhoR
cds_wt_6568	phoR	two-component hybrid sensor and regulator
cds_wt_6569	-	3-oxoacyl-
cds_wt_6570	-	putative DNA-binding protein
cds_wt_6571	-	C-type lectin domain family 4 member G;
cds_wt_6572	-	putative hydrolase
cds_wt_6573	polA	DNA polymerase I
cds_wt_6574	yneD	3-oxoacyl-
cds_wt_6575	-	putative lipoprotein
cds_wt_6576	pelX	putative exopolysaccharide lyase
cds_wt_6577	-	Homoserine kinase; HSK; HK;
cds_wt_6578	PHY1	sensor histidine kinase/response regulator
cds_wt_6579	dapA	dihydrodipicolinate synthase
cds_wt_6580	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6581	arsR	Arsenical resistance operon repressor;
cds_wt_6582	-	hypothetical protein
cds_wt_6583	-	Uncharacterized protein Mb0911c;
cds_wt_6584	nadE	NAD synthase
cds_wt_6585	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6586	-	N-acyl-phosphatidylethanolamine-hydrolyzing phospholipase D; N-acyl phosphatidylethanolamine phospholipase D; NAPE-hydrolyzing phospholipase D; NAPE-PLD;
cds_wt_6587	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6588	prpH	hypothetical protein
cds_wt_6589	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6590	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6591	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6592	ybcL	UPF0098 protein ybhB;
cds_wt_6593	-	hypothetical protein
cds_wt_6594	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6595	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6596	-	Sulfurtransferase tusA; tRNA 2-thiouridine synthesizing protein A;
cds_wt_6597	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6598	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6599	-	hypothetical protein
cds_wt_6600	mtrR	HTH-type transcriptional regulator mtrR;
cds_wt_6601	-	Uncharacterized HTH-type transcriptional regulator yobV;
cds_wt_6602	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6603	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6604	-	Alkanesulfonate monooxygenase; FMNH ₂ -dependent aliphatic sulfonate monooxygenase;

cds_wt_6605	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6606	-	putative acetyltransferase
cds_wt_6607	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6608	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6609	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6610	adh	putative dehydrogenase
cds_wt_6611	ytfH	Uncharacterized HTH-type transcriptional regulator ydeP;
cds_wt_6612	p20	Uncharacterized N-acetyltransferase p20;
cds_wt_6613	fabG	hypothetical protein
cds_wt_6614	-	Multiple antibiotic resistance protein marR; Uncharacterized transcriptional regulatory protein yxjL;
cds_wt_6615	yvqC	two-component system, sensor protein
cds_wt_6616	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6617	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6618	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6619	-	Uncharacterized protein aq_1494;
cds_wt_6620	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6621	-	UPF0104 membrane protein MTH_1261;
cds_wt_6622	-	Pleiotropic drug resistance protein 1; NtPDR1;
cds_wt_6623	PDR1	Spermidine/putrescine import ATP-binding protein potA;
cds_wt_6624	-	hypothetical protein
cds_wt_6625	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6626	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6627	-	Uncharacterized protein Mb1389c;
cds_wt_6628	morA	hypothetical protein predicted by Glimmer/Critica
cds_wt_6629	-	Protein piccolo; Aczonin; Multidomain presynaptic cytomatrix protein;
cds_wt_6630	Pclo	acyl-CoA synthase
cds_wt_6631	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6632	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6633	-	Methyl-accepting chemotaxis protein 3;
cds_wt_6634	-	hypothetical protein
cds_wt_6635	-	hypothetical protein
cds_wt_6636	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6637	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6638	-	glycosyl transferase family 2 protein
cds_wt_6639	-	HTH-type transcriptional regulator maltT; ATP-dependent transcriptional activator maltT;
cds_wt_6640	-	Oxygen regulatory protein nreC; Nitrogen regulation protein C;
cds_wt_6641	nreC	hypothetical protein predicted by Glimmer/Critica
cds_wt_6642	-	Serine/threonine-protein kinase SNF1-like kinase 1; Serine/threonine-protein kinase SNF1LK; Salt-inducible kinase 1; SIK-1; SIK1;
cds_wt_6643	amfT	Dipeptidyl-peptidase 5; Dipeptidyl-peptidase V; DPP V; DppV; AltName: Allergen=Tri r 4;
cds_wt_6644	DPPV	hypothetical protein predicted by Glimmer/Critica
cds_wt_6645	-	

cds_wt_6646	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6647	amfB	multidrug resistance protein
cds_wt_6648	iroC	putative ABC transporter
cds_wt_6649	-	Probable auxin efflux carrier component 6; OsPIN6;
cds_wt_6650	betI	HTH-type transcriptional regulator betI;
cds_wt_6651	nonF	ThiJ/PfpI
cds_wt_6652	tetR	transcriptional regulator, TetR family
cds_wt_6653	mmyQ	Metalloreductase STEAP3; Six-transmembrane
cds_wt_6654	-	epithelial antigen of prostate 3; pHyde;
cds_wt_6655	-	RNA polymerase sigma factor sigM;
cds_wt_6656	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6657	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6658	-	hypothetical protein
		cellulase., cellulose 1,4-beta-cellobiosidase
		Uncharacterized HTH-type transcriptional regulator
cds_wt_6659	-	ywhA;
cds_wt_6660	sdaA	L-serine dehydratase
cds_wt_6661	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6662	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6663	aceE	pyruvate dehydrogenase E1 component
cds_wt_6664	bhp	Protocadherin beta-6; PCDH-beta-6;
cds_wt_6665	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6666	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6667	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6668	-	Putative multidrug resistance protein mdtD;
cds_wt_6669	rcaC	Protein rcaC;
cds_wt_6670	-	Collagen alpha-3
cds_wt_6671	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6672	fadH	2,4-dienoyl-CoA reductase
cds_wt_6673	-	enoyl-CoA hydratase
cds_wt_6674	-	Negative transcription regulator padR;
		Hepatocyte growth factor receptor; HGF receptor;
		Scatter factor receptor; SF receptor; HGF/SF
cds_wt_6675	MET	receptor; Met proto-oncogene tyrosine kinase; c-Met;
cds_wt_6676	-	putative enoyl-CoA hydratase/isomerase
cds_wt_6677	-	HTH-type protein slmA;
cds_wt_6678	-	putative membrane protein
cds_wt_6679	-	alpha amylase
		Sterol 3-beta-glucosyltransferase; Autophagy-related
cds_wt_6680	-	protein 26; UDP-glycosyltransferase 51;
cds_wt_6681	-	hypothetical protein
cds_wt_6682	-	UPF0135 protein ybgl;
cds_wt_6683	-	hypothetical protein predicted by Glimmer/Critica
		Ankyrin-2; Brain ankyrin; Ankyrin-B; Non-erythroid
cds_wt_6684	ANK2	ankyrin;
cds_wt_6685	-	Uncharacterized protein R665;
cds_wt_6686	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6687	NOD3	Protein NLRC3;
cds_wt_6688	-	hypothetical protein
cds_wt_6689	-	hypothetical protein predicted by Glimmer/Critica

cds_wt_6690	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6691	tas	Methyl-accepting chemotaxis aspartate transducer; Membrane-bound lytic murein transglycosylase F; EC=4.2.2.n1; Murein lyase F;
cds_wt_6692	glnH	EC=4.2.2.n1; Murein lyase F;
cds_wt_6693	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6694	yycE	Uncharacterized protein yycE; Riboflavin biosynthesis protein ribD; Includes: Diaminohydroxyphosphoribosylaminopyrimidine deaminase; DRAP deaminase; Riboflavin-specific deaminase; Includes: 5-amino-6-
cds_wt_6695	-	Inner membrane protein ybjJ;
cds_wt_6696	-	putative secreted protein
cds_wt_6697	-	hypothetical protein
cds_wt_6698	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6699	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6700	-	Metallothiol transferase fosB; Fosfomycin resistance protein;
cds_wt_6701	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6702	-	Transcription elongation factor SPT5; DRB sensitivity-inducing factor large subunit; DSIF large subunit; Protein foggy;
cds_wt_6703	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6704	-	2-hydroxy-6-oxononadienedioate/2-hydroxy-6- oxononatrienedioate hydrolase 2; EC=3.7.1.n1; 2- hydroxy-6-oxonona-2,4-diene-1,9-dioic acid 5,6- hydrolase 2; 2-hydroxy-6-ketonona-2,4-diene-1,9- dioic acid 5,6-hydrolase 2; 2-hydroxy-6-oxonona- 2,4,7-triene-1,9-dioic acid 5,6-hydrolase 2;
cds_wt_6705	lipJ	hypothetical protein predicted by Glimmer/Critica
cds_wt_6706	-	UPF0161 protein MS0482;
cds_wt_6707	hlyA	Cold shock protein cspA; CSP-A; 7.4 kDa cold shock protein; CS7.4;
cds_wt_6708	cspA	hypothetical protein predicted by Glimmer/Critica
cds_wt_6709	-	Carboxylesterase bioH; Biotin synthesis protein bioH;
cds_wt_6710	mhpC	hypothetical protein predicted by Glimmer/Critica
cds_wt_6711	-	Ubiquinone/menaquinone biosynthesis methyltransferase ubiE;
cds_wt_6712	-	Probable ubiquinone biosynthesis protein ubiB;
cds_wt_6713	aarF	Aminoglycoside acetyltransferase regulator; 2,3-bisphosphoglycerate-dependent phosphoglycerate mutase; Phosphoglyceromutase; PGAM; BPG-dependent PGAM; dPGM;
cds_wt_6714	-	short chain dehydrogenase
cds_wt_6715	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6716	-	Uncharacterized protein Mb1292c;
cds_wt_6717	-	Uncharacterized N-acetyltransferase ycf52-like;
cds_wt_6718	wecD	probable secreted serine protease
cds_wt_6719	pepA	hypothetical protein predicted by Glimmer/Critica
cds_wt_6720	-	glutathione-dependent formaldehyde dehydrogenase
cds_wt_6721	fdh	hypothetical protein
cds_wt_6722	-	

cds_wt_6723	-	Probable HTH-type transcriptional regulator yttP;
cds_wt_6724	-	Stress response protein yttP;
cds_wt_6725	-	Zeaxanthin epoxidase, chloroplastic;
cds_wt_6726	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6727	-	Phosphoglycolate phosphatase; PGPase; PGP;
		Hemoglobin-like protein yjbl; Truncated BHb; trBHb;
		Non-hemolytic phospholipase C; PLC-N;
		Phosphatidylcholine cholinephosphohydrolase;
cds_wt_6728	-	Phosphatidylcholine-hydrolyzing phospholipase C;
cds_wt_6729	-	PC-PLC;
		hypothetical protein predicted by Glimmer/Critica
		Spermidine/putrescine import ATP-binding protein
cds_wt_6730	-	potA;
cds_wt_6731	tcmG	putative rifampin monooxygenase
		HTH-type transcriptional regulator tcmR;
cds_wt_6732	tcmR	Tetracenomycin C transcriptional repressor;
cds_wt_6733	TCNA	Sialidase; Neuraminidase; NA; Major surface antigen;
cds_wt_6734	-	hypothetical protein
cds_wt_6735	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6736	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6737	-	putative DNA-binding protein
cds_wt_6738	-	ATP-dependent RNA helicase DBP10;
cds_wt_6739	-	Uncharacterized protein Rv0966c/MT0994;
cds_wt_6740	-	hypothetical protein
cds_wt_6741	-	hypothetical protein
cds_wt_6742	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6743	-	Peroxidase ycdB;
cds_wt_6744	ycdO	UPF0409 protein ycdO;
		Ferrous iron permease efeU; Ferrous iron uptake
cds_wt_6745	ycdN	protein;
cds_wt_6746	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6747	bacE	Putative bacilysin exporter bacE;
cds_wt_6748	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6749	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6750	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6751	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6752	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6753	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6754	-	hypothetical protein
cds_wt_6755	-	hypothetical protein
cds_wt_6756	-	putative DNA-binding protein
		Ubiquinone/menaquinone biosynthesis
cds_wt_6757	-	methyltransferase ubiE;
cds_wt_6758	-	Uncharacterized protein MJ0002;
cds_wt_6759	-	Uncharacterized protein MJ0002;
cds_wt_6760	yghZ	Uncharacterized protein yghZ;
cds_wt_6761	gcvP	glycine dehydrogenase
cds_wt_6762	-	hypothetical protein
cds_wt_6763	pabB	para-aminobenzoate synthase, component I
cds_wt_6764	-	RNA polymerase sigma-E factor;

cds_wt_6765	-	hypothetical protein
cds_wt_6766	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6767	def	putative polypeptide deformylase
		3-demethylubiquinone-9 3-methyltransferase; 3,4-dihydroxy-5-hexaprenylbenzoate methyltransferase; DHHB methyltransferase;
cds_wt_6768	-	
cds_wt_6769	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6770	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6771	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6772	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6773	-	hypothetical protein
cds_wt_6774	-	putative transposase
cds_wt_6775	-	Probable ctpA-like serine protease;
cds_wt_6776	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6777	-	putative integral membrane protein
		Metallothiol transferase fosB; Fosfomycin resistance protein;
cds_wt_6778	-	
cds_wt_6779	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6780	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6781	-	putative oxidoreductase
cds_wt_6782	-	putative DNA-binding protein
cds_wt_6783	-	hypothetical protein
cds_wt_6784	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6785	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6786	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6787	-	Collagen alpha-5
cds_wt_6788	-	hypothetical protein
		Amino-acid acetyltransferase; N-acetylglutamate synthase; AGS; NAGS;
cds_wt_6789	yycN	
cds_wt_6790	ydbC	putative dehydrogenase
cds_wt_6791	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6792	hisK	Probable histidinol-phosphatase; HolPase;
cds_wt_6793	-	putative integral membrane protein
		Phytochrome-like protein cph2; Bacteriophytochrome cph2;
cds_wt_6794	-	
cds_wt_6795	-	Uncharacterized protein MJ1623;
cds_wt_6796	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6797	arcB	ornithine cyclodeaminase
cds_wt_6798	ereB	Erythromycin esterase type II;
cds_wt_6799	-	pyridoxal-dependent decarboxylase decarboxylase
cds_wt_6800	-	Rhizobactin siderophore biosynthesis protein rhbF;
cds_wt_6801	-	Osmotic growth protein 1;
cds_wt_6802	-	uridine kinase
cds_wt_6803	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6804	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6805	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6806	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6807	-	Aerotaxis receptor;
cds_wt_6808	-	Agglutinin receptor; SSP-5;
cds_wt_6809	-	putative secreted ATP/GTP binding protein

cds_wt_6810	ohr	Organic hydroperoxide resistance protein-like 2;
cds_wt_6811	ykmA	HTH-type transcriptional regulator mgrA;
cds_wt_6812	-	Uncharacterized N-acetyltransferase yjdG;
cds_wt_6813	-	UPF0721 transmembrane protein HI0198;
cds_wt_6814	-	UPF0303 protein RHE_CH02903;
cds_wt_6815	-	hypothetical protein
cds_wt_6816	yjhP	tRNA
cds_wt_6817	tetX	Tetracycline resistance protein from transposon Tn4351/Tn4400;
cds_wt_6818	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6819	-	Glyoxalase domain-containing protein 4;
cds_wt_6820	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6821	sugE	Quaternary ammonium compound-resistance protein sugE;
cds_wt_6822	plsC	putative 1-acylglycerol-3-phosphate O-acyltransferase
cds_wt_6823	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6824	-	acetyltransferase, GNAT family
cds_wt_6825	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6826	ytrA	HTH-type transcriptional repressor yvoA;
cds_wt_6827	-	Autophagy-related protein 22;
cds_wt_6828	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6829	iniA	Uncharacterized protein in xynA 3'region; ORF6;
cds_wt_6830	iniC	Flags: Fragment;
cds_wt_6831	-	GTP-binding protein engA;
cds_wt_6832	phzR	Uncharacterized AAA domain-containing protein C16E9.10c;
cds_wt_6833	-	Transcriptional activator protein phzR;
cds_wt_6834	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6835	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6836	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6837	-	Otogelin;
cds_wt_6838	ydbC	hypothetical protein
cds_wt_6839	-	putative dehydrogenase
cds_wt_6840	dhIE	Uncharacterized HTH-type transcriptional regulator sll1512;
cds_wt_6841	-	leucine dehydrogenase
cds_wt_6842	-	Leucine-responsive regulatory protein;
cds_wt_6843	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6844	sdr2	putative DNA-binding protein
cds_wt_6845	-	dehydrogenase
cds_wt_6846	qor	hypothetical protein
cds_wt_6847	-	quinone oxidoreductase
cds_wt_6848	-	hypothetical protein
cds_wt_6849	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6850	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6851	-	hypothetical protein predicted by Glimmer/Critica

		3-demethylubiquinone-9 3-methyltransferase; 3,4-dihydroxy-5-hexaprenylbenzoate methyltransferase; DHHB methyltransferase;
cds_wt_6852	-	
cds_wt_6853	p20	Uncharacterized N-acetyltransferase p20;
cds_wt_6854	-	carboxymethylenebutenolidase
cds_wt_6855	xerD	Tyrosine recombinase xerD;
cds_wt_6856	-	RNA pyrophosphohydrolase;
cds_wt_6857	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6858	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6859	bacA	undecaprenyl-diphosphatase
cds_wt_6860	xerD	Tyrosine recombinase xerD;
cds_wt_6861	uup	Ribose import ATP-binding protein rbsA;
cds_wt_6862	avtA	putative aminotransferase
cds_wt_6863	-	Uncharacterized protein yyaP;
cds_wt_6864	fliA	RNA polymerase sigma factor rpoD;
		Uncharacterized transcriptional regulatory protein yfiK;
cds_wt_6865	-	
cds_wt_6866	yvfT	putative two-component system sensor kinase
cds_wt_6867	yvfS	Putative transport permease yvfS;
		Spermidine/putrescine import ATP-binding protein potA;
cds_wt_6868	yvfR	
cds_wt_6869	-	UPF0477 protein RBAM_011910;
cds_wt_6870	-	hypothetical protein
cds_wt_6871	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6872	gph	Phosphoglycolate phosphatase; PGPase; PGP;
cds_wt_6873	-	similar to methionine adenosyltransferase
cds_wt_6874	dapA	dihydrodipicolinate synthase
cds_wt_6875	-	Probable RuBisCO transcriptional regulator;
cds_wt_6876	-	hypothetical protein
		Glutamyl aminopeptidase; EAP; Aminopeptidase A; APA; AltName: CD_antigen=CD249;
cds_wt_6877	-	
cds_wt_6878	-	Uncharacterized protein Mb0510;
cds_wt_6879	-	thiolase
cds_wt_6880	-	HTH-type transcriptional regulator betI;
cds_wt_6881	terC	Inner membrane protein alx;
cds_wt_6882	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6883	-	conserved hypothetical protein
cds_wt_6884	-	3-oxoacyl-
cds_wt_6885	tnpA	Tn5045 transposase
cds_wt_6886	tnpA	Tn5045 transposase
cds_wt_6887	czcD	Cation-efflux pump fieF;
		Cadmium efflux system accessory protein; Cadmium resistance regulatory protein;
cds_wt_6888	cadC	
cds_wt_6889	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6890	lppY	hypothetical protein
cds_wt_6891	chrA	Probable chromate transport protein;
cds_wt_6892	pin	Transposon Tn552 DNA-invertase binR;
cds_wt_6893	-	hypothetical protein
cds_wt_6894	-	hypothetical protein predicted by Glimmer/Critica

cds_wt_6895	-	oxidoreductase, short chain
cds_wt_6896	-	dehydrogenase/reductase family
cds_wt_6897	adh	hypothetical protein predicted by Glimmer/Critica
cds_wt_6898	pin	sorbitol dehydrogenase
cds_wt_6899	-	DNA-invertase from lambdoid prophage e14;
cds_wt_6900	rsbU	Uncharacterized protein Rv1364c/MT1410;
cds_wt_6901	-	Uncharacterized protein Rv1364c/MT1410;
cds_wt_6902	-	Transposase for transposon Tn1546;
cds_wt_6903	pspE	hypothetical protein predicted by Glimmer/Critica
		Uncharacterized protein yibN;
cds_wt_6904	tetR	Tetracycline repressor protein class B from
cds_wt_6905	dmpI	transposon Tn10;
cds_wt_6906	-	Probable tautomerase K2;
cds_wt_6907	fabG	hypothetical protein
cds_wt_6908	-	short-chain dehydrogenase/reductase SDR
cds_wt_6909	metR	hypothetical protein predicted by Glimmer/Critica
cds_wt_6910	lepB	Probable RuBisCO transcriptional regulator;
cds_wt_6911	-	signal peptidase I
cds_wt_6912	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6913	-	hypothetical protein
cds_wt_6914	-	Uncharacterized protein R00370;
cds_wt_6915	-	Uncharacterized protein R00369;
cds_wt_6916	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6917	-	putative hydrolase
cds_wt_6918	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6919	-	hypothetical protein
cds_wt_6920	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6921	degU	hypothetical protein predicted by Glimmer/Critica
cds_wt_6922	-	Transcriptional regulatory protein degU;
		hypothetical protein
cds_wt_6923	yezE	Uncharacterized HTH-type transcriptional regulator
		yezE;
cds_wt_6924	-	Protein piccolo; Aczonin; Multidomain presynaptic
cds_wt_6925	-	cytomatrix protein; Brain-derived HLMN protein;
cds_wt_6926	nodN	hypothetical protein
cds_wt_6927	-	UPF0336 protein SAV_4901;
cds_wt_6928	-	hypothetical protein predicted by Glimmer/Critica
		hypothetical protein predicted by Glimmer/Critica
cds_wt_6929	sdr2	Retinol dehydrogenase 12; All-trans and 9-cis retinol
		dehydrogenase;
cds_wt_6930	ycdF	Uncharacterized HTH-type transcriptional regulator
cds_wt_6931	-	yvdT;
cds_wt_6932	-	Probable RuBisCO transcriptional regulator;
cds_wt_6933	-	Uncharacterized protein ycf39; ORF319;
cds_wt_6934	-	Uncharacterized protein R00370;
cds_wt_6935	-	Uncharacterized protein R00369;
cds_wt_6936	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6937	-	GAF
		hypothetical protein predicted by Glimmer/Critica

cds_wt_6938	tlpA	Methyl-accepting chemotaxis protein I; MCP-I; Serine chemoreceptor protein;
cds_wt_6939	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6940	-	hypothetical protein
cds_wt_6941	-	hypothetical protein
cds_wt_6942	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6943	-	RNA polymerase sigma-E factor;
cds_wt_6944	-	hypothetical protein
cds_wt_6945	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6946	ubiE	putative methyltransferase
cds_wt_6947	insA	transposase
cds_wt_6948	p20	Uncharacterized N-acetyltransferase p20;
Beta-galactoside-specific lectin 3; Beta-galactoside-specific lectin III; Beta-galactoside-specific lectin II; Contains: Beta-galactoside-specific lectin 3 chain A isoform 1; ML-3 A; Beta-galactoside-specific lectin III chain A isoform 1; ML-III A; Lectin chain A isoform 2; rRNA N-glycosidase; Contains: Beta-galactoside-specific lectin 3 chain B; ML-3 B; Beta-galactoside-specific lectin III chain B; ML-III B;		
cds_wt_6949	-	
cds_wt_6950	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6951	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6952	cadC	Cadmium efflux system accessory protein homolog;
cds_wt_6953	-	Cation-efflux pump fieF;
cds_wt_6954	-	Uncharacterized N-acetyltransferase C550.08;
Peptidyl-glycine alpha-amidating monooxygenase; PAM; Includes: Peptidylglycine alpha-hydroxylating monooxygenase; PHM; Includes: Peptidyl-alpha-hydroxyglycine alpha-amidating lyase;		
cds_wt_6955	PAM	Peptidylamidoglycolate lyase; PAL;
cds_wt_6956	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6957	salY	Macrolide export ATP-binding/permease protein macB;
cds_wt_6958	phnL	Spermidine/putrescine import ATP-binding protein potA;
cds_wt_6959	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6960	-	hypothetical protein predicted by Glimmer/Critica
Probable transcriptional regulator ycf27; OmpR-like protein;		
cds_wt_6961	baeR	
cds_wt_6962	baeS	sensor histidine kinase
2-hydroxy-6-oxononadienedioate/2-hydroxy-6-oxononatrienedioate hydrolase; EC=3.7.1.n1; 2-hydroxy-6-oxonona-2,4-diene-1,9-dioic acid 5,6-hydrolase; 2-hydroxy-6-ketonona-2,4-diene-1,9-dioic acid 5,6-hydrolase; 2-hydroxy-6-oxonona-2,4,7-triene-1,9-dioic acid 5,6-hydrolase;		
cds_wt_6963	-	
cds_wt_6964	dgoR	Fatty acid metabolism regulator protein;
cds_wt_6965	-	putative integral membrane protein
NAD-dependent epimerase/dehydratase:short-chain dehydrogenase/reductase SDR		
cds_wt_6966	-	

cds_wt_6967	-	hypothetical protein
cds_wt_6968	dgoR	Fatty acid metabolism regulator protein;
cds_wt_6969	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6970	-	HTH-type transcriptional regulator betI;
cds_wt_6971	-	Cyclic AMP-inducible protein BP74;
cds_wt_6972	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6973	-	hypothetical protein
cds_wt_6974	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6975	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6976	-	Uncharacterized signaling protein PA1727;
cds_wt_6977	pleD	Uncharacterized signaling protein PA3311;
cds_wt_6978	tlpB	Methyl-accepting chemotaxis protein II; MCP-II; Aspartate chemoreceptor protein;
cds_wt_6979	-	NAD-dependent epimerase/dehydratase:short-chain dehydrogenase/reductase SDR
cds_wt_6980	dgoR	Fatty acid metabolism regulator protein;
cds_wt_6981	yjjN	putative oxidoreductase
cds_wt_6982	pdhR	Fatty acid metabolism regulator protein;
cds_wt_6983	-	Autoinducer 2-binding protein lsrB; AI-2-binding protein lsrB;
cds_wt_6984	ydeZ	Autoinducer 2 import system permease protein lsrD; AI-2 import system permease protein lsrD;
cds_wt_6985	lsrC	Autoinducer 2 import system permease protein lsrC; AI-2 import system permease protein lsrC;
cds_wt_6986	rbsA	putative ABC transporter ATP-binding protein
cds_wt_6987	-	putative D-isomer specific 2-hydroxyacid dehydrogenase family protein
cds_wt_6988	hpcE	RIKEN cDNA B430104H02 gene
cds_wt_6989	ykgF	Uncharacterized electron transport protein ykgF;
cds_wt_6990	-	UPF0707 protein yvbY;
cds_wt_6991	nrm	Nurim; Nuclear rim protein; Nuclear envelope membrane protein;
cds_wt_6992	hpcE	putative 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase
cds_wt_6993	ponA	putative penicillin-binding protein
cds_wt_6994	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6995	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_6996	devR	Transcriptional regulatory protein degU; Protease production enhancer protein;
cds_wt_6997	devS	two-component system, NarL family, sensor kinase
cds_wt_6998	-	Uncharacterized protein Rv1355c/MT1398;
cds_wt_6999	-	Uncharacterized protein Mb0644c;
cds_wt_7000	-	Heme-regulated cyclic di-GMP, cyclic AMP phosphodiesterase.; Direct oxygen sensor protein; Ec DOS;
cds_wt_7001	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7002	gadB	glutamate decarboxylase
cds_wt_7003	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7004	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7005	-	hypothetical protein

cds_wt_7006	dpm	dolichol-phosphate mannosyltransferase
cds_wt_7007	-	hypothetical protein
cds_wt_7008	-	hypothetical protein
cds_wt_7009	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7010	-	RNA polymerase sigma factor rpoD; Sigma-42;
cds_wt_7011	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7012	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7013	-	2',3'-cyclic-nucleotide 2'-phosphodiesterase;
cds_wt_7014	-	Putative HTH-type transcriptional regulator yhjB; Uncharacterized transcriptional regulatory protein yhcZ;
cds_wt_7015	-	
cds_wt_7016	ectB	diaminobutyrate-2-oxoglutarate transaminase
cds_wt_7017	argF	ornithine carbamoyltransferase
cds_wt_7018	-	Uncharacterized MFS-type transporter yfiS;
cds_wt_7019	-	hypothetical protein Acetyl-coenzyme A synthetase; Acetate--CoA ligase; Acyl-activating enzyme;
cds_wt_7020	-	Gramicidin S synthetase 2; Gramicidin S synthetase II; Includes: ATP-dependent proline adenylation; ProA; Proline activase; Includes: ATP-dependent valine adenylation; ValA; Valine activase; Includes: ATP-dependent ornithine adenylation; OrnA; Ornithine activase; Includes: ATP-dependent leucine adenylation; LeuA; Leucine activase;
cds_wt_7021	-	
cds_wt_7022	-	hypothetical protein
cds_wt_7023	-	hypothetical protein
cds_wt_7024	-	hypothetical protein predicted by Glimmer/Critica RNA-binding protein 6; RNA-binding motif protein 6; RNA-binding protein DEF-3; Lung cancer antigen NY-LU-12; Protein G16;
cds_wt_7025	-	
cds_wt_7026	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7027	sypC	putative non-ribosomal peptide synthetase
cds_wt_7028	CBS	pyridoxal-phosphate dependent enzyme
cds_wt_7029	-	putative ornithine cyclodeaminase
cds_wt_7030	-	extracellular protease
cds_wt_7031	PRB1	putative subtilase-type peptidase
cds_wt_7032	-	hypothetical protein predicted by Glimmer/Critica Transcriptional regulatory protein degU; Protease production enhancer protein;
cds_wt_7033	amfR	Polycystic kidney disease protein 1-like 3; Polycystin-1L3; PC1-like 3 protein;
cds_wt_7034	-	
cds_wt_7035	-	Protein mbtH; adenylyl cyclase class-3/4/guanylyl cyclase:tetratricopeptide TPR_4
cds_wt_7036	-	
cds_wt_7037	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7038	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7039	cylM	Lactacin 481/lactococcin biosynthesis protein lcnDR2;

		Linear gramicidin synthetase subunit B; Includes: ATP-dependent alanine adenylyase; AlaA; Alanine activase; Includes: ATP-dependent D-leucine adenylyase; D-LeuA; D-leucine activase; Includes: Leucine racemase
cds_wt_7040	lgrB	
cds_wt_7041	G7c	Protein G7c;
cds_wt_7042	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7043	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7044	ACF2	Endo-1,3
cds_wt_7045	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7046	bcsA	cellulose synthase (UDP-forming)
cds_wt_7047	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7048	-	hypothetical protein
cds_wt_7049	-	Uncharacterized protein Mb1315;
		Endoglucanase E-4; Endo-1,4-beta-glucanase E-4;
cds_wt_7050	celD	Cellulase E-4; Cellulase E4;
cds_wt_7051	celA	cellulase
cds_wt_7052	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7053	-	Urease operon transcriptional activator;
cds_wt_7054	-	hypothetical protein
		Phosphoserine phosphatase rsbU; Sigma factor sigB
cds_wt_7055	rsbU	regulation protein rsbU;
cds_wt_7056	-	hypothetical protein
cds_wt_7057	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7058	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7059	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7060	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7061	-	hypothetical protein
cds_wt_7062	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7063	-	UPF0076 protein PH0854;
		Macrolide export ATP-binding/permease protein
cds_wt_7064	-	macB;
		Macrolide export ATP-binding/permease protein
cds_wt_7065	phnL	macB;
cds_wt_7066	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7067	-	hypothetical protein
cds_wt_7068	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7069	-	hypothetical protein predicted by Glimmer/Critica
		Uncharacterized HTH-type transcriptional regulator
cds_wt_7070	catR	ywbl;
cds_wt_7071	gabT	4-aminobutyrate aminotransferase
cds_wt_7072	gabD	putative succinate-semialdehyde dehydrogenase
cds_wt_7073	pknA	putative serine/threonine protein kinase
cds_wt_7074	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7075	Nat9	N-acetyltransferase 9;
cds_wt_7076	-	3-
cds_wt_7077	-	HTH-type transcriptional regulator betI;
		Bifunctional AAC/APH; Includes: 6'-aminoglycoside
cds_wt_7078	aph	N-acetyltransferase; AAC
cds_wt_7079	-	hypothetical protein predicted by Glimmer/Critica

cds_wt_7080	pteR	HTH-type transcriptional regulator malT; ATP-dependent transcriptional activator malT;
cds_wt_7081	luxR	Response regulator protein vraR;
cds_wt_7082	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7083	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7084	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7085	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7086	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7087	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7088	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7089	-	Zeaxanthin epoxidase, chloroplastic;
cds_wt_7090	-	HTH-type transcriptional regulator betI;
cds_wt_7091	-	Uncharacterized signaling protein CC_0091;
cds_wt_7092	-	hypothetical protein
cds_wt_7093	-	hypothetical protein
cds_wt_7094	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7095	-	Deoxyhypusine hydroxylase; Deoxyhypusine monooxygenase;
cds_wt_7096	-	hypothetical protein
cds_wt_7097	yheG	Lysophospholipase NTE1; Neuropathy target esterase homolog; Intracellular phospholipase B;
cds_wt_7098	chiA	extracellular exochitinase Chi36
cds_wt_7099	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7100	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7101	phoR	sensory box histidine kinase PhoR
cds_wt_7102	cheY	Transcriptional regulatory protein yycF;
cds_wt_7103	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7104	-	Uncharacterized HTH-type transcriptional regulator Mb2017c;
cds_wt_7105	yesE	Uncharacterized phzA/B-like protein PA3332;
cds_wt_7106	-	hypothetical protein
cds_wt_7107	gltC	Probable RuBisCO transcriptional regulator;
cds_wt_7108	-	UPF0076 protein PH0854;
cds_wt_7109	-	UPF0118 membrane protein Rv0205/MT0215;
cds_wt_7110	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7111	mshB	3-phosphoshikimate 1-carboxyvinyltransferase; 5-enolpyruvylshikimate-3-phosphate synthase; EPSP synthase; EPSPS;
cds_wt_7112	-	Heavy metal-dependent transcription regulator 2;
cds_wt_7113	pcaC	gamma-carboxymuconolactone decarboxylase
cds_wt_7114	-	Uncharacterized protein yesE;
cds_wt_7115	dedA	Uncharacterized membrane protein Mb2670;
cds_wt_7116	-	Uncharacterized protein R00370;
cds_wt_7117	-	Uncharacterized protein R00369;
cds_wt_7118	-	2,3-bisphosphoglycerate-dependent phosphoglycerate mutase; Phosphoglyceromutase; PGAM; BPG-dependent PGAM; dPGM;
cds_wt_7119	yjeF	Uncharacterized protein R107.2;
cds_wt_7120	ykoW	Uncharacterized protein Mb1389c;
cds_wt_7121	-	hypothetical protein predicted by Glimmer/Critica

cds_wt_7122	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7123	pepE	putative peptidase
cds_wt_7124	-	Multidrug resistance protein B;
cds_wt_7125	-	Uncharacterized protein C16A10.01;
cds_wt_7126	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7127	-	Glutamate/gamma-aminobutyrate antiporter;
cds_wt_7128	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7129	-	WD repeat-containing protein YBR281C;
cds_wt_7130	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7131	-	unknown protein
cds_wt_7132	-	putative membrane protein
cds_wt_7133	-	putative integral membrane protein
cds_wt_7134	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7135	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7136	-	Probable protease htpX homolog;
cds_wt_7137	-	Probable lipid kinase yegS-like;
cds_wt_7138	-	hypothetical protein
cds_wt_7139	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7140	-	hypothetical protein
cds_wt_7141	varS	Uncharacterized transporter C3H1.06c;
cds_wt_7142	-	proline rich protein (putative membrane protein)
cds_wt_7143	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7144	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7145	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7146	cpdA	probable DNA repair exonuclease
cds_wt_7147	arcC	carbamate kinase
cds_wt_7148	arcB	ornithine carbamoyltransferase
cds_wt_7149	arcA	arginine deiminase
cds_wt_7150	yjdE	Uncharacterized amino-acid permease P7G5.06;
cds_wt_7151	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7152	malT	HTH-type transcriptional regulator malT; ATP-dependent transcriptional activator malT;
cds_wt_7153	-	putative integral membrane protein
cds_wt_7154	luxR	transcriptional regulator, LuxR family
cds_wt_7155	-	1,4-alpha-glucan-branching enzyme; Glycogen-branching enzyme; BE; 1,4-alpha-D-glucan:1,4-alpha-D-glucan 6-glucosyl-transferase;
cds_wt_7156	-	Uncharacterized protein YMR196W;
cds_wt_7157	-	hypothetical protein
cds_wt_7158	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7159	yhhT	UPF0118 membrane protein HI0338;
cds_wt_7160	-	hypothetical protein
cds_wt_7161	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7162	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7163	-	Uncharacterized WD repeat-containing protein alr3466;
cds_wt_7164	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7165	-	putative integral membrane protein
cds_wt_7166	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7167	-	hypothetical protein

cds_wt_7168	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7169	-	Carboxylate-amine ligase Mmcs_0573; Protein FAM8A1; Autosomal highly conserved protein;
cds_wt_7170	-	cation-transporting ATPase
cds_wt_7171	pacL	hypothetical protein
cds_wt_7172	-	fatty acid alpha hydroxylase
cds_wt_7173	cypC	Myc-induced nuclear antigen;
cds_wt_7174	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7175	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7176	-	HTH-type transcriptional regulator glxA;
cds_wt_7177	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7178	-	Uncharacterized protein yndH;
cds_wt_7179	yndH	hypothetical protein
cds_wt_7180	yndG	hypothetical protein predicted by Glimmer/Critica
cds_wt_7181	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7182	-	Flavin reductase; FR; NADPH-dependent diaphorase; NADPH-flavin reductase; FLR; Biliverdin reductase B; BVR-B; Biliverdin-IX beta-reductase; Green heme-binding protein; GHBP;
cds_wt_7183	-	inositol-1-monophosphatase
cds_wt_7184	suhB	Nodulation protein D 1;
cds_wt_7185	lysR	hypothetical protein predicted by Glimmer/Critica
cds_wt_7186	-	Y+L amino acid transporter 2; y
cds_wt_7187	-	Uncharacterized HTH-type transcriptional regulator ycgE;
cds_wt_7188	-	Multidrug resistance protein Y;
cds_wt_7189	-	geranylgeranyl pyrophosphate synthase
cds_wt_7190	gds	hypothetical protein predicted by Glimmer/Critica
cds_wt_7191	-	putative integral membrane protein
cds_wt_7192	-	HTH-type transcriptional regulator glxA;
cds_wt_7193	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7194	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7195	-	Uncharacterized membrane protein SE_0528;
cds_wt_7196	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7197	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7198	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7199	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7200	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7201	-	Prestalk A differentiation protein A; Putative S-adenosyl-L-methionine-dependent methyltransferase MAV_4444;
cds_wt_7202	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7203	-	HTH-type transcriptional regulator betI;
cds_wt_7204	-	3-
cds_wt_7205	-	Ubiquinone/menaquinone biosynthesis methyltransferase ubiE;
cds_wt_7206	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7207	-	hypothetical protein
cds_wt_7208	-	RNA pyrophosphohydrolase;
cds_wt_7209	-	hypothetical protein
cds_wt_7210	-	

cds_wt_7211	Abp1	copper amine oxidase, putative
cds_wt_7212	-	hypothetical protein
cds_wt_7213	-	MutT/NUDIX family protein
cds_wt_7214	livK	Leu/Ile/Val-binding protein homolog 1;
cds_wt_7215	-	Signaling protein ykoW;
cds_wt_7216	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7217	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7218	-	probable short-chain type dehydrogenase/reductase
cds_wt_7219	ethA	putative monooxygenase
cds_wt_7220	-	Carbohydrate diacid regulator; Sugar diacid regulator;
cds_wt_7221	-	Uncharacterized protein R00369;
cds_wt_7222	-	Uncharacterized protein R00370;
cds_wt_7223	glpK	glycerol kinase
cds_wt_7224	glpK	Glycerol kinase; ATP:glycerol 3-phosphotransferase;
cds_wt_7225	kdgR	Glycerokinase; GK;
cds_wt_7226	glpK	Pectin degradation repressor protein kdgR;
cds_wt_7227	glpK	glycerol kinase
cds_wt_7228	glpD	glycerol kinase
cds_wt_7229	-	glycerol-3-phosphate dehydrogenase
cds_wt_7230	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7231	ydch	hypothetical protein predicted by Glimmer/Critica
cds_wt_7232	-	Uncharacterized HTH-type transcriptional regulator ydch;
cds_wt_7233	ncch	Aggrecan core protein; Cartilage-specific proteoglycan core protein; CSPCP;
cds_wt_7234	-	RNA polymerase sigma factor ncch;
cds_wt_7235	-	hypothetical protein
cds_wt_7236	ucpA	hypothetical protein predicted by Glimmer/Critica
cds_wt_7237	-	putative oxidoreductase
cds_wt_7238	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7239	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7240	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7241	estA	hypothetical protein predicted by Glimmer/Critica
cds_wt_7242	-	Esterase;
cds_wt_7243	prsR	3-demethylubiquinone-9 3-methyltransferase; 3,4-dihydroxy-5-hexaprenylbenzoate methyltransferase; DHHB methyltransferase;
cds_wt_7244	prpD	hypothetical protein
cds_wt_7245	-	Phosphoserine phosphatase rsbU; Sigma factor sigB regulation protein rsbU;
cds_wt_7246	yofA	hypothetical protein predicted by Glimmer/Critica
cds_wt_7247	mmr	Probable RuBisCO transcriptional regulator;
cds_wt_7248	-	Multidrug resistance protein B homolog;
cds_wt_7249	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7250	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7251	-	putative DNA-binding protein
cds_wt_7252	-	hypothetical protein
cds_wt_7253	-	hypothetical protein
		hypothetical protein predicted by Glimmer/Critica

cds_wt_7254	-	putative integral membrane protein
cds_wt_7255	-	hypothetical protein
cds_wt_7256	doxX	Uncharacterized protein HI0886;
cds_wt_7257	-	hypothetical fusion protein
cds_wt_7258	ydhT	mannan endo-1,4-beta-mannosidase
cds_wt_7259	lpqC	polyhydroxybutyrate depolymerase
cds_wt_7260	-	putative RNA polymerase ECF-subfamily sigma factor
cds_wt_7261	msbA	Lipid A export ATP-binding/permease protein msbA;
cds_wt_7262	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7263	MAN1	Mannan endo-1,4-beta-mannosidase 1; Beta-mannanase 1; Endo-beta-1,4-mannanase 1; LeMAN1;
cds_wt_7264	manB	beta-mannosidase
cds_wt_7265	malG	Maltose transport system permease protein malG; sn-glycerol-3-phosphate transport system permease
cds_wt_7266	yurN	protein ugpA;
cds_wt_7267	msmE	Putative binding protein BruAb2_0484;
cds_wt_7268	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7269	glcK	glucose kinase
cds_wt_7270	cytR	HTH-type transcriptional repressor purR; Purine nucleotide synthesis repressor; Pur regulon repressor;
cds_wt_7271	yihS	Uncharacterized sugar isomerase yihS;
cds_wt_7272	cscK	fructokinase
cds_wt_7273	lpqC	polyhydroxybutyrate depolymerase
cds_wt_7274	-	putative serine/threonine protein kinase
cds_wt_7275	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7276	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7277	-	Signal peptidase I W; SPase I; Leader peptidase I;
cds_wt_7278	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7279	-	Leukocyte common antigen; L-CA; Lymphocyte antigen 5; Ly-5; T200; AltName: CD_antigen=CD45; Response regulator pleD; Stalked cell differentiation-controlling protein; Includes: Diguanylate cyclase; DGC; Diguanylate kinase;
cds_wt_7280	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7281	-	Probable E3 ubiquitin-protein ligase HERC4; HECT domain and RCC1-like domain-containing protein 4;
cds_wt_7282	-	putative secreted hydrolase
cds_wt_7283	ydhT	Uncharacterized protein yegE;
cds_wt_7284	-	Xylose repressor;
cds_wt_7285	xylR	Nitrate/nitrite sensor protein narQ;
cds_wt_7286	-	Transcriptional regulatory protein degU; Protease production enhancer protein;
cds_wt_7287	-	Cysteine desulfurase; Selenocysteine lyase; Selenocysteine reductase; Selenocysteine beta-lyase; SCL;
cds_wt_7288	-	Carboxylesterase bioH; Biotin synthesis protein bioH;
cds_wt_7289	-	Protein ydcF;
cds_wt_7290	ydcF	Uncharacterized N-acetyltransferase yoaA;
cds_wt_7291	-	

cds_wt_7292	thrC	threonine synthase
cds_wt_7293	hylP	Hyaluronoglucosaminidase; Hyaluronidase;
cds_wt_7294	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7295	xysA	endo-1,4-beta-xylanase
cds_wt_7296	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7297	-	putative membrane protein
cds_wt_7298	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7299	-	hypothetical protein
cds_wt_7300	-	Multidrug-efflux transporter 2 regulator;
cds_wt_7301	tfxG	Trifolitoxin immunity protein;
cds_wt_7302	-	hypothetical protein
cds_wt_7303	-	Uncharacterized 17.2 kDa protein in melC2-rnhH intergenic region; ORF3;
cds_wt_7304	-	Uncharacterized HTH-type transcriptional regulator Rv1255c/MT1294;
cds_wt_7305	todF	Carboxylesterase bioH; Biotin synthesis protein bioH;
cds_wt_7306	-	Uncharacterized N-acetyltransferase ycf52;
cds_wt_7307	tetR	Uncharacterized HTH-type transcriptional regulator yuxN;
cds_wt_7308	-	hypothetical protein
cds_wt_7309	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7310	-	RNA pyrophosphohydrolase;
cds_wt_7311	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7312	-	hypothetical protein
cds_wt_7313	-	Negative transcription regulator padR;
cds_wt_7314	phnL	Spermidine/putrescine import ATP-binding protein potA;
cds_wt_7315	-	hypothetical protein
cds_wt_7316	lytE	Probable N-acetylmuramoyl-L-alanine amidase; Cell wall hydrolase; Autolysin; ORFL3;
cds_wt_7317	-	Transcriptional regulatory protein uhpA;
cds_wt_7318	-	putative two-component system sensor kinase
cds_wt_7319	-	hypothetical protein
cds_wt_7320	-	Spermidine/putrescine import ATP-binding protein potA;
cds_wt_7321	-	Putative esterase ytxM;
cds_wt_7322	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7323	-	Carboxylesterase bioH; Biotin synthesis protein bioH;
cds_wt_7324	nerA	GTN reductase
cds_wt_7325	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7326	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7327	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7328	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7329	dppD	putative ABC transporter ATP-binding subunit
cds_wt_7330	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7331	-	helix-turn-helix motif
cds_wt_7332	-	Abhydrolase domain-containing protein 11;
cds_wt_7333	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7334	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7335	-	hypothetical protein

cds_wt_7336	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7337	-	UPF0410 protein ymge; Transglycosylase-associated gene protein;
cds_wt_7338	phr	tRNA uridine 5-carboxymethylaminomethyl modification enzyme mnmG; Glucose-inhibited division protein A;
cds_wt_7339	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7340	pleD	Probable diguanylate cyclase yeaP; DGC;
cds_wt_7341	ydeS	Uncharacterized HTH-type transcriptional regulator ydeS;
cds_wt_7342	-	Uncharacterized protein MJ0531;
cds_wt_7343	-	cyanophycinase and related exopeptidase-like
cds_wt_7344	cphB	Cyanophycinase;
cds_wt_7345	-	HTH-type transcriptional regulator hexR; Hex regulon repressor;
cds_wt_7346	-	Membrane-bound lytic murein transglycosylase F; EC=4.2.2.n1; Murein lyase F;
cds_wt_7347	-	putative ABC transporter permease
cds_wt_7348	-	carboxypeptidase G2
cds_wt_7349	-	Uncharacterized protein y4IL;
cds_wt_7350	-	Uncharacterized signaling protein PA3311;
cds_wt_7351	-	Putative diflavin flavoprotein A 1;
cds_wt_7352	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7353	-	hypothetical protein
cds_wt_7354	-	Arabinan endo-1,5-alpha-L-arabinosidase; Endo-1,5-alpha-L-arabinanase; ABN; Endo-arabinanase;
cds_wt_7355	-	putative lipoprotein
cds_wt_7356	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7357	nhaA	Na
cds_wt_7358	-	Laminin-like protein epi-1;
cds_wt_7359	-	putative integral membrane protein
cds_wt_7360	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7361	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7362	-	hypothetical protein
cds_wt_7363	-	Sensor histidine kinase yycG;
cds_wt_7364	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7365	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7366	albD	putative membrane protein
cds_wt_7367	-	PI-PLC X domain-containing protein At5g67130;
cds_wt_7368	glpD	glycerol-3-phosphate dehydrogenase
cds_wt_7369	-	Uncharacterized HTH-type transcriptional regulator Rv2250c/MT2310;
cds_wt_7370	adaS	alkyl-dihydroxyacetonephosphate synthase, putative
cds_wt_7371	bmrU	Probable lipid kinase yegS-like;
cds_wt_7372	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7373	bchE	hypothetical protein
cds_wt_7374	-	hypothetical protein
cds_wt_7375	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7376	-	lantibiotic biosynthesis protein

cds_wt_7377	-	hypothetical protein, putative lanthionine biosynthesis protein
cds_wt_7378	-	UPF0142 protein ycaO;
cds_wt_7379	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7380	-	hypothetical protein
cds_wt_7381	-	hypothetical protein
cds_wt_7382	-	hypothetical protein
cds_wt_7383	-	UPF0142 protein MJ1094;
cds_wt_7384	bscv	Adipocyte plasma membrane-associated protein; BSCv protein;
cds_wt_7385	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7386	-	Extracellular matrix-binding protein ebh; ECM-binding protein homolog;
cds_wt_7387	ydfJ	Membrane protein ydfJ;
cds_wt_7388	phoR	sensor histidine kinase
cds_wt_7389	phoP	Response regulator arlR;
cds_wt_7390	adp	D-alanyl-D-alanine carboxypeptidase
cds_wt_7391	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7392	sigG	RNA polymerase sigma-H factor; Sigma-30;
cds_wt_7393	chiC	putative sugar hydrolase
cds_wt_7394	yheB	chitinase
cds_wt_7395	-	HTH-type transcriptional regulator glnR;
cds_wt_7396	-	hypothetical protein
cds_wt_7397	cspD	Cold shock protein cspA; CSP-A; 7.4 kDa cold shock protein; CS7.4;
cds_wt_7398	-	Ferrous iron transport protein A;
cds_wt_7399	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7400	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7401	-	Disease resistance protein RPP8; Resistance to Peronospora parasitica protein 8;
cds_wt_7402	-	hypothetical protein
cds_wt_7403	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7404	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7405	xylS	alpha-xylosidase
cds_wt_7406	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7407	spaF	Spermidine/putrescine import ATP-binding protein potA; Retinol-binding protein 3; Interphotoreceptor retinoid-binding protein; IRBP; Interstitial retinol-binding protein;
cds_wt_7408	Rbp3	
cds_wt_7409	-	hypothetical protein
cds_wt_7410	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7411	-	hypothetical protein
cds_wt_7412	-	hypothetical protein
cds_wt_7413	ctpD	putative cation-transporting P-type ATPase D
cds_wt_7414	cadC	Cadmium efflux system accessory protein;
cds_wt_7415	ctpA	putative cation transporter
cds_wt_7416	-	hypothetical protein
cds_wt_7417	-	Cation-transporting ATPase pacS;
cds_wt_7418	-	hypothetical protein predicted by Glimmer/Critica

cds_wt_7419	gpsA	glycerol-3-phosphate dehydrogenase (NAD(P)+)
cds_wt_7420	rbsB	Basic membrane protein A1; Immunodominant antigen P39;
cds_wt_7421	tlpB	Methyl-accepting chemotaxis protein mcpB; H3;
cds_wt_7422	sigF	RNA polymerase sigma factor rpoD; Sigma-70;
cds_wt_7423	-	putative two-component system sensor kinase
cds_wt_7424	-	Hybrid signal transduction histidine kinase J;
cds_wt_7425	-	hypothetical protein
cds_wt_7426	-	hypothetical protein
cds_wt_7427	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7428	ADH5	quinone reductase
cds_wt_7429	-	Uncharacterized HTH-type transcriptional regulator yeaM;
cds_wt_7430	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7431	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7432	phy	sensory transduction histidine kinase
cds_wt_7433	-	Uncharacterized protein MJ0240;
cds_wt_7434	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7435	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7436	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7437	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7438	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7439	cadD	cadmium resistance transporter
cds_wt_7440	-	hypothetical protein
cds_wt_7441	ykrU	Nitrilase homolog 2;
cds_wt_7442	-	Uncharacterized HTH-type transcriptional regulator ydeP;
cds_wt_7443	ytfG	Uncharacterized oxidoreductase ytfG;
cds_wt_7444	GALC	similar to Galactocerebrosidase precursor (GALCERase) (Galactosylceramidase) (Galactosylceramide beta-galactosidase) (Galactocerebroside beta-galactosidase)
cds_wt_7445	acbH	Uncharacterized ABC transporter extracellular-binding protein yurO;
cds_wt_7446	acbF	Probable ABC transporter permease protein yurN;
cds_wt_7447	acbG	Probable ABC transporter permease protein yurM;
cds_wt_7448	acbD	alpha-amylase
cds_wt_7449	acbE	alpha-amylase family protein
cds_wt_7450	acbA	glucose-1-phosphate thymidyltransferase
cds_wt_7451	acbB	dTDP-glucose 4,6-dehydratase
cds_wt_7452a	acbC	Fe-ADH, Iron-containing alcohol dehydrogenase
cds_wt_7452b	acbO	Xylose isomerase-like TIM barrel
cds_wt_7453	acbN	3-oxoacyl-
cds_wt_7454	acbL	L-threonine 3-dehydrogenase;
cds_wt_7455	acbM	N-acetyl-D-glucosamine kinase; GlcNAc kinase;
cds_wt_7456	acbK	sugar kinase of the ribokinase family
cds_wt_7457	acbQ	putative 4-alpha-glucanotransferase
cds_wt_7458	acbJ	HMP-PP phosphatase;
cds_wt_7459	acbl	hypothetical protein predicted by Glimmer/Critica
cds_wt_7460	acbP	ADP-ribose pyrophosphatase

cds_wt_7461	acbR	glucose-1-phosphate adenylyltransferase
cds_wt_7462	acbS	Glycogen synthase 1; Starch
cds_wt_7463	acbU	hypothetical protein predicted by Glimmer/Critica
cds_wt_7464	acbV	4-aminobutyrate aminotransferase
		Spermidine/putrescine import ATP-binding protein
cds_wt_7465	acbW	potA;
cds_wt_7466	acbX	conserved hypothetical protein
cds_wt_7467	acbY	conserved hypothetical protein
		Alpha-amylase; 1,4-alpha-D-glucan
cds_wt_7468	acbZ	glucanohydrolase;
		Phytochrome-like protein cph2; Bacteriophytochrome
cds_wt_7469	-	cph2;
		Alpha-N-arabinofuranosidase 2; Alpha-N-
cds_wt_7470	-	arabinofuranosidase II; Arabinosidase II; Alpha-N-
cds_wt_7471	-	AFase II;
cds_wt_7472	-	Uncharacterized signaling protein CC_0091;
		Uncharacterized protein C4H3.03c;
		HTH-type transcriptional regulator hpr; Protease
cds_wt_7473	marR	production regulatory protein hpr;
cds_wt_7474	prsR	Anti-sigma F factor; Stage II sporulation protein AB;
cds_wt_7475	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7476	xylR	Xylose repressor;
		HTH-type transcriptional repressor purR; Purine
		nucleotide synthesis repressor; Pur regulon
		repressor;
cds_wt_7477	rbsR	
cds_wt_7478	ydhT	mannan endo-1,4-beta-mannosidase
cds_wt_7479	lpqC	polyhydroxybutyrate depolymerase
cds_wt_7480	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7481	-	Uncharacterized protein Rv0048c/MT0054;
cds_wt_7482	pksA	HTH-type transcriptional regulator betI;
cds_wt_7483	tlpB	Methyl-accepting chemotaxis protein tlpB;
cds_wt_7484	-	Protein adrA;
cds_wt_7485	-	hypothetical protein
cds_wt_7486	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7487	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7488	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7489	yokD	aminoglycoside N3-acetyltransferase
cds_wt_7490	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7491	rhsA	Protein rhsC;
cds_wt_7492	-	hypothetical protein 2SCD4.09c
cds_wt_7493	-	hypothetical protein
cds_wt_7494	-	hypothetical protein
cds_wt_7495	-	Protein essC;
cds_wt_7496	-	putative integral membrane protein
cds_wt_7497	-	putative integral membrane protein
cds_wt_7498	-	HTH-type protein slmA;
cds_wt_7499	-	Uncharacterized protein yndB;
cds_wt_7500	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7501	-	hypothetical protein
cds_wt_7502	-	hypothetical protein

cds_wt_7503	-	hydrolase, alpha/beta fold family HTH-type transcriptional repressor purR; Purine nucleotide synthesis repressor; Pur regulon
cds_wt_7504	lacI	repressor;
cds_wt_7505	-	hypothetical protein predicted by Glimmer/Critica Transmembrane and TPR repeat-containing protein
cds_wt_7506	-	2;
cds_wt_7507	-	hypothetical protein predicted by Glimmer/Critica Uncharacterized WD repeat-containing protein
cds_wt_7508	-	alr3466;
cds_wt_7509	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7510	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7511	-	hypothetical protein
cds_wt_7512	ppiB	peptidyl-prolyl cis-trans isomerase Uncharacterized WD repeat-containing protein
cds_wt_7513	-	alr3466;
cds_wt_7514	-	Regulatory protein afsR; Abhydrolase domain-containing protein 11; Williams- Beuren syndrome chromosomal region 21 protein
cds_wt_7515	-	homolog;
cds_wt_7516	-	Uncharacterized signaling protein CC_0091;
cds_wt_7517	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7518	ANK3	putative ankyrin-like protein
cds_wt_7519	tetR	Tetracycline repressor protein class C;
cds_wt_7520	-	Aminoglycoside N
cds_wt_7521	-	putative secreted protein Insertion element IS110 uncharacterized 43.6 kDa protein;
cds_wt_7522	-	hypothetical protein
cds_wt_7523	-	hypothetical protein
cds_wt_7524	tetR	Tetracycline repressor protein class H;
cds_wt_7525	lipG	hydrolase, alpha/beta fold family
cds_wt_7526	adh2	alcohol dehydrogenase Uncharacterized isochorismatase family protein
cds_wt_7527	-	ywoC;
cds_wt_7528	-	DnaK suppressor protein homolog;
cds_wt_7529	-	putative secreted protein
cds_wt_7530	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7531	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7532	-	Regulatory protein afsR;
cds_wt_7533	-	hypothetical protein
cds_wt_7534	metG	methionyl-tRNA synthetase
cds_wt_7535	-	sarcosine oxidase
cds_wt_7536	-	Uncharacterized MFS-type transporter yttB;
cds_wt_7537	-	hypothetical protein Short-chain specific acyl-CoA dehydrogenase, mitochondrial; SCAD; Butyryl-CoA dehydrogenase;
cds_wt_7538	-	Short-chain specific acyl-CoA dehydrogenase, mitochondrial; SCAD; Butyryl-CoA dehydrogenase;
cds_wt_7539	-	Anaerobic magnesium-protoporphyrin IX monomethyl ester
cds_wt_7540	-	

cds_wt_7541	-	hypothetical protein
cds_wt_7542	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7543	BBE1	putative lipoprotein
cds_wt_7544	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7545	-	hypothetical protein
cds_wt_7546	-	Thioredoxin reductase; TRXR;
cds_wt_7547	-	Anti-sigma F factor antagonist; Stage II sporulation protein AA;
cds_wt_7548	-	Uncharacterized protein ydaM;
cds_wt_7549	-	Oxygen sensor histidine kinase nreB; Nitrogen regulation protein B;
cds_wt_7550	-	Lipoprotein-releasing system ATP-binding protein lolD;
cds_wt_7551	-	Spermidine/putrescine import ATP-binding protein potA;
cds_wt_7552	-	Macrolide export ATP-binding/permease protein macB;
cds_wt_7553	draG	putative hydrolase
cds_wt_7554	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7555	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7556	tetR	Tetracycline repressor protein class H;
cds_wt_7557	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7558	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7559	orfA	probable transposase for insertion sequence element IS1533
cds_wt_7560	-	Response regulator gacA; Global activator;
cds_wt_7561	-	Phytochrome D;
cds_wt_7562	-	Uncharacterized protein R00370;
cds_wt_7563	-	Signaling protein ykoW;
cds_wt_7564	-	Uncharacterized signaling protein PA1727;
cds_wt_7565	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7566	-	Polypeptide N-acetylgalactosaminyltransferase 6; Polypeptide GalNAc transferase 6; pp-GaNTase 6; GalNAc-T6; Protein-UDP acetylgalactosaminyltransferase 6; UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase 6;
cds_wt_7567	hstK	serine/threonine protein kinase and signal transduction histidine kinase (STHK) with GAF sensor
cds_wt_7568	tcmR	HTH-type transcriptional regulator tcmR;
cds_wt_7569	-	Tetracenomycin C transcriptional repressor;
cds_wt_7570	-	Response regulator arlR;
cds_wt_7571	-	Uncharacterized signaling protein PA3311;
cds_wt_7572	-	hypothetical protein
cds_wt_7573	ydeS	Prestalk A differentiation protein A;
cds_wt_7574	-	Uncharacterized HTH-type transcriptional regulator Mb1581;
cds_wt_7575	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7575	-	hypothetical protein predicted by Glimmer/Critica

cds_wt_7576	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7577	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7578	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7579	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7580	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7581	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7582	tnp	Putative transposase insK for insertion sequence element IS150;
cds_wt_7583	-	hypothetical protein
cds_wt_7584	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7585	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7586	-	Muscle M-line assembly protein unc-89;
cds_wt_7587	-	Uncoordinated protein 89;
cds_wt_7588	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7589	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7590	-	hypothetical protein
cds_wt_7591	cad	hypothetical protein predicted by Glimmer/Critica
cds_wt_7592	-	lysine decarboxylase
cds_wt_7593	PHY1	two-component hybrid sensor and regulator
cds_wt_7594	ybiA	two-component sensor histidine kinase
cds_wt_7595	-	Swarming motility protein ybiA;
cds_wt_7596	-	hypothetical protein
cds_wt_7597	tlpB	hypothetical protein predicted by Glimmer/Critica
cds_wt_7598	-	Methyl-accepting chemotaxis protein mcpB; H3;
cds_wt_7599	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7600	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7601	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7602	kdpD	hypothetical protein
cds_wt_7603	metG	sensory transduction histidine kinase
cds_wt_7604	-	methionyl-tRNA synthetase
cds_wt_7605	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7606	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7607	-	Nephrocystin-3;
cds_wt_7608	-	Heme-regulated cyclic di-GMP, cyclic AMP phosphodiesterase,; Direct oxygen sensor protein; Ec DOS;
cds_wt_7609	prsR	hypothetical protein predicted by Glimmer/Critica
cds_wt_7610	-	Anti-sigma F factor; Stage II sporulation protein AB;
cds_wt_7611	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7612	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7613	smf	hypothetical protein predicted by Glimmer/Critica
cds_wt_7614	-	Protein smf;
cds_wt_7615	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7616	-	hypothetical protein
cds_wt_7617	-	Uncharacterized signaling protein PA1727;
cds_wt_7618	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7619	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7620	dnaK	hypothetical protein predicted by Glimmer/Critica
		Chaperone protein dnaK; Heat shock protein 70; Heat shock 70 kDa protein; HSP70;

cds_wt_7621	-	Otogelin;
cds_wt_7622	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7623	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7624	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7625	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7626	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7627	sulA	cell-division inhibitor
cds_wt_7628	-	transposase
cds_wt_7629	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7630	-	hypothetical protein
cds_wt_7631	traE	Uncharacterized protein pXO2-09/BXB0008/GBAA_pXO2_0008;
cds_wt_7632	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7633	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7634	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7635	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7636	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7637	-	putative DNA-binding protein
cds_wt_7638	-	hypothetical protein
cds_wt_7639	-	Phosphoglycolate phosphatase; PGPase; PGP;
cds_wt_7640	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7641	-	hypothetical protein
cds_wt_7642	marR	Uncharacterized HTH-type transcriptional regulator ykoM;
cds_wt_7643	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7644	-	Tetratricopeptide repeat protein 28; TPR repeat protein 28;
cds_wt_7645	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7646	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7647	-	Uncharacterized protein Mb2601c;
cds_wt_7648	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7649	-	Inner membrane protein yrbG;
cds_wt_7650	-	Uncharacterized HTH-type transcriptional regulator ywhA;
cds_wt_7651	rre7	Probable transcriptional regulator ycf27; OmpR-like protein;
cds_wt_7652	kaiC	Circadian clock protein kinase kaiC;
cds_wt_7653	-	putative secreted protein
cds_wt_7654	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7655	-	putative serine/threonine protein kinase
cds_wt_7656	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7657	NIA2	probable sulfite oxidase
cds_wt_7658	-	Transforming growth factor-beta-induced protein ig-h3; Beta ig-h3; Kerato-epithelin; RGD-containing collagen-associated protein; RGD-CAP;
cds_wt_7659	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7660	stuC	sensor histidine kinase
cds_wt_7661	-	Cyanobacterial phytochrome B;
cds_wt_7662	-	Beta-Ala-His dipeptidase; Carnosine dipeptidase 1; CNDP dipeptidase 1;

cds_wt_7663	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7664	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7665	-	Neurocan core protein; Chondroitin sulfate proteoglycan 3;
cds_wt_7666	-	Uncharacterized signaling protein PA3311;
cds_wt_7667	-	Uncharacterized protein DR_1314;
cds_wt_7668	-	Uncharacterized protein DR_1314;
cds_wt_7669	tetR	Tetracycline repressor protein class H;
cds_wt_7670	-	ribonuclease BN, putative
cds_wt_7671	-	putative integral membrane protein
cds_wt_7672	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7673	-	hypothetical protein
cds_wt_7674	-	Laminin subunit gamma-3; Laminin 12 gamma 3 subunit;
cds_wt_7675	-	Anti-sigma F factor antagonist; Stage II sporulation protein AA;
cds_wt_7676	-	hypothetical protein
cds_wt_7677	ucpA	3-oxoacyl-
cds_wt_7678	phoR	sensory box histidine kinase PhoR
cds_wt_7679	nodC	N-acetylglucosaminyltransferase; Nodulation protein C;
cds_wt_7680	nmoT	Transposase;
cds_wt_7681	istB	Chromosomal replication initiator protein dnaA;
cds_wt_7682	-	Probable mannan synthase 9; Cellulose synthase-like protein A9; OsCslA9;
cds_wt_7683	-	glycosyl transferase, group 2 family protein
cds_wt_7684	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7685	pleD	Uncharacterized signaling protein PA1727;
cds_wt_7686	-	Inner membrane protein yfiN;
cds_wt_7687	bhp	Extracellular matrix-binding protein ebh; ECM-binding protein homolog;
cds_wt_7688	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7689	-	Beta-galactoside-specific lectin 3; Beta-galactoside-specific lectin III; Beta-galactoside-specific lectin II; Contains: Beta-galactoside-specific lectin 3 chain A isoform 1; ML-3 A; Beta-galactoside-specific lectin III chain A isoform 1; ML-III A; Lectin chain A isoform 2; rRNA N-glycosidase; Contains: Beta-galactoside-specific lectin 3 chain B; ML-3 B; Beta-galactoside-specific lectin III chain B; ML-III B;
cds_wt_7690	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7691	-	Uncharacterized protein L153;
cds_wt_7692	-	Uncharacterized protein L153;
cds_wt_7693	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7694	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7695	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7696	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7697	-	Probable transcriptional regulator ycf27; OmpR-like protein;
cds_wt_7698	ETR1	Ethylene receptor; MEETR1; Cm-ETR1;

cds_wt_7699	-	Uncharacterized signaling protein CC_0091;
cds_wt_7700	phoR	phosphate regulon sensor protein
cds_wt_7701	-	hypothetical protein predicted by Glimmer/Critica
		Probable transcriptional regulator ycf27; OmpR-like protein;
cds_wt_7702	mtrA	hypothetical protein predicted by Glimmer/Critica
cds_wt_7703	-	Chaperone protein dnaK; Heat shock protein 70; Heat shock 70 kDa protein; HSP70;
cds_wt_7704	dnaK	hypothetical protein predicted by Glimmer/Critica
cds_wt_7705	-	Signal transduction histidine-protein kinase/phosphatase mprB; Mycobacterial persistence regulator B;
cds_wt_7706	cckA	hypothetical protein predicted by Glimmer/Critica
cds_wt_7707	-	hypothetical protein
cds_wt_7708	-	hypothetical protein
cds_wt_7709	-	hypothetical protein
cds_wt_7710	otsA	alpha,alpha-trehalose-phosphate synthase
cds_wt_7711	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7712	-	Uncharacterized signaling protein PA1727;
cds_wt_7713	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7714	ybfG	Uncharacterized protein fadG;
cds_wt_7715	-	hypothetical protein predicted by Glimmer/Critica
		serine/threonine protein kinase and signal transduction histidine kinase (STHK) with GAF sensor
cds_wt_7716	-	Uncharacterized protein yhcK;
cds_wt_7717	-	Uncharacterized protein R00370;
cds_wt_7718	-	hypothetical protein
cds_wt_7719	-	hypothetical protein
cds_wt_7720	-	Uncharacterized protein Rv2667/MT2741;
cds_wt_7721	-	Chaperone protein clpB;
cds_wt_7722	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7723	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7724	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7725	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7726	-	Uncharacterized signaling protein PA1727;
cds_wt_7727	morA	Cellulose synthesis regulatory protein;
cds_wt_7728	-	Membrane-bound lytic murein transglycosylase F; EC=4.2.2.n1; Murein lyase F;
cds_wt_7729	-	sensory box histidine kinase/response regulator
cds_wt_7730	virA	Putative Xaa-Pro dipeptidyl-peptidase; X-Pro dipeptidyl-peptidase; X-prolyl-dipeptidyl aminopeptidase; X-PDAP;
cds_wt_7731	-	phosphinothricin N-acetyltransferase
cds_wt_7732	pat	Microtubule-associated protein 1A; MAP-1A; Proliferation-related protein p80; Contains: MAP1 light chain LC2;
cds_wt_7733	-	Uncharacterized oxidoreductase yesF;
cds_wt_7734	-	hypothetical protein
cds_wt_7735	-	Uncharacterized protein slr1717;
cds_wt_7736	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7737	-	

cds_wt_7738	-	hypothetical protein
cds_wt_7739	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7740	-	hypothetical protein
cds_wt_7741	-	hypothetical protein
cds_wt_7742	phoA	acid phosphatase
cds_wt_7743	-	UPF0014 inner membrane protein ybbM;
cds_wt_7744	-	membrane protein, putative
cds_wt_7745	-	Protein icfG;
cds_wt_7746	phoB	Probable transcriptional regulator ycf27; OmpR-like protein;
cds_wt_7747	-	Blue-light-activated protein; Includes: Blue-light-activated histidine kinase; Includes: Response regulator;
cds_wt_7748	-	hypothetical protein
cds_wt_7749	-	multi-sensor hybrid histidine kinase
cds_wt_7750	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7751	-	Uncharacterized signaling protein CC_0091;
cds_wt_7752	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7753	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7754	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7755	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7756	-	Thrombin-like enzyme gussurobin;
cds_wt_7757	xynD	arabinosidase
cds_wt_7758	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7759	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7760	-	Aminopeptidase 2, mitochondrial; Aminopeptidase II; AP-II; YscII;
cds_wt_7761	bacC	Bacitracin synthetase 3; BA3; Includes: ATP-dependent isoleucine adenylation; IleA; Isoleucine activase; Includes: ATP-dependent D-phenylalanine adenylation; D-PheA; D-phenylalanine activase; Includes: ATP-dependent histidine adenylation; HisA; Histidine activase; Includes: ATP-dependent D-aspartate adenylation; D-AspA; D-aspartate activase; Includes: ATP-dependent asparagine adenylation; AsnA; Asparagine activase; Includes: Aspartate racemase; Includes: Phenylalanine racemase
cds_wt_7762	-	Insertion element IS402 uncharacterized 16.2 kDa protein;
cds_wt_7763	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7764	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7765	PHY1	Phytochrome 1;
cds_wt_7766	-	Putative S-adenosyl-L-methionine-dependent methyltransferase MAV_4444;
cds_wt_7767	-	hypothetical protein
cds_wt_7768	copG	hypothetical protein
cds_wt_7769	-	hypothetical protein predicted by Glimmer/Critica

		2-hydroxy-6-oxononadienedioate/2-hydroxy-6-oxononatrienedioate hydrolase; EC=3.7.1.n1; 2-hydroxy-6-oxonona-2,4-diene-1,9-dioic acid 5,6-hydrolase; 2-hydroxy-6-ketonona-2,4-diene-1,9-dioic acid 5,6-hydrolase; 2-hydroxy-6-oxonona-2,4,7-triene-1,9-dioic acid 5,6-hydrolase;
cds_wt_7770	-	
cds_wt_7771	-	hypothetical protein
		HTH-type transcriptional activator rhaS; L-rhamnose operon regulatory protein rhaS;
cds_wt_7772	pobR	
cds_wt_7773	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7774	-	Uncharacterized protein Rv1364c/MT1410;
cds_wt_7775	hspX	17.5 kDa class I heat shock protein; HSP 17.5-E;
cds_wt_7776	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7777	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7778	p20	Uncharacterized N-acetyltransferase p20;
cds_wt_7779	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7780	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7781	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7782	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7783	tcaB	Multidrug resistance protein mdtL;
cds_wt_7784	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7785	-	hypothetical protein predicted by Glimmer/Critica
		Uncharacterized sensor-like histidine kinase
cds_wt_7786	-	Caur_0899;
cds_wt_7787	pin	Transposon Tn552 DNA-invertase binR;
		Phosphoserine phosphatase rsbU; Sigma factor sigB
cds_wt_7788	prpD	regulation protein rsbU;
cds_wt_7789	-	Uncharacterized protein AF_2041;
cds_wt_7790	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7791	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7792	mtrR	HTH-type transcriptional regulator mtrR;
cds_wt_7793	pepD	putative aminopeptidase
		Response regulator mprA; Mycobacterial persistence
cds_wt_7794	tcra	regulator A;
cds_wt_7795	-	sensor histidine kinase
cds_wt_7796	cheB	protein-glutamate methylesterase
cds_wt_7797	benR	XylIDLEGF operon transcriptional activator 1;
cds_wt_7798	-	Tolloid-like protein 1; mTII;
cds_wt_7799	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7800	-	hypothetical protein
		Tetratricopeptide repeat protein 28; TPR repeat
cds_wt_7801	-	protein 28;
cds_wt_7802	-	hypothetical protein
cds_wt_7803	-	Putative peptidoglycan O-acetyltransferase yrhL;
cds_wt_7804	-	hypothetical protein
		UDP-N-acetylglucosamine--peptide N-
		acetylglucosaminyltransferase 110 kDa subunit; O-
cds_wt_7805	Ogt	linked N-acetylglucosamine transferase 110 kDa
cds_wt_7806	estA	subunit; O-GlcNAc transferase subunit p110;
		putative secreted hydrolase

cds_wt_7807	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7808	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7809	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7810	-	hypothetical protein
cds_wt_7811	lysX	lysyl-tRNA synthetase
cds_wt_7812	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7813	-	Endo-1,4-beta-xylanase Z; Xylanase Z; 1,4-beta-D-xylan xylanohydrolase Z;
cds_wt_7814	-	Carbon catabolite-derepressing protein kinase;
cds_wt_7815	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7816	-	RNA pyrophosphohydrolase;
cds_wt_7817	-	Uncharacterized signaling protein PA3311;
cds_wt_7818	-	putative serine/threonine protein kinase (putative secreted protein)
cds_wt_7819	pepX	hydrolase, CocE/NonD family
cds_wt_7820	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7821	APE3	probable aminopeptidase
cds_wt_7822	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7823	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7824	-	hypothetical protein
cds_wt_7825	-	Uncharacterized protein Rv2915c/MT2982.1;
cds_wt_7826	-	Uncharacterized protein in ftr 5'region; ORFU; Flags: Fragment;
cds_wt_7827	-	Uncharacterized membrane protein Rv0364/MT0380;
cds_wt_7828	pdxY	pyridoxal kinase
cds_wt_7829	-	Phosphoglycolate phosphatase; PGPase; PGP;
cds_wt_7830	-	Phytochrome-like protein cph2; Bacteriophytochrome cph2;
cds_wt_7831	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7832	bacA	undecaprenyl-diphosphatase
cds_wt_7833	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7834	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7835	spaF	Spermidine/putrescine import ATP-binding protein potA;
cds_wt_7836	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7837	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7838	-	hypothetical protein
cds_wt_7839	-	hypothetical protein
cds_wt_7840	-	hypothetical protein
cds_wt_7841	-	hypothetical protein
cds_wt_7842	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7843	-	Aldo-keto reductase yakc
cds_wt_7844	-	sensor histidine kinase
cds_wt_7845	phoB	Phosphate regulon transcriptional regulatory protein phoB;
cds_wt_7846	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7847	lysX	lysyl-tRNA synthetase
cds_wt_7848	-	Zeaxanthin epoxidase, chloroplastic;
cds_wt_7849	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7850	cax	Putative vacuolar cation/proton exchanger 4; Ca

cds_wt_7851	-	Uncharacterized protein Mb0911c;
cds_wt_7852	-	Putative araC-like transcription regulator;
cds_wt_7853	-	Cellulose synthesis regulatory protein;
cds_wt_7854	-	putative secreted protein
cds_wt_7855	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7856	-	Uncharacterized protein R00370;
cds_wt_7857	-	Uncharacterized protein R00369;
		FMN-dependent NADH-azoreductase; FMN-dependent NADH-azo compound oxidoreductase;
cds_wt_7858	-	Azo-dye reductase;
cds_wt_7859	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7860	-	hypothetical protein
cds_wt_7861	-	hypothetical protein
cds_wt_7862	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7863	-	putative glycosyl transferase
cds_wt_7864	celA	putative endo-1,4-beta-glucanase
cds_wt_7865	-	Galactose oxidase; GAO; GOase; GO;
cds_wt_7866	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7867	-	Anti-sigma F factor; Stage II sporulation protein AB;
cds_wt_7868	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7869	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7870	lamA	putative secreted hydrolase
cds_wt_7871	scoB	3-oxoacid CoA-transferase subunit B
cds_wt_7872	scoA	putative 3-oxoadipate CoA-transferase subunit A
cds_wt_7873	iclR	Acetate operon repressor;
cds_wt_7874	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7875	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7876	-	Uncharacterized signaling protein CC_0091;
		DNA-directed RNA polymerase II subunit RPB1; RNA polymerase II subunit B1; DNA-directed RNA polymerase III largest subunit;
cds_wt_7877	RPII	
cds_wt_7878	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7879	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7880	-	hypothetical protein
cds_wt_7881	-	Otogelin;
cds_wt_7882	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7883	-	Glycogen synthase 2; Starch
cds_wt_7884	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7885	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7886	icsA	glycosyltransferase
cds_wt_7887	yticB	UDP-glucose 4-epimerase
cds_wt_7888	caiB	CaiB/BaiF family protein
cds_wt_7889	adp	D-alanyl-D-alanine carboxypeptidase
cds_wt_7890	-	Nodulation protein V;
cds_wt_7891	-	Response regulator gacA; Global activator;
cds_wt_7892	-	hypothetical protein
cds_wt_7893	-	UPF0353 protein MAP_1207;
cds_wt_7894	-	HTH-type transcriptional regulator betI;
cds_wt_7895	aofH	putative flavin-containing monoamine oxidase
cds_wt_7896	-	Uncharacterized membrane protein MJ0091;

cds_wt_7897	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7898	-	conserved hypothetical protein
cds_wt_7899	-	conserved hypothetical protein
cds_wt_7900	drmA	Spermidine/putrescine import ATP-binding protein potA;
cds_wt_7901	galE	UDP-glucose 4-epimerase
cds_wt_7902	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7903	cut4	Cutinase; Cutin hydrolase;
cds_wt_7904	-	Uncharacterized transporter AF_1552;
cds_wt_7905	-	Uncharacterized HTH-type transcriptional regulator ywbl;
cds_wt_7906	-	Probable nitrogen assimilation transcriptional activator;
cds_wt_7907	-	Thrombin-like enzyme gussurobin;
cds_wt_7908	cutR	Alkaline phosphatase synthesis transcriptional regulatory protein sphR;
cds_wt_7909	lip1	putative hydrolase
cds_wt_7910	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7911	-	membrane protein, putative
cds_wt_7912	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7913	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7914	yurM	sn-glycerol-3-phosphate transport system permease protein ugpE;
cds_wt_7915	yurN	Maltose transport system permease protein malF;
cds_wt_7916	-	Maltose-binding periplasmic protein; MMBP;
cds_wt_7917	ampC	Maltodextrin-binding protein;
cds_wt_7918	ybbC	putative beta-lactamase
cds_wt_7919	rpiR	Uncharacterized protein ybbC; ORF2;
cds_wt_7920	-	Uncharacterized HTH-type transcriptional regulator CA_C0191;
cds_wt_7921	-	N-acetylmuramic acid 6-phosphate etherase 1;
cds_wt_7922	-	MurNAc-6-P etherase 1;
cds_wt_7923	-	Putative zinc metalloprotease MJ0611;
cds_wt_7924	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7925	-	Putative nitroreductase MJ1384;
cds_wt_7926	-	Putative nitroreductase MJ1384;
cds_wt_7927	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7928	-	UPF0142 protein ycaO;
cds_wt_7929	-	hypothetical protein
cds_wt_7930	chiR	hypothetical protein predicted by Glimmer/Critica
cds_wt_7931	-	Transcriptional regulatory protein degU; Protease production enhancer protein;
cds_wt_7932	rfbD	Histidine protein kinase divJ;
cds_wt_7933	-	dTDP-4-dehydrorhamnose reductase
cds_wt_7934	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7935	-	Homoserine O-acetyltransferase; Homoserine O-trans-acetylase; Homoserine transacetylase; HTA;
cds_wt_7936	-	hypothetical protein predicted by Glimmer/Critica

cds_wt_7937	abfB	putative secreted protein
cds_wt_7938	-	hypothetical protein
cds_wt_7939	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7940	-	Putative multidrug resistance protein mdtD;
cds_wt_7941	ssuD	putative FMNH2-utilizing oxygenase
cds_wt_7942	nrd	Alkanesulfonate monooxygenase; FMNH2-dependent aliphatic sulfonate monooxygenase;
cds_wt_7943	-	Alpha-lytic protease; Alpha-lytic endopeptidase;
cds_wt_7944	-	putative integral membrane protein
cds_wt_7945	-	Uncharacterized protein R617;
cds_wt_7946	-	hypothetical protein
cds_wt_7947	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7948	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7949	fprC	putative ferredoxin reductase
cds_wt_7950	pteD	cytochrome P450 hydroxylase
cds_wt_7951	-	hypothetical protein
cds_wt_7952	pknL	serine/threonine protein kinase
cds_wt_7953	acdH	acyl-CoA dehydrogenase
cds_wt_7954	-	propionyl-CoA carboxylase alpha chain
cds_wt_7955	-	putative acetyl/propionyl CoA carboxylase, beta subunit
cds_wt_7956	-	hypothetical protein
cds_wt_7957	dhaR	HTH-type transcriptional repressor dhaR;
cds_wt_7958	yqjF	Uncharacterized protein yqjF;
cds_wt_7959	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7960	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7961	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7962	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7963	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7964	iga	IgA-specific serine endopeptidase; IgA protease;
cds_wt_7965	katG	catalase
cds_wt_7966	-	Glycerol-3-phosphate dehydrogenase
cds_wt_7967	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7968	-	Putative disease resistance protein At4g10780;
cds_wt_7969	-	Probable disease resistance protein At1g61180;
cds_wt_7970	-	putative oxidoreductase
cds_wt_7971	ypeA	Acetyltransferase ECA0875;
cds_wt_7972	-	Mucin and cadherin-like protein; Mu-protocadherin; GP100;
cds_wt_7973	katE	catalase
cds_wt_7974	lig	DNA ligase
cds_wt_7975	-	Polycystic kidney disease protein 1-like 3; Polycystin-1L3; PC1-like 3 protein;
cds_wt_7976	-	Ubiquinone/menaquinone biosynthesis methyltransferase ubiE;
cds_wt_7977	rhaR	HTH-type transcriptional activator rhaS; L-rhamnose operon regulatory protein rhaS;
cds_wt_7978	livS	L-glutamine:2-deoxy-scylo-inosose aminotransferase; L-glutamine:DOI aminotransferase;

cds_wt_7979	gmd	UDP-glucose 4-epimerase
cds_wt_7980	-	hypothetical protein
cds_wt_7981	wbpD	putative acetyltransferase
cds_wt_7982	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_7983	wbiA	Putative peptidoglycan O-acetyltransferase yrhL;
cds_wt_7984	-	Uncharacterized MFS-type transporter MJ1317;
cds_wt_7985	wecE	pleiotropic regulatory protein
		putative pyruvate dehydrogenase E1 component,
cds_wt_7986	pdhA	alpha subunit
cds_wt_7987	acoB	putative pyruvate dehydrogenase E1 beta subunit
		Bifunctional protein glmU; Includes: UDP-N-
		acetylglucosamine pyrophosphorylase; N-
		acetylglucosamine-1-phosphate uridyltransferase;
		Includes: Glucosamine-1-phosphate N-
cds_wt_7988	cysE	acetyltransferase;
cds_wt_7989	lip	hypothetical protein
cds_wt_7990	mbtH	Protein mbtH;
		Tyrosidine synthetase 3; Tyrosidine synthetase III;
		Includes: ATP-dependent asparagine adenylase;
		AsnA; Asparagine activase; Includes: ATP-
		dependent glutamine adenylase; GlnA; Glutamine
		activase; Includes: ATP-dependent tyrosine
		adenylase; TyrA; Tyrosine activase; Includes: ATP-
		dependent valine adenylase; ValA; Valine activase;
		Includes: ATP-dependent ornithine adenylase; OrnA;
		Ornithine activase; Includes: ATP-dependent leucine
		adenylase; LeuA; Leucine activase;
cds_wt_7991	tycC	amino acid adenylation
cds_wt_7992	dhbF	putative non-ribosomal peptide synthetase
cds_wt_7993	dhbF	permease, putative
cds_wt_7994	-	glycosyl transferase, family 2
cds_wt_7995	pssF	Protein piccolo; Aczonin;
cds_wt_7996	-	Polypeptide N-acetylgalactosaminyltransferase 5; pp-
		GaNTase 5; Protein-UDP
		acetylgalactosaminyltransferase 5; UDP-
		GalNAc; polypeptide N-
cds_wt_7997	-	acetylgalactosaminyltransferase 5;
cds_wt_7998	wzxC	Lipopolysaccharide biosynthesis protein wzxC;
cds_wt_7999	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_8000	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_8001	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_8002	-	glycosyltransferase
cds_wt_8003	yxkH	Putative polysaccharide deacetylase yxkH;
cds_wt_8004	-	hypothetical protein
		Uncharacterized HTH-type transcriptional regulator
cds_wt_8005	lrp	ybaO;
cds_wt_8006	-	hypothetical protein predicted by Glimmer/Critica

		Polypeptide N-acetylgalactosaminyltransferase 6; Polypeptide GalNAc transferase 6; pp-GaNTase 6; GalNAc-T6; Protein-UDP acetylgalactosaminyltransferase 6; UDP- GalNAc:polypeptide N- acetylgalactosaminyltransferase 6;
cds_wt_8007	wbbL	hypothetical protein
cds_wt_8008	-	UDP-glucose 6-dehydrogenase
cds_wt_8009	udgA	sugar transferase
cds_wt_8010	rfbP	dTDP-4-dehydrorhamnose 3,5-epimerase
cds_wt_8011	rmlC	dTDP-glucose 4,6-dehydratase
cds_wt_8012	spsJ	dTDP-4-dehydrorhamnose reductase
cds_wt_8013	rfbD	hypothetical protein predicted by Glimmer/Critica
cds_wt_8014	-	Prestalk A differentiation protein A;
cds_wt_8015	-	acetyltransferase, GNAT family
cds_wt_8016	cysE	serine/threonine kinase with two-component sensor domain
cds_wt_8017	hstK	hypothetical protein predicted by Glimmer/Critica
cds_wt_8018	-	hypothetical protein predicted by Glimmer/Critica
cds_wt_8019	-	Multiple sugar-binding periplasmic receptor chvE;
cds_wt_8020	chvE	Methyl-accepting chemotaxis protein mcpB; H3;
cds_wt_8021	-	hypothetical protein
cds_wt_8022	-	Chaperone protein dnaK; Heat shock protein 70; Heat shock 70 kDa protein; HSP70;
cds_wt_8023	-	LexA repressor;
cds_wt_8024	-	Tetracycline resistance protein, class H; TetA
cds_wt_8025	tetA	resolvase
cds_wt_8026	rsd	

FIGURES

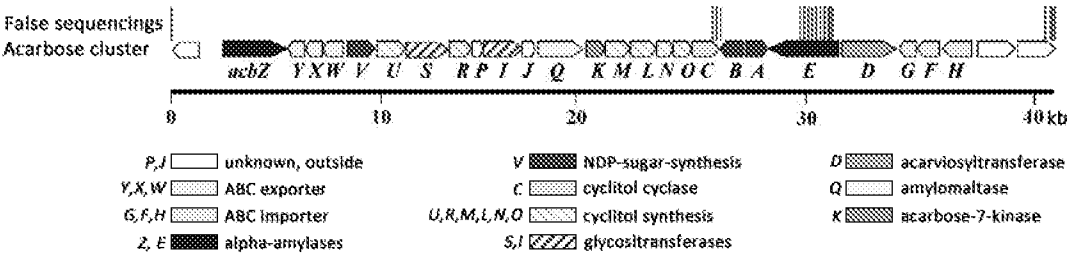


Figure 1

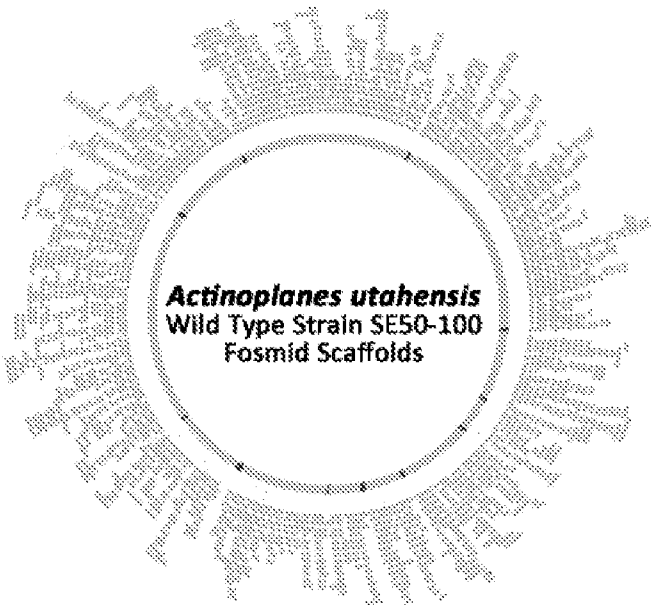


Figure 2

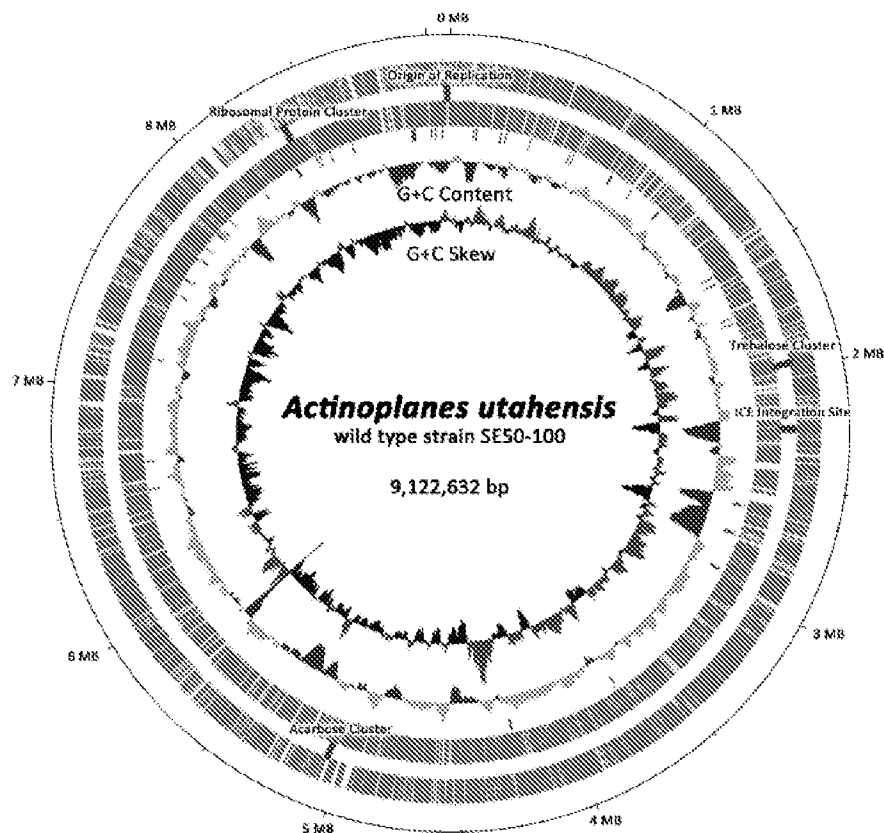


Figure 3

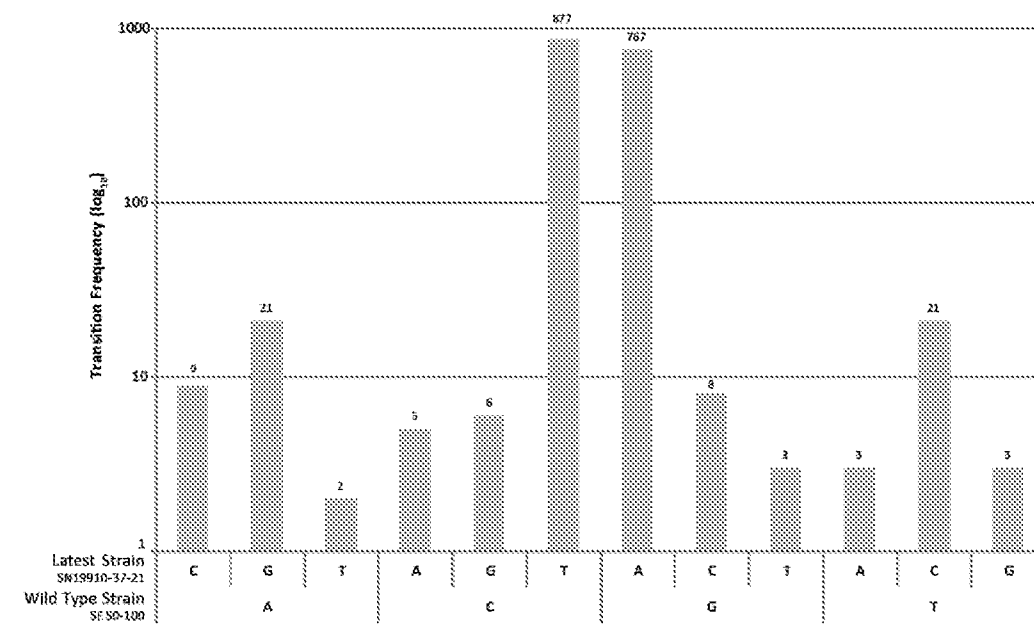


Figure 4

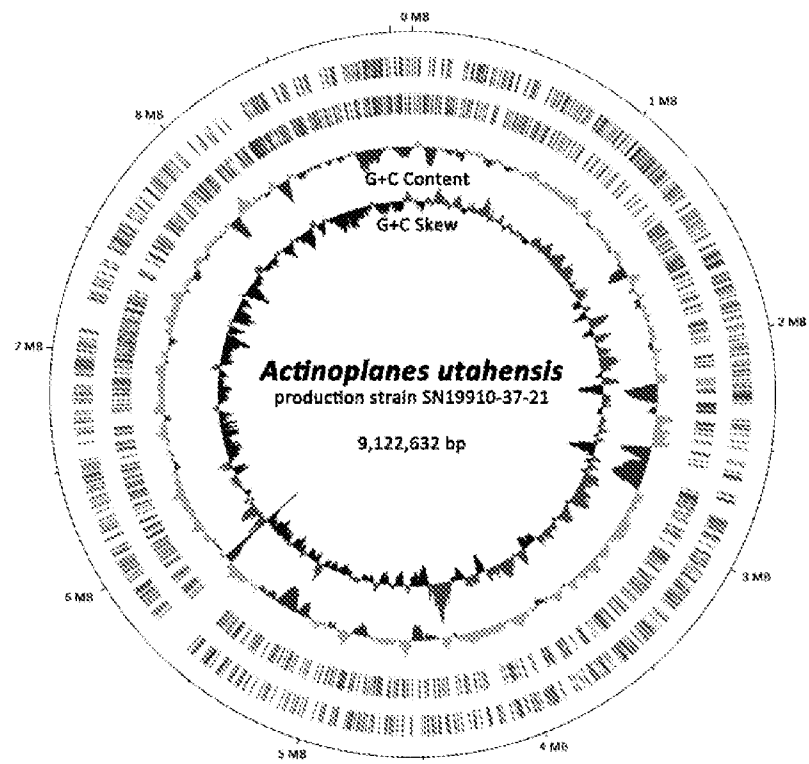


Figure 5

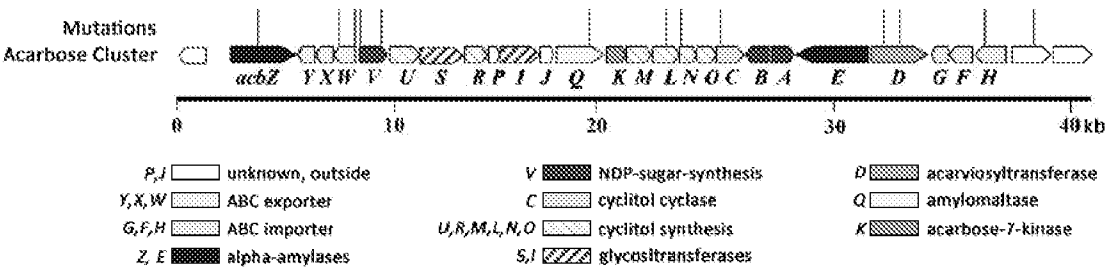


Figure 6

INTERNATIONAL SEARCH REPORT

International application No
PCT/EP2011/063243

A. CLASSIFICATION OF SUBJECT MATTER

INV. C07K14/365 C12N15/11 C12P19/26
ADD.

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

C07K C12N C12P

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EPO-Internal, BIOSIS, Sequence Search, WPI Data

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	DE 100 21 667 A1 (BAYER AG [DE]) 8 November 2001 (2001-11-08) page 2, lines 1-2 claims 1-9 sequences 1-57	1-3
X	DE 197 08 127 A1 (BAYER AG [DE]) 3 September 1998 (1998-09-03) abstract page 2, paragraph 1 claims 1-2 ----- -/-	1-3



Further documents are listed in the continuation of Box C.



See patent family annex.

* Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

Date of the actual completion of the international search

5 October 2011

Date of mailing of the international search report

30/11/2011

Name and mailing address of the ISA/

European Patent Office, P.B. 5818 Patentlaan 2
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Authorized officer

Herrmann, Klaus

INTERNATIONAL SEARCH REPORT

International application No

PCT/EP2011/063243

C(Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	HYUN CHANG-GU ET AL: "Molecular detection of alpha-glucosidase inhibitor-producing actinomycetes", JOURNAL OF MICROBIOLOGY, vol. 43, no. 3, June 2005 (2005-06), pages 313-318, XP002660585, ISSN: 1225-8873 figure 3 table 1 -----	1-3

INTERNATIONAL SEARCH REPORT

International application No.
PCT/EP2011/063243

Box No. II Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box No. III Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fees, this Authority did not invite payment of additional fees.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

1-3(partially)

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest and, where applicable, the payment of a protest fee.
- ☐ The additional search fees were accompanied by the applicant's protest but the applicable protest fee was not paid within the time limit specified in the invitation.
- ☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. claims: 1-3(partially)

A DNA having essentially the sequence of SEQ ID 16053 or fragments thereof characterized in that it contains at least the mutation G7102A (first mutation depicted in table 9), and subject-matter relating thereto.

2-2622. claims: 1-3(partially)

Idem as subject 1 but limited to each of the individual mutations listed in table 9. Invention 2 is limited to mutation G11919A etc. The present application is directed to numerous mutations in numerous (potential) genes (see Tables 9 and 11). If the Applicant intends to pay further search fees he is asked to exactly define the nucleotide sequence/mutation for which a search is to be carried out (Attention is drawn to Art. 19(2), 5 and 6 PCT).

INTERNATIONAL SEARCH REPORT

Information on patent family members

International application No

PCT/EP2011/063243

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
DE 10021667	A1	08-11-2001	NONE
DE 19708127	A1	03-09-1998	AU 6296898 A 18-09-1998
		BG 103672 A 31-05-2000	
		BR 9807640 A 21-03-2000	
		CA 2282735 A1 03-09-1998	
		CN 1249001 A 29-03-2000	
		CZ 9903054 A3 17-11-1999	
		WO 9838313 A1 03-09-1998	
		EP 0968294 A1 05-01-2000	
		HU 0000889 A2 28-07-2000	
		NO 994164 A 27-08-1999	
		PL 335369 A1 25-04-2000	
		ZA 9801659 A 10-09-1998	