Defence Research and Development Canada
Recherche et développement pour la défense Canada

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The genome of *Bacillus cereus* 14579: a local analysis

B.J. Berger
Defence R&D Canada – Suffield

Technical Memorandum
DRDC Suffield TM 2003-114
October 2003

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Author

Dr Bradley J. Berger

Approved by

A/H/CBDS for

Dr Jacques Lavigne

HCBDS

Approved for release by

Dr Robin G. Clewley

DRP Chair

Abstract

Due to its close genetic and biochemical identity to *Bacillus anthracis*, *B. cereus* can be used as a lower risk pathogen in order to model anthrax biochemistry. The recent sequencing of the *B. cereus* 14579 genome has assisted in this process. This report presents the results of a locally performed analysis and annotation of the *B. cereus* 14579 genome. 4885 putative open reading frames were detected, with 2946 of these identified through homology searching. These identified gene products were then used for metabolic reconstruction of the organism, with an emphasis on potential enzymes involved in regenerating methionine from methylthioadenosine. The present results demonstrate the ease and utility of local genome analysis as a tool for assisting in research studies at DRDC Suffield.

Résumé

L'identité génétique et biochimique du *Bacillus anthracis* étant proche de celle du *B. cereus,* ce dernier peut être utilisé comme pathogène de risque faible et servir de modèle en biochimie du charbon. Le récent séquençage du génome 14579 du *B. cereus* a rendu cette démarche possible. Ce rapport présente les résultats des analyses effectuées localement et des annotations du génome 14579 du *B. cereus*. 4885 cadres ouverts de lecture putatifs ont été détectés et 2946 de ces derniers ont été identifiés par une recherche d'homologie. Ces produits génétiques identifiés ont ensuite été utilisés pour la reconstruction métabolique de l'organisme, axée sur les enzymes potentiels qui interviennent pour régénérer la méthionine à partir de la méthylthioadénosine. Les résultats présents indiquent que les analyses génomiques locales sont un outil facile et utile pour appuyer les projets de recherche au RDDC Suffield.

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Executive summary

One of the most powerful recent advances in the biological sciences is the availability of incomplete and complete genome sequences for organisms relevent to individual researchers. For organisms relevent to biological defence research, complete genomes are already known for *Bacillus anthracis* (anthrax), *Yersinia pestis* (plague), *Brucella melitenisis* and *Brucella suis* (brucellosis), *Coxiella burnetii* (Q fever), *Mycobacterium tuberculosis* (tuberculosis), and *Plasmodium falciparum* (malaria). The other biological threat agents of interest, such as *Francisella tularensis* (tularemia) and *Burkholderia mallei* (glanders), have incomplete, on-going genome projects underway. The data from all these projects is available to researchers at DRDC Suffield and is being employed in both detection and countermeasures research.

One of the weaknesses of the standard approach to dealing with genomic data is the willingness of individual researchers to completely accept the genome annotation generated by the sequencing laboratory without any local analysis. In general, most researchers only exhaustively and critically examine potential gene products directly relevent to their particular studies, without a similar analysis of larger metabolic issues. As most sequencing laboratories do not actually work on the organisms being sequenced, sequencing and annotation errors often remain uncorrected. Some organisms, such as *Bacillus subtilis*, *Mycobacterium tuberculosis*, and *Plasmodium falciparum* have communities of researchers integrating the results of their local genome analyses into a more robust annotated genome. The vast majority of genomes are not so well served.

Bacillus cereus and *B. anthracis* are almost completely identical at the genome sequence level, allowing *B. cereus* to be used as a lower risk model for many questions relating to anthrax biochemistry. In this laboratory, for example, *B. cereus* is used as a surrogate model for characterising enzymes which might serve as antimicrobial targets in anthrax. In this report, the DNA sequence of *B. cereus* 14579 made available by Integrated Genomics is subjected to an analysis of the putative gene products and resulting metabolic reconstruction. The results clearly show the ease with which both incomplete and complete genome sequences can be analysed for local laboratory use, and provides a complete bench resource which complements the genomic analysis performed by the sequencing institution.

Berger, B. J. 2003. The genome of *Bacillus cereus* 14579: a local analysis. DRDC Suffield TM2003-114. Defence R&D Canada – Suffield.

Sommaire

Un des plus importants progrès récents en sciences biologiques est que les chercheurs ont chacun à leur disposition des séquences génomiques complètes et incomplètes d'organismes. En ce qui concerne les organismes qui intéressent la recherche pour la défense biologique, les génomes complets sont déjà connus pour *Bacillus anthracis* (le charbon), *Yersinia pestis* (la peste), *Brucella melitenisis* et *Brucella suis* (la brucellose), *Coxiella burnetii* (la fièvre Q), *Mycobacterium tuberculosis* (la tuberculose), et *Plasmodium falciparum* (la malaria). Des projets de profilage de génome ont été entrepris et sont encore incomplets pour d'autres agents comportant un risque biologique tels que *Francisella tularensis* (tularémie) et *Burkholderia mallei* (morve). Les données provenant de ces projets ont été mises à la disposition des chercheurs au RDDC Suffield et sont employées pour la recherche dans le domaine de la détection et celui des contre-mesures.

Une des faiblesses de la démarche standard à propos des données génomiques est le manque de volonté de chaque chercheur à accepter complètement l'annotation génomique générée par le laboratoire de séquençage, dans d'autres analyses au niveau local. En général, la plupart des chercheurs examinent des produits génétiques ayant le potentiel de relever directement de leurs études particulières, mais ceci seulement de manière exhaustive et éclairée, sans effectuer d'analyses similaires pour les problèmes plus importants liés au métabolisme. Comme la plupart des laboratoires de séquençage ne travaillent actuellement pas sur les organismes qui sont mis en séquences, les erreurs de séquençage et d'annotation ne sont souvent pas corrigées. Pour certains organismes tels que *Bacillus subtilis*, *Mycobacterium tuberculosis* et *Plasmodium falciparum*, une collectivité de chercheurs intègre les résultats des analyses effectuées localement, ce qui produit une annotation génomique plus robuste. Mais une grande majorité de génomes ne sont pas aussi bien traités.

Bacillus cereus et *B. anthracis* sont presque complètement identiques au niveau de la séquence génomique et ceci permet d'utiliser le *B. cereus* comme modèle comportant un risque plus faible pour beaucoup de questions liées à la biochimie du charbon. Dans ce laboratoire, par exemple, *B. cereus* est utilisé comme modèle de substitution pour la caractérisation des enzymes pouvant servir de cibles antimicrobiennes dans le charbon. Dans ce rapport, on soumet la séquence ADN du *B. cereus*14579, rendue disponible par integrated Genomics, à des analyses de produits génétiques putatifs et de reconstruction métabolique qui en résulte. Les résultats montrent clairement la facilité avec laquelle les séquences génomiques à la fois complètes et incomplètes peuvent être analysées par les laboratoires locaux, fournissant ainsi une ressource de travail complète qui complémente les analyses génomiques effectuées par les institutions de séquençage.

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Acknowledgements

Genomic data for *Bacillus cereus* 14579 was made available by Integrated Genomics (Chicago, IL, USA), and was funded by DARPA. Genomic data for *Bacillus anthracis* Ames and for *B. anthracis* Florida A2012 was made available by The Institute for Genomic Research (Rockville, MD, USA), and was funded by DARPA.

This work was funded in part by a Defence R&D Canada Technology Investment Fund award.

Introduction

The recent revolution in genomic analysis of microorganisms has led to an exponential increase in the amount of information available to researchers interested in microbial proteins and biochemical pathways. Optimal exploitation of this information requires that a researcher should be capable of analysing, interpreting, and annotating incomplete and complete genomic data relating to the particular organism(s) of interest in that laboratory. While the sequencing laboratory is, almost always, interested in publishing their own account of the annotation of a given genome, user-generated annotations provide a useful counterpoint for comparison and also allow for a focus on biochemical processes of particular local interest. This report represents an example of such an analysis on both incomplete and complete genomic information available for a model organism of considerable local utility.

Bacillus cereus is an opportunistic, gram-positive, sporulating bacterial pathogen that is a common cause of food poisoning, and also a source of serious ocular infections. In addition, *B. cereus* is known to be almost identical to *B. anthracis* and *B. thuringiensis*, and the three organisms are now widely viewed as a single species which differ in plasmid content [1]. *B. cereus* contains no large circular plasmids, while *B. anthracis* carries the 182 kbp pXO1, which encodes the three toxin genes, and the 93 kbp pXO2, which encodes the genes for the poly-glutamate capsule [2]. *B. thuringiensis* carries the 128 kbp pBtoxis, which encodes the insecticidal crystalline toxins [3]. The chromosomal DNA of *B. cereus* and *B. anthracis* have been judged as 92-99% identical by DNA hybridization and sequence analysis of selected genes [1,4]. One of the few key differences in chromosomal DNA between the two species is the transcriptional regulator gene *plcR*, which is intact in *B. cereus* but contains a single base frame shift in *B. anthracis* [5]. PlcR appears to upregulate a large set of genes in *B. cereus*, particularly those relating to the expression of phospholipases and cold-shock response [6,7]. Therefore, the lack of functional PlcR in *B. anthracis* explains the lack of lecithinase activity and the inability of the organism to grow well at lower temperatures. Recent studies have implicated incompatability between PlcR and pXO2 as the driving force behind the maintainance of *plcR* inactivation in *B. anthracis* [8]. However, aside from *plcR*, there are few obvious differences between *B. cereus* and *B. anthracis* uncovered to date.

B. anthracis is one of the central concerns of the Canadian Forces in the area of biological weapon defence. The ease of growth and dissemination, and very long persistance of this organism make it highly attractive to both sophisticated governmental and small-scale terrorist biological weapon development and utilisation. Numerous governments are known to have weaponised anthrax, and there remains an untested scientific report of the generation of vaccine-resistant genetically-modified anthrax [9]. In addition, the recent dissemination of anthrax-laced letters and subsequent deaths of several people, have highlighted the effectiveness of a small amount of anthrax to create mortality and wide-spread panic. One of the key aims of Defence R&D Canada, and other biodefence organisations, is to develop new antibacterial compounds effective against anthrax in order to counter natural or engineered resistance to established antibacterial agents.

In order to uncover new classes of antimicrobials, it is necessary to examine both known and novel targets in the organism. As the chromosomal gene content of *B. anthracis* and *B. cereus* are essentially identical as known to date, it is possible to utilise *B. cereus* as a lower-pathogenicity model system for *B. anthracis* enzymology and metabolism. In this manner, studies involving larger amounts of biomass can be done more safely, and time pressures on over-burdened biohazard level 3 suites can be eased. New enzyme targets can be defined in *B. cereus*, and any effective inhibitors can then be verified in small-scale *B. anthracis* drug-inhibition assays. The most important aid for the discovery, cloning, expression, and characterisation of novel enzyme targets is the presence of chromosomal DNA sequence information for the organism of interest. For *B. anthracis*, there has been a recent publication and general release of the complete genome for *B. anthracis* Florida isolate A2012 [10], and there is also a complete genome sequence available from The Institute for Genome Research for *B. anthracis* Ames (www.tigr.org). These genomes are identical, as outlined in Read et al. [10]. For *B. cereus*, Integrated Genomics made a public release of an incomplete, gapped genome for the type strain 14579 in 2001 (www.integratedgenomics.com). Recently, the same company has allowed access to a completed version of the same genome via their website. At the time, it was unclear how long this information would remain in the public domain, as this company has previously made unavailable large amounts of genome information once openly accessible via their web server. As it turned out, as soon as the analyses presented below were completed, Integrated Genomics published their annotation of the *B. cereus* 14579 genome [11], and The Institute for Genomic Research published a similar study on the genome of *B. anthracis* Ames [12]. A short discussion comparing the present analysis with the published information has therefore been appended.

The presence of completed genome sequences for both *B. cereus* and *B. anthracis* provides a unique opportunity for the use of model systems to solve key problems in biodefence research. Similar approaches may one day be available for *Yersinia pseudotuberculosis*/*Y. pestis* and *Ochrobactrum intermedium*/*Brucella melitensis*, which also have similarly close chromosomal DNA relationships [13,14]. The purpose of this memorandum is to provide a laboratory reference to the genome of *B. cereus* 14579, with an emphasis on the potential gene products and on the relationship to the *B. anthracis* Ames genome. In addition, the present analysis will provide a useful comparative counterpart to any potential publication by Integrated Genomics. Having multiple sources of genome annotation will then strengthen individual gene identifications and highlight ambiguous conclusions. This report is intended to act as a bench reference for this laboratory and other research work at Defence R&D Canada, and also presents an example of the type of complete genome analysis easily performed from available data.

Materials and Methods

The 2001 gapped genome data release and 2003 complete genome data release for *B. cereus* 14579 were obtained from Integrated Genomics (www.integratedgenomics.com). The sequencing was performed by Integrated Genomics and was funded by DARPA. The 2002 complete genome data release for *B. anthracis* Florida A2012 [10], and the complete *B. anthracis* Ames genome data was obtained from TIGR (www.tigr.org). The anthrax genomes were sequenced by TIGR and was funded by DARPA. The 2000 complete genome data release for *B. halodurans* C-125 was obtained from the Japan Marine and Science Technology Centre (www.jamstec.go.jp), and was sequenced by that organisation with funding from the Japanese government [15]. The 1997 complete genome data release for *B. subtilis* 168 was obtained from the Pasteur Institute (www.pasteur.fr/Bio/SubtiList.html). The *B. subtilis* genome was sequenced by a European and Japanese academic consortium with funding by the European Commission [16].

The *B. cereus* 14579 gapped genome contigs were ordered and aligned to the complete *B. anthracis* Ames genome using the NUCmer component of MUMmer 2.1 (The Institute for Genomic Research; Rockville, MD, USA) [17,18]. The initial base identity length was set to 50 nucleotides, a maximum gap length of 90 nucleotides, and extension was performed with an identity threshold of 70%. The gaps and overlaps in the alignments were manually examined and the resulting contig map visualised using Sigmaplot 8.0 (SPSS; Chicago, IL, USA).

The complete *B. cereus* 14579 genome was directly compared individually with the complete *B. anthracis* Ames, *B. halodurans* C-125, and *B. subtilis* 168 genomes using the MUMmer and PROmer components of MUMmer 2.1. For DNA-DNA comparisons, MUMmer was used with a threshold of 25 nucleotides for an exact match length. For protein-protein comparisons, PROmer was used with an initial complete identity match length of 5 amino acids, a maximal gap length of 30 amino acids, and an identity threshold of 35%. The resulting matches were plotted using Sigmaplot.

Gene finding within the complete *B. cereus* 14579 genome data was performed using Glimmer 2.02 (The Institute for Genomic Research) [19], and full training on the subject data set. The resulting putative open reading frames were searched against the Swissprot and Genbank non-redundant databases (www.ncbi.nlm.nih.gov) run locally using the blastfasta perl module (The Institute for Genomic Research) (REF) and both stand-alone BLAST (www.ncbi.nlm.nih.gov) and stand-alone WU-BLAST (www.wustl.edu) [20]. The resulting BLAST matches for each open reading frame were then manually examined to confirm identity and eliminate spurious open reading frames. Ribosomal RNA sequences were detected by BLAST homology searching of the *B. cereus* genome data using *B. subtilis* 168 rDNA sequences. Putative tRNA genes were detected in the *B. cereus* 14579 genome data by the tRNAscanSE program [21]. Metabolic reconstruction was then performed by manually examining the genome annotation for the presence of enzymes as defined for particular metabolic steps by the KEGG metabolic database (www.genome.ad.jp/kegg) [22]. Metabolic steps in a given pathway set with no obvious *B. cereus* homolog were manually removed from pathway map image files downloaded from KEGG.

Results and Discussion

Ordering of Contigs in Gapped Data Release

For several years, an incomplete, gapped genome data set has been available for *B. cereus* 14579 via Integrated Genomics. The existence and availability of this dataset was a key factor in the decision by this laboratory to use *B. cereus* 14579 as the metabolic surrogate model for *B. anthracis*. By replacing *B. subtilis* 168 with *B. cereus* 14579, a much closer and more relevent model of anthrax metabolism can be studied outside of biohazard level 3 containment. Indeed, with the exception of plasmid content, *B. cereus* and *B. anthracis* are almost identical [1].

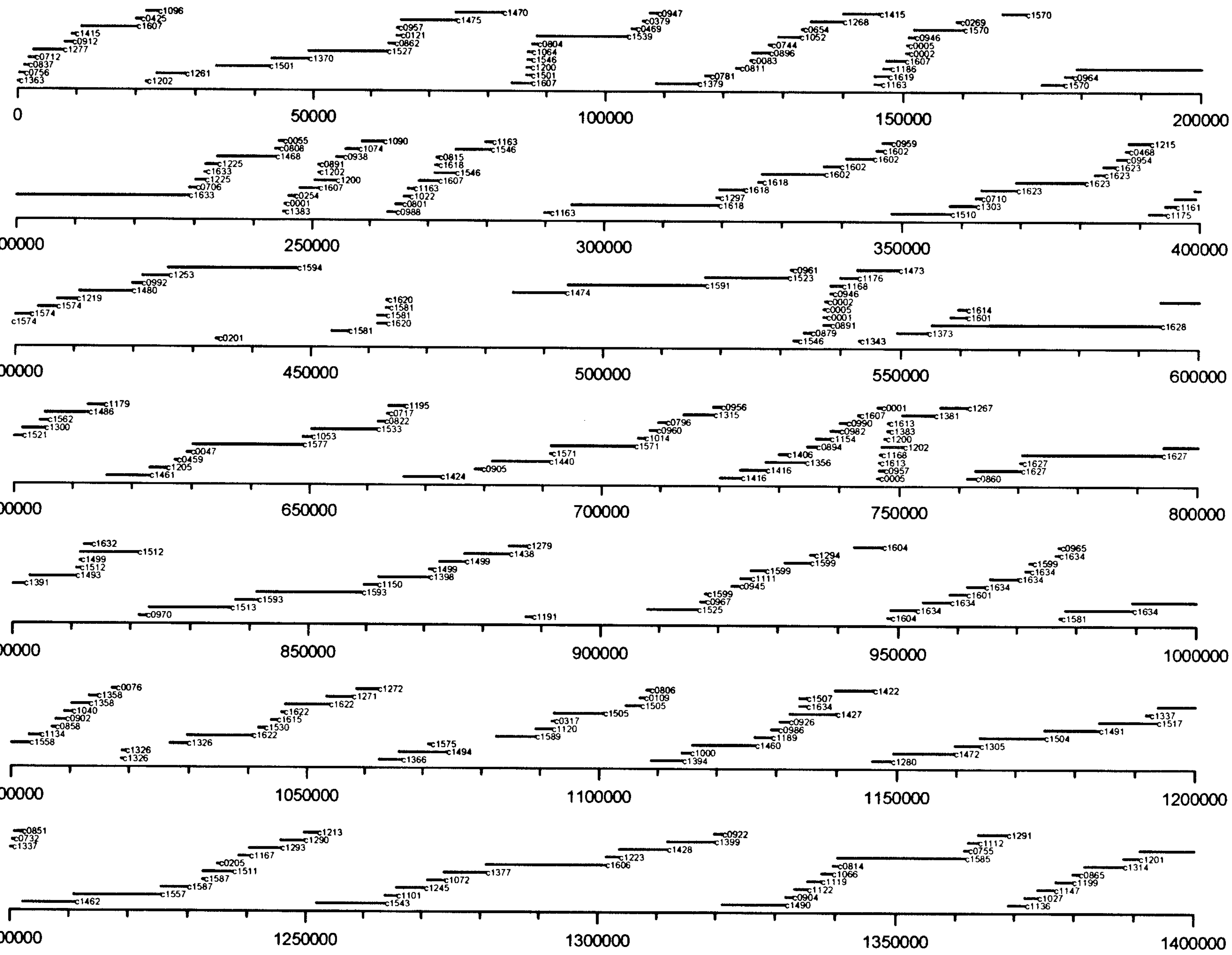
Unfortunately, the existence of the *B. cereus* genome data in incomplete, unordered form created difficulties in certain aspects of experimentation. In a recent study on *Bacillus spp.* aminotransferases [23], we found that a key branched-chain amino acid aminotransferase of interest was only present as 5' and 3' portions of two different DNA contigs, with the intervening sequence missing. In such a case, there is no guarantee that the two end sequences actually belong to the same enzyme. It is necessary to perform PCR using primers to the end sequences and hope for a successful PCR reaction. Ordering of the *B. cereus* DNA contigs would allow one to determine if the end sequences were on adjacent contigs, the approximate size of the missing intervening sequence, and thus allow for more confident troubleshooting of the PCR reaction.

In another study on *B. cereus* spore proteins [24], the N-terminal amino acids of numerous spore proteins were determined and used to search the *B. cereus* genome data for identification. In many cases, the N-terminus of the target sequence was not present in the gapped genome data, forcing us to use the more recent *B. anthracis* Ames and Florida A2012 genome data to identify the protein. In addition, many *B. cereus* proteins which did have N-terminal sequence present were lacking the C-terminal sequence, complicating calculation of the theoretical size and pI of the target protein. Again, in the absence of a complete *B. cereus* genome sequence, an ordering of the existing contigs would allow for an estimate of the size of the missing information.

The recent release of the *B. anthracis* Ames genome sequence provided a full length sequence from an extremely closely related organism to act as a scaffold to order the *B. cereus* 14579 contigs. Using the NUCmer program, the 1528 *B. cereus* contigs were ordered into 1269 matches (Figure 1). Numerous contigs overlapped and several contigs did not have a high-enough homology to the *B. anthracis* sequence to enter the assembly. The match length which exceeded 70% identity ranged from 77 to 49751 nucleotides in length, with an average match size of 3556.58 ± 127.33 nucleotides (mean ± standard error, n = 1269). Togethor all 1269 matches covered 4513302 nucleotides. The gaps between the matches ranged from 0 to 39008 nucleotides, with an average gap length of 1334.73 ± 113.50 nucleotides (mean ± standard error, n = 831). The total gap length amounted to 1109160 nucleotides. The overlap between matches ranged from 0 to 3817 nucleotides, and averaged 273.71 ± 22.78 nucleotides (mean ± standard error, n = 441). The total overlap amongst the matches amounted to 120706 nucleotides. The complete match and gap value (minus overlaps) amounted to 5501756, which compared well with the value of 5227297 for the complete *B. anthracis* genome (minus plasmids) [10].

As a simple test of the ordering of the contigs, the placement of the contigs containing the ends of the *B. cereus* 14579 branched-chain amino acid aminotransferase 2 was examined. Our previous work found the 5' of the sequence on contig 1066 and the 3' on contig 0814. In the ordered contigs, contig 1066 does indeed immediately precede contig 0814. The intervening gap is 182 nucleotides, which matches well with the value of 174 nucleotides actually found after PCR of the entire gene from *B. cereus* 14579 genomic DNA [23]. The difference of 8 nucleotides is due to the exact point at the end of the contig where NUCmer stopped the extension.

Figure 1 (next 4 pages). *Ordering of B. cereus genome contigs. The individual DNA contigs from the 2001 release of B. cereus 14579 genome data were aligned and ordered against the 2002 complete B. anthracis Ames genome data using the NUCmer program as described in the Material and Methods section. In the figure, the numbered axis reflects the B. anthracis genome and the red bars the B. cereus DNA contigs. The number after each bar (eg: c1606) refers to the contig number assigned by Integrated Genomics. Individual contigs may appear in multiple locations due to close identity to multicopy or high homology orthologues, or due to DNA rearrangements between B. cereus and B. anthracis. Gaps may appear in an individual contig due to localised drifting of the DNA sequence, or due to insertion, deletion, inversion, or transversion of DNA stretches.*


c1363
c0756
c0837
c0712
c1277
c0912
c1415
c1607
c0425
c1096
c1202
c1261
c1501
c1370
c1527
c0862
c0121
c0957
c1475
c1470
c1607
c1501
c1200
c1546
c1064
c0804
c1539
c0469
c0379
c0947
c1379
c0781
c0811
c0083
c0896
c0744
c1052
c0654
c1268
c1415
c1163
c1619
c1186
c1607
c0002
c0005
c0946
c1570
c0269
c1570
c0964
c1570
0
50000
100000
150000
200000
c1633
c0706
c1225
c1633
c1225
c1468
c0808
c0055
c1383
c0001
c0254
c1607
c1200
c1202
c0891
c0938
c1074
c1090
c0988
c0801
c1022
c1163
c1607
c1546
c1618
c0815
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c1163
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c1297
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c0959
c1510
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c0710
c1623
c1623
c1623
c1623
c0954
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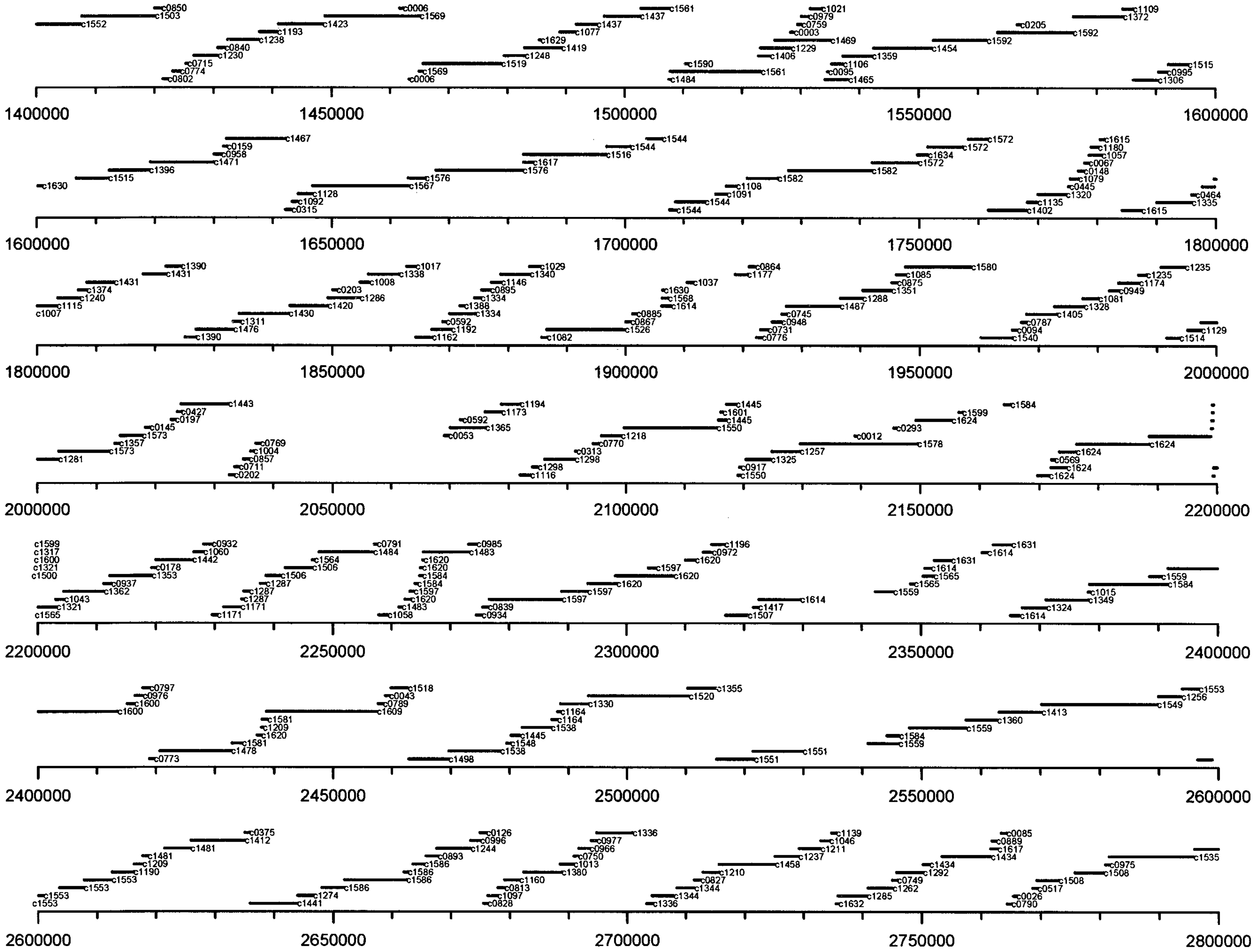
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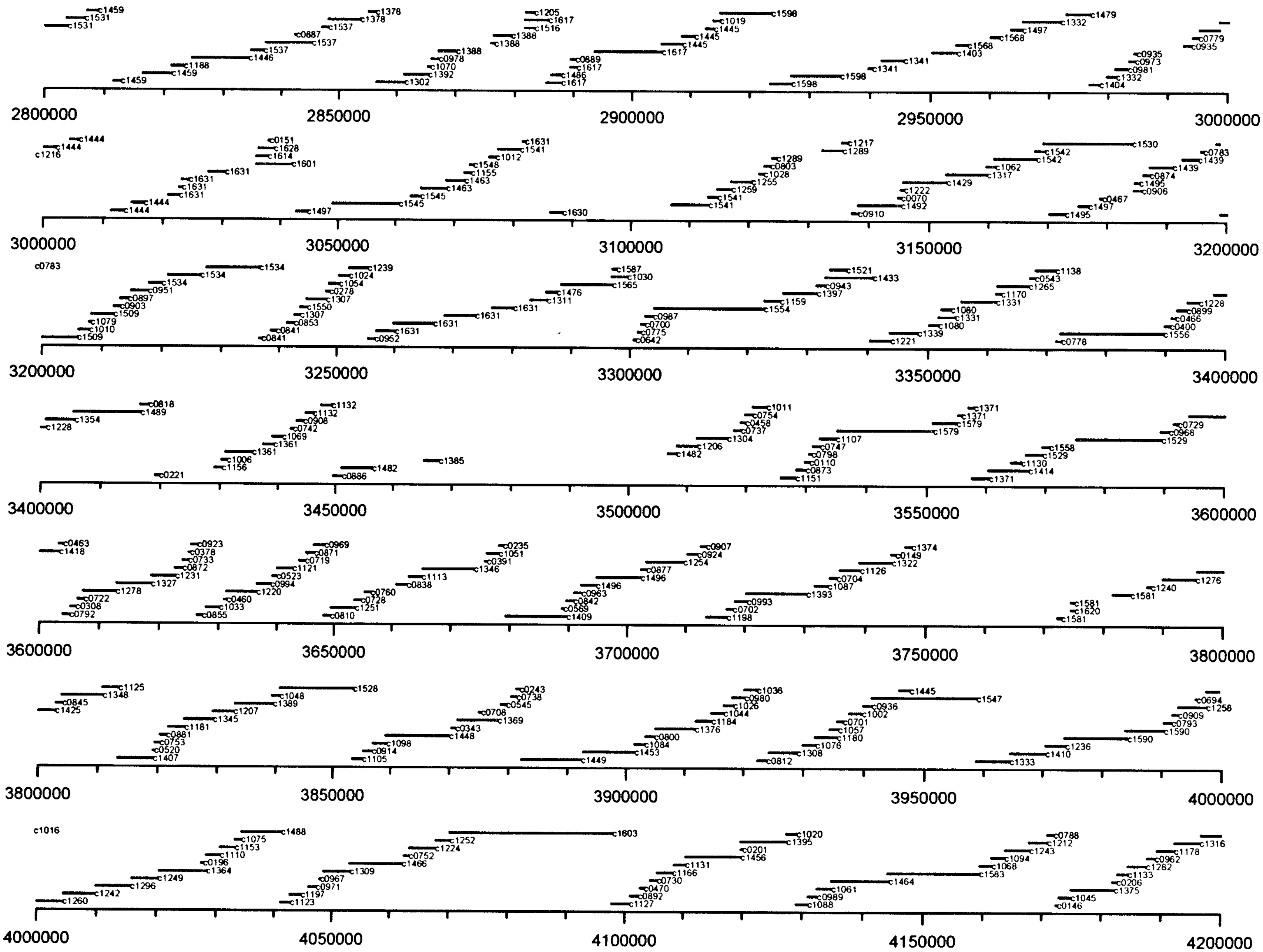

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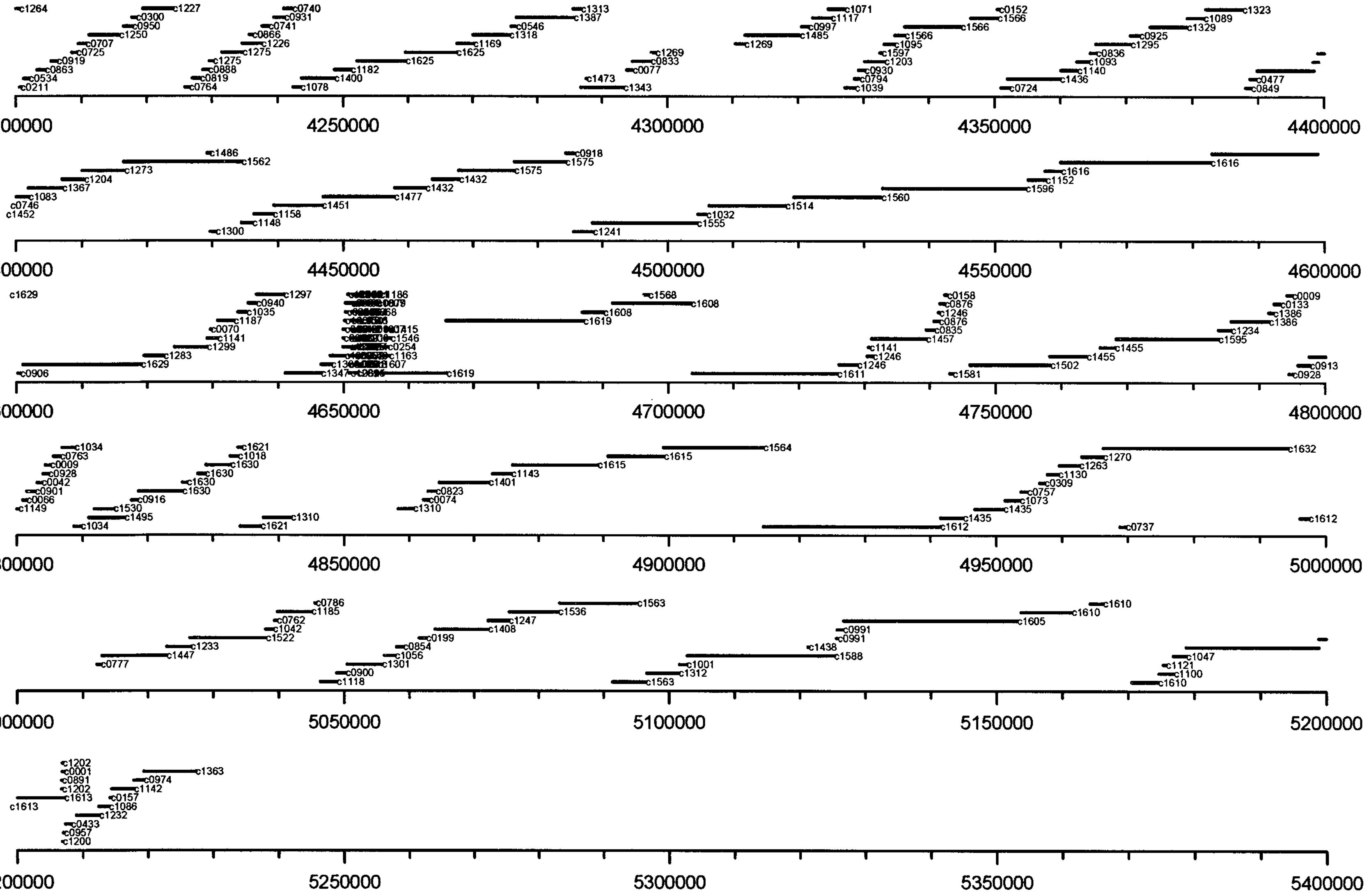
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Comparison of *B. cereus* Genome Structure With Other *Bacillus spp.*

Very recently, a completed genome sequence for *B. cereus* 14579 has been made available by Integrated Genomics. This data set will replace the gapped genome contigs ordered above, but the ordering is still of value in interpreting experiments previously performed using the gapped data. The *B. cereus* 14579 chromosome consists of a single circular molecule of 5411460 base pairs, which is very similar to *B. anthracis* Ames at 5227297 base pairs, and significantly longer than *B. subtilis* 168 (4214810 base pairs) [16] and *B. halodurans* C-125 (4202353 base pairs) [15]. The GC% of the *B. cereus* genome is 35.28%, which is nearly identical to *B. anthracis* Ames (35.38%) [10], but lower than *B. subtilis* 168 (43.5%) [16] and *B. halodurans* (43.7%) [15].

Whole genome alignment of *B. cereus* 14579 and *B. anthracis* Ames showed the expected near total conservation of primary sequence structure (Figure 2). There was a reasonable amount of background noise when the match threshold was 25 nucleotides, and this background could be significantly reduced by raising the match threshold to 50 nucleotides (data not shown). However, at this more stringent level, *B. subtilis* and *B. halodurans* (see below) yielded few matches. Therefore, for comparative purposes, the data from the 25 nucleotide threshold was used for *B. cereus and B. anthracis*. There are no obvious large insertions, deletions, or transversions between the two organisms, although there are several small gaps suggestive of insertion or deletion of genetic material. There were 43302 identical DNA stretches between *B. cereus* 14579 and *B. anthracis* Ames, with an average size of 48.72 ± 0.25 base pairs (mean ± standard error, n = 43302). The largest identical DNA match between the two organisms was 1981 base pairs, and there were 11983 matches exceeding 50 base pairs, 2405 exceeding 100 base pairs, and 87 exceeding 500 base pairs. The matches combined for 2109628 base pairs, which indicated that approximately 39% of the *B. cereus* genome is completely identical to the *B. anthracis* genome.

When the *B. cereus* and *B. anthracis* genomes were compared at amino acid level, there was an even more striking conservation of information (Figure 3). Out of 4855 putative open-reading frames matched and extended by PROmer, there was an overall amino acid sequence identity of 80.15 ± 0.18% (mean ± standard error). Of these 4855 matching sequences, 100 had an amino acid identity of 35-50%, 1262 had an identity of 50-75%, 2363 an identity of 75-90%, and 1130 an identity of 90-100%. In addition, examination of Figure 3 showed that there was an equal distribution of lower identity proteins across the genome.

When compared with *B. subtilis* 168, *B. cereus* shared a much lower identity at the nucleic acid level (Figure 4). There are only about five regions with significant identity between the two organisms, with one being in the opposite orientation and suggestive of a large transversion of genetic material. Using a 25 nucleotide match threshold, there were only 818 identical sequences between *B. cereus* 14579 and *B. subtilis* 168, with an average length of 47.87 ± 1.26 base pairs (mean ± standard error, n = 818). The longest identical stretch was 287 base pairs, with only 198 matches exceeding 50 base pairs and 56 exceeding 100 base pairs. The total identical sequence detected between the two organisms amounted to 39154 base pairs. It is clear that, despite the apparent close relationship between the *B. cereus* and *B. subtilis* complexes as judged by alignment of ribosomal DNA sequences [25], there is little immediate identity between the chromosomes of these organisms.

When examining conservation of protein sequences encoded by the genomes, *B. cereus* 14579 and *B. subtilis* 168 maintain a fairly high degree of relatedness (Figure 5). PROmer was able to detect and extend 2691 sequences which exceeded 35% amino acid identity, with an overall identity of 65.15 ± 11.10% (mean ± standard error, n = 2691). Of the 2702 sequences, 179 had an identity of 35-50%, 2037 an identity of 50-75%, 430 an identity of 75-90%, and 45 an identity exceeding 90%. Therefore, while there is little direct relationship bewteen the two organisms at the DNA level, there is a striking conservation of encoded protein sequence (and, presumably, function).

B. halodurans C-125 is an alkaliphilic organism that is distantly related to the *B. cereus* and *B. subtilis* complexes when alignments are constructed using ribosomal DNA sequences [25]. Alignment of the entire genomes for the two organisms showed a pattern very similar to the *B. cereus – B. subtilis* alignment (Figure 6), with only a few regions of sequence identity. Interestingly, *B. halodurans* does not share with *B. cereus* the region of transverse identity seen in *B. subtilis*. Using a 25 nucleotide match threshold, there were only 620 matches between *B. cereus* 14579 and *B. halodurans* C-125, with an average length of 44.59 ± 0.95 (mean ± standard error, n = 620). The longest identical DNA sequence was 204 base pairs in length, with only 175 matches exceeding 50 base pairs and 23 exceeding 100 base pairs. The total identical sequence between the two organisms amounted to 27647 base pairs. On the DNA level, one would get the impression that *B. halodurans* is not much more distantly related to *B. cereus* than *B. subtilis*.

At the protein sequence level, the picture is similar to that seen with *B. subtilis* (Figure 7). PROmer detected and extended 3122 sequences which exceeded 35% amino acid identity, with an overall identity of 65.16 ± 0.18% (mean ± standard error, n = 3122). Of these sequences, 173 had an identity of 35-50%, 2461 and identity of 50-75%, 431 an identity of 75-90%, and 57 an identity exceeding 90%. Again, at the protein level, *B. halodurans* is not much more distantly related to *B. cereus* than *B. subtilis*.

The lack of a closer relationship between *B. cereus* 14579 and *B. subtilis* 168 at both the DNA and protein level than is seen with *B. halodurans* is an intriguing result. When one examines a single molecule such as ribosomal DNA ,which has very strong evolutionary selective pressures against mutation [25], *B. subtilis* is considerably more closely related to *B. cereus*. However, the exact relationship between two microorganisms is highly dependent on the target molecule chosen for examination. Our own study on branched-chain amino acid aminotransferases has also shown an equivalent distance between *B. cereus* and *B. subtilis/B. halodurans* when examining enzymes that catalyse methionine regeneration [23]. The

PROmer results discussed here would seem to support a generalisation of our finding on branched-chain amino acid aminotransferases. These homology results clearly highlight the important conclusion that *B. cereus* is, by far, the most appropriate model for *B. anthracis* metabolism and physiology modelling. Indeed, the possibility that the *B. subtilis* complex is more distantly related to the *B. cereus* complex than originally thought calls into question the use of *B. globigii* (*B. atrophaeous*) as a field simulant for *B. anthracis* studies. While *B. cereus* remains too pathogenic to use in open field trials, certain strains of *B. thuringiensis* (as another member of the *B. cereus* complex) would certainly be more biologically and biochemically relevent than *B. globigii.*

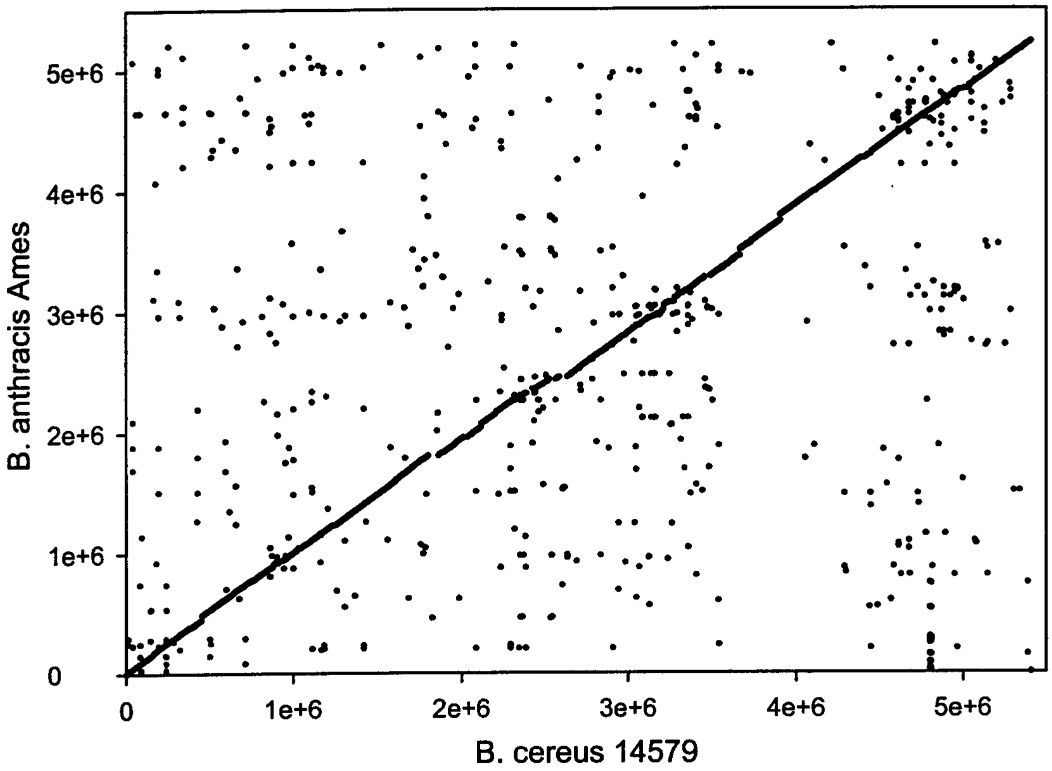

Figure 2. *Whole genome alignment of B. cereus 14579 and B. anthracis Ames. The complete genomes for both organisms were aligned using the MUMmer 2.1 program as described in the Materials and Methods section. Each data point represents a stretch of identical base pairs, regardless of length, mapped to the location in each organism (as shown on the axis by the distance, in nucleotides, from the origin of replication for the chromosome).*

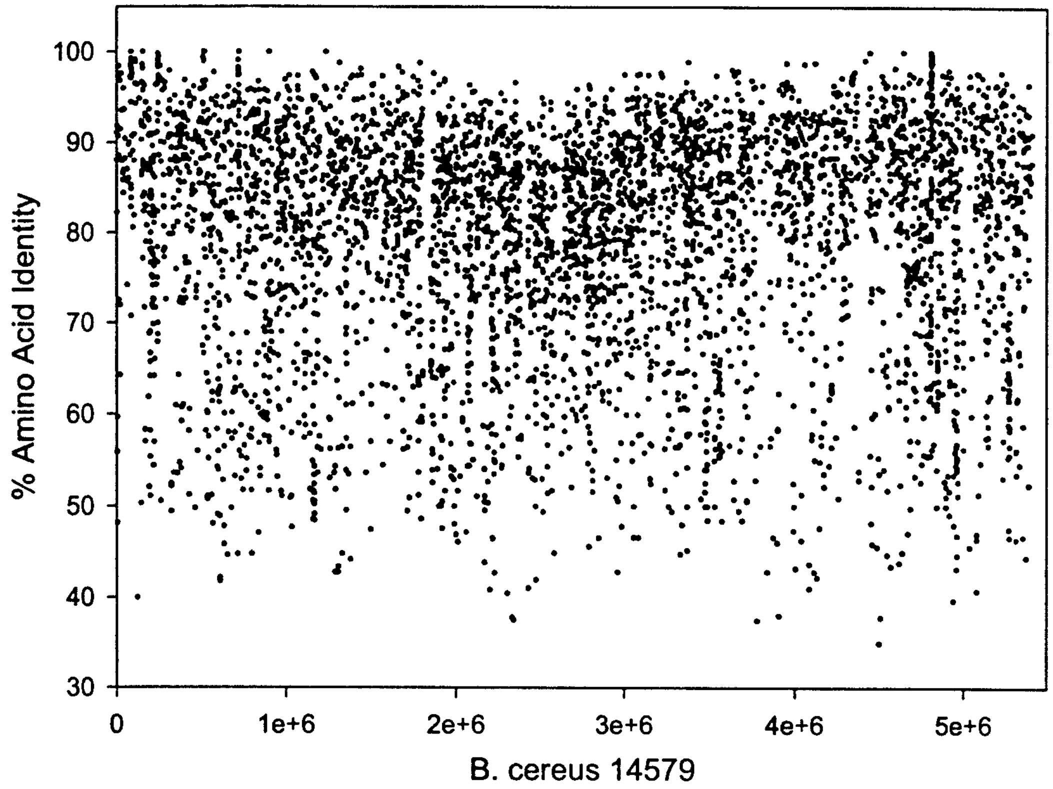

***Figure 3**. Identity of B. cereus 14579 and B. anthracis Ames at the amino acid level. The complete six-frame translations for both organisms were aligned using the PROmer program as described in the Materials and Methods section. Each data point represents a putative open reading frame in B. cereus 14579 that has a match in B. anthracis Ames with an amino acid identity exceeding 35%. Each match is mapped to the location on the B. cereus chromosome, as shown on the X-axis as nucleotide distance from the origin of replication. The Y-axis show the overall amino acid identity for each match.*

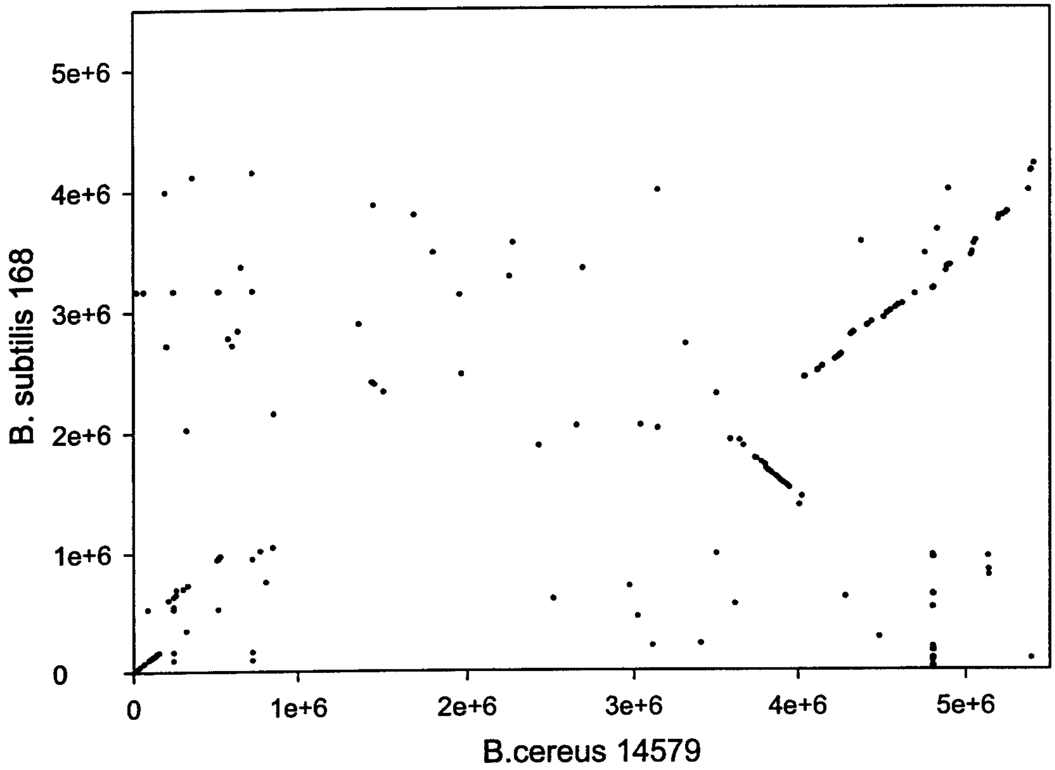

Figure 4. *Whole genome alignment of B. cereus 14579 and B. subtilis 168. The complete genomes for both organisms were aligned using the MUMmer 2.1 program as described in the Materials and Methods section. Each data point represents a stretch of identical base pairs, regardless of length, mapped to the location in each organism (as shown on the axis by the distance, in nucleotides, from the origin of replication for the chromosome).*

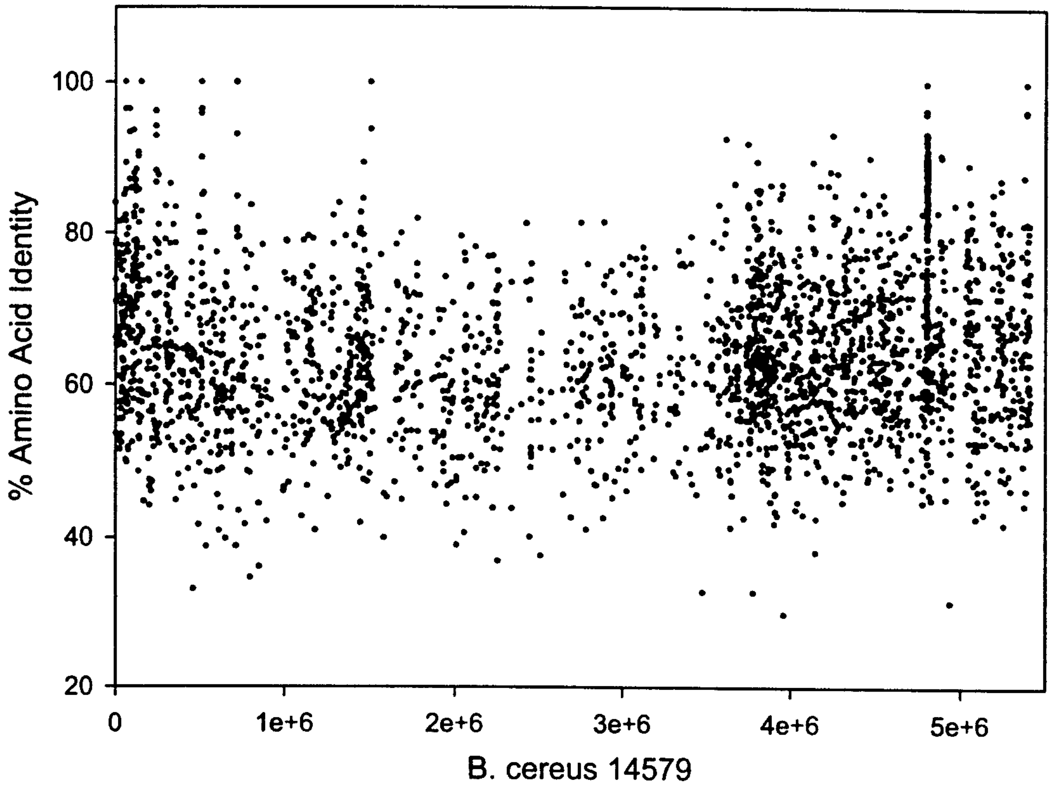

Figure 5. *Identity of B. cereus 14579 and B. subtilis 168 at the amino acid level. The complete six-frame translations for both organisms were aligned using the PROmer program as described in the Materials and Methods section. Each data point represents a putative open reading frame in B. cereus 14579 that has a match in B. subtilis 168 with an amino acid identity exceeding 35%. Each match is mapped to the location on the B. cereus chromosome, as shown on the X-axis as nucleotide distance from the origin of replication. The Y-axis show the overall amino acid identity for each match.*

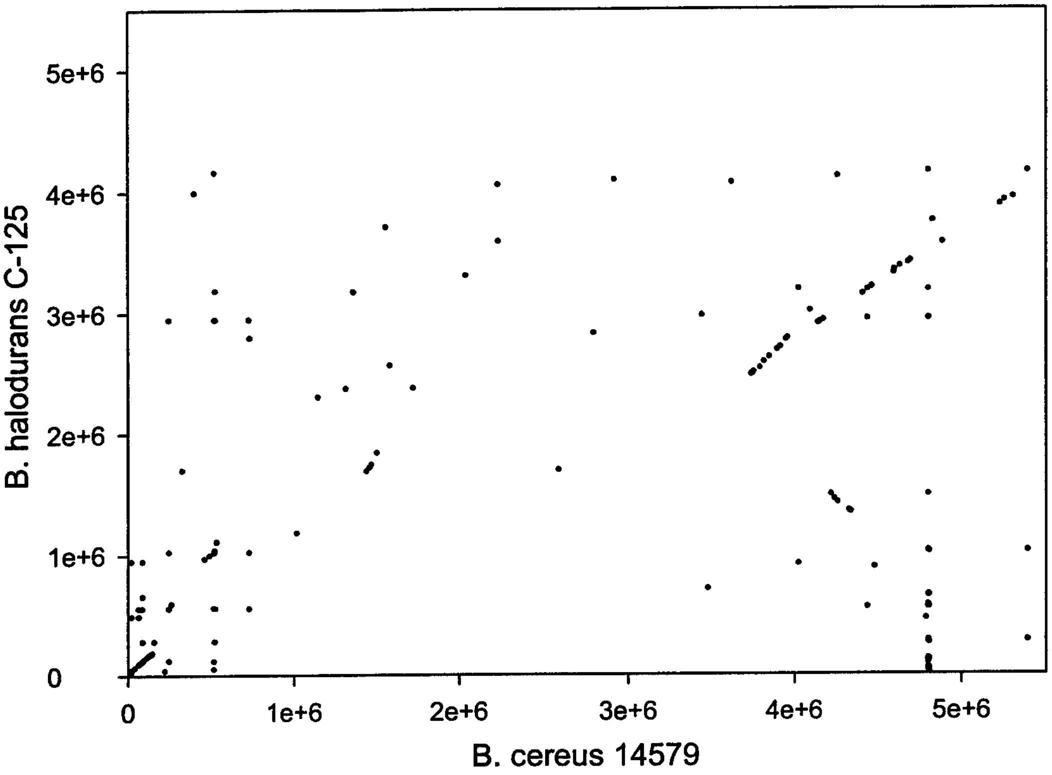

Figure 6. *Whole genome alignment of B. cereus 14579 and B. halodurans C-125. The complete genomes for both organisms were aligned using the MUMmer 2.1 program as described in the Materials and Methods section. Each data point represents a stretch of identical base pairs, regardless of length, mapped to the location in each organism (as shown on the axis by the distance, in nucleotides, from the origin of replication for the chromosome).*

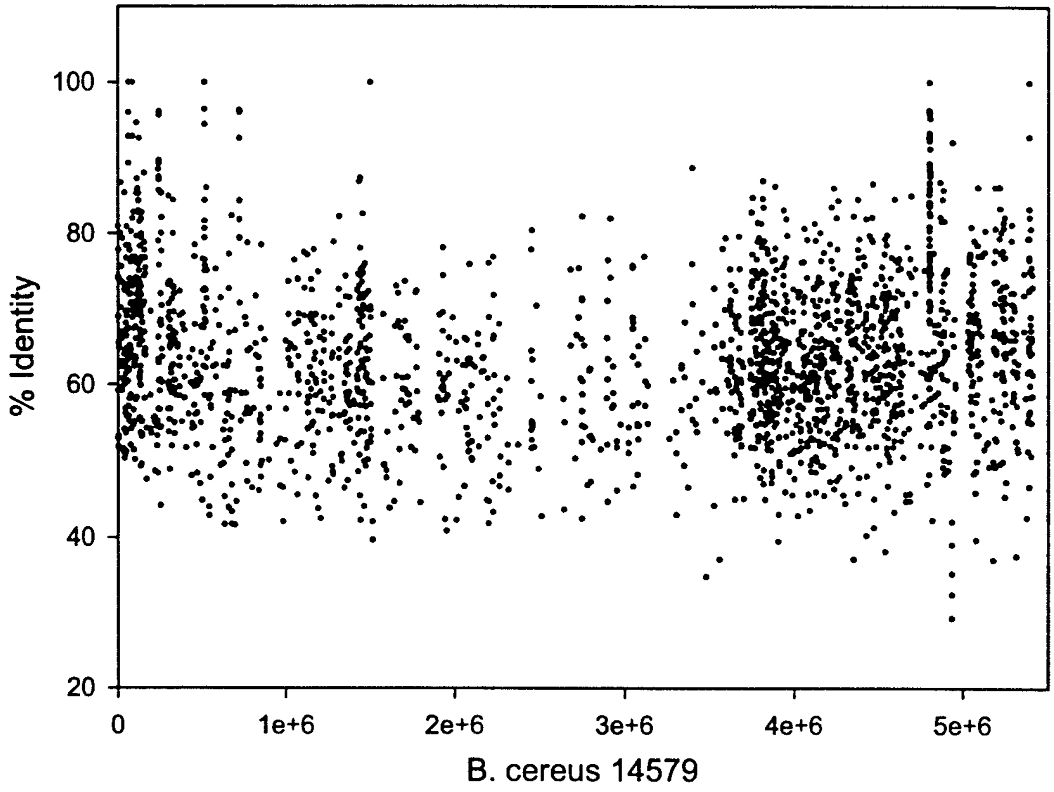

Figure 7. *Identity of B. cereus 14579 and B. halodurans C-125 at the amino acid level. The complete six-frame translations for both organisms were aligned using the PROmer program as described in the Materials and Methods section. Each data point represents a putative open reading frame in B. cereus 14579 that has a match in B. halodurans C-125 with an amino acid identity exceeding 35%. Each match is mapped to the location on the B. cereus chromosome, as shown on the X-axis as nucleotide distance from the origin of replication. The Y-axis show the overall amino acid identity for each match.*

Predicted Gene Products in *B. cereus*

B. cereus 14579 was found to contain 13 rRNA gene clusters (Table 1), with all in the orientation 16S-23S-5S. This number of rRNAs compares with 10 sets for *B. subtilis*, 8 sets for *B. halodurans*, and 11 sets for *B. anthracis* A2012 [10,15,16]. Using the tRNAscan-SE program, 108 tRNAs were found in *B. cereus* 14579 (Table 2), located primarily in seven clusters. In comparison, *B. subtilis* 168 was found to contain 86 tRNA genes, *B. halodurans* C-125 78, and *B. anthracis* A2012 95 [10,15,16].

The *B. cereus* 14579 genome was subjected to open-reading frame analysis by the Glimmer program, and the resulting putative open-reading frames subjected to BLAST analysis against both the Swiss-Prot protein database and the Genbank non-redundant DNA database. The resulting identifications and alignments were manually examined using a conservative cutoff of $E>1^{10}$ as the threshold for a positive match. Using this criterion, 4885 putative protein-encoding genes were identified. Of these, 1940 (39.7%) matched to other hypothetical proteins with no known function. The remaining 2946 genes encoded proteins with a high homology to known proteins or protein families. All 4885 putative protein-encoding genes are shown in Table 3, which is also available as a searchable Excel file. As expected, most *B. cereus* open-reading frames had a high identity match with proteins from *B. anthracis* Florida A2012 [10]. However, the existing annotation for this *B. anthracis* strain is a lower detail, gene family level documentation. Therefore, the existence of published genome data for a very closely related organism to *B. cereus* 14579 provided less assistance than would normally be expected. Most high quality, solid gene identifications for *B. cereus* tended to be due to matches with annotated genes from *B. subtilis* 168 and *B. halodurans* C-250.

Within the genome of *B. cereus* 14579 were found 8 regions where the predicted gene products had significant homology with phage proteins (at positions 929487, 1248750, 1417854, 2361679, 2530170, 2542990, 3674717, 4676013). These regions are likely to represent integrated prophages in the *B. cereus* genome. In addition, there were 14 predicted gene products with high homology to transposase (at positions 588975, 1499343, 1781379, 2291385, 2459772, 2575694, 2587573, 2623493, 2784887, 3140548, 3262997, 4728620, 5076164, 5093457). This number is likely representative of the number of insertion elements, and other transposons, present in the *B. cereus* genome. As a comparison, *B. subtilis* 168 was predicted to contain 27 prophages and10 transposons, while *B. halodurans* was predicted to contain 2 prophages and 112 transposons [15,16].

The genome was found to contain 64 genes encoding ribosomal proteins (35 for 50S and 20 for 30S components), and 39 tRNA synthetase genes. In addition, a large number (245) of transcriptional regulators were uncovered, with 12 LysR, 9 ArsR, 11 MarR, 18 GntR, 6 AraC, 24 TetR, 7 MerR, 1 MocR, 6 DeoR, 2 IclR, and 1 PlcR regulators found. This latter transcriptional regulator has been found to be central to the regulation of a number of *B. cereus* virulence factors and toxins [6]. The presence of only one clear PlcR regulator suggests that regulation of PlcR targets is tightly controlled. *B. cereus* was also found to contain 61 genes encoding two-component signal transduction proteins and 132 genes encoding ABC transporter components. Therefore, the organism has a large number of processes for interacting with its environment.

The genome was found to contain only one copy each of cereolysin A, cereolysin B, and cereolysin O. In addition, five other proteins with high homology to enterotoxins and cytotoxins were discovered. The genome also contained a single cephalosporinase and five proteins with high homology to tetracycline resistance proteins. The organism also contained the operon for the synthesis of bacitracin/gramicidin, along with the associated bacitracin resistance genes.

Even though the overall structure of the *B. cereus* and *B. subtilis* genomes is quite disimilar (see above), it was interesting to note that a number of putative *B. subtilis* operons consisting primarily of hypothetical proteins are replicated in the *B. cereus* genome. Examples of this conservation are yheA-D, yjcD-H, ylmC-F, ylaH-O, ylbJ-N, ykuJ-R, yvcI-L, and ykrS-Z. Clearly, the function of these gene products is important enough to the bacterium to remain conserved, and deserve closer examination of their biochemical and physiological function.

Of the gene products currently of interest in this laboratory, *B. cereus* was found to contain 24 putative aminotransferase sequences. Amongst these sequences were two branched-chain amino acid aminotransferases and two D-amino acid aminotransferases, as found previously [23]. One of these branched-chain aminotransferases is responsible for the last step of methionine regeneration from methylthioadenosine [23]. As was found in *B. subtilis* [23], there were six putative aspartate aminotransferases in the *B. cereus* genome, all of which were found to be members of the If subfamily of aminotransferases. However, not all of the putative aspartate aminotransferases were directly homologous to particular *B. subtilis* enzymes. In addition, two N-acetylornithine aminotransferases and one ornithine aminotransferase were discovered. These enzymes normally play a role in the availability of ornithine for polyamine biosynthesis, as well as the production and degradation of proline. As the *B. cereus* genome was found to contain no ornithine decarboxylase, but instead contained arginine decarboxylase, the ornithine and N-acetylornithine aminotransferases likely only function in proline metabolism.

The enzymes involved or implicated in the methylthioadenosine pathway were highly conserved with those previously identified in *B. subtilis* [26,27]. Table 4 summarizes the gene products and their locations in both *B. cereus* 14579 and *B. subtilis* 168. Both organisms appear to have all the enzymes required for the methylthioadenosine cycle [23]. The ykrS – ykrZ genes, which have been implicated in silico and by gene deletion to be involved in methylthioadenosine salvage [26,27], are very similarly organised in *B. cereus* (Figure 8). Therefore, conservation of function is likely, and these genes should be further examined for functional activity in both *B. cereus* and *B. anthracis*.

***Table 1**. The ribosomal RNA genes of B. cereus 14579. All rRNA genes were identified by homology searching of the B. cereus 14579 genome data using the BLAST program [20] and the B. subtilis rRNA genes [16].*

16S		23S		5S	
Start	Stop	Start	Stop	Start	Stop
9187	10741	14032	12882	14099	14197
28928	30482	32610	32079	33840	33938
82215	83769	86834	85684	86953	87042
87923	89477	92542	91392	92608	92706
151137	152691	155756	154606	155865	155954
245178	246732	249796	248646	249863	249961
265743	267297	270362	269212	270429	270527
273016	274570	277635	276485	277702	277800
286313	287867	290932	289782	290998	291096
293420	294974	298039	296889	298105	298203
510017	511571	514635	513485	514753	514842
718440	719994	723058	721908	723178	723267
4808648	4807094	4805742	4806951	4803911	4803822

***Table 2**. The tRNA genes of B. cereus 14579. The putative tRNA encoding genes were identified by the tRNAscan-SE program [21].*

tRNA		tRNA	Anti	tRNA		tRNA	Anti	tRNA		tRNA	Anti
Start	Stop	Type	Codon	Start	Stop	Type	Codon	Start	Stop	Type	Codon
10870	10946	Ile	GAT	245032	245102	Gly	TCC	724860	724936	Ile	GAT
10955	11030	Ala	TGC	249974	250050	Met	CAT	724945	725019	Asn	GTT
21647	21739	Ser	TGA	250054	250129	Asp	GTC	725021	725092	Glu	TTC
30611	30687	Ile	GAT	514860	514934	Asn	GTT	2422653	2422723	Pseudo	CCA
30696	30771	Ala	TGC	514937	515028	Ser	GGA	5391433	5391358	Lys	TTT
64189	64262	Met	CAT	515046	515120	Glu	TTC	5391344	5391273	Glu	TTC
64276	64347	Glu	TTC	515125	515200	Val	TAC	5391250	5391175	Asp	GTC
87057	87132	Val	TAC	515227	515303	Met	CAT	5391133	5391061	Phe	GAA
87137	87212	Thr	TGT	515307	515382	Asp	GTC	5046768	5046690	Arg	CCG
87226	87301	Lys	TTT	515392	515467	Phe	GAA	4803808	4803733	Val	TAC
87315	87395	Leu	TAG	515486	515561	Thr	TGT	4803728	4803653	Thr	TGT
87425	87499	Gly	GCC	515572	515655	Tyr	GTA	4803643	4803568	His	GTG
87516	87604	Leu	TAA	515663	515736	Trp	CCA	4803545	4803465	Leu	TAG
87608	87681	Arg	ACG	515756	515831	His	GTG	4803435	4803361	Gly	GCC
87690	87763	Pro	TGG	515895	515969	Gln	TTG	4803344	4803256	Leu	TAA
87773	87848	Ala	TGC	515975	516049	Gly	GCC	4803252	4803179	Arg	ACG
155973	156047	Asn	GTT	516064	516134	Cys	GCA	4803168	4803095	Pro	TGG
156052	156124	Thr	GGT	516145	516229	Leu	CAA	4803079	4803007	Ala	TGC
156149	156223	Glu	TTC	520659	520732	Gly	TCC	4802986	4802910	Met	CAT
156229	156304	Val	TAC	723282	723357	Val	TAC	4802905	4802829	Met	CAT
156322	156405	Tyr	GTA	723366	723449	Tyr	GTA	4802811	4802719	Ser	TGA
156471	156545	Gln	TTG	723461	723535	Gln	TTG	4802691	4802615	Met	CAT
156551	156626	Lys	TTT	723540	723615	Lys	TTT	4802611	4802536	Asp	GTC
156632	156703	Gly	GCC	723630	723710	Leu	TAG	4802523	4802448	Phe	GAA
156714	156786	Ala	TGC	723740	723814	Gly	GCC	4802433	4802358	Thr	TGT
243925	243999	Asn	GTT	723831	723919	Leu	TAA	4802347	4802272	Lys	TTT
244003	244093	Ser	GCT	723923	723996	Arg	ACG	4802258	4802188	Gly	TCC
244102	244176	Glu	TTC	724007	724080	Pro	TGG	4802177	4802101	Ile	GAT
244181	244256	Val	TAC	724097	724169	Ala	TGC	4802093	4802019	Asn	GTT
244282	244358	Met	CAT	724190	724282	Ser	TGA	4802011	4801921	Ser	GCT
244362	244437	Asp	GTC	724338	724430	Ser	TGA	4801915	4801844	Glu	TTC
244525	244599	Gln	TTG	724451	724527	Met	CAT	4438504	4438431	Gly	TCC
244605	244677	Lys	TTT	724531	724606	Asp	GTC	4438429	4438353	Arg	TCT
244694	244779	Leu	GAG	724615	724690	Phe	GAA	4220245	4220172	Met	CAT
244873	244949	Arg	ACG	724700	724775	Thr	TGT	1251020	1250948	Val	GAC
244954	245030	Pro	TGG	724779	724849	Trp	CCA	1236366	1236294	Val	GAC

Table 3. *The protein-coding genes of the B. cereus 14579 chromosome. Putative open reading frames were detected, checked, and annotated as described in the Materials and Methods section. Where gene identity can be conclusively determined, common gene labels are used. Gene labels beginning with "y" (such as "ykrV") denote a significant match to a hypothetical or putative protein encoding gene from B. subtilis 168. Gene labels beginning with "x" or "z" (such as "xxaD") are hypothetical or putative protein encoding genes with significant homology to only B. anthracis Florida A2012, or homology to no other known organisms. Gaps in the gene numbers are indicative of sequences removed by Glimmer during the gene-finding process or via manual curation.*

Gene No.	Start	End	Frame and Length	Label / Identification
1	281	1618	[+2 L=1338]	dnaA / Chromosomal replication initiator protein
2	1800	2942	[+3 L=1143]	dnaN / DNA polymerase III, beta chain
3	3298	3735	[+1 L= 438]	recF / DNA replication and repair protein
4	4458	6392	[+3 L=1935]	gyrB / DNA topoisomerase subunit B
5	6472	8943	[+1 L=2472]	gyrA / DNA topoisomerase subunit A
7	11580	11152	[-1 L= 429]	zzzA / Hypothetical protein
8	15233	14235	[-3 L= 999]	yaaC / Hypothetical protein
9	15349	16809	[+1 L=1461]	imdH / Inosine-5'-monophosphate dehydrogenase (IMP dehydrogenase)
11	16902	18230	[+3 L=1329]	dacA / D-alanyl-D-alanine carboxypeptidase precursor (penicillin-binding protein 5)
12	18388	19278	[+1 L= 891]	yaaD / Superoxide-inducible protein 7
13	19300	19887	[+1 L= 588]	yaaE / amidotransferase
14	20218	21489	[+1 L=1272]	sys / Seryl-tRNA synthetase (Serine--tRNA ligase)
15	21747	22295	[+3 L= 549]	zzzB / Hypothetical protein
16	22531	22337	[-2 L= 195]	yaaF / deoxypurine kinase subunit
17	23002	22616	[-2 L= 387]	yaaF / deoxypurine kinase subunit
18	23658	23008	[-1 L= 651]	yaaG / deoxypurine kinase subunit
19	24305	23769	[-3 L= 537]	yaaI / Isochorismatase
20	24415	24912	[+1 L= 498]	yaaJ / Cytidine and deoxycytidylate deaminase
21	25392	27077	[+3 L=1686]	dnaX / DNA polymerase III subunit gamma/tau
22	27103	27429	[+1 L= 327]	yaaK / Hypothetical protein
23	27447	28040	[+3 L= 594]	recR / Recombination protein
24	28058	28276	[+2 L= 219]	yaaL / Hypothetical protein
26	28441	28707	[+1 L= 267]	bofA / Sigma-K factor processing regulatory protein
28	34129	34305	[+1 L= 177]	csfB / sigma-F transcribed protein
29	34380	35798	[+3 L=1419]	yaaO / lysine decarboxylase
30	35803	36426	[+1 L= 624]	kthY / Thymidylate kinase (dTMP kinase)
31	36465	37445	[+3 L= 981]	holB / DNA polymerase III, delta' subunit
32	37445	38278	[+2 L= 834]	yaaT / signal peptidase-like protein
33	38281	38643	[+1 L= 363]	yabA / Hypothetical protein
34	38729	39466	[+2 L= 738]	yabB / Hypothetical protein
35	39456	39743	[+3 L= 288]	yazA / Hypothetical protein
36	39715	40587	[+1 L= 873]	yabC / Hypothetical protein
37	40991	40614	[-3 L= 378]	abrB / Transition state regulatory protein
38	41354	43360	[+2 L=2007]	sym / Methionyl-tRNA synthetase (Methionine--tRNA ligase)
39	43530	44294	[+3 L= 765]	yabD / Putative deoxyribonuclease
40	44494	45066	[+1 L= 573]	yabF / Hypothetical protein
41	45066	45941	[+3 L= 876]	ksgA / Dimethyladenosine transferase (16S rRNA dimethylase)
42	46055	46915	[+2 L= 861]	yabG / Hypothetical protein
44	47145	47402	[+3 L= 258]	veg / Veg protein
45	47497	47673	[+1 L= 177]	sspF / Small, acid-soluble spore proteins, alpha/beta type
46	47864	48739	[+2 L= 876]	ispE / 4-diphosphocytidyl-2-C-methyl-D-erythritol kinase (CMK)
47	48797	49642	[+2 L= 846]	purR / Pur operon repressor
48	49757	50137	[+2 L= 381]	yabJ / Putative regulator of purine biosynthesis
49	50239	50583	[+1 L= 345]	spoG / Stage V sporulation protein G
50	50882	52276	[+2 L=1395]	gcaD / UDP-N-acetylglucosamine pyrophosphorylase (N-acetylglucosamine-1-phosphate uridyltransferase)
51	52298	53248	[+2 L= 951]	kprS / Ribose-phosphate pyrophosphokinase (PRPP synthetase)
52	53252	53881	[+2 L= 630]	spoC / Peptidyl-tRNA hydrolase (PTH) (Stage V sporulation protein c)
53	53955	54176	[+3 L= 222]	yabK / Hypothetical protein
54	54255	57812	[+3 L=3558]	mfd / Transcription-repair coupling factor (TRCF)
55	57952	58485	[+1 L= 534]	spoT / Stage V sporulation protein T
56	58719	60317	[+3 L=1599]	yabM / Hypothetical protein

57	60333	61790	[+3 L=1458]	yabN / Hypothetical protein
58	61763	62080	[+2 L= 318]	yabO / Hypothetical protein
59	62142	62447	[+3 L= 306]	yabP / Hypothetical protein
60	62447	63097	[+2 L= 651]	yabQ / Hypothetical protein
61	63097	63453	[+1 L= 357]	divC / cell division initiation protein
62	63544	64026	[+1 L= 483]	yabR / polyribonucleotide nucleotidyltransferase
63	64607	67075	[+2 L=2469]	spoE / Stage II sporulation protein E, serine phosphatase
64	67297	68736	[+1 L=1440]	yacA / cell-cycle protein
65	68736	69275	[+3 L= 540]	hprT / Hypoxanthine-guanine phosphoribosyltransferase (HGPRTase)
66	69364	71262	[+1 L=1899]	ftsH / Cell division protein and general stress protein
67	71510	72295	[+2 L= 786]	yacB / Hypothetical protein
68	72305	73177	[+2 L= 873]	hslO / 33 kDa chaperonin (Heat shock protein 33 homolog) (HSP33)
69	73276	74214	[+1 L= 939]	cysK / Cysteine synthase (O-acetylserine sulfhydrylase)
70	74440	75834	[+1 L=1395]	pabB / Para-aminobenzoate synthase component I (ADC synthase)
71	75834	76427	[+3 L= 594]	pabA / Para-aminobenzoate synthase component II (ADC synthase)
72	76424	77293	[+2 L= 870]	pabC / 4-amino-4-deoxychorismate lyase (ADC lyase)
73	77238	78128	[+3 L= 891]	dhpS / Dihydropteroate synthase (DHPS) (Dihydropteroate pyrophosphorylase)
74	78132	78491	[+3 L= 360]	folB / Dihydroneopterin aldolase (DHNA)
75	78491	79003	[+2 L= 513]	hppK / 2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase (HPPK)
76	78958	79158	[+1 L= 201]	yazB / Hypothetical protein
78	79185	80180	[+3 L= 996]	yacF / transcriptional regulator involved in nitrogen regulation
79	80343	81839	[+3 L=1497]	syK / Lysyl-tRNA synthetase (Lysine--tRNA ligase) (LysRS)
84	92915	93373	[+2 L= 459]	ctsR / Transcriptional regulator
85	93535	94092	[+1 L= 558]	yacH / Hypothetical protein
86	94043	95161	[+2 L=1119]	yacI / Hypothetical ATP:guanido phosphotransferase (creatine kinase)
87	95187	97619	[+3 L=2433]	clpC / class III stress response-related ATPase
88	97718	99091	[+2 L=1374]	radA / DNA repair protein
89	99098	100168	[+2 L=1071]	yacK / Hypothetical protein
90	100332	101438	[+3 L=1107]	yacL / Hypothetical protein
91	101458	102135	[+1 L= 678]	ispD / 2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase
92	102255	102728	[+3 L= 474]	ispF / 2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase (MECPS)
93	102788	104275	[+2 L=1488]	gltX / Glutamyl-tRNA synthetase (Glutamate--tRNA ligase)
94	104723	105385	[+2 L= 663]	cysE / Serine acetyltransferase (SAT)
95	105369	106763	[+3 L=1395]	cysS / Cysteinyl-tRNA synthetase (Cysteine--tRNA ligase)
96	106751	107173	[+2 L= 423]	zzzC / Hypothetical protein
97	107173	107913	[+1 L= 741]	yacO / tRNA/rRNA methyltransferase
98	107920	108429	[+1 L= 510]	yacP / Hypothetical protein
99	108500	109156	[+2 L= 657]	rpsH / RNA Polymerase sigma-H factor
100	109474	109650	[+1 L= 177]	secE / Preprotein translocase secE subunit
101	109785	110315	[+3 L= 531]	nusG / Transcription antitermination protein
102	110477	110908	[+2 L= 432]	rplK / 50S ribosomal protein L11 (BL11)
103	111001	111777	[+1 L= 777]	rplA / 50S ribosomal protein L1 (BL1)
105	111936	112511	[+3 L= 576]	rplJ / 50S ribosomal protein L10 (BL5)
106	112582	112938	[+1 L= 357]	rplG / 50S ribosomal protein L7/L12 (BL13)
107	112976	113614	[+2 L= 639]	ybxB / Hypothetical protein
108	113899	117438	[+1 L=3540]	rpoB / DNA-directed RNA polymerase beta chain (RNA polymerase beta subunit)
109	117479	121087	[+2 L=3609]	rpoC / DNA-directed RNA polymerase beta' chain (RNA polymerase beta' subunit)
110	121171	121449	[+1 L= 279]	ybxF / Putative ribosomal protein L7Ae
111	121546	121986	[+1 L= 441]	rpsL / ribosomal protein S12 (BS12)
112	122019	122486	[+3 L= 468]	rpsG / 30S ribosomal protein S7 (BS7)
113	122635	124773	[+1 L=2139]	efg / Elongation factor G (EF-G) (Vegetative protein 19)
114	124894	126078	[+1 L=1185]	tufA / Elongation factor Tu (EF-Tu)
115	126480	126785	[+3 L= 306]	rpsJ / 30S ribosomal protein S10
116	126823	127452	[+1 L= 630]	rplC / 50S ribosomal protein L3 (BL3)
117	127481	128101	[+2 L= 621]	rplD / 50S ribosomal protein L4
118	128104	128391	[+1 L= 288]	rplW / 50S ribosomal protein L23
119	128423	129250	[+2 L= 828]	rplB / 50S ribosomal protein L2 (BL2)
120	129314	129589	[+2 L= 276]	rpsS / 30S ribosomal protein S19 (BS19)
121	129592	129948	[+1 L= 357]	rplV / 50S ribosomal protein L22
122	129955	130611	[+1 L= 657]	rpsC / 30S ribosomal protein S3
123	130616	131047	[+2 L= 432]	rplP / 50S ribosomal protein L16
124	131050	131238	[+1 L= 189]	rpmC / 50S ribosomal protein L29

125	131262	131522 [+3 L= 261]	rpsQ / 30S ribosomal protein S17 (BS16)
126	131569	131934 [+1 L= 366]	rplP / 50S ribosomal protein L14
127	131952	132284 [+3 L= 333]	rplX / 50S Ribosomal protein L24
128	132314	132850 [+2 L= 537]	rplE / 50S ribosomal protein L5 (BL6)
129	132887	133069 [+2 L= 183]	rpsP / 30S ribosomal protein S14-1 (BS-A)
130	133066	133497 [+1 L= 432]	rpsH / 30S ribosomal protein S8 (BS8)
131	133533	134069 [+3 L= 537]	rplF / 50S ribosomal protein L6 (BL10)
132	134095	134463 [+1 L= 369]	rplR / 50S ribosomal protein L18
133	134485	134985 [+1 L= 501]	rpsE / 30S ribosomal protein S5 (BS5)
134	135002	135181 [+2 L= 180]	rpmD / 50S ribosomal protein L30
135	135218	135655 [+2 L= 438]	rplO / 50S ribosomal protein L15
136	135658	135936 [+1 L= 279]	secY / Preprotein translocase subunit
137	135908	136957 [+2 L=1050]	secY / Preprotein translocase subunit
138	137017	137664 [+1 L= 648]	kad / Adenylate kinase (ATP-AMP transphosphorylase)
139	137667	138410 [+3 L= 744]	ampM / Methionine aminopeptidase (MAP)
140	138482	138697 [+2 L= 216]	tifl / Translation initiation factor IF-1
141	138736	138846 [+1 L= 111]	rpmJ / 50S ribosomal protein L36 (Ribosomal protein II) (Ribosomal protein B) (BL38)
142	138871	139233 [+1 L= 363]	rpsM / 30S ribosomal protein S13 (BS14)
144	139261	139647 [+1 L= 387]	rpsK / 30S ribosomal protein S11 (BS11)
145	139831	140772 [+1 L= 942]	rpoA / DNA-directed RNA polymerase alpha chain (RNA polymerase alpha subunit)
146	140811	141170 [+3 L= 360]	rplR / 50S Ribosomal protein L17 (BL21)
147	141217	142116 [+1 L= 900]	ybxA / Hypothetical ABC transporter ATP-binding protein
148	142095	142973 [+3 L= 879]	atpB / Hypothetical ABC transporter ATP-binding protein MG180
149	142964	143755 [+2 L= 792]	ybaF / Hypothetical protein
150	143722	144513 [+1 L= 792]	truA / tRNA pseudouridine synthase A (Uracil hydrolyase)
151	144669	145103 [+3 L= 435]	rpsM / 50S ribosomal protein L13
152	145128	145517 [+3 L= 390]	rpsl / 30S ribosomal protein S9
153	145683	146108 [+3 L= 426]	ybaK / Hypothetical protein
154	146178	146888 [+3 L= 711]	cwlD / Germination-specific N-acetylmuramoyl-L-alanine amidase (Autolysin)
155	147036	148100 [+3 L=1065]	ybxl / Mrp protein homolog
156	148892	148278 [-3 L= 615]	gerD / Spore germination protein precursor
157	149032	149640 [+1 L= 609]	kbaA / KinB signaling pathway activation protein
158	150717	149764 [-1 L= 954]	ybaN / Hypothetical polysaccharide deacetylase homolog
163	156904	158046 [+1 L=1143]	yxaA / Glycerate kinase
164	158260	159150 [+1 L= 891]	argl / Arginase
165	159402	160220 [+3 L= 819]	ybbP / Hypothetical protein
166	160162	161694 [+1 L=1533]	ybbR / Hypothetical protein
167	161651	163033 [+2 L=1383]	ybbT / Phosphoglucomutase (glycolysis) homolog
169	163523	165322 [+2 L=1800]	glmS / Glucosamine--fructose-6-phosphate aminotransferase (Hexosephosphate aminotransferase)
173	167053	169116 [+1 L=2064]	yuxL / Probable acylaminoacyl-peptidase
174	169227	169790 [+3 L= 564]	xxxA / Hypothetical protein
175	170372	169869 [-3 L= 504]	xxxB / Hypothetical protein
176	170738	171538 [+2 L= 801]	fabG / 3-oxoacyl-[acyl-carrier protein] reductase (dehydrogenase/reductase)
177	172249	171584 [-2 L= 666]	metl / Probable D-methionine transport system permease protein
178	173264	172227 [-3 L=1038]	metN / Probable D-methionine transport ATP-binding protein
180	174089	173280 [-3 L= 810]	metQ / Probable D-methionine-binding lipoprotein
181	175338	174373 [-1 L= 966]	adhZ / Zinc-binding dehydrogenases
182	175436	176197 [+2 L= 762]	xxxC / Hypothetical protein
183	176267	177700 [+2 L=1434]	yitY / L-gulonolactone oxidase (LGO)
184	177700	178230 [+1 L= 531]	yitZ / Multidrug resistance protein homolog
185	178303	180027 [+1 L=1725]	xxxD / Hypothetical protein
186	180157	181404 [+1 L=1248]	ydgK / Bicyclomycin resistance protein homolog
188	182161	182661 [+1 L= 501]	xxxE / Hypothetical protein
190	182896	182684 [-2 L= 213]	xxxF / Hypothetical Protein
191	183306	184220 [+3 L= 915]	dppB / Dipeptide transport system permease protein
192	184240	185241 [+1 L=1002]	dppC / Dipeptide transport system permease protein
194	185201	186208 [+2 L=1008]	appD / Oligopeptide transport ATP-binding protein
195	186208	186978 [+1 L= 771]	oppF / Oligopeptide transport ATP-binding protein
196	186995	188602 [+2 L=1608]	dppE / Dipeptide-binding protein precursor
197	189125	188625 [-3 L= 501]	yusW / Hypothetical protein
198	189263	190159 [+2 L= 897]	ybfP / Transcriptional regulator homolog
199	190263	190643 [+3 L= 381]	yhgE / Phage infection protein homolog
200	192331	190694 [-2 L=1638]	dppE / Dipeptide-binding protein precursor

201	194385	192748 [-1 L=1638]	dppE / Dipeptide-binding protein precursor
202	195608	194778 [-3 L= 831]	yvgN / Plant-metabolite dehydrogenase homolog
203	196413	195613 [-1 L= 801]	proI / Pyrroline-5-carboxylate reductase 2 (P5CR 2) (P5C reductase 2)
204	197550	196702 [-1 L= 849]	ycxE / Hypothetical protein
207	198525	197854 [-1 L= 672]	modB / Molybdenum transport system permease protein
208	199355	198534 [-3 L= 822]	modA / Molybdate-binding periplasmic protein precursor
209	199417	200415 [+1 L= 999]	yvgK / Molybdenum-binding protein homolog
212	201889	200996 [-2 L= 894]	yrdQ / Transcription regulator LysR family homolog
213	201927	202952 [+3 L=1026]	yrDr / Hypothetical transport protein
218	203611	204213 [+1 L= 603]	plsC / Probable 1-acyl-sn-glycerol-3-phosphate acyltransferase (1-AGP acyltransferase)
221	204690	205664 [+3 L= 975]	ccpB / Catabolite control protein B
222	205829	206155 [+2 L= 327]	xxxG / Hypothetical protein
223	206277	207110 [+3 L= 834]	yqfU / Hypothetical protein
224	207213	207605 [+3 L= 393]	yxeA / Hypothetical protein
226	208277	209107 [+2 L= 831]	xxxH / Hypothetical protein
227	210987	209230 [-1 L=1758]	ydaL / Hypothetical protein
228	211116	211646 [+3 L= 531]	xxxI / Hypothetical protein
229	212561	211689 [-3 L= 873]	xxxJ / Hypothetical protein
231	213296	215269 [+2 L=1974]	ydiF / Hypothetical ABC transporter ATP-binding protein
234	216220	217953 [+1 L=1734]	appA / Oligopeptide-binding protein precursor
235	218012	219013 [+2 L=1002]	appB / Oligopeptide transport system permease protein
236	219029	219946 [+2 L= 918]	oppC / Oligopeptide transport system permease protein
238	219960	220937 [+3 L= 978]	appD / Oligopeptide transport ATP-binding protein
239	220937	221899 [+2 L= 963]	appF / Oligopeptide transport ATP-binding protein
240	222839	221940 [-3 L= 900]	yxeH / Hypothetical protein
246	224308	225474 [+1 L=1167]	hppD / Putative 4-hydroxyphenylpyruvate dioxygenase
247	225544	226497 [+1 L= 954]	xxxK / putative hydrolase
249	226457	227635 [+2 L=1179]	xxxL / Hypothetical protein
250	227870	229282 [+2 L=1413]	yfnA / Metabolite transporter homolog
251	229391	230662 [+2 L=1272]	yqjV / Hypothetical transport protein
252	230876	231976 [+2 L=1101]	ddlA / D-alanine--D-alanine ligase (D-alanylalanine synthetase)
253	232012	233415 [+1 L=1404]	murF / uDP-N-acetylmuramoylalanyl-D-glutamyl-2,6-diaminopimelate--D-alanyl -D-alanyl ligase (UDP-MurNAc-pentapeptide synthetase)
254	233782	235323 [+1 L=1542]	ydbR / Probable RNA helicase
255	235422	236381 [+3 L= 960]	uvsE / UV DNA damage endonuclease
256	236949	236380 [-1 L= 570]	ydcA / Hypothetical protein
257	237043	237399 [+1 L= 357]	acpS / Holo-[acyl-carrier protein] synthase (Holo-ACP synthase)
258	237421	238506 [+1 L=1086]	ydcC / Hypothetical protein
259	238627	239793 [+1 L=1167]	alaR / Alanine racemase
260	240105	240389 [+3 L= 285]	xxxM / Hypothetical protein
261	240397	240744 [+1 L= 348]	ydcE / Hypothetical protein
262	240809	242980 [+2 L=2172]	xxxN / Hypothetical Protein
263	243347	243808 [+2 L= 462]	ydcK / Hypothetical protein
264	247344	246916 [-1 L= 429]	xxxO / Hypothetical protein
265	250295	250774 [+2 L= 480]	ydiB / Hypothetical protein
266	250740	251447 [+3 L= 708]	ydiC / Glycoprotein endopeptidase homolog
267	251455	251904 [+1 L= 450]	ydiD / Ribosomal-protein-alanine acetyltransferase (Acetylating enzyme ribosomal protein S18)
268	251892	252920 [+3 L=1029]	ydiE / Glycoprotein endopeptidase homolog
270	255383	253407 [-3 L=1977]	ydiF / Hypothetical ABC transporter ATP-binding protein
271	255517	256143 [+1 L= 627]	ydiH / Hypothetical protein
272	256367	256179 [-3 L= 189]	xxxP / Hypothetical protein
273	257113	256367 [-2 L= 747]	ydiL / Hypothetical protein
275	257452	257784 [+1 L= 333]	cpnS / 10 kDa chaperonin (groES protein)
277	257826	259457 [+3 L=1632]	cpnL / 60 kDa chaperonin (groEL protein)
278	259858	261402 [+1 L=1545]	guaA / Putative GMP synthase [glutamine-hydrolyzing] (Glutamine amidotransferase)
280	261790	263112 [+1 L=1323]	yebD / Hypothetical protein
281	263260	263958 [+1 L= 699]	xxxQ / Hypothetical two-component response regulator
282	263945	265447 [+2 L=1503]	xxxR / Hypothetical histidine kinase
285	270798	271754 [+3 L= 957]	xxxS / Hypothetical protein
286	271958	272686 [+2 L= 729]	xxxT / Hypothetical protein
289	278891	277818 [-3 L=1074]	xxxU / Hypothetical protein
291	279988	279119 [-2 L= 870]	xxxV / Hypothetical protein
292	280738	280019 [-2 L= 720]	xxxW / Hypothetical protein

293	281751	280960 [-1 L= 792]	xxxX / Hypothetical protein
294	282045	282986 [+3 L= 942]	xxxY / Putative UDP-glucose 4-epimerase (Galactowaldenase)
295	283867	283031 [-2 L= 837]	xxxZ / Hypothetical protein
296	285803	283875 [-3 L=1929]	xxyA / Putative glycosyl transferase
299	291296	292225 [+2 L= 930]	ybhF / Hypothetical transport protein
300	293106	292318 [-1 L= 789]	xxyB / Hypothetical protein
304	298965	299468 [+3 L= 504]	purE / Phosphoribosylaminoimidazole carboxylase catalytic subunit (AIR carboxylase)
305	299468	300616 [+2 L=1149]	purK / Phosphoribosylaminoimidazole carboxylase ATPase subunit (AIR carboxylase)
306	300580	301920 [+1 L=1341]	purB / Adenylosuccinate lyase (Adenylosuccinase)
307	301955	302728 [+2 L= 774]	purC / Phosphoribosylaminoimidazole-succinocarboxamide synthase (SAICAR synthetase)
308	302724	302975 [+3 L= 252]	yexA / Hypothetical protein
309	302975	303655 [+2 L= 681]	purQ / Phosphoribosylformylglycinamidine synthase I (FGAM synthase I)
310	303642	305858 [+3 L=2217]	purL / Phosphoribosylformylglycinamidine synthase II (FGAM synthase II)
311	305828	307258 [+2 L=1431]	purA / Amidophosphoribosyltransferase precursor (Glutamine phosphoribosylpyrophosphate amidotransferase)
313	307367	308404 [+2 L=1038]	purM / Phosphoribosylformylglycinamidine cyclo-ligase (AIRS)
315	308404	308988 [+1 L= 585]	purN / Phosphoribosylglycinamide formyltransferase (GART)
316	309016	310548 [+1 L=1533]	purH / Bifunctional purine biosynthesis protein [Includes: phosphoribosylaminoimidazolecarboxamide formyltransferase (AICAR transformylase); IMP cyclohydrolase (ATIC)]
317	310974	312242 [+3 L=1269]	purD / Phosphoribosylamine--glycine ligase (GARS)
318	312446	312285 [-3 L= 162]	xxyC / Hypothetical protein
319	313307	312465 [-3 L= 843]	xxyD / Hypothetical protein
321	313997	313530 [-3 L= 468]	xxyE / Hypothetical protein
323	314242	314928 [+1 L= 687]	pcrB / PcrB protein homolog
324	314932	317190 [+1 L=2259]	pcrA / ATP-dependent DNA helicase
325	317208	319214 [+3 L=2007]	dnlJ / DNA ligase (Polydeoxyribonucleotide synthase [NAD+])
326	319234	320427 [+1 L=1194]	yerH / Hypothetical protein
327	320527	321294 [+1 L= 768]	xxyF / Hypothetical protein
328	321452	322996 [+2 L=1545]	rocA / 1-pyrroline-5-carboxylate dehydrogenase (P5C dehydrogenase)
329	323815	323273 [-2 L= 543]	yddQ / Hypothetical isochorismatase family protein
330	324186	325304 [+3 L=1119]	xxyG / Hypothetical ABC transporter ATP-binding protein
332	325297	325959 [+1 L= 663]	xxyH / Hypothetical ABC transporter permease
334	325984	326832 [+1 L= 849]	xxyI / Hypothetical lipoprotein
335	327175	327438 [+1 L= 264]	yubF / Hypothetical protein
337	327583	327870 [+1 L= 288]	gatC / Glutamyl-tRNA(Gln) amidotransferase subunit C (Glu-ADT subunit C)
338	327889	329343 [+1 L=1455]	gatA / Glutamyl-tRNA(Gln) amidotransferase subunit A (Glu-ADT subunit A)
339	329361	330785 [+3 L=1425]	gatB / Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit b (Asp/Glu-ADT subunit B)
340	331346	332248 [+2 L= 903]	yerQ / Hypothetical protein
341	332392	333132 [+1 L= 741]	xxyJ / Hypothetical protein
342	333215	334651 [+2 L=1437]	gabT / 4-aminobutyrate aminotransferase (GABA aminotransferase)
343	334743	336134 [+3 L=1392]	xxyK / Hypothetical transcriptional regulator
344	336130	337578 [+1 L=1449]	gabD / Succinate-semialdehyde dehydrogenase [NADP+] (SSDH)
345	337629	337949 [+3 L= 321]	xxyL / Hypothetical protein
347	339947	338625 [-3 L=1323]	ampS / Aminopeptidase
348	341059	339971 [-2 L=1089]	xxyM / Hypothetical polysaccharide deacetylase
351	343543	342350 [-2 L=1194]	nupC / Pyrimidine nucleoside transport protein
352	343948	345342 [+1 L=1395]	yefA / RNA methyltransferase
353	345485	346492 [+2 L=1008]	yfjN / Hypothetical protein
356	349078	349593 [+1 L= 516]	xxyN / Hypothetical protein
357	349677	350396 [+3 L= 720]	xxyO / Hypothetical protein
358	351314	350622 [-3 L= 693]	xxyP / Hypothetical protein
359	352438	351332 [-2 L=1107]	xxyQ / Muconate cycloisomerase
360	352532	353800 [+2 L=1269]	xxyR / Hypothetical protein
362	355213	353795 [-2 L=1419]	nhaC / Na(+)/H(+) antiporter (Sodium/proton antiporter)
363	355507	356619 [+1 L=1113]	amhX / Amidohydrolase (Aminoacylase)
364	356857	357459 [+1 L= 603]	xxyS / Hypothetical methyltransferase
365	359023	357500 [-2 L=1524]	dhnA / NADH dehydrogenase (alkyl hydroperoxide reductase)
366	359601	359041 [-1 L= 561]	ahpC / Alkyl hydroperoxide reductase C22 protein (General stress protein 22)
368	360193	361419 [+1 L=1227]	xxyT / 5-methylthioribose kinase
369	361432	362475 [+1 L=1044]	tifB / Putative translation initiation factor eIF-2B

370	362526	363170 [+3 L= 645]	fucA / L-fuculose-1-phosphate aldolase
371	364222	363218 [-2 L=1005]	fhuG / Ferrichrome transport system permease protein
373	365259	364222 [-1 L=1038]	fhuB / Ferrichrome transport system permease protein
374	366228	365311 [-1 L= 918]	yxeB / Ferrichrome ABC transporter (ferrichrome-binding protein)
375	366562	367608 [+1 L=1047]	trxB / Thioredoxin reductase
376	368175	367810 [-1 L= 366]	xxyU / Hypothetical protein
377	368362	368598 [+1 L= 237]	yoeD / Hypothetical protein
378	368837	369349 [+2 L= 513]	cotB / Spore coat protein B
380	369373	369819 [+1 L= 447]	cotB / Spore coat protein B
381	369985	370650 [+1 L= 666]	ywrJ / Hypothetical protein
382	370886	372154 [+2 L=1269]	xxyV / Hypothetical protein
383	372295	373518 [+1 L=1224]	ykrQ / Two-component sensor histidine kinase homolog
385	374837	374163 [-3 L= 675]	xxyW / Hypothetical protein
386	375131	376246 [+2 L=1116]	xxyX / Hypothetical protein
387	376310	377140 [+2 L= 831]	ycgL / Hypothetical protein
388	378467	377160 [-3 L=1308]	xxyY / Hypothetical protein
389	380128	378605 [-2 L=1524]	yhfW / Hypothetical protein
390	380710	381792 [+1 L=1083]	xxyZ / Putative fatty acid desaturase (Delta 12 desaturase)
391	382604	381852 [-3 L= 753]	xxzA / Putative glutamine transport system permease protein
392	383442	382651 [-1 L= 792]	yxeM / Probable amino-acid ABC transporter binding protein precursor
394	384287	383568 [-3 L= 720]	yqiZ / Probable amino-acid ABC transporter ATP-binding protein
395	384471	385787 [+3 L=1317]	tlpA / Methyl-accepting chemotaxis protein
396	385928	386383 [+2 L= 456]	argR / Putative arginine repressor
398	386730	387884 [+3 L=1155]	arcA / Arginine deiminase (ADI)
399	387918	388913 [+3 L= 996]	otcC / Ornithine carbamoyltransferase, catabolic (OTCase)
400	389007	390428 [+3 L=1422]	arcD / Arginine/ornithine antiporter
402	390469	391428 [+1 L= 960]	arcC / Carbamate kinase
403	391591	392319 [+1 L= 729]	xxzB / Hypothetical protein
404	392479	393159 [+1 L= 681]	xxzC / Hypothetical protein
405	394621	393290 [-2 L=1332]	ygaK / Reticuline oxidase homolog
406	394770	396527 [+3 L=1758]	xxzD / Putative exo-alpha-1,4-glucosidase
407	396736	398370 [+1 L=1635]	ptgA / Probable PTS system, glucose-specific IIABC component (Glucose-permease IIABC component)
408	398366	399166 [+2 L= 801]	xxzE / Hypothetical protein
409	399463	402333 [+1 L=2871]	xxzF / Putative membrane protein
410	404565	402379 [-1 L=2187]	topB / DNA topoisomerase III
411	404951	405766 [+2 L= 816]	thiM / Hydroxyethylthiazole kinase (TH kinase)
412	405776	406441 [+2 L= 666]	thiE / Thiamine-phosphate pyrophosphorylase (TMP pyrophosphorylase)
413	407873	406563 [-3 L=1311]	dcuB / Putative anaerobic C4-dicarboxylate transporter
414	408375	410114 [+3 L=1740]	tlpA / Methyl-accepting chemotaxis protein
415	410203	413829 [+1 L=3627]	xxzG / Hypothetical protein
416	413992	414405 [+1 L= 414]	xxzH / Hypothetical protein
417	414377	415150 [+2 L= 774]	xxzI / Putative ABC transporter permease protein
418	415150	416145 [+1 L= 996]	xxzJ / Hypothetical protein
419	416145	416891 [+3 L= 747]	xxzK / Putative ABC transporter ATP-binding protein
422	419610	417532 [-1 L=2079]	chiT / Chitinase A1 Precursor
423	419925	420293 [+3 L= 369]	xxzL / Hypothetical protein
424	420307	420618 [+1 L= 312]	ydfQ / Thioredoxin homolog
428	421224	421808 [+3 L= 585]	qacR / Transcriptional regulator
429	421872	423107 [+3 L=1236]	ykuC / Hypothetical protein
431	424771	423491 [-2 L=1281]	yxiO / Hypothetical protein
432	426193	424883 [-2 L=1311]	xxzM / Putative phosphodiesterase
433	426330	426638 [+3 L= 309]	yesK / Hypothetical protein
434	426911	428416 [+2 L=1506]	hgtP / Prolyl-tRNA synthetase (Proline--tRNA ligase)
435	429557	428538 [-3 L=1020]	xxzN / Hypothetical protein
436	429759	430634 [+3 L= 876]	xxzO / Hypothetical protein
437	430766	431359 [+2 L= 594]	yceC / Stress response protein SCP2
438	431337	431966 [+3 L= 630]	yceD / General stress protein 16U (GSP16U)
440	432334	432630 [+1 L= 297]	yceE / Tellurium resistance protein homolog
441	432706	433494 [+1 L= 789]	yceF / Tellurium resistance protein homolog
442	433607	435235 [+2 L=1629]	yceG / Hypothetical protein
443	435257	436336 [+2 L=1080]	yceH / Toxic anion resistance protein homolog
444	439194	436531 [-1 L=2664]	xxzP / Putative cation-transporting ATPase
445	439612	439391 [-2 L= 222]	yfkK / Hypothetical protein
446	439787	440248 [+2 L= 462]	yfkJ / Protein-tyrosine phosphatase homolog
448	440305	440817 [+1 L= 513]	xxzQ / Hypothetical protein

449	440827	441690 [+1 L= 864]	yfkH / Transporter homolog
451	443806	441884 [-2 L=1923]	ykvW / Heavy metal-transporting ATPase homolog
452	444078	445025 [+3 L= 948]	xxzR / Hypothetical protein
453	445149	445826 [+3 L= 678]	xxzS / Hypothetical protein
454	446007	446540 [+3 L= 534]	sipS / Signal peptidase I S (Leader peptidase I)
456	449343	446584 [-1 L=2760]	xxzT / Hypothetical protein
457	449830	450420 [+1 L= 591]	ybfM / Alkaline phosphatase homolog
459	450863	450438 [-3 L= 426]	xxzU / Hypothetical protein
461	451239	451075 [-1 L= 165]	xxzV / Hypothetical protein
462	451790	451377 [-3 L= 414]	ydaG / General stress protein 26 (GSP26)
464	451961	453022 [+2 L=1062]	yfkE / H+/Ca2+ exchanger homolog
465	453105	453899 [+3 L= 795]	ykfD / Hypothetical protein
466	455065	453941 [-2 L=1125]	xxzW / Hypothetical protein
468	455635	457185 [+1 L=1551]	fumA / Fumarate hydratase class I, aerobic (Fumarase)
469	457298	458095 [+2 L= 798]	xxzX / Putative polysaccharide deacetylase
470	458146	459018 [+1 L= 873]	yfjP / DNA-3-methyladenine glycosylase
471	459032	459634 [+2 L= 603]	yfjO / RNA methyltransferase homolog
472	459754	460407 [+1 L= 654]	yfjO / RNA methyltransferase homolog
473	460659	461549 [+3 L= 891]	xxzY / Hypothetical cell-wall amidase
474	461667	462401 [+3 L= 735]	truA / tRNA pseudouridine synthase A (Pseudouridylate synthase I)
476	464139	462739 [-1 L=1401]	rocR / Arginine utilization regulatory protein
477	464405	464665 [+2 L= 261]	xxzZ / Hypothetical protein
478	464775	465392 [+3 L= 618]	rocC / Amino-acid permease
479	465365	466195 [+2 L= 831]	rocE / Amino-acid permease
480	466247	467566 [+2 L=1320]	ylmB / Acetylornithine deacetylase homolog
481	468364	467672 [-2 L= 693]	xxaA / Hypothetical protein
484	468452	469060 [+2 L= 609]	xxaB / Hypothetical protein
486	469700	469362 [-3 L= 339]	xxaC / Hypothetical protein
487	469890	469798 [-1 L= 93]	ylaM / Glutaminase homolog
488	470804	469878 [-3 L= 927]	yflF / Phosphotransferase system enzyme II homolog
489	471130	472629 [+1 L=1500]	ybfS / Putative PTS system IIABC component
490	472859	474130 [+2 L=1272]	pbpE / Penicillin-binding protein 4*
491	474290	474688 [+2 L= 399]	xxaD / Hypothetical protein
492	474708	474899 [+3 L= 192]	xxaE / Hypothetical protein
493	474877	476457 [+1 L=1581]	xxaF / Putative glycosyltransferase
494	476453	477691 [+2 L=1239]	xxaG / UDP-glucose:GDP-mannose dehydrogenase homolog
495	477691	478653 [+1 L= 963]	xxaH / Putative UDP-glucose 4-epimerase (Galactowaldenase)
496	478637	480190 [+2 L=1554]	xxaI / Putative glycosyltransferase
497	480521	482782 [+2 L=2262]	pflB / Formate acetyltransferase 1 (Pyruvate formate-lyase 1)
498	482856	483584 [+3 L= 729]	pflA / Pyruvate formate-lyase activating enzyme (PFL-activating enzyme)
499	484000	485163 [+1 L=1164]	ypfP / Putative glycosyl transferase
501	486322	485768 [-2 L= 555]	xxaJ / Hypothetical protein
502	487695	486568 [-1 L=1128]	hutI / Probable imidazolonepropionase (Imidazolone-5-propionate hydrolase)
503	488740	487838 [-2 L= 903]	yfhF / Cell-division inhibitor homolog
504	488822	489631 [+2 L= 810]	recX / Regulatory protein recX
505	489645	489959 [+3 L= 315]	yhfH / Hypothetical protein
508	490498	490761 [+1 L= 264]	yfhJ / Hypothetical protein
510	491769	490792 [-1 L= 978]	yfhP / Hypothetical protein
511	491919	493013 [+3 L=1095]	yfhQ / A/G-specific adenine glycosylase homolog
512	493338	493054 [-1 L= 285]	yfhS / Hypothetical protein
513	493368	493679 [+3 L= 312]	sasG / Small, acid-soluble spore protein gamma-type (SASP)
515	493871	494128 [+2 L= 258]	ygaB / Hypothetical protein
518	494406	494933 [+3 L= 528]	xxaK / Hypothetical protein
519	494991	496724 [+3 L=1734]	ygaD / ABC transporter (ATP-binding protein) homolog
520	497910	496768 [-1 L=1143]	ygaE / Hypothetical protein
521	502646	498213 [-3 L=4434]	gltB / Glutamate synthase [NADPH] large chain precursor (Glutamate synthase alpha subunit) (NADPH-GOGAT)
522	504143	502848 [-3 L=1296]	gsaB / Glutamate-1-semialdehyde 2,1-aminomutase 2 (Glutamate-1-semialdehyde aminotransferase)
523	504271	505281 [+1 L=1011]	natA / ATP-binding transport protein (Na(+) ABC transporter)
524	505259	506065 [+2 L= 807]	xxaL / Hypothetical protein
525	506052	506855 [+3 L= 804]	xxaM / Hypothetical protein
526	506922	507332 [+3 L= 411]	lctB / LCTB protein
528	507371	507832 [+2 L= 462]	bcpA / Bacterioferritin comigratory protein homolog
529	508130	508561 [+2 L= 432]	perR / Peroxide operon regulator

530	508735	509151	[+1 L= 417]	xxaN / Hypothetical protein
531	509626	509264	[-2 L= 363]	xxaO / Hypothetical protein
534	512183	511755	[-3 L= 429]	xxaP / Hypothetical protein
535	516756	516439	[-1 L= 318]	xxaQ / Hypothetical protein
536	517099	517824	[+1 L= 726]	yeeI / Hypothetical protein
537	517974	518432	[+3 L= 459]	mutT / MutT-like protein
538	518902	519702	[+1 L= 801]	pbpA / Penicillin-binding protein 1A homolog
539	519887	520540	[+2 L= 654]	yvgV / Hypothetical protein
540	520932	522071	[+3 L=1140]	yhbA / Hypothetical protein
541	522119	523003	[+2 L= 885]	xxaR / Hypothetical protein
542	523065	523550	[+3 L= 486]	cspR / rRNA methylase homolog
543	523682	525748	[+2 L=2067]	xxaS / Hypothetical protein
546	526137	528029	[+3 L=1893]	prkA / Serine protein kinase
547	528485	529657	[+2 L=1173]	yhbH / Stress response protein
549	529789	532866	[+1 L=3078]	xxaT / Hypothetical protein
550	532951	533322	[+1 L= 372]	xxaU / Hypothetical protein
551	533316	533552	[+3 L= 237]	xxaV / Hypothetical protein
552	535207	533660	[-2 L=1548]	opuD / Glycine betaine transporter
553	535454	538348	[+2 L=2895]	colA / Collagenase
554	538656	539201	[+3 L= 546]	yuaF / Hypothetical protein
555	539217	540788	[+3 L=1572]	yuaG / Epidermal surface antigen homolog
556	541041	543014	[+3 L=1974]	mcpA / Methyl-accepting chemotaxis protein
557	543169	544773	[+1 L=1605]	citS / Two-component sensor histidine kinase
558	544779	545468	[+3 L= 690]	citT / Transcriptional regulatory protein
559	546822	545521	[-1 L=1302]	citN / Mg2+/citrate complex transporter homolog
560	547038	547328	[+3 L= 291]	xxaW / Hypothetical protein
561	547464	547967	[+3 L= 504]	xxaX / Hypothetical protein
562	548257	549123	[+1 L= 867]	xxaY / Hypothetical ANK-repeats protein
563	549595	550158	[+1 L= 564]	glpP / Glycerol uptake operon antiterminator regulatory protein
565	550125	551252	[+3 L=1128]	msmX / Probable multiple sugar-binding transport ATP-binding protein
566	551255	552184	[+2 L= 930]	ugpA / SN-glycerol-3-phosphate transport system permease protein
567	552184	553002	[+1 L= 819]	ugpE / SN-glycerol-3-phosphate transport system permease protein
568	553027	554400	[+1 L=1374]	ugpB / Glycerol-3-phosphate-binding periplasmic protein precursor
569	554841	555542	[+3 L= 702]	xxaZ / Protein phosphatase 2A homolog
570	555714	556409	[+3 L= 696]	xxbA / Hypothetical protein
571	556409	557656	[+2 L=1248]	xxbB / Hypothetical protein
573	557891	558709	[+2 L= 819]	corA / Mg2+ transporter protein
574	558720	559472	[+3 L= 753]	yvpB / Hypothetical protein
575	559757	561736	[+2 L=1980]	mcpA / Methyl-accepting chemotaxis protein
576	561758	563419	[+2 L=1662]	xxbC / Two-component sensor histidine kinase
577	563419	564123	[+1 L= 705]	yufM / Two-component response regulator homolog
578	564249	565592	[+3 L=1344]	marN / Na(+)-malate symporter (Sodium-dependent malate transporter)
579	565655	566851	[+2 L=1197]	maoX / NAD-Dependent malic enzyme (malate oxidoreductase)
580	567671	567150	[-3 L= 522]	xxbD / Hypothetical protein
581	568830	567862	[-1 L= 969]	ydeD / Hypothetical transport protein
582	568906	570303	[+1 L=1398]	gntR / Helix_turn_helix gluconate operon transcriptional repressor
583	570851	570342	[-3 L= 510]	xxbE / Hypothetical protein
584	572451	571000	[-1 L=1452]	resE / Sensor protein
585	573200	572520	[-3 L= 681]	xxbF / Hypothetical protein
588	574546	574001	[-2 L= 546]	xxbG / Hypothetical acetyltransferase
589	575611	574739	[-2 L= 873]	fdhD / Required for formate dehydrogenase activity
590	575819	578776	[+2 L=2958]	yrhE / Formate dehydrogenase chain A
591	578792	579271	[+2 L= 480]	yrhD / Hypothetical protein
593	579418	581293	[+1 L=1881]	xxbH / Glycerophosphoryl diester phosphodiesterase
594	581671	582801	[+1 L=1131]	dhaA / alanine dehydrogenase
596	582908	584320	[+2 L=1413]	xxbI / Putative amino acid transporter
597	584652	585026	[+3 L= 375]	xxbJ / Arsenical resistance operon repressor homolog
598	585053	587416	[+2 L=2364]	yvgW / Zinc-transporting ATPase
599	589086	587626	[-1 L=1461]	yueK / Nicotinate phosphoribosyltransferase homolog
600	589286	589876	[+2 L= 591]	nprA / Transcriptional activator
601	589962	590366	[+3 L= 405]	xxbK / Transposase
602	590366	591451	[+2 L=1086]	xxbL / Transposase
604	591628	592359	[+1 L= 732]	rapD / Response regulator aspartate phosphatase D
606	592663	594360	[+1 L=1698]	nprE / Bacillolysin precursor (Neutral protease)
607	594975	594430	[-1 L= 546]	yqeD / Hypothetical protein
608	595371	595889	[+3 L= 519]	xxbM / Hypothetical protein

609	595909	596178 [+1 L= 270]	xxbN / Hypothetical protein
610	597486	596227 [-1 L=1260]	xxbO / Hypothetical protein
611	598791	597724 [-1 L=1068]	lytR / Membrane-bound protein
612	600102	598927 [-1 L=1176]	nupC / Pyrimidine nucleoside transport protein
613	600092	600577 [+2 L= 486]	ywkD / Hypothetical protein
614	600689	601984 [+2 L=1296]	yrkA / Hemolysin homolog
615	602152	603591 [+1 L=1440]	aspA / Aspartate ammonia-lyase (Aspartase)
616	605253	603637 [-1 L=1617]	xxbP / Lactate permease homolog
617	606075	606359 [+3 L= 285]	xxbQ / Transcriptional repressor homolog
618	606554	606730 [+2 L= 177]	yfjU / Hypothetical protein
619	608120	606774 [-3 L=1347]	yclF / Permease homolog
620	609342	608503 [-1 L= 840]	xxbR / Periplasmic binding protein homolog
622	609623	610468 [+2 L= 846]	yfiZ / Iron(III) dicitrate transport permease homolog
623	610374	610643 [+3 L= 270]	yfiZ / Iron(III) dicitrate transport permease homolog
624	610643	611698 [+2 L=1056]	yfhA / Iron(III) dicitrate transport permease homolog
625	611708	612532 [+2 L= 825]	yusV / Iron(III) dicitrate transport permease homolog
626	613295	612567 [-3 L= 729]	xxbS / Hypothetical protein
627	613494	614696 [+3 L=1203]	kblA / 2-amino-3-ketobutyrate coenzyme A ligase (Glycine acetyltransferase)
628	614735	615706 [+2 L= 972]	xxbT / UDP-glucose 4-epimerase homolog
629	615769	616188 [+1 L= 420]	xxbU / Hypothetical protein
630	618112	616232 [-2 L=1881]	yojO / Hypothetical protein
631	619117	618119 [-2 L= 999]	yojN / Nitric-oxide reductase homolog
633	620666	619140 [-3 L=1527]	pldC / Phospholipase D
635	621709	623415 [+1 L=1707]	xxbV / Hypothetical protein
636	624847	623453 [-2 L=1395]	yvSH / ABC transporter (amino acid permease) homolog
637	625300	626007 [+1 L= 708]	treR / Trehalose operon transcriptional repressor
638	626152	627576 [+1 L=1425]	treP / Trehalose-permease IIBC component (Phosphotransferase enzyme II, BC component)
639	627554	629251 [+2 L=1698]	treC / Trehalose-6-phosphate hydrolase (Alpha,alpha-phosphotrehalase)
640	630412	629291 [-2 L=1122]	xxbW / Hypothetical protein
641	631508	630396 [-3 L=1113]	grbB / Spore germination protein
642	632991	631483 [-1 L=1509]	grkA / Spore germination protein KA
643	633132	633815 [+3 L= 684]	xxbX / Amino terminal protease homolog
644	633842	634810 [+2 L= 969]	yerl / Hypothetical protein
645	634970	636430 [+2 L=1461]	yrbD / Sodium/proton-dependent alanine carrier protein homolog
646	636468	637301 [+3 L= 834]	glnQ / Glutamine transport ATP-binding protein
647	637317	638144 [+3 L= 828]	glnH / Glutamine-binding protein precursor
648	638248	638901 [+1 L= 654]	glnM / Glutamine ABC transporter permease protein
649	638905	639546 [+1 L= 642]	glnP / Glutamine ABC transporter permease protein
650	639752	641176 [+2 L=1425]	rocE / Arginine permease
651	641154	641528 [+3 L= 375]	xxbY / Hypothetical protein
652	641568	641783 [+3 L= 216]	xxbZ / Cell-cycle regulation histidine triad (Hit family) homolog
653	641768	642019 [+2 L= 252]	xxbZ / Cell-cycle regulation histidine triad (Hit family) homolog
654	642203	642757 [+2 L= 555]	sigW / RNA polymerase sigma factor
655	642726	644147 [+3 L=1422]	xxcA / Hypothetical protein
656	645142	644183 [-2 L= 960]	xxcB / Hypothetical protein
657	645238	645756 [+1 L= 519]	ywjB / Hypothetical protein
658	647164	645776 [-2 L=1389]	xxcC / Histidine kinase-like ATPase homolog
660	648003	647179 [-1 L= 825]	xxcD / Two-component response regulator homolog
661	648029	649273 [+2 L=1245]	xxcE / Hypothetical protein
662	649433	650881 [+2 L=1449]	ybaR / Sulfate transporter
663	650950	651369 [+1 L= 420]	xxcF / Hypothetical protein
665	653160	651814 [-1 L=1347]	glpT / Glycerol-3-phosphate transporter (G-3-P permease)
666	653421	653885 [+3 L= 465]	yusO / Transcription regulator MarR family homolog
667	653908	655518 [+1 L=1611]	yusP / Multidrug-efflux transporter homolog
669	655659	656627 [+3 L= 969]	rbsR / Ribose operon repressor
670	656635	657537 [+1 L= 903]	rbsK / Ribokinase
671	657537	657929 [+3 L= 393]	rbsD / High affinity ribose transport protein
673	657942	659432 [+3 L=1491]	rbsA / Ribose transport ATP-binding protein
674	659438	660370 [+2 L= 933]	rbsC / Ribose transport system permease protein
675	660373	660675 [+1 L= 303]	rbsD / D-ribose-binding protein precursor
676	660828	661310 [+3 L= 483]	rbsB / D-ribose-binding protein precursor
677	661321	661992 [+1 L= 672]	talA / Transaldolase
679	662377	664773 [+1 L=2397]	xxcG / Zinc-metalloprotease homolog
680	666589	665438 [-2 L=1152]	xxcH / Multidrug-efflux transporter homolog

681	666806	667864	[+2 L=1059]	ydjL / Sorbitol dehydrogenase (L-iditol 2-dehydrogenase) homolog
682	667966	668328	[+1 L= 363]	xxcI / Hypothetical protein
683	668585	669433	[+2 L= 849]	phlD / Phospholipase C precursor (PLC) (Phosphatidylcholine cholinephosphohydrolase) (Cereolysin A)
684	669513	670511	[+3 L= 999]	phlC / Sphingomyelinase C precursor (Sphingomyelin phosphodiesterase) (Cereolysin B)
686	670601	671791	[+2 L=1191]	xxcJ / Hypothetical protein
687	671782	673095	[+1 L=1314]	gglO / L-gulonolactone oxidase (L-gulono-gamma-lactone oxidase)
688	674303	673155	[-3 L=1149]	xxcK / Hypothetical protein
691	676085	675276	[-3 L= 810]	upkA / Putative undecaprenol kinase 1 (Bacitracin resistance protein 1)
692	677163	676225	[-1 L= 939]	xxcL / Methyl-accepting chemotaxis protein homolog
693	677384	678673	[+2 L=1290]	ycvE / Hypothetical protein
694	678780	679004	[+3 L= 225]	xxcM / Transcriptional regulator protein homolog
695	679000	679470	[+1 L= 471]	ygaO / Hypothetical protein
696	679591	680220	[+1 L= 630]	xxcN / Hypothetical protein
698	682922	681519	[-3 L=1404]	yclF / Hypothetical transporter
701	683160	684452	[+3 L=1293]	brnQ / Branched-chain amino acid transport system carrier protein
702	684596	686314	[+2 L=1719]	xxcO / Hypothetical protein
704	687900	686356	[-1 L=1545]	xxcP / Hypothetical protein
705	689473	688085	[-2 L=1389]	ybxG / Proline transport protein
706	689755	691044	[+1 L=1290]	ytiP / Hypothetical protein
707	691179	691376	[+3 L= 198]	xxcR / Transcriptional regulator protein homolog
708	691351	691809	[+1 L= 459]	xxcS / Hypothetical protein
709	692289	691855	[-1 L= 435]	yitI / Hypothetical protein
711	694548	692617	[-1 L=1932]	yjbQ / Na(+)/H(+) antiporter homolog
712	694972	694664	[-2 L= 309]	qoxD / Quinol oxidase polypeptide IV
713	695575	694976	[-2 L= 600]	qoxC / Quinol oxidase polypeptide III
714	697532	695592	[-3 L=1941]	qoxB / Quinol oxidase polypeptide I
715	698570	697560	[-3 L=1011]	qoxA / Quinol oxidase polypeptide II precursor
716	700130	698718	[-3 L=1413]	rocC / Amino-acid permease
717	700498	701214	[+1 L= 717]	yvpB / Hypothetical protein
718	701326	702522	[+1 L=1197]	amaA / N-acyl-L-amino acid amidohydrolase (L-aminoacylase)
719	702527	702721	[+2 L= 195]	yhjC / Hypothetical protein
720	702721	704190	[+1 L=1470]	yhjB / Metabolite permease homolog
721	704416	704805	[+1 L= 390]	xxcT / Hypothetical protein
722	704815	705891	[+1 L=1077]	xxcU / Hypothetical protein
724	705895	707016	[+1 L=1122]	graB / Spore germination protein A2
725	706994	708166	[+2 L=1173]	graC / Spore germination protein A3 precursor
727	709781	708384	[-3 L=1398]	feoB / Ferrous iron transport protein B homolog
728	710481	709762	[-1 L= 720]	feoB / Ferrous iron transport protein B homolog
729	710735	710481	[-3 L= 255]	feoA / Ferrous iron transport protein A
731	711218	712144	[+2 L= 927]	pstS / Phosphate-binding protein homolog
732	712216	713106	[+1 L= 891]	xxcV / Phosphate permease homolog
733	713112	714029	[+3 L= 918]	xxcW / Permease component of ATP-dependent phosphate uptake system
734	714168	714689	[+3 L= 522]	xxcX / Hypothetical protein
735	717781	714740	[-2 L=3042]	yerP / Acriflavin resistance protein homolog
736	720606	720178	[-1 L= 429]	xxcY / Hypothetical protein
737	725197	725637	[+1 L= 441]	yhcV / IMP dehydrogenase homolog
738	725962	727110	[+1 L=1149]	xxcZ / Hypothetical protein
739	727686	727357	[-1 L= 330]	ykvI / Hypothetical protein
740	728846	727695	[-3 L=1152]	xxdA / Peptidase homolog
741	729459	730169	[+3 L= 711]	tenA / Transcriptional activator
742	730141	730887	[+1 L= 747]	xxdB / ABC transporter ATP-binding protein homolog
743	730887	731639	[+3 L= 753]	xxdC / ABC transporter permease protein homolog
744	731624	732637	[+2 L=1014]	xxdD / Thiamine biosynthesis protein homolog
745	732645	733268	[+3 L= 624]	tenI / Thiamine phosphate pyrophosphorylase
746	733264	734370	[+1 L=1107]	yjbR / Sarcosine oxidase homolog
747	734389	734589	[+1 L= 201]	xxdE / Hypothetical protein
748	734589	735362	[+3 L= 774]	thiG / Thiazole biosynthesis protein
751	735358	736374	[+1 L=1017]	thiF / Adenylyltransferase
752	736384	737202	[+1 L= 819]	yjbV / Phosphomethylpyrimidine kinase (HMP-phosphate kinase)
757	738869	740533	[+2 L=1665]	atkA / Potassium-transporting ATPase A chain
760	740547	742637	[+3 L=2091]	atkB / Potassium-transporting ATPase B chain
761	742621	743235	[+1 L= 615]	atkC / Potassium-transporting ATPase C chain
762	743295	744446	[+3 L=1152]	kdpD / Osmosensitive K+ channel His kinase sensor homolog
763	745656	744478	[-1 L=1179]	yvmA / Transporter homolog

764	745797	746255	[+3 L= 459]	yvmB / Hypothetical protein
765	746387	747238	[+2 L= 852]	xxdF / Phosphodiesterase homolog
771	750238	750885	[+1 L= 648]	xxdG / ABC transporter homolog
774	752539	751481	[-2 L=1059]	rbsC / Ribose transport system permease protein
775	754004	752460	[-3 L=1545]	rbsA / Ribose transport ATP-binding protein
776	755053	753944	[-2 L=1110]	rbsB / D-ribose-binding protein precursor
777	756637	755339	[-2 L=1299]	ytiP / Hypothetical protein
778	756828	757703	[+3 L= 876]	yhxC / Alcohol dehydrogenase homolog
780	757875	758531	[+3 L= 657]	xxdH / Hypothetical protein
782	759844	758906	[-2 L= 939]	ydjE / Fructokinase homolog
783	761316	759844	[-1 L=1473]	xxdI / Sucrose-6-phosphate hydrolase homolog
784	762710	761337	[-3 L=1374]	ptsB / PTS system, sucrose-specific IIBC component (Sucrose-permease IIBC component)
785	763832	762849	[-3 L= 984]	xxdJ / Sucrose operon repressor homolog
786	764165	763953	[-3 L= 213]	xxdK / Hypothetical protein
787	764690	764241	[-3 L= 450]	xxdL / Thioredoxin
789	765122	764706	[-3 L= 417]	dsbH / Protein-disulfide oxidoreductase homolog
790	765535	765290	[-2 L= 246]	yhdB / Hypothetical protein
791	766168	765659	[-2 L= 510]	xxdM / Hypothetical protein
792	767323	766217	[-2 L=1107]	grqB / Spore germination protein
793	768425	767343	[-3 L=1083]	grqC / Spore germination protein
795	769963	768425	[-2 L=1539]	grqA / Spore germination protein
797	770834	771457	[+2 L= 624]	yhfC / Hypothetical protein
798	771575	772990	[+2 L=1416]	spvR / Stage V sporulation protein R
800	773101	774369	[+1 L=1269]	xxdN / Hypothetical protein
801	774547	775515	[+1 L= 969]	mprA / Extracellular metalloprotease precursor
804	776184	777878	[+3 L=1695]	naoX / NADH oxidase homolog
805	778066	778326	[+1 L= 261]	ykrD / Hypothetical protein
806	778403	778975	[+2 L= 573]	ykrF / Hypothetical protein yrkF
807	778954	780144	[+1 L=1191]	ykrH / Hypothetical protein
808	780163	780402	[+1 L= 240]	ykrI / Hypothetical protein
809	780486	780800	[+3 L= 315]	ykrF / Hypothetical protein
810	780800	781111	[+2 L= 312]	xxdO / Hypothetical protein
811	781175	781651	[+2 L= 477]	ykrE / Hypothetical protein
812	781687	782448	[+1 L= 762]	ykrJ / Hypothetical protein
814	782925	782488	[-1 L= 438]	xxdP / Hypothetical protein
815	784309	783077	[-2 L=1233]	xxdQ / Hypothetical protein
816	784498	785580	[+1 L=1083]	xxdR / Zinc-binding dehydrogenase homolog
817	787284	785623	[-1 L=1662]	xxdS / Hypothetical protein
819	788829	787630	[-1 L=1200]	xxdT / Multi-drug resistance efflux pump homolog
820	789149	790234	[+2 L=1086]	xxdU / Hypothetical protein
822	790314	792251	[+3 L=1938]	licR / lichenan operon transcription antiterminator
823	792350	792682	[+2 L= 333]	licA / PTS system, lichenan-specific IIA component (Lichenan-permease IIA component)
824	792687	792989	[+3 L= 303]	licB / PTS system, lichenan-specific IIB component (Lichenan-permease IIB component)
825	793073	794383	[+2 L=1311]	licC / PTS system, lichenin-specific IIC component (Lichenin-permease IIC component)
827	794630	795712	[+2 L=1083]	xxdV / Hypothetical protein
829	798182	796803	[-3 L=1380]	xxdW / Hypothetical protein
830	799833	798643	[-1 L=1191]	xxdX / ABC-transporter permease homolog
831	800495	799824	[-3 L= 672]	yknY /ABC transporter (ATP-binding protein) homolog
832	801595	800495	[-2 L=1101]	xxdY / Hypothetical protein
833	801807	802538	[+3 L= 732]	ywaF / Hypothetical protein
834	802631	803494	[+2 L= 864]	xxdZ / Hypothetical protein
835	803499	804500	[+3 L=1002]	xxeA / Hypothetical protein
837	805861	804548	[-2 L=1314]	brnQ / Branched-chain amino acid transport system carrier protein
838	806649	806083	[-1 L= 567]	ctjC / Spore coat peptide assembly protein
839	806937	806665	[-1 L= 273]	ctjB / Spore coat peptide assembly protein
840	807149	806937	[-3 L= 213]	ctjA / Spore coat peptide assembly protein
841	807184	807609	[+1 L= 426]	xxeB / Glyoxalase homolog
842	807627	808403	[+3 L= 777]	xxeC / Hypothetical protein
843	809237	808428	[-3 L= 810]	xxeD / Hypothetical protein
844	809520	809867	[+3 L= 348]	xxeE / Hypothetical protein
845	809888	810490	[+2 L= 603]	ykoX / Alkaline phosphatase homolog
846	810600	810965	[+3 L= 366]	xxeF / Hypothetical protein

847	810989	811330 [+2 L= 342]	xxeG / Hypothetical protein
848	811866	811393 [-1 L= 474]	xxeH / Hypothetical protein
850	812152	812973 [+1 L= 822]	xxeI / Purple acid phosphatase
851	812966	814624 [+2 L=1659]	xxeJ / Purple acid phosphatase
852	814707	814907 [+3 L= 201]	xxeK / Hypothetical protein
854	815421	815125 [-1 L= 297]	xxeL / Amino acid permease
855	816578	815418 [-3 L=1161]	yfnA / Metabolite transporter homolog
856	816669	817904 [+3 L=1236]	gerN / Na_H_Exchanger, Sodium/hydrogen exchanger homolog
857	818032	818343 [+1 L= 312]	xxeM / Hypothetical protein
858	818376	819236 [+3 L= 861]	xxeN / Transcriptional regulator
859	819517	820428 [+1 L= 912]	xxeO / Hypothetical protein
860	820456	821817 [+1 L=1362]	yfeV / PTS system, sucrose phosphotransferase enzyme II, BC component
861	821869	822939 [+1 L=1071]	xxeP / Hypothetical protein
862	823095	823496 [+3 L= 402]	yfiD / Hypothetical protein
864	823654	824052 [+1 L= 399]	xxeQ / Hypothetical protein
865	824055	824537 [+3 L= 483]	xxeR / Hypothetical protein
867	825537	824578 [-1 L= 960]	xxeS / Hypothetical protein
868	825693	826184 [+3 L= 492]	asnC / Transcriptional regulator
869	826317	826769 [+3 L= 453]	xxeT / Hypothetical protein
870	827650	826856 [-2 L= 795]	xxeU / Oxidoreductase homolog
871	827758	828114 [+1 L= 357]	xxeV / Transcriptional regulator homolog
873	828521	828871 [+2 L= 351]	ykkC / Hypothetical protein
874	828877	829188 [+1 L= 312]	ykkD / Chaperonin homolog
875	829343	829918 [+2 L= 576]	yvdT / transcription regulator TetR/AcrR family homolog
876	830134	831333 [+1 L=1200]	bltA / Multidrug resistance protein 2 (Multidrug-efflux transporter 2)
877	831723	831373 [-1 L= 351]	xxeW / Hypothetical protein
878	831866	832414 [+2 L= 549]	xxeX / Hypothetical protein
879	832441	832986 [+1 L= 546]	xxeY / NAD(P)H dehydrogenase (quinone)
880	834812	833055 [-3 L=1758]	xxeZ / Bacterial extracellular solute-binding proteins
881	834897	836156 [+3 L=1260]	xxfA / Transporter homolog
883	837240	836728 [-1 L= 513]	yfkM / General stress protein 18 (GSP18)
884	839256	837262 [-1 L=1995]	katB / Catalase 2
885	840739	839534 [-2 L=1206]	xxfB / Hypothetical protein
886	842314	840794 [-2 L=1521]	yvsH / ABC transporter (amino acid permease) homolog
888	842746	843573 [+1 L= 828]	murI / Glutamate racemase
889	843681	844769 [+3 L=1089]	xxfC / Hypothetical protein
890	846365	844854 [-3 L=1512]	gapN / NADP-dependent glyceraldehyde-3-phosphate dehydrogenase
892	846887	848644 [+2 L=1758]	yheI / ABC transporter (amino acid permease) homolog
893	848644	850641 [+1 L=1998]	yheH / ABC transporter (ATP-binding protein) homolog
894	850939	851733 [+1 L= 795]	yckK / Probable amino-acid ABC transporter extracellular binding protein precursor
896	851717	852418 [+2 L= 702]	yckJ / Probable amino-acid ABC transporter permease protein
897	852450	853181 [+3 L= 732]	yckI / Probable amino-acid ABC transporter ATP-binding protein
898	853439	853239 [-3 L= 201]	sspA / SMALL, ACID-SOLUBLE SPORE PROTEIN 1 (SASP)
899	853895	854140 [+2 L= 246]	xxfD / Hypothetical protein
900	855641	854166 [-3 L=1476]	yheD / Hypothetical protein
901	856702	855644 [-2 L=1059]	yheC / Hypothetical protein
902	856814	857956 [+2 L=1143]	yheB / Hypothetical protein
903	858102	858455 [+3 L= 354]	yheA / Hypothetical protein
904	859008	861308 [+3 L=2301]	comP / Two-component sensor histidine kinase
905	861347	862000 [+2 L= 654]	comA / Competence two-component regulator
906	862782	864467 [+3 L=1686]	ilvX / Acetolactate synthase (Acetohydroxy-acid synthase)
907	864487	865242 [+1 L= 756]	aldC / Alpha-acetolactate decarboxylase
908	866083	865469 [-2 L= 615]	xxfE / 3-methyladenine DNA glycosylase homolog
909	866104	867087 [+1 L= 984]	yhaX / Stress response protein
910	867437	871447 [+2 L=4011]	xxfF / Hypothetical protein
911	873263	871548 [-3 L=1716]	yqeE / N-acetylmuramoyl-L-alanine amidase precursor (Cell wall hydrolase) (Autolysin)
912	873494	874987 [+2 L=1494]	hemN / Oxygen-independent coproporphyrinogen III oxidase (Coproporphyrinogenase)
913	875313	876866 [+3 L=1554]	xxfG / Long-chain fatty-acid-CoA ligase
915	878218	877757 [-2 L= 462]	xxfH / Hypothetical protein
916	878364	879872 [+3 L=1509]	ybaR / Sulfate transporter
917	880172	881728 [+2 L=1557]	yabM / Amino acid transport protein homolog
918	881875	882960 [+1 L=1086]	xxfI / Pyruvyl-transferase homolog
919	883110	884969 [+3 L=1860]	xxfJ / N-acetylmuramoyl-L-alanine amidase homolog

920	886413	885022 [-1 L=1392]	xxfK / Hypothetical protein
922	886610	887524 [+2 L= 915]	echH / 3-hydroxbutyryl-CoA dehydratase homolog
924	887981	888307 [+2 L= 327]	xxfL / Hypothetical protein
926	888638	889684 [+2 L=1047]	yhfE / Glucanase homolog
927	889955	891583 [+2 L=1629]	xxfM / N-acetylmuramoyl-L-alanine amidase homolog
928	891735	892685 [+3 L= 951]	xxfN / Methyltransferase homolog
929	893105	892797 [-3 L= 309]	yflJ / Hypothetical protein
930	893127	894176 [+3 L=1050]	xxfO / Hypothetical protein
931	894223	895317 [+1 L=1095]	ocdB / Ornithine cyclodeaminase 2 homolog
932	895682	895822 [+2 L= 141]	xxfP / Hypothetical protein
933	895842	897263 [+3 L=1422]	appA / Oligopeptide-binding protein precursor
934	897322	898269 [+1 L= 948]	appB / Oligopeptide transport system permease protein
935	898279	899127 [+1 L= 849]	appC / Oligopeptide transport system permease protein
936	899139	900146 [+3 L=1008]	dppD / Dipeptide transport ATP-binding protein
937	900133	901110 [+1 L= 978]	appF / Oligopeptide transport ATP-binding protein
939	902684	903502 [+2 L= 819]	xxfQ / Hypothetical protein
940	903510	903899 [+3 L= 390]	xxfR / Hypothetical protein
941	904054	904575 [+1 L= 522]	xxfS / Hypothetical protein
945	906295	906594 [+1 L= 300]	xxfT / Hypothetical protein
947	907101	907460 [+3 L= 360]	xxfU / Hypothetical protein
948	907460	909094 [+2 L=1635]	yokI / Hypothetical protein
949	909131	909481 [+2 L= 351]	xxfV / Hypothetical protein
956	911123	911314 [+2 L= 192]	xxfW / Hypothetical protein
957	911332	911784 [+1 L= 453]	xxfX / Hypothetical protein
960	912865	913080 [+1 L= 216]	xxfY / Hypothetical protein
961	913132	913635 [+1 L= 504]	xxfZ / Hypothetical protein
968	917553	916234 [-1 L=1320]	xxgA / Dicarboxylate transporter homolog
970	917908	919392 [+1 L=1485]	citS / Two-component sensor histidine kinase
971	919389	920063 [+3 L= 675]	citT / Two-component response regulator
972	920063	921073 [+2 L=1011]	yflP / Hypothetical protein
974	921545	923161 [+2 L=1617]	ydiS / 5-methylcytosine-specific restriction enzyme homolog
975	923157	924488 [+3 L=1332]	ydjA / Hypothetical protein
976	924579	925697 [+3 L=1119]	xxgB / Site-specific DNA methylase homolog
980	928608	930188 [+3 L=1581]	xxgC / Hypothetical protein
981	930474	931520 [+3 L=1047]	intR / Phage integrase
985	935648	940018 [+2 L=4371]	xxgD / Hypothetical protein
988	941038	941289 [+1 L= 252]	xxgE / Hypothetical protein
989	941301	942035 [+3 L= 735]	xxgF / Transcriptional regulator homolog
991	942294	943037 [+3 L= 744]	xxgG / Hypothetical protein
992	943646	944506 [+2 L= 861]	xxgH / Hypothetical protein
993	944497	945789 [+1 L=1293]	dnaC / Replicative DNA helicase
994	945837	946001 [+3 L= 165]	xxgI / Hypothetical protein
995	946992	946147 [-1 L= 846]	xxgJ / Hypothetical protein
997	947148	947957 [+3 L= 810]	xxgK / Hypothetical protein
998	949162	948590 [-2 L= 573]	tetR / Bacterial regulatory protein tetR homolog
999	949305	950777 [+3 L=1473]	lmrB / Lincomycin resistance protein
1000	951126	951677 [+3 L= 552]	xxgL / Hypothetical protein
1003	952361	952903 [+2 L= 543]	yjcK / Ribosomal-protein-alanine N-acetyltransfer homolog
1005	954149	954817 [+2 L= 669]	yhcS / Hypothetical protein
1007	957005	955626 [-3 L=1380]	xxgM / Hypothetical protein
1009	958033	958371 [+1 L= 339]	xxgN / Hypothetical protein
1010	960049	958646 [-2 L=1404]	xxgO / Hypothetical protein
1012	960477	961058 [+3 L= 582]	xxgP / Hypothetical protein
1013	961178	961729 [+2 L= 552]	xxgQ / Hypothetical protein
1014	962288	961914 [-3 L= 375]	xxgR / Hypothetical protein
1015	962566	963072 [+1 L= 507]	xxgS / Transcriptional regulator homolog
1016	963059	963649 [+2 L= 591]	pssA / CDP-diacylglycerol--serine O-phosphatidyltransferase (Phosphatidylserine synthase)
1017	963668	964060 [+2 L= 393]	xxgT / Hypothetical protein
1018	964378	965010 [+1 L= 633]	xxgU / Hypothetical protein
1019	966123	965116 [-1 L=1008]	dakA / Dihydroxyacetone kinase
1021	966706	966134 [-2 L= 573]	xxgV / Transcriptional regulator
1022	966876	968624 [+3 L=1749]	dakB / Dihydroxyacetone kinase
1027	971287	972393 [+1 L=1107]	xxgW / Response regulator homolog
1029	972775	973179 [+1 L= 405]	xxgX / Hypothetical protein
1031	974577	973807 [-1 L= 771]	xxgY / Hypothetical protein

1032	975066	975344	[+3 L= 279]	xxgZ / Hypothetical protein
1035	976466	978211	[+2 L=1746]	slaA / S-layer protein sap precursor (Surface array protein)
1037	979121	979450	[+2 L= 330]	xxhA / Hypothetical protein
1038	979467	980075	[+3 L= 609]	xxhB / Hypothetical protein
1041	980946	981356	[+3 L= 411]	xxhC / Hypothetical protein
1042	981899	981447	[-3 L= 453]	xxhD / Hypothetical protein
1043	982113	982499	[+3 L= 387]	yflT / Hypothetical protein
1045	982544	982750	[+2 L= 207]	xxhE / Hypothetical protein
1046	982829	983077	[+2 L= 249]	xxhF / Hypothetical protein
1048	983659	983994	[+1 L= 336]	rsbV / Anti-sigma B factor antagonist
1049	984004	984483	[+1 L= 480]	rsbW / Anti-sigma B factor
1050	984449	985222	[+2 L= 774]	rpsB / RNA polymerase sigma-B factor
1051	985290	985733	[+3 L= 444]	bfrA / Bacterioferritin
1052	985909	987048	[+1 L=1140]	rsbP / SigmaB regulation protein phosphatase 2C
1053	987948	987094	[-1 L= 855]	cheR / Methyltransferase
1054	990655	987968	[-2 L=2688]	cheY / Homologous receiver homolog
1057	991525	992052	[+1 L= 528]	xxhG / Hypothetical protein
1058	992096	992395	[+2 L= 300]	xxhH / Hypothetical protein
1059	992526	992843	[+3 L= 318]	xxhI / Hypothetical protein
1062	994818	993829	[-1 L= 990]	xxhJ / Zinc-binding dehydrogenase homolog
1063	994994	995977	[+2 L= 984]	cbaH / Choloylglycine hydrolase
1064	996260	996105	[-3 L= 156]	yflJ / Hypothetical protein
1065	996334	996756	[+1 L= 423]	xxhK / Hypothetical protein
1067	997181	998419	[+2 L=1239]	yhaO / DNA repair exonuclease
1068	998419	1001340	[+1 L=2922]	yhaN / Hypothetical protein
1069	1001385	1002326	[+3 L= 942]	yhaM / CMP-binding factor homolog
1070	1002590	1002961	[+2 L= 372]	xxhL / Hypothetical protein
1071	1004051	1003428	[-3 L= 624]	yrhP / Dihydrodipicolinate reductase homolog
1072	1004923	1005864	[+1 L= 942]	yckA / ABC transporter homolog
1073	1005908	1006897	[+2 L= 990]	xxhM / ABC transporter substrate-binding protein homolog
1074	1007106	1008233	[+3 L=1128]	xxhN / Response regulator homolog
1076	1008593	1009465	[+2 L= 873]	xxhO / Hypothetical protein
1078	1009547	1009744	[+2 L= 198]	yhaL / Hypothetical protein
1079	1009962	1010810	[+3 L= 849]	xxhP / Hypothetical protein
1082	1012100	1013293	[+2 L=1194]	oxdD / Oxalate decarboxylase
1083	1013680	1014126	[+1 L= 447]	xxhQ / Hypothetical protein
1084	1014227	1014784	[+2 L= 558]	glpP / Glycerol uptake operon antiterminator regulatory protein
1085	1014999	1015832	[+3 L= 834]	glpF / Glycerol uptake facilitator protein
1086	1015849	1017336	[+1 L=1488]	glpK / Glycerol kinase (ATP:glycerol 3-phosphotransferase)
1088	1017434	1019152	[+2 L=1719]	glpD / Aerobic glycerol-3-phosphate dehydrogenase
1089	1019234	1019599	[+2 L= 366]	xxhR / Hypothetical protein
1090	1019595	1020368	[+3 L= 774]	xxhS / Hypothetical protein
1093	1021842	1021282	[-1 L= 561]	xxhT / Hypothetical protein
1094	1024264	1021934	[-2 L=2331]	uvrD / Helicase
1095	1024437	1024787	[+3 L= 351]	xxhU / Hypothetical protein
1096	1025733	1024876	[-1 L= 858]	lipA / Rotamase, PPIC-type
1099	1026455	1026799	[+2 L= 345]	yhaI / Hypothetical protein
1100	1027365	1026811	[-1 L= 555]	hprA / Protease production regulatory protein
1102	1028110	1027667	[-2 L= 444]	yhaH / Hypothetical protein
1103	1028704	1028210	[-2 L= 495]	hitC / Cell-cycle regulation histidine triad (HIT) protein
1105	1029203	1029943	[+2 L= 741]	ecsA / ABC-type transporter ATP-binding protein
1106	1029939	1031147	[+3 L=1209]	ecsB / ABC transporter permease
1107	1031164	1031868	[+1 L= 705]	ecsC / Hypothetical protein
1110	1032181	1032771	[+1 L= 591]	xxhV / Bacterial regulatory proteins, tetR family
1112	1033024	1033485	[+1 L= 462]	ydbS / Hypothetical protein
1114	1033485	1034942	[+3 L=1458]	ydbT / Hypothetical protein
1116	1035472	1035735	[+1 L= 264]	xxhW / Hypothetical protein
1117	1036077	1036610	[+3 L= 534]	xxhX / Transcriptional regulator
1118	1036938	1044269	[+3 L=7332]	xxhY / Hypothetical protein, possible collagen adhesin precursor
1121	1045485	1046228	[+3 L= 744]	xxhZ / Hypothetical protein
1122	1046321	1047259	[+2 L= 939]	yxxF / Hypothetical transport protein
1123	1047493	1047966	[+1 L= 474]	ydbS / Hypothetical protein
1124	1047953	1049374	[+2 L=1422]	ydbT / Hypothetical protein
1125	1050086	1049592	[-3 L= 495]	yixC / Hypothetical protein
1126	1050214	1052328	[+1 L=2115]	pbpF / Penicillin-binding protein 1F (PBP-1F)
1127	1052485	1053552	[+1 L=1068]	dcuP / Uroporphyrinogen decarboxylase (URO-D)

1128	1053570	1054502	[+3 L= 933]	hemZ / Ferrochelatase (Heme synthetase)
1130	1054524	1055942	[+3 L=1419]	ppoX / Protoporphyrinogen oxidase (PPO)
1131	1057372	1056005	[-2 L=1368]	xxiA / Hypothetical protein
1132	1057596	1059959	[+3 L=2364]	xxiB / Hypothetical protein
1133	1060096	1060392	[+1 L= 297]	xxiC / Hypothetical protein
1136	1061313	1060453	[-1 L= 861]	xxiD / Hypothetical protein
1137	1061514	1061924	[+3 L= 411]	blaI / Beta-lactamase repressor protein
1138	1061930	1063876	[+2 L=1947]	blaR / Membrane-associated Zn-dependent protease homolog
1139	1064129	1064722	[+2 L= 594]	yhgD / Transcription regulator TetR/AcrR family homolog
1140	1064943	1068044	[+3 L=3102]	xxiE / Hypothetical protein
1142	1068392	1068712	[+2 L= 321]	xxiF / Hypothetical protein
1143	1069137	1068745	[-1 L= 393]	xxiG / Hypothetical protein
1145	1069229	1069735	[+2 L= 507]	xxiH / Acetyltransferase homolog
1146	1069864	1070943	[+1 L=1080]	yhjM / Transcription regulator LacI family homolog
1147	1071183	1070989	[-1 L= 195]	yhfH / Hypothetical protein
1148	1071324	1072055	[+3 L= 732]	blaB / Lactamase_B, metallo-beta-lactamase superfamily
1149	1072068	1073054	[+3 L= 987]	lplA / Lipoate-protein ligase homolog
1151	1073176	1073622	[+1 L= 447]	xxiI / Hypothetical protein
1152	1073787	1075316	[+3 L=1530]	lcfA / Long-chain-fatty-acid--CoA ligase (Long-chain acyl-CoA synthetase)
1153	1075322	1075660	[+2 L= 339]	xxiJ / Hypothetical surface layer protein
1154	1075838	1076401	[+2 L= 564]	subI / Sulfate ABC transporter (sulfate-binding protein)
1155	1076361	1076888	[+3 L= 528]	subI / Sulfate ABC transporter (sulfate-binding protein)
1157	1076926	1077750	[+1 L= 825]	cysT / Sulfate ABC transporter (permease)
1159	1077765	1078619	[+3 L= 855]	cysW / Sulfate ABC transporter (permease)
1160	1078594	1079706	[+1 L=1113]	cysA / Sulfate transport ATP-binding protein
1162	1080977	1081261	[+2 L= 285]	xxiK / Hypothetical protein
1168	1084290	1085078	[+3 L= 789]	xxiL / Hypothetical protein
1173	1087083	1087460	[+3 L= 378]	xxiM / Hypothetical protein
1177	1089730	1090608	[+1 L= 879]	xxiN / Hypothetical protein
1181	1092555	1091452	[-1 L=1104]	cytK / Cytotoxin K
1182	1092751	1093854	[+1 L=1104]	xxiO / Hypothetical protein
1183	1093991	1094965	[+2 L= 975]	ydhJ / Hypothetical protein
1184	1096145	1095015	[-3 L=1131]	yhdL / Hypothetical protein
1185	1096627	1096145	[-2 L= 483]	yhdM / RNA polymerase sigma factor
1186	1096765	1097664	[+1 L= 900]	xxiP / Transcriptional regulator (AraC/XylS family)
1187	1097686	1098090	[+1 L= 405]	xxiQ / Glyoxalase/Bleomycin resistance protein homolog
1189	1100639	1098900	[-3 L=1740]	yvrG / Two-component sensor histidine kinase homolog
1190	1101359	1100652	[-3 L= 708]	yvrH / Two-component response regulator homolog
1191	1101488	1102339	[+2 L= 852]	xxiR / Amino terminal protease homolog
1192	1102344	1102604	[+3 L= 261]	xxiS / Hypothetical protein
1194	1102732	1103028	[+1 L= 297]	xxiT / Hypothetical protein
1195	1103219	1104535	[+2 L=1317]	yhfN / Putative metalloprotease
1196	1104673	1106397	[+1 L=1725]	mcpA / Methyl-accepting chemotaxis protein
1198	1106840	1107493	[+2 L= 654]	xxiU / S-layer protein precursor (surface layer protein)
1200	1107581	1108399	[+2 L= 819]	xxiV / S-layer protein precursor (surface layer protein)
1201	1108622	1110208	[+2 L=1587]	masY / Malate synthase
1202	1110226	1111509	[+1 L=1284]	aceA / Isocitrate lyase (Isocitratase)
1203	1112470	1111625	[-2 L= 846]	xxiW / Choline/ethanolamine kinase homolog
1205	1113211	1113411	[+1 L= 201]	cspD / Cold shock protein
1210	1114632	1115210	[+3 L= 579]	comK / Competence transcription factor (Competence protein k)
1211	1115649	1116239	[+3 L= 591]	yhjE / Hypothetical protein
1212	1116299	1116859	[+2 L= 561]	lepI / Signal peptidase I (Leader peptidase I)
1213	1116979	1120491	[+1 L=3513]	addB / ATP-dependent deoxyribonuclease chain B
1214	1120491	1124213	[+3 L=3723]	addA / ATP-dependent deoxyribonuclease chain A
1215	1124229	1124513	[+3 L= 285]	xxiX / Hypothetical protein
1216	1124870	1124652	[-3 L= 219]	gepF / Probable spore germination protein
1217	1125294	1124911	[-1 L= 384]	gepE / Probable spore germination protein
1218	1125504	1125313	[-1 L= 192]	gepD / Probable spore germination protein
1219	1126125	1125514	[-1 L= 612]	gepC / Probable spore germination protein
1220	1126399	1126196	[-2 L= 204]	gepB / Probable spore germination protein
1221	1126644	1126417	[-1 L= 228]	gepA / Probable spore germination protein
1222	1126926	1126735	[-1 L= 192]	yisI / Hypothetical protein
1224	1127150	1128055	[+2 L= 906]	yisK / 5-oxo-1,2,5-tricarboxilic-3-penten acid decarboxylase homolog
1225	1128376	1128098	[-2 L= 279]	xxiY / Hypothetical protein
1226	1129677	1128490	[-1 L=1188]	rocD / Ornithine aminotransferase
1227	1129828	1130190	[+1 L= 363]	yisL / Hypothetical protein

1228	1130878	1130327	[-2 L= 552]	yisN / Hypothetical protein
1229	1131109	1132122	[+1 L=1014]	asnO / Asparagine synthetase [glutamine-hydrolyzing]
1230	1132169	1132963	[+2 L= 795]	asnO / Asparagine synthetase [glutamine-hydrolyzing]
1231	1133155	1134111	[+1 L= 957]	hemH / Ferrochelatase (Heme synthetase)
1232	1134174	1135637	[+3 L=1464]	catA / Catalase
1233	1137140	1135911	[-3 L=1230]	nrgA / Probable ammonium transporter
1234	1137299	1138651	[+2 L=1353]	xxiZ / Alpha amylase
1236	1139080	1139853	[+1 L= 774]	xxjA / Hypothetical protein
1237	1141216	1140713	[-2 L= 504]	yitK / Hypothetical protein
1238	1141432	1142283	[+1 L= 852]	yitL / Hypothetical protein
1239	1143197	1142343	[-3 L= 855]	xxjB / Rotamase homolog
1242	1143516	1144412	[+3 L= 897]	yitT / Hypothetical protein
1246	1145694	1144888	[-1 L= 807]	xxjC / Hypothetical protein
1247	1146180	1146362	[+3 L= 183]	yjcZ / Hypothetical protein
1249	1146518	1149172	[+2 L=2655]	clpB / endopeptidase Clp ATP-binding chain B
1250	1149396	1149217	[-1 L= 180]	yjzD / Hypothetical protein
1251	1149553	1150284	[+1 L= 732]	yjaU / Hypothetical protein
1252	1150305	1151186	[+3 L= 882]	xxjD / Hypothetical protein
1253	1151244	1151417	[+3 L= 174]	yjzA / Hypothetical protein
1254	1152127	1153056	[+1 L= 930]	fabH / 3-oxoacyl-[acyl-carrier-protein] synthase III (Beta-ketoacyl-ACP synthase III)
1255	1153091	1154326	[+2 L=1236]	fabF / 3-oxoacyl-[acyl-carrier-protein] synthase II (Beta-ketoacyl-ACP synthase II)
1256	1154437	1155222	[+1 L= 786]	yjaZ / Hypothetical protein
1257	1155369	1156112	[+3 L= 744]	yjbA / Hypothetical protein
1259	1157079	1156477	[-1 L= 603]	ywbS / Tryptophanyl-tRNA synthetase (Tryptophan--tRNA ligase)
1260	1157462	1157082	[-3 L= 381]	ywbT / Tryptophanyl-tRNA synthetase (Tryptophan--tRNA ligase)
1261	1158259	1157864	[-2 L= 396]	xxjE / Hypothetical protein
1264	1158609	1160213	[+3 L=1605]	oppA / Extracellular solute-binding proteins, family 5
1265	1160334	1161269	[+3 L= 936]	oppB / Oligopeptide transport system permease protein
1266	1161269	1162282	[+2 L=1014]	oppC / Dipeptide transport system permease protein
1268	1162304	1163344	[+2 L=1041]	oppD / Oligopeptide transport ATP-binding protein
1269	1163331	1164272	[+3 L= 942]	oppF / Oligopeptide transport ATP-binding protein
1270	1165864	1164422	[-2 L=1443]	yisQ / Hypothetical protein
1271	1166202	1167860	[+3 L=1659]	oppE / Dipeptide-binding protein precursor
1273	1168622	1169083	[+2 L= 462]	yjbD / Hypothetical protein
1274	1169810	1169139	[-3 L= 672]	yjbE / Hypothetical protein
1275	1170156	1170836	[+3 L= 681]	mecA / Negative regulator of genetic competence
1276	1170912	1172453	[+3 L=1542]	clsA / Cardiolipin synthetase (CL synthase)
1277	1172537	1173778	[+2 L=1242]	yjbF / Hypothetical protein
1278	1173833	1175656	[+2 L=1824]	pepF / Oligoendopeptidase F homolog
1280	1177085	1176195	[-3 L= 891]	xxjF / Hypothetical protein
1281	1177483	1177088	[-2 L= 396]	glbO / Hemoglobin-like protein HbO
1282	1178230	1177655	[-2 L= 576]	yjbK / Hypothetical protein
1283	1178375	1178743	[+2 L= 369]	yjbL / Hypothetical protein
1284	1178756	1179412	[+2 L= 657]	xxjG / GTP pyrophosphokinase
1285	1179434	1180228	[+2 L= 795]	ppnK / Probable inorganic polyphosphate/ATP-NAD kinase
1286	1180246	1181136	[+1 L= 891]	yjbO / Hypothetical protein
1287	1181328	1181191	[-1 L= 138]	xxjH / Hypothetical protein
1288	1182575	1181412	[-3 L=1164]	xxjI / Hypothetical protein
1289	1183566	1182715	[-1 L= 852]	apaH / Bis(5'-nucleosyl)-tetraphosphatase, symmetrical (Diadenosine tetraphosphatase)
1290	1184689	1183532	[-2 L=1158]	xxjJ / Stage V sporulation protein E
1291	1185854	1184931	[-3 L= 924]	xxjK / Glycosyltransferase homolog
1292	1186677	1185871	[-1 L= 807]	xxjL / Hypothetical protein
1293	1187650	1186808	[-2 L= 843]	xxjM / O-methyltransferase homolog
1294	1188159	1187776	[-1 L= 384]	bclA / BclA protein
1295	1188403	1188149	[-2 L= 255]	bclA / BclA protein
1297	1188548	1189663	[+2 L=1116]	xxjN / Hypothetical protein
1298	1189869	1190564	[+3 L= 696]	pcmT / Protein-L-isoD(D-D) O-methyltransferase
1299	1190564	1191247	[+2 L= 684]	xxjO / Hypothetical protein
1300	1191265	1191942	[+1 L= 678]	xxjP / Hypothetical protein
1301	1191960	1192694	[+3 L= 735]	goeI / Glucose-1-phosphate thymidylyltransferase
1302	1192706	1193248	[+2 L= 543]	rfbC / dTDP-4-dehydrorhamnose 3,5-epimerase (dTDP-4-keto-6-deoxyglucose 3,5-epimerase)
1303	1193261	1194235	[+2 L= 975]	rfbB / dTDP-glucose 4,6-dehydratase

1304	1194251	1195102	[+2 L= 852]	rfbD / dTDP-dehydrorhamnose reductase
1305	1195214	1195981	[+2 L= 768]	fabI / Enoyl-[acyl-carrier-protein] reductase [NADH] (NADH-dependent enoyl-ACP reductase)
1307	1196074	1196667	[+1 L= 594]	xxjQ / Hypothetical protein
1308	1197198	1196734	[-1 L= 465]	xxjR / Hypothetical protein
1309	1197192	1197671	[+3 L= 480]	xxjS / Hypothetical protein
1311	1198548	1198039	[-1 L= 510]	xxjT / Hypothetical protein
1312	1199258	1198710	[-3 L= 549]	xxjU / Hypothetical protein
1313	1201386	1199323	[-1 L=2064]	yjcD / ATP-dependent DNA helicase pcrA
1314	1201930	1201490	[-2 L= 441]	yjcF / Acetyltransferase homolog
1315	1202429	1201914	[-3 L= 516]	yjcG / Hypothetical protein
1316	1203488	1202526	[-3 L= 963]	yjcH / Hypothetical protein
1317	1203458	1204366	[+2 L= 909]	xxjV / Hypothetical protein
1318	1204369	1204590	[+1 L= 222]	xxjW / Hypothetical protein
1319	1204597	1204839	[+1 L= 243]	xxjX / Hypothetical protein
1320	1205127	1204870	[-1 L= 258]	xxjY / Hypothetical protein
1322	1206899	1205424	[-3 L=1476]	opuE / Osmoregulated proline transporter (Sodium/proline symporter)
1325	1207677	1209197	[+3 L=1521]	trpE / Anthranilate/para-aminobenzoate synthases component I
1326	1209197	1209781	[+2 L= 585]	trpG / Anthranilate synthase component II [Includes: Glutamine amidotransferase; Anthranilate phosphoribosyltransferase]
1327	1209781	1210803	[+1 L=1023]	trpD / Anthranilate phosphoribosyltransferase
1328	1210808	1211566	[+2 L= 759]	trpC / Indole-3-glycerol phosphate synthase (IGPS)
1330	1211566	1212177	[+1 L= 612]	trpF / N-(5'-phosphoribosyl)anthranilate isomerase (PRAI)
1331	1212168	1213367	[+3 L=1200]	trpB / Tryptophan synthase beta chain
1333	1213374	1214147	[+3 L= 774]	trpA / Tryptophan synthase alpha chain
1334	1214224	1214580	[+1 L= 357]	xxjZ / Hypothetical protein
1336	1214698	1216194	[+1 L=1497]	lctP / L-lactate permease
1337	1216279	1216971	[+1 L= 693]	yukJ / Hypothetical protein
1338	1217819	1216989	[-3 L= 831]	xxkA / Hypothetical protein
1339	1218016	1218783	[+1 L= 768]	xxkB / Hypothetical protein
1340	1218806	1220038	[+2 L=1233]	yvbJ / Hypothetical protein
1341	1220527	1220090	[-2 L= 438]	xxkC / Hypothetical protein
1344	1220716	1222047	[+1 L=1332]	naoX / NADH oxidase (NOXASE)
1346	1222211	1222618	[+2 L= 408]	xxkD / Hypothetical protein
1347	1224193	1222655	[-2 L=1539]	xxkE / Hypothetical protein
1348	1226158	1224212	[-2 L=1947]	xxkF / Hypothetical protein
1349	1228074	1226158	[-1 L=1917]	xxkG / Hypothetical protein
1350	1229458	1228202	[-2 L=1257]	odhB / Dihydrolipoamide succinyltransferase component of 2-oxoglutarate dehydrogenase complex (E2)
1351	1232459	1229595	[-3 L=2865]	odhA / 2-oxoglutarate dehydrogenase E1 component (Alpha-ketoglutarate dehydrogenase)
1354	1233283	1233489	[+1 L= 207]	xxkH / Transcriptional regulator
1355	1233495	1233869	[+3 L= 375]	xxkI / Hypothetical protein
1357	1234217	1234576	[+2 L= 360]	xxkJ / Hypothetical protein
1363	1236890	1238404	[+2 L=1515]	xxkK / Hypothetical protein
1366	1240375	1241616	[+1 L=1242]	yonV / Bacillus subtilis phage SPBc2 protein
1369	1244803	1244609	[-2 L= 195]	yetN / Hypothetical protein
1373	1247690	1249381	[+2 L=1692]	xxkL / Hypothetical protein
1374	1249737	1250846	[+3 L=1110]	xxkM / Phage integrase homolog
1377	1253570	1252755	[-3 L= 816]	radC / Ribosomal RNA adenine dimethylase homolog
1378	1254029	1254253	[+2 L= 225]	xxkN / Hypothetical protein
1379	1254354	1255691	[+3 L=1338]	dacB / Penicillin-binding protein 5* precursor (D-alanyl-D-alanine carboxypeptidase)
1381	1255840	1256451	[+1 L= 612]	lepW / Signal peptidase I W (Leader peptidase I)
1382	1256509	1257099	[+1 L= 591]	xxkO / Hypothetical protein
1383	1257218	1258054	[+2 L= 837]	xxkP / Hypothetical protein
1385	1258438	1259034	[+1 L= 597]	cotN / Spore coat-associated protein N (camelysin)
1388	1259454	1259113	[-1 L= 342]	sinR / Regulator protein
1389	1259647	1259516	[-2 L= 132]	sinI / Regulator protein
1392	1259990	1262377	[+2 L=2388]	inaA / Immune inhibitor A precursor
1393	1262552	1263916	[+2 L=1365]	ywdH / Aldehyde dehydrogenase
1395	1264160	1265140	[+2 L= 981]	potA / Spermidine/putrescine transport ATP-binding protein
1396	1265140	1265985	[+1 L= 846]	potB / Spermidine/putrescine transport system permease protein
1397	1265995	1266792	[+1 L= 798]	potC / Spermidine/putrescine transport system permease protein
1399	1266834	1267880	[+3 L=1047]	potD / Spermidine/putrescine-binding periplasmic protein precursor
1400	1267943	1268587	[+2 L= 645]	xxkQ / Hypothetical protein

1401	1268701	1270890	[+1 L=2190]	xxkR / Hypothetical protein
1403	1270986	1271408	[+3 L= 423]	yodN / Hypothetical protein
1404	1271500	1272432	[+1 L= 933]	yhcT / Pseudouridine synthase homolog
1405	1272527	1273141	[+2 L= 615]	xxkS / Hypothetical protein
1406	1274012	1273188	[-3 L= 825]	ykwD / Hypothetical protein
1407	1275796	1274471	[-2 L=1326]	glcF / Glycolate oxidase iron-sulfur subunit
1408	1277205	1275796	[-1 L=1410]	glcD / Glycolate oxidase subunit
1409	1278447	1277326	[-1 L=1122]	ysfB / Hypothetical protein
1410	1278365	1279546	[+2 L=1182]	xxkT / Hypothetical protein
1411	1279542	1280210	[+3 L= 669]	resD / Two-component transcriptional regulatory protein
1412	1280217	1281614	[+3 L=1398]	resE / Two-component sensor protein
1413	1282033	1282686	[+1 L= 654]	xxkU / Transcriptional regulator
1414	1282858	1283574	[+1 L= 717]	yvfV / Glycolate oxidase subunit homolog
1415	1283594	1285012	[+2 L=1419]	yvfW / Iron-sulfur protein
1416	1285015	1285722	[+1 L= 708]	yvbY / Hypothetical protein
1417	1285812	1286558	[+3 L= 747]	comC / Type 4 prepilin-like proteins leader peptide processing enzyme (Late competence protein comC)
1419	1287766	1286918	[-2 L= 849]	ywcJ / Nitrite transport protein homolog
1422	1288900	1287971	[-2 L= 930]	xxkV / Hypothetical protein
1424	1290500	1289061	[-3 L=1440]	yubG / Na+-transporting ATP synthase homolog
1425	1290690	1290496	[-1 L= 195]	sasD / Small acid-soluble spore protein C-3 (SASP)
1426	1291365	1290829	[-1 L= 537]	maoC / 3-hydroxybutyryl-CoA dehydratase
1427	1291895	1291374	[-3 L= 522]	xxkW / Hypothetical protein
1429	1292388	1292107	[-1 L= 282]	xxkX / Hypothetical protein
1430	1292538	1293065	[+3 L= 528]	phaR / Poly-beta-hydroxybutyrate polymerase (PHA synthase) (Polyhydroxyalkanoic acid synthase)
1431	1293219	1293959	[+3 L= 741]	fabG / 3-oxoacyl-[acyl-carrier protein] reductase (3-ketoacyl-acyl carrier protein reductase)
1432	1294045	1295127	[+1 L=1083]	PhaC / Poly-beta-hydroxybutyrate polymerase (PHA synthase) (Polyhydroxyalkanoic acid synthase)
1433	1295225	1296418	[+2 L=1194]	xxkY / FAD dependent oxidoreductase homolog
1435	1296445	1297791	[+1 L=1347]	ykrM / Na+-transporting ATP synthase homolog
1436	1298174	1297836	[-3 L= 339]	xxkZ / Hypothetical protein
1438	1298308	1298466	[+1 L= 159]	xxlA / Hypothetical protein
1441	1298698	1299771	[+1 L=1074]	xxlB / Hypothetical protein
1442	1299779	1300792	[+2 L=1014]	xxlC / ABC transporter homolog
1443	1300796	1302550	[+2 L=1755]	xxlD / ABC transporter permease homolog
1444	1302563	1303255	[+2 L= 693]	ppaZ / Phosphonoacetaldehyde Hydrolase
1445	1303385	1304479	[+2 L=1095]	aepT / 2-aminoethylphosphonate:pyruvate aminotransferase
1446	1304479	1305660	[+1 L=1182]	xxlE / Hypothetical protein
1447	1305704	1306483	[+2 L= 780]	yulB / Transcriptional regulator
1449	1306908	1309205	[+3 L=2298]	xxlF / Hypothetical protein
1450	1309541	1309987	[+2 L= 447]	ykrY / Hypothetical protein
1451	1310050	1310166	[+1 L= 117]	xxlG / Class II aldolase homolog
1452	1310269	1310916	[+1 L= 648]	xxlH / CBS, Domain in cystathionine beta-synthase and other proteins
1454	1311862	1311095	[-2 L= 768]	xxlI / Hypothetical protein
1455	1312344	1312622	[+3 L= 279]	ynzD / Hypothetical protein
1456	1314181	1312658	[-2 L=1524]	ykvD / Two-component sensor histidine kinase homolog
1457	1314347	1314790	[+2 L= 444]	ykvE / Transcriptional regulator
1458	1314950	1316641	[+2 L=1692]	xxlM / Oligoendopeptidase F homolog
1459	1316730	1317311	[+3 L= 582]	yuaE / Hypothetical protein
1463	1318752	1317547	[-1 L=1206]	kinB / Sporulation kinase B
1464	1319087	1319755	[+2 L= 669]	ykvJ / Hypothetical protein
1465	1319758	1320246	[+1 L= 489]	ptpS / 6-pyruvoyl tetrahydropterin synthase
1466	1320239	1320955	[+2 L= 717]	ykvL / Coenzyme PQQ synthesis homolog
1467	1320968	1321471	[+2 L= 504]	ykvM / Hypothetical protein
1468	1321714	1321526	[-2 L= 189]	ykvS / Hypothetical protein
1470	1322204	1322812	[+2 L= 609]	xxlN / Hypothetical protein
1471	1323465	1322854	[-1 L= 612]	xxlO / Acetyltransferase homolog
1472	1323710	1323955	[+2 L= 246]	xxlP / Hypothetical protein
1473	1324059	1324373	[+3 L= 315]	xxlQ / Hypothetical protein
1475	1324854	1325210	[+3 L= 357]	ymaA / Phage ribonucleoprotein homolog
1476	1325200	1327281	[+1 L=2082]	rirA / Phage ribonucleoside-diphosphate reductase alpha chain (Ribonucleotide reductase)
1477	1327366	1328331	[+1 L= 966]	rirB / Phage ribonucleoside-diphosphate reductase beta chain (Ribonucleotide reductase small subunit)

1478	1328551	1328928	[+1 L= 378]	yhcF / Transcriptional regulator homolog
1479	1328928	1329623	[+3 L= 696]	yhcG / ABC transporter ATP-binding protein homolog
1480	1329623	1330411	[+2 L= 789]	xxlR / Hypothetical protein
1481	1330429	1331328	[+1 L= 900]	yhcH / ABC transporter ATP-binding protein homolog
1482	1331331	1332104	[+3 L= 774]	yhcI / Hypothetical protein
1483	1332295	1333320	[+1 L=1026]	xxlS / Hypothetical protein
1484	1334151	1333639	[-1 L= 513]	lrpC / Transcriptional regulator
1485	1334152	1334622	[+1 L= 471]	xxlT / Hypothetical protein
1486	1334594	1335187	[+2 L= 594]	yrdC / Hypothetical protein
1487	1335277	1335672	[+1 L= 396]	xxlU / Hypothetical protein
1488	1336623	1335706	[-1 L= 918]	ykfA / Hypothetical protein
1489	1336736	1337824	[+2 L=1089]	npdO / 2-nitropropane dioxygenase
1490	1339024	1337852	[-2 L=1173]	dltD / undecaprenol-phosphate-poly(glycerophosphate chain) D-alanine transfer protein
1491	1339260	1339024	[-1 L= 237]	dltC / D-alanine--poly(phosphoribitol)ligase subunit 2 (D-alanyl carrier protein)
1492	1340503	1339331	[-2 L=1173]	dltB / protein for D-alanine esterification of lipoteichoic acid
1493	1342014	1340503	[-1 L=1512]	dltA / D-alanine--poly(phosphoribitol)ligase subunit 1 (D-alanine-D-alanyl carrier protein ligase)
1497	1342511	1343677	[+2 L=1167]	amaA / N-acyl-L-amino acid amidohydrolase (L-aminoacylase)
1498	1343905	1344078	[+1 L= 174]	xxlV / Hypothetical protein
1499	1344074	1344517	[+2 L= 444]	flaW / Flavodoxin homolog
1500	1344545	1345315	[+2 L= 771]	xxlW / Hypothetical protein
1502	1346568	1345669	[-1 L= 900]	aphT / Aminoglycoside phosphotransferase
1503	1346652	1347173	[+3 L= 522]	xxlX / Hypothetical protein
1508	1349076	1347679	[-1 L=1398]	norM / Multidrug resistance protein homolog (Na(+)/drug antiporter)
1510	1349221	1350009	[+1 L= 789]	bacA / Undecaprenol kinase (Bacitracin resistance protein)
1511	1350629	1350045	[-3 L= 585]	xxlY / Hypothetical protein
1513	1351253	1351672	[+2 L= 420]	ypoP / Transcriptional regulator
1515	1353405	1352011	[-1 L=1395]	gltT / Proton/sodium-glutamate symport protein (Glutamate-aspartate carrier protein)
1517	1354483	1355862	[+1 L=1380]	yubJ / V-type sodium ATP synthase homolog
1518	1356374	1355904	[-3 L= 471]	yqfX / Hypothetical protein
1519	1356464	1356820	[+2 L= 357]	ytfJ / Hypothetical protein
1520	1356830	1356928	[+2 L= 99]	xxlZ / Hypothetical protein
1523	1357730	1357485	[-3 L= 246]	ykuS / Hypothetical protein
1524	1358069	1357812	[-3 L= 258]	xxmA / Hypothetical protein
1526	1358466	1359359	[+3 L= 894]	ilvE / Branched-chain amino acid aminotransferase
1527	1359678	1360076	[+3 L= 399]	ilvB / Acetolactate synthase large subunit (Acetohydroxy-acid synthase large subunit)
1528	1360060	1361376	[+1 L=1317]	ilvB / Acetolactate synthase large subunit (Acetohydroxy-acid synthase large subunit)
1529	1361376	1361882	[+3 L= 507]	ilvH / Acetolactate synthase small subunit (Acetohydroxy-acid synthase small subunit)
1530	1361906	1362919	[+2 L=1014]	ilvC / Ketol-acid reductoisomerase (Acetohydroxy-acid isomeroreductase)
1531	1362924	1364441	[+3 L=1518]	leuA / 2-isopropylmalate synthase (Alpha-isopropylmalate synthase)
1532	1364456	1365583	[+2 L=1128]	leuC / 3-isopropylmalate dehydrogenase (Beta-IPM dehydrogenase)
1533	1365586	1366977	[+1 L=1392]	leuB / 3-isopropylmalate dehydratase large subunit (Alpha-IPM isomerase)
1534	1366922	1367536	[+2 L= 615]	leuD / 3-isopropylmalate dehydratase small subunit (Alpha-IPM isomerase)
1535	1367850	1369109	[+3 L=1260]	hisZ / Histidyl-tRNA synthetase
1536	1369058	1369720	[+2 L= 663]	hisG / ATP phosphoribosyltransferase
1537	1369735	1371021	[+1 L=1287]	hisX / Histidinol dehydrogenase
1538	1371024	1371605	[+3 L= 582]	hisE / Imidazoleglycerol-phosphate dehydratase (IGPD)
1539	1371609	1372235	[+3 L= 627]	hisH / Imidazole glycerol phosphate synthase subunit (IGP synthase glutamine amidotransferase subunit)
1540	1372211	1372927	[+2 L= 717]	hisA / 1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino] imidazole-4-carboxamide isomerase
1541	1372924	1373679	[+1 L= 756]	hisF / Imidazole glycerol phosphate synthase subunit hisF (IGP synthase cyclase subunit)
1542	1373679	1373981	[+3 L= 303]	hisI / Phosphoribosyl-AMP cyclohydrolase (PRA-CH)

1543	1373995	1374315	[+1 L= 321]	hisB / Phosphoribosyl-ATP pyrophosphatase (PRA-PH)
1544	1374406	1375344	[+1 L= 939]	hisP / Histidinol-phosphatase (HolPase)
1547	1375719	1376696	[+3 L= 978]	xxmB / Glycerate dehydrogenase homolog
1548	1377431	1376733	[-3 L= 699]	pssA / CDP-diacylglycerol--serine O-phosphatidyltransferase (Phosphatidylserine synthase)
1549	1379506	1377623	[-2 L=1884]	yqgS / Hypothetical protein
1550	1379707	1380153	[+1 L= 447]	xxmC / Hypothetical protein
1552	1380608	1381921	[+2 L=1314]	lysA / Diaminopimelate decarboxylase (DAP decarboxylase)
1553	1382222	1382362	[+2 L= 141]	xxmD / Hypothetical protein
1554	1382453	1383154	[+2 L= 702]	cysH / Phosphoadenosine phosphosulfate reductase (PAPS sulfotransferase)
1555	1383197	1384330	[+2 L=1134]	ylnB / Sulfate adenylyltransferase (Sulfate adenylate transferase) homolog
1556	1384346	1384936	[+2 L= 591]	apsK / Adenylylsulfate kinase (Adenosine-5'phosphosulfate kinase)
1557	1384951	1386570	[+1 L=1620]	nirA / Nitrite and sulphite reductase
1559	1386866	1387642	[+2 L= 777]	sumT / Uroporphyrin-III C-methyltransferase
1560	1387632	1388399	[+3 L= 768]	ylnE / Hypothetical protein
1561	1388377	1388988	[+1 L= 612]	cysG / Siroheme synthase
1562	1389413	1390768	[+2 L=1356]	xxmE / Sodium-dependent transporter homolog
1564	1392392	1391061	[-3 L=1332]	xxmF / Peptidase homolog
1565	1392819	1394090	[+3 L=1272]	gltT / Proton/sodium-glutamate symport protein (Glutamate-aspartate carrier protein)
1566	1394162	1394677	[+2 L= 516]	xxmG / Hypothetical protein
1567	1394836	1396314	[+1 L=1479]	xxmH / Hypothetical protein
1568	1396499	1396852	[+2 L= 354]	xxmI / Hypothetical protein
1569	1396903	1397562	[+1 L= 660]	yvqH / Hypothetical protein
1570	1397627	1398409	[+2 L= 783]	yvqF / Hypothetical protein
1571	1398412	1399464	[+1 L=1053]	yvqE / Two-component sensor histidine kinase homolog
1572	1399464	1400093	[+3 L= 630]	yvqC / Two-component response regulator protein homolog
1573	1400270	1400605	[+2 L= 336]	xxmJ / Hypothetical protein
1574	1402024	1400636	[-2 L=1389]	braB / Branched-chain amino acid transport system carrier protein
1575	1402565	1402780	[+2 L= 216]	xxmK / Hypothetical protein
1576	1403600	1402827	[-3 L= 774]	xxmL / Methyltransferase homolog
1577	1403583	1404560	[+3 L= 978]	xxmM / Hypothetical protein
1578	1404868	1404674	[-2 L= 195]	xxmN / Hypothetical protein
1580	1405020	1406114	[+3 L=1095]	xxmO / Hypothetical protein
1581	1406133	1406747	[+3 L= 615]	xxmP / Hypothetical protein
1582	1406910	1408115	[+3 L=1206]	hmpA / Flavohemoprotein (Hemoglobin-like protein) (Flavohemoglobin)
1583	1408648	1408139	[-2 L= 510]	xxmQ / Hypothetical protein
1584	1408819	1409043	[+1 L= 225]	xxmR / Hypothetical protein
1585	1410149	1409343	[-3 L= 807]	yunE / Hypothetical protein
1586	1411262	1410261	[-3 L=1002]	ykaB / Low-affinity inorganic phosphate transport homolog
1587	1411903	1411271	[-2 L= 633]	ykaA / Hypothetical protein
1588	1412200	1414239	[+1 L=2040]	pbpF / Penicillin-binding protein 1F (PBP-1F)
1590	1414801	1414370	[-2 L= 432]	xxmS / Hypothetical protein
1592	1416804	1415518	[-1 L=1287]	xxmT / Histidine kinase homolog
1593	1416926	1417768	[+2 L= 843]	yunF / Hypothetical protein
1594	1418180	1417989	[-3 L= 192]	xxmU / Hypothetical protein
1595	1418841	1418305	[-1 L= 537]	xxmV / Phage integrase
1596	1419431	1418943	[-3 L= 489]	xxmW / Histidine kinase-like ATPase
1597	1420515	1419385	[-1 L=1131]	xxmX / Histidine kinase homolog
1599	1421697	1420993	[-1 L= 705]	deoD / Purine nucleoside phosphorylase
1600	1421875	1422660	[+1 L= 786]	xxmY / Hypothetical protein
1601	1425307	1422671	[-2 L=2637]	yfiX / Hypothetical protein
1602	1425417	1425818	[+3 L= 402]	xxmZ / Hypothetical protein
1603	1425823	1426332	[+1 L= 510]	ypuI / Hypothetical protein
1604	1426402	1427352	[+1 L= 951]	sodF / Superoxide dismutase [Fe]
1605	1427318	1428589	[+2 L=1272]	dacB / Penicillin-binding protein 5* precursor (D-alanyl-D-alanine carboxypeptidase)
1606	1428573	1429178	[+3 L= 606]	spmA / Spore maturation protein A
1608	1429178	1429705	[+2 L= 528]	spmB / Spore maturation protein B

1609	1429998	1430723	[+3 L= 726]	rluB / Ribosomal large subunit pseudouridine synthase B (Uracil hydrolyase)
1610	1430833	1431351	[+1 L= 519]	resA / Cytochrome c biogenesis protein (thioredoxin)
1612	1431428	1432447	[+2 L=1020]	resB / Cytochrome c biogenesis protein
1613	1432447	1433094	[+1 L= 648]	resB / Cytochrome c biogenesis protein
1614	1433112	1434266	[+3 L=1155]	resC / Cytochrome c biogenesis protein
1615	1434573	1435286	[+3 L= 714]	resD / Transcriptional regulatory protein
1616	1435289	1437061	[+2 L=1773]	resE / Two-component sensor histidine kinase
1617	1437201	1437779	[+3 L= 579]	yvqK / Hypothetical protein
1618	1437837	1438478	[+3 L= 642]	xxnA / Peptidase homolog
1621	1439856	1440458	[+3 L= 603]	ypaA / Hypothetical protein
1622	1440873	1440586	[-1 L= 288]	ferA / Ferredoxin
1623	1441118	1442188	[+2 L=1071]	ypbB / Hypothetical protein
1624	1442181	1443707	[+3 L=1527]	recQ / ATP-dependent DNA helicase (Recombination protein S)
1625	1443659	1444270	[+2 L= 612]	ypbD / Hypothetical protein
1626	1444281	1444772	[+3 L= 492]	ypbE / Hypothetical protein
1627	1444842	1445615	[+3 L= 774]	ypbG / Phosphoesterase homolog
1628	1445603	1446490	[+2 L= 888]	xxnB / Transcriptional regulator
1629	1446571	1447176	[+1 L= 606]	ypbH / negative regulation of competence MecA homolog
1630	1447491	1448627	[+3 L=1137]	gudB / NAD-specific glutamate dehydrogenase (NAD-GDH)
1632	1448767	1449063	[+1 L= 297]	xxnC / Hypothetical protein
1634	1449547	1450002	[+1 L= 456]	cwlL / Phage N-acetylmuramoyl-L-alanine amidase cwlL precursor (Cell wall hydrolase) (Autolysin)
1635	1450114	1451091	[+1 L= 978]	ypdA / Thioredoxin reductase
1636	1452104	1451133	[-3 L= 972]	aspG / L-asparaginase (L-asparagine amidohydrolase)
1638	1452588	1453262	[+3 L= 675]	kcyA / Cytidylate kinase (Cytidine monophosphate kinase)
1639	1453600	1454745	[+1 L=1146]	rslH / 30S ribosomal protein S1
1640	1454761	1455807	[+1 L=1047]	ipdI / Isopentenyl-diphosphate delta-isomerase (IPP isomerase)
1642	1456361	1456978	[+2 L= 618]	yphA / Hypothetical protein
1644	1456974	1457864	[+3 L= 891]	yphB / Hypothetical protein
1646	1458174	1459481	[+3 L=1308]	engA / GTP-binding protein homolog
1647	1459503	1460522	[+3 L=1020]	gpdA / Glycerol-3-phosphate dehydrogenase [NAD(P)+] (NAD(P)H-dependent dihydroxyacetone-phosphate reductase)
1648	1460632	1460889	[+1 L= 258]	xxnD / Hypothetical protein
1650	1461154	1461360	[+1 L= 207]	yphE / Hypothetical protein
1651	1461418	1462134	[+1 L= 717]	yphF / Hypothetical protein
1652	1462383	1463858	[+3 L=1476]	spfA / Stage IV sporulation protein A
1654	1464080	1464430	[+2 L= 351]	dbhA / DNA-binding protein HU (DNA-binding protein II)
1655	1464554	1465120	[+2 L= 567]	mtrA / GTP cyclohydrolase I (GTP-CH-I)
1657	1465307	1466038	[+2 L= 732]	hepA / Heptaprenyl diphosphate synthase component I (Spore germination protein C1)
1658	1466062	1466790	[+1 L= 729]	menH / Menaquinone biosynthesis methyltransferase (Spore germination protein C2)
1659	1466816	1467784	[+2 L= 969]	hepB / Heptaprenyl diphosphate synthase component II (Spore germination protein C3)
1660	1467831	1468355	[+3 L= 525]	ndpK / Nucleoside diphosphate kinase (Nucleoside-2-P kinase)
1661	1468623	1469792	[+3 L=1170]	aroC / Chorismate synthase (5-enolpyruvylshikimate-3-phosphate phospholyase)
1662	1469795	1470877	[+2 L=1083]	aroB / 3-dehydroquinate synthase
1663	1470986	1472122	[+2 L=1137]	hisH / Histidinol-phosphate aminotransferase (Imidazole acetol-phosphate transaminase)
1664	1472381	1473712	[+2 L=1332]	ypiA / Hypothetical protein
1665	1473732	1474322	[+3 L= 591]	ypiB / Hypothetical protein
1666	1474462	1474935	[+1 L= 474]	ypiF / Hypothetical protein
1667	1475079	1475588	[+3 L= 510]	qcrA / Menaquinol-cytochrome C reductase iron-sulfur subunit (Rieske iron-sulfur protein)
1668	1475592	1476263	[+3 L= 672]	qcrB / Menaquinol-cytochrome C reductase cytochrome B subunit
1669	1476310	1477074	[+1 L= 765]	qcrC / Menaquinol-cytochrome C reductase cytochrome B/C subunit
1670	1477170	1477784	[+3 L= 615]	ypjA / Hypothetical protein
1671	1477813	1478496	[+1 L= 684]	xxnE / Hypothetical protein
1672	1478606	1479391	[+2 L= 786]	ypjB / Hypothetical protein
1674	1479541	1480176	[+1 L= 636]	xxnF / Hypothetical protein

1676	1480311	1480919	[+3 L= 609]	xxnG / Hypothetical protein
1677	1481832	1480954	[-1 L= 879]	ypjC / Hypothetical protein
1678	1482268	1482663	[+1 L= 396]	ypjD / Hypothetical protein
1679	1482666	1483463	[+3 L= 798]	dapB / Dihydrodipicolinate reductase (DHPR)
1680	1483481	1483873	[+2 L= 393]	mgsA / Methylglyoxal synthase (MGS)
1681	1483873	1484589	[+1 L= 717]	ypjG / Hypothetical protein
1682	1484589	1485731	[+3 L=1143]	ypjH / Lipopolysaccharide biosynthesis-related protein homolog
1683	1485712	1486911	[+1 L=1200]	papS / Poly(A) polymerase (PAP)
1684	1486887	1487876	[+3 L= 990]	birA / BirA bifunctional protein (Biotin--[acetyl-CoA-carboxylase] synthetase)
1685	1488429	1488010	[-1 L= 420]	xxnH / Hypothetical protein
1686	1488879	1489712	[+3 L= 834]	panB / 3-methyl-2-oxobutanoate hydroxymethyltransferase (Ketopantoate hydroxymethyltransferase)
1687	1489685	1490560	[+2 L= 876]	panC / Pantoate--beta-alanine ligase (Pantothenate synthetase)
1688	1490576	1490956	[+2 L= 381]	panD / Aspartate 1-decarboxylase precursor (Aspartate alpha-decarboxylase)
1689	1491091	1493463	[+1 L=2373]	din Probable ATP-dependent helicase dinG homolog
1690	1493463	1493891	[+3 L= 429]	dinG / ATP-dependent helicase homolog
1691	1494145	1494312	[+1 L= 168]	ypmA / Hypothetical protein
1692	1494323	1494823	[+2 L= 501]	ypmB / Hypothetical protein
1693	1494845	1496029	[+2 L=1185]	aspB / Aspartate aminotransferase
1694	1496147	1496857	[+2 L= 711]	dnaD / DNA replication protein
1695	1496876	1497520	[+2 L= 645]	endC / Endonuclease III (DNA-(apurinic or apyrimidinic site) lyase)
1696	1497527	1498042	[+2 L= 516]	ypoC / Hypothetical protein
1697	1500110	1498074	[-3 L=2037]	pbpA / Penicillin-binding protein 1A/1B (PBP1)
1698	1500330	1500734	[+3 L= 405]	xxnI / Transposase homolog
1699	1500734	1501819	[+2 L=1086]	xxnJ / Transposase
1700	1502572	1501913	[-2 L= 660]	pbpA / Penicillin-binding protein 1A/1B (PBP1)
1701	1503241	1502642	[-2 L= 600]	recU / Recombination protein U homolog
1702	1503282	1504367	[+3 L=1086]	yppC / Hypothetical protein
1707	1505045	1505386	[+2 L= 342]	yppD / Hypothetical protein
1708	1505607	1505419	[-1 L= 189]	yppF / Hypothetical protein
1709	1505785	1506348	[+1 L= 564]	yppG / Hypothetical protein
1710	1506507	1506932	[+3 L= 426]	cotD / Spore coat protein D
1711	1506992	1507543	[+2 L= 552]	ypsA / Hypothetical protein
1712	1507635	1507976	[+3 L= 342]	ypsB / Hypothetical protein
1713	1508631	1509773	[+3 L=1143]	ypsC / Hypothetical protein
1715	1509817	1510017	[+1 L= 201]	xxnL / Hypothetical protein
1716	1510103	1512094	[+2 L=1992]	ypvA / ATP-dependent helicase homolog
1718	1512148	1513713	[+1 L=1566]	ypwA / Carboxypeptidase homolog
1719	1513764	1514234	[+3 L= 471]	xxnM / Acetyltransferase homolog
1720	1514376	1515119	[+3 L= 744]	ampM / Methionine aminopeptidase (Peptidase M)
1722	1515314	1516039	[+2 L= 726]	xprT / Xanthine phosphoribosyltransferase
1723	1516046	1517365	[+2 L=1320]	pbuX / Xanthine permease
1725	1518547	1517387	[-2 L=1161]	yrkO / Hypothetical protein
1728	1519125	1522754	[+3 L=3630]	ypbR / Hypothetical protein
1730	1523051	1522764	[-3 L= 288]	xxnN / Hypothetical protein
1731	1523088	1523552	[+3 L= 465]	yvbK / Hypothetical protein
1732	1523576	1523845	[+2 L= 270]	ypbS / Hypothetical protein
1733	1523851	1524681	[+1 L= 831]	thtM / Thiosulfate sulfurtransferase
1735	1525692	1525246	[-1 L= 447]	xxnP / Hypothetical protein
1737	1526091	1527326	[+3 L=1236]	xxnQ / Hypothetical protein
1738	1527322	1527705	[+1 L= 384]	yshE / Hypothetical protein
1739	1528414	1529136	[+1 L= 723]	atmB / Mg(2+) transport ATPase, P-type 2
1740	1529272	1530135	[+1 L= 864]	ypcP / 5'-3' exonuclease
1742	1530964	1532154	[+1 L=1191]	xxnR / Hypothetical protein
1743	1532158	1532898	[+1 L= 741]	ywqC / Capsular polysaccharide biosynthesis protein
1744	1532855	1533505	[+2 L= 651]	yveL / Tyrosine-protein kinase homolog
1745	1533527	1534162	[+2 L= 636]	xxnS / Glycosyltransferase homolog
1746	1534204	1535655	[+1 L=1452]	xxnT /Polysaccharide biosynthesis protein
1747	1535662	1536873	[+1 L=1212]	yvhE / Hypothetical protein

1748	1536851	1537648	[+2 L= 798]	tuaG / Teichuronic acid biosynthesis protein
1749	1537648	1538697	[+1 L=1050]	xxnU / Glycosyltransferase homolog
1750	1538761	1540338	[+1 L=1578]	xxnV / Hypothetical protein
1757	1555507	1540457	[-2 L=15051]	xxnW / Hypothetical protein
1758	1555630	1556487	[+1 L= 858]	yitH / Hypothetical protein
1759	1557085	1556528	[-2 L= 558]	xxnX / Isochorismatase homolog
1760	1557268	1557525	[+1 L= 258]	xxnY / Hypothetical protein
1761	1558442	1557534	[-3 L= 909]	xxnZ / Transporter homolog
1762	1558836	1558453	[-1 L= 384]	rnhL / 14.7 kDa ribonuclease H-like protein
1763	1559778	1558909	[-1 L= 870]	xxoA / Aldose 1-epimerase homolog
1764	1559962	1560444	[+1 L= 483]	xxoB / Hypothetical protein
1765	1560599	1561255	[+2 L= 657]	xxoC / Rnase H homolog
1768	1561729	1561484	[-2 L= 246]	xxoD / Hypothetical protein
1769	1562082	1561852	[-1 L= 231]	cspB / Cold shock protein
1771	1562311	1563036	[+1 L= 726]	yqcI / Hypothetical protein
1772	1563054	1563794	[+3 L= 741]	ycgF / Hypothetical protein
1773	1563766	1564107	[+1 L= 342]	xxoE / Hypothetical protein
1774	1564189	1564815	[+1 L= 627]	xxoF / Hypothetical protein
1775	1565041	1565379	[+1 L= 339]	ywcB / Hypothetical protein
1776	1565385	1566932	[+3 L=1548]	ywcA / Na+-dependent symport homolog
1777	1567040	1568473	[+2 L=1434]	yhxA / Adenosylmethionine-8-amino-7-oxononanoate homolog
1778	1568517	1568816	[+3 L= 300]	xxoG / Hypothetical protein
1779	1570045	1568885	[-2 L=1161]	gerN / Na(+)/H(+) antiporter homolog
1780	1570356	1572047	[+3 L=1692]	ykqC / Hypothetical protein
1781	1572144	1572971	[+3 L= 828]	ydfL / Multidrug-efflux transporter 2 regulator homolog
1782	1573117	1574469	[+1 L=1353]	xxoH / Hypothetical protein
1783	1575195	1574512	[-1 L= 684]	xxoI / Hypothetical protein
1784	1575329	1575910	[+2 L= 582]	xxoJ / Hypothetical protein
1785	1576053	1576376	[+3 L= 324]	yvlA / Hypothetical protein
1786	1576520	1577260	[+2 L= 741]	xxoK / NADPH-flavin oxidoreductase homolog
1787	1578364	1577642	[-2 L= 723]	xxoL / Hypothetical protein
1790	1579785	1578589	[-1 L=1197]	xxoM / Hypothetical protein
1794	1580699	1580884	[+2 L= 186]	ymaH / Host factor-1 protein homolog
1795	1581532	1580918	[-2 L= 615]	xxoN / Hypothetical protein
1796	1581690	1582520	[+3 L= 831]	ytxD / Flagellar motor apparatus homolog
1797	1582540	1583217	[+1 L= 678]	xxoO / Hypothetical protein
1798	1583371	1583736	[+1 L= 366]	cheY / Chemotactic tumbling protein
1799	1583869	1585884	[+1 L=2016]	cheA / Chemotaxis protein
1800	1586057	1587694	[+2 L=1638]	fliY / Flagellar motor switch protein
1801	1587727	1589094	[+1 L=1368]	xxoP / Hypothetical protein
1802	1589125	1589838	[+1 L= 714]	xxoQ / Hypothetical protein
1803	1590670	1589876	[-2 L= 795]	cheR / Chemotaxis protein methyltransferase
1804	1591264	1590698	[-2 L= 567]	xxoR / Hypothetical protein
1805	1591327	1591797	[+1 L= 471]	xxoS / Hypothetical protein
1806	1591816	1592265	[+1 L= 450]	xxoT / Hypothetical protein
1807	1592286	1593581	[+3 L=1296]	flgK / Flagellar hook-associated protein 1
1808	1593609	1594496	[+3 L= 888]	flgL / Flagellar hook-associated protein 3
1809	1594510	1595892	[+1 L=1383]	fliD / Flagellar hook-associated protein 2 (Flagellar cap protein)
1810	1595918	1596283	[+2 L= 366]	fliS / Flagellar protein
1811	1596261	1596545	[+3 L= 285]	xxoU / Hypothetical protein
1812	1596867	1597322	[+3 L= 456]	flgB / Flagellar basal-body rod protein
1813	1597347	1597757	[+3 L= 411]	flgC / Flagellar basal-body rod protein
1814	1597777	1598073	[+1 L= 297]	fliE / Flagellar hook-basal body complex protein
1815	1598099	1599670	[+2 L=1572]	fliF / Flagellar M-ring protein
1817	1599687	1600688	[+3 L=1002]	fliG / Flagellar motor switch protein
1818	1600669	1601364	[+1 L= 696]	xxoV / Hypothetical protein
1819	1601364	1602665	[+3 L=1302]	fliI / Flagellum-specific ATP synthase
1820	1602785	1603192	[+2 L= 408]	xxoW / Hypothetical protein
1821	1603188	1603748	[+3 L= 561]	xxoX / Hypothetical protein
1822	1603723	1604313	[+1 L= 591]	xxoY / Hypothetical protein
1823	1604320	1604889	[+1 L= 570]	xxoZ / Flagellar hook assembly protein homolog

1824	1604914	1606224	[+1 L=1311]	flgE / Flagellar hook protein
1825	1606276	1606608	[+1 L= 333]	xxpA / Hypothetical protein
1826	1606808	1607299	[+2 L= 492]	xxpB / Hypothetical protein
1827	1607426	1608331	[+2 L= 906]	cheV / Chemotaxis protein
1828	1609046	1610002	[+2 L= 957]	xxpC / Hypothetical protein
1829	1610910	1610104	[-1 L= 807]	flaA / Flagellin
1830	1611973	1611143	[-2 L= 831]	flaB / Flagellin
1832	1612879	1612046	[-2 L= 834]	flaC / Flagellin
1834	1613880	1613023	[-1 L= 858]	flaD / Flagellin
1835	1614026	1614808	[+2 L= 783]	xxpD / Transglycosylase homolog
1836	1614874	1615095	[+1 L= 222]	fliN / Flagellar motor switch protein
1837	1615113	1616096	[+3 L= 984]	fliM / Flagellar motor switch protein
1838	1616110	1616466	[+1 L= 357]	spoA / Surface presentation of antigens (SPOA) protein
1839	1616482	1616799	[+1 L= 318]	xxpE / Hypothetical protein
1840	1616799	1617554	[+3 L= 756]	fliP / Flagellar biosynthetic protein
1841	1617591	1617863	[+3 L= 273]	fliQ / Flagellar biosynthetic protein
1843	1617882	1618640	[+3 L= 759]	fliR / Flagellar biosynthetic protein
1844	1618654	1619697	[+1 L=1044]	flhB / Flagellar biosynthetic protein
1845	1619709	1621100	[+3 L=1392]	flhA / Flagellar biosynthesis protein
1846	1621107	1621787	[+3 L= 681]	flhA / Flagellar biosynthesis protein
1847	1621805	1622704	[+2 L= 900]	flhF / Flagellar biosynthesis protein
1849	1622830	1623123	[+1 L= 294]	flhF / Flagellar biosynthesis protein
1850	1623169	1623939	[+1 L= 771]	flgG / Flagellar basal-body rod protein (Distal rod protein)
1851	1624060	1624767	[+1 L= 708]	syaI / Alanyl-tRNA synthetase (Alanine--tRNA ligase)
1852	1624788	1625621	[+3 L= 834]	yrhO / Cyclodextrin metabolism homolog
1853	1625608	1626339	[+1 L= 732]	xxpF / Hypothetical protein
1854	1626333	1626641	[+3 L= 309]	xxpG / Hypothetical protein
1857	1627868	1627266	[-3 L= 603]	xxpH / Dienelactone hydrolase homolog
1858	1628206	1627874	[-2 L= 333]	yqjZ / Hypothetical protein
1859	1628570	1628394	[-3 L= 177]	yfjU / Hypothetical protein
1860	1629851	1628640	[-3 L=1212]	xxpI / Transcriptional regulator
1861	1629971	1631236	[+2 L=1266]	xxpJ / Hypothetical protein
1862	1631336	1631887	[+2 L= 552]	xxpK / Hypothetical protein
1863	1632824	1631934	[-3 L= 891]	xxpL / Transcriptional regulator
1864	1632987	1633976	[+3 L= 990]	xxpM / ABC transporter
1865	1633957	1634979	[+1 L=1023]	xxpN / ABC transporter, substrate binding protein
1867	1634995	1637922	[+1 L=2928]	xxpO / Metallo-beta-lactamase homolog
1868	1637946	1638776	[+3 L= 831]	xxpP / Hypothetical protein
1869	1639251	1638832	[-1 L= 420]	yfmQ / Hypothetical protein
1872	1639814	1640905	[+2 L=1092]	xxpQ / D-alanyl-D-alanine carboxypeptidase homolog
1873	1641022	1641594	[+1 L= 573]	xxpR / Phosphoglycerate mutase homolog
1874	1641666	1642055	[+3 L= 390]	xxpS / Hypothetical protein
1875	1642994	1642080	[-3 L= 915]	xxpT / Hydrolase homolog
1876	1643299	1642973	[-2 L= 327]	xxpU / Hypothetical protein
1877	1643693	1643286	[-3 L= 408]	xxpV / Hypothetical protein
1878	1643815	1644639	[+1 L= 825]	xxpW / Hypothetical protein
1879	1646514	1644688	[-1 L=1827]	asnO / Asparagine synthetase [glutamine-hydrolyzing]
1880	1646761	1647324	[+1 L= 564]	sigZ / RNA polymerase sigma factor sigZ
1881	1647324	1648427	[+3 L=1104]	xxpX / Hypothetical protein
1882	1649545	1648475	[-2 L=1071]	xxpY / Hypothetical protein
1883	1649756	1650652	[+2 L= 897]	xxpZ / Cation transport protein
1885	1651795	1651079	[-2 L= 717]	ydhC / Transcriptional regulator
1886	1652729	1651767	[-3 L= 963]	ydeD / Transport protein
1888	1654400	1653216	[-3 L=1185]	cobW / Cobalamin synthesis protein
1890	1654682	1655557	[+2 L= 876]	xxqA / Hypothetical protein
1891	1655574	1656455	[+3 L= 882]	xxqB / Hypothetical protein
1892	1656550	1657227	[+1 L= 678]	xxqC / Hypothetical protein
1893	1657694	1659094	[+2 L=1401]	mleN / Malate-2H(+)/Na(+)-lactate antiporter
1894	1659575	1659141	[-3 L= 435]	xxqD / Hypothetical protein
1895	1660245	1659538	[-1 L= 708]	xxqE / Hypothetical protein
1896	1660437	1661822	[+3 L=1386]	fumH / Fumarate hydratase, class-II (Fumarase)

1897	1662352	1661924 [-2 L= 429]	xxqF / Hypothetical protein
1898	1662971	1663795 [+2 L= 825]	xxqG / Transcriptional regulator
1899	1663896	1665302 [+3 L=1407]	yoeA / Hypothetical protein
1900	1666138	1665365 [-2 L= 774]	xxqH / Hypothetical protein
1901	1666444	1666848 [+1 L= 405]	xxqI / Hypothetical protein
1902	1666959	1667372 [+3 L= 414]	xxqJ / Hypothetical protein
1903	1667377	1668186 [+1 L= 810]	xxqK / Hypothetical protein
1905	1668243	1668953 [+3 L= 711]	ccdA / Cytochrome c-type biogenesis protein
1906	1668975	1669526 [+3 L= 552]	resA / ResA protein
1907	1669538	1670224 [+2 L= 687]	lgtA / Prolipoprotein diacylglyceryl transferase
1908	1670827	1670285 [-2 L= 543]	xxqL / Transcriptional regulator
1910	1670978	1672306 [+2 L=1329]	sdhD / D-serine dehydratase (D-serine deaminase)
1911	1672454	1673707 [+2 L=1254]	xxqM / Hypothetical protein
1913	1674698	1674021 [-3 L= 678]	xxqN / Hypothetical protein
1914	1675765	1674698 [-2 L=1068]	xxqO / Hypothetical protein
1916	1676222	1675761 [-3 L= 462]	xxqP / Hypothetical protein
1917	1676536	1676201 [-2 L= 336]	sigW / RNA polymerase sigma factor
1919	1676928	1677599 [+3 L= 672]	yxjL / Response regulator
1920	1677607	1678704 [+1 L=1098]	yxjM / Sensor-like histidine kinase
1921	1678837	1679781 [+1 L= 945]	xxqR / ABC-type multidrug transporter, ATPase component homolog
1922	1679822	1680928 [+2 L=1107]	xxqS / ABC-type multidrug transporter, permease homolog
1923	1680933	1682075 [+3 L=1143]	xxqT / ABC-type multidrug transporter, permease homolog
1924	1682138	1683397 [+2 L=1260]	ywjE / Phospholipase D
1925	1684198	1683458 [-2 L= 741]	pyrH / Uridylate kinase (Uridine monophosphate kinase)
1927	1684575	1685843 [+3 L=1269]	gltT / Proton/sodium-glutamate symport protein (Glutamate-aspartate carrier protein)
1928	1685871	1687307 [+3 L=1437]	aspA / Aspartate ammonia-lyase (Aspartase)
1929	1687356	1689089 [+3 L=1734]	malS / Malate dehydrogenase (malic enzyme)
1930	1689164	1690459 [+2 L=1296]	ycbA / Sensor-like histidine kinase homolog
1931	1690465	1691394 [+1 L= 930]	ycbB / Response regulator homolog
1932	1691516	1694707 [+2 L=3192]	snfB / Helicase homolog
1936	1695679	1696659 [+1 L= 981]	asnA / Aspartate--ammonia ligase (Asparagine synthetase A)
1937	1697173	1696724 [-2 L= 450]	xxqU / Glyoxalase/Bleomycin resistance protein homolog
1938	1698632	1697406 [-3 L=1227]	aakB / Aspartokinase 2 [Contains: Aspartokinase II alpha subunit; Aspartokinase II beta subunit]
1939	1699206	1700120 [+3 L= 915]	yndG / Hypothetical protein
1940	1700128	1700736 [+1 L= 609]	yndH / Hypothetical protein
1941	1700761	1702368 [+1 L=1608]	yndJ / Hypothetical protein
1942	1702928	1702404 [-3 L= 525]	xxqV / Mutator protein homolog
1943	1703024	1704283 [+2 L=1260]	xxqW / Hypothetical protein
1944	1704966	1704505 [-1 L= 462]	xxqX / Hypothetical protein
1946	1705372	1706172 [+1 L= 801]	xxqY / UDP-galactose-lipid carrier transferase homolog
1947	1706292	1706864 [+3 L= 573]	yfiO / Hypothetical protein
1948	1706904	1708649 [+3 L=1746]	xxqZ / Transporter homolog
1950	1710729	1712000 [+3 L=1272]	ydeG / Metabolite transport protein homolog
1951	1713033	1712053 [-1 L= 981]	yhfB / 3-Oxoacyl-carrier protein synthase
1952	1713726	1714982 [+3 L=1257]	feoB / Ferrous iron transport protein B
1953	1715199	1716407 [+3 L=1209]	yfnC / Fosmidomycin resistance protein homolog
1954	1716421	1717335 [+1 L= 915]	cysM / Cysteine synthase (O-acetylserine sulfhydrylase)
1955	1717384	1717926 [+1 L= 543]	xxrA / Acetyltransferase homolog
1956	1718022	1718846 [+3 L= 825]	xxrB / Hypothetical protein
1958	1720214	1721548 [+2 L=1335]	xxrC / Sodium-dependent transporter
1959	1722295	1721594 [-2 L= 702]	xxrD / Polysaccharide deacetylase
1960	1722622	1722882 [+1 L= 261]	yraL / Hypothetical protein
1961	1723046	1723729 [+2 L= 684]	yetF / Hypothetical protein
1962	1723825	1724481 [+1 L= 657]	xxrE / Hypothetical protein
1964	1724735	1725511 [+2 L= 777]	xxrF / Hypothetical protein
1967	1726703	1726107 [-3 L= 597]	msrA / Peptide methionine sulfoxide reductase msrA (Protein-methionine-S-oxide reductase)
1969	1727147	1726734 [-3 L= 414]	xxrG / Reductase homolog
1970	1727490	1727179 [-1 L= 312]	xxrH / Reductase homolog

1971	1728428	1729324 [+2 L= 897]	ilvE / Branched-chain amino acid aminotransferase
1972	1729344	1731062 [+3 L=1719]	ilvB / Acetolactate synthase large subunit (Acetohydroxy-acid synthase large subunit)
1974	1731053	1731289 [+2 L= 237]	ilvH /Acetolactate synthase small subunit (Acetohydroxy-acid synthase small subunit)
1975	1731307	1732311 [+1 L=1005]	ilvC / Ketol-acid reductoisomerase (Acetohydroxy-acid isomeroreductase)
1976	1732361	1734031 [+2 L=1671]	ilvD / Dihydroxy-acid dehydratase (DAD)
1977	1734066	1735325 [+3 L=1260]	ilvA / Threonine dehydratase biosynthetic (Threonine deaminase)
1978	1736792	1735692 [-3 L=1101]	capA / Capsule biosynthesis protein
1979	1736996	1737709 [+2 L= 714]	xxrI / Hypothetical protein
1980	1737719	1738588 [+2 L= 870]	xxrJ / Acetyltransferase homolog
1981	1738753	1739970 [+1 L=1218]	xxrK / Transporter protein
1982	1740788	1740030 [-3 L= 759]	ligB / Catalytic subunit of aromatic ring-opening dioxygenase
1983	1740985	1741920 [+1 L= 936]	xxrL / Lysophospholipase homolog
1984	1742189	1742830 [+2 L= 642]	xxrM / Hypothetical protein
1985	1742943	1744472 [+3 L=1530]	xxrN / Acetyl-coA hydrolase/transferase homolog
1986	1744714	1745154 [+1 L= 441]	xxrO / Acetyltransferase homolog
1987	1745185	1745541 [+1 L= 357]	yunG / Hypothetical protein
1988	1745598	1746920 [+3 L=1323]	yorC / Hypothetical protein
1989	1747077	1748702 [+3 L=1626]	xxrP / Extracellular solute-binding protein, family 5 homolog
1990	1749050	1749847 [+2 L= 798]	xxrQ / Hypothetical protein
1991	1749974	1750351 [+2 L= 378]	xxrR / Hypothetical protein
1994	1750683	1752725 [+3 L=2043]	xxrS / Methyltransferase homolog
1995	1752864	1753049 [+3 L= 186]	pqqE / Coenzyme PPQ synthesis protein homolog
1996	1753770	1753243 [-1 L= 528]	yoaA / Alanine acetyltransferase homolog
1997	1753855	1754595 [+1 L= 741]	xxrT / Two-component response regulator protein
1998	1754577	1755674 [+3 L=1098]	xxrU / Histidine kinase-like ATPase
1999	1755749	1756606 [+2 L= 858]	xxrV / Peptidase homolog
2000	1757965	1756673 [-2 L=1293]	mntH / Manganese transport protein (NRAMP)
2001	1758444	1759400 [+3 L= 957]	ybfQ / Hypothetical protein
2002	1761079	1759607 [-2 L=1473]	xxrW / Hypothetical protein
2003	1761255	1762196 [+3 L= 942]	ykpB / 2-dehydropantoate 2-reductase (Ketopantoate reductase) homolog
2006	1762823	1764646 [+2 L=1824]	ydaO / Hypothetical protein
2007	1765248	1766405 [+3 L=1158]	etxA / Enterotoxin A
2008	1766446	1767351 [+1 L=1206]	etxB / Enterotoxin B
2009	1767753	1768838 [+3 L=1086]	etxC / Enterotoxin C
2011	1769350	1770666 [+1 L=1317]	ampS / Aminopeptidase
2012	1770816	1772183 [+3 L=1368]	xxrX / Hypothetical protein
2014	1772414	1773031 [+2 L= 618]	xxrY / Hypothetical protein
2015	1773077	1773718 [+2 L= 642]	xxrZ / Acetyltransferase homolog
2016	1774326	1774009 [-1 L= 318]	xxsA / Hypothetical protein
2017	1775117	1774470 [-3 L= 648]	xxsB / Amino terminal protease homolog
2019	1775907	1776398 [+3 L= 492]	xxsC / Transcriptional regulator
2020	1776772	1777716 [+1 L= 945]	deoR / Deoxyribonucleoside regulator
2023	1778015	1778692 [+2 L= 678]	deoC / Deoxyribose-phosphate aldolase (Phosphodeoxyriboaldolase)
2024	1778795	1779973 [+2 L=1179]	nupC / Pyrimidine nucleoside transport protein
2025	1780001	1781311 [+2 L=1311]	pynP / Pyrimidine-nucleoside phosphorylase (PYNP)
2026	1781383	1781739 [+1 L = 357]	cddA / Cytidine deaminase (Cytidine aminohydrolase)
2028	1781757	1782347 [+3 L= 591]	xxsD / Hypothetical protein
2029	1782366	1783184 [+3 L= 819]	xxsE / Transposase
2030	1783395	1783880 [+3 L= 486]	yneJ / Hypothetical protein
2032	1784170	1783934 [-2 L= 237]	xxsF / Hypothetical protein
2033	1784351	1785631 [+2 L=1281]	xxsG / Metallopeptidase homolog
2034	1786364	1785732 [-3 L= 633]	xxsH / Hypothetical protein
2035	1786698	1788368 [+3 L=1671]	xxsI / Multicopper oxidase homolog
2037	1789302	1791443 [+3 L=2142]	topB / DNA topoisomerase III
2038	1791588	1792895 [+3 L=1308]	xxsJ / Hypothetical protein
2039	1794104	1793106 [-3 L= 999]	yqcL / Hypothetical protein
2040	1794352	1795050 [+1 L= 699]	yocJ / Acyl carrier protein phosphodiesterase 1 (ACP phosphodiesterase

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2041	1795274	1796647	[+2 L=1374]	brnQ / Branched-chain amino acid transport system carrier protein
2042	1796735	1797151	[+2 L= 417]	xxsK / Hypothetical protein
2044	1797483	1799129	[+3 L=1647]	ycnJ / Copper export protein homolog
2045	1799216	1799839	[+2 L= 624]	ycnI / Hypothetical protein
2046	1800790	1799888	[-2 L= 903]	yvbV / Transport protein
2047	1800888	1801754	[+3 L= 867]	yvbU / Transcriptional regulator
2048	1801815	1802306	[+3 L= 492]	xxsL / Hypothetical protein
2050	1802380	1803027	[+1 L= 648]	ywbO / 2-Hydroxychromene-2-carboxylate isomerase homolog
2052	1803088	1803687	[+1 L= 600]	xxsM / Nitroreductase homolog
2054	1804060	1804689	[+1 L= 630]	xxsN / Amidase homolog
2055	1805132	1804791	[-3 L= 342]	xxsO / Hypothetical protein
2056	1805567	1806661	[+2 L=1095]	xxsP / Hypothetical protein
2059	1807470	1807135	[-1 L= 336]	yobD / Phage-related transcriptional regulator homolog
2062	1808360	1809919	[+2 L=1560]	xxsQ / Hypothetical protein
2064	1810238	1810468	[+2 L= 231]	xxsR / Hypothetical protein
2065	1810485	1811117	[+3 L= 633]	xxsS / Hypothetical protein
2067	1811560	1812540	[+1 L= 981]	xxsT / Hypothetical protein
2071	1813896	1815086	[+3 L=1191]	xxsU / Hypothetical protein
2076	1816722	1819805	[+3 L=3084]	xxsV / Hypothetical protein
2077	1819832	1822255	[+2 L=2424]	xxsW / Hypothetical protein
2083	1823460	1823792	[+3 L= 333]	xxsX / Hypothetical protein
2092	1827046	1827273	[+1 L= 228]	xxsY / Phage protein
2093	1827279	1827863	[+3 L= 585]	xxsZ / Phage protein
2104	1831298	1831576	[+2 L= 279]	abrB / Transition state regulatory protein
2110	1834922	1836634	[+2 L=1713]	xxtA / Hypothetical protein
2111	1836654	1838168	[+3 L=1515]	xxtB / Hypothetical protein
2113	1838230	1839009	[+1 L= 780]	xxtC / Phage protein
2114	1839072	1840193	[+3 L=1122]	xxtD / Phage protein
2121	1842812	1843315	[+2 L= 504]	xxtE / Hypothetical protein
2124	1843911	1844345	[+3 L= 435]	xxtF / Hypothetical protein
2126	1844702	1848622	[+2 L=3921]	xxtG / Phage protein
2127	1848640	1849653	[+1 L=1014]	xxtH / Hypothetical protein
2128	1849613	1850134	[+2 L= 522]	xxtI / Hypothetical protein
2129	1850134	1855107	[+1 L=4974]	xxtJ / Hypothetical protein
2131	1855193	1855435	[+2 L= 243]	xxtK / Hypothetical protein
2132	1855438	1855674	[+1 L= 237]	xxtL / Hypothetical protein
2133	1855674	1856735	[+3 L=1062]	xxtM / Hypothetical protein
2134	1858951	1857323	[-2 L=1629]	xxtN / Hypothetical protein
2139	1860792	1860595	[-1 L= 198]	xxtO / Transcriptional regulator
2141	1861244	1861543	[+2 L= 300]	xxtP / Hypothetical protein
2143	1861841	1862200	[+2 L= 360]	xxtQ / SpoIIIE homolog
2144	1862230	1863021	[+1 L= 792]	xxtR / SpoIIIE homolog
2145	1862966	1863586	[+2 L= 621]	xxtS / Hypothetical protein
2149	1864564	1866033	[+1 L=1470]	cisA / Chromosome recombinase
2150	1866263	1867063	[+2 L= 801]	xxtT / Amidase homolog
2152	1867245	1868255	[+3 L=1011]	xxtU / Hypothetical protein
2153	1869289	1868348	[-2 L= 942]	ldhX / L-lactate dehydrogenase X
2154	1869490	1870923	[+1 L=1434]	yobN / L-amino acid oxidase homolog
2156	1871033	1871953	[+2 L= 921]	xxtV / Cobalamin synthesis related protein homolog
2157	1872204	1873433	[+3 L=1230]	xxtW / ABC transporter substrate-binding protein
2158	1873526	1874275	[+2 L= 750]	xxtX / ABC transporter
2159	1874278	1874976	[+1 L= 699]	xxtY / ABC transporter ATP-binding protein
2160	1874992	1875858	[+1 L= 867]	xxtZ / ABC transporter permease protein
2162	1875842	1876861	[+2 L=1020]	xxuA / ABC transporter permease protein
2163	1877756	1876929	[-3 L= 828]	yofA / Transcriptional regulator
2164	1877826	1878380	[+3 L= 555]	xxuB / Hypothetical protein
2166	1879520	1880056	[+2 L= 537]	yjhA / Hypothetical protein
2167	1880427	1880867	[+3 L= 441]	xxuC / Transcriptional regulator, MarR family
2168	1880989	1882041	[+1 L=1053]	xxuD / Oxidoreductase homolog
2169	1882637	1884037	[+2 L=1401]	cydA / Cytochrome D ubiquinol oxidase subunit I

2170	1883931	1885040	[+3 L=1110]	cydB / Cytochrome D ubiquinol oxidase subunit II
2171	1885043	1886761	[+2 L=1719]	cydC / Transport ATP-binding protein
2172	1886761	1888482	[+1 L=1722]	cydD / Transport ATP-binding protein
2174	1889851	1892433	[+1 L=2583]	xxuE / Glycosyltransferase homolog
2175	1892456	1893583	[+2 L=1128]	xxuF / Hypothetical protein
2176	1893579	1894142	[+3 L= 564]	xxuG / Acetyltransferase homolog
2178	1894642	1895085	[+1 L= 444]	yybP / Hypothetical protein
2179	1895462	1895127	[-3 L= 336]	xxuH / Hypothetical protein
2181	1896941	1895943	[-3 L= 999]	xxuI / Hypothetical protein
2182	1897203	1898153	[+3 L= 951]	dacA / Serine-type D-Ala-D-Ala carboxypeptidase
2183	1898392	1899003	[+1 L= 612]	xxuJ / Nitroreductase homolog
2185	1899963	1901252	[+3 L=1290]	xxuK / Enterotoxin
2186	1902137	1901358	[-3 L= 780]	xxuL / Hypothetical protein
2188	1902360	1902527	[+3 L= 168]	yvcC / ABC transporter ATP-binding protein
2189	1902505	1904118	[+1 L=1614]	yvcC / ABC transporter ATP-binding protein
2190	1904180	1904881	[+2 L= 702]	xxuM / Response regulator
2191	1904881	1905951	[+1 L=1071]	xxuN / Two-component histidine kinase homolog
2192	1906235	1906960	[+2 L= 726]	yoxD / 3-Oxoacyl-acyl carrier protein reductase homolog
2194	1907254	1908123	[+1 L= 870]	aadK / Aminoglycoside 6-adenylyltransferase
2195	1908245	1909069	[+2 L= 825]	notB / chitooligosaccharide deacetylase
2196	1909141	1909479	[+1 L= 339]	yfhL / Hypothetical protein
2197	1910138	1909533	[-3 L= 606]	xxuO / Hydrolase homolog, MutT family
2198	1910220	1910855	[+3 L= 636]	xxuP / Hypothetical protein
2200	1911628	1912920	[+1 L=1293]	dhoM / Homoserine dehydrogenase (HDH)
2201	1912898	1913971	[+2 L=1074]	thrC / Threonine synthase
2202	1913971	1914861	[+1 L= 891]	khsE / Homoserine kinase (HK)
2203	1914998	1915204	[+2 L= 207]	xxuQ / Hypothetical protein
2204	1915361	1917715	[+2 L=2355]	xxuR / Hypothetical protein
2205	1918033	1919037	[+1 L=1005]	xxuS / Hypothetical protein
2206	1919205	1919999	[+3 L= 795]	xxuT / Hypothetical protein
2207	1919962	1920450	[+1 L= 489]	xxuU / Hypothetical protein
2208	1920457	1921152	[+1 L= 696]	xxuV / Hypothetical protein
2209	1921116	1922507	[+3 L=1392]	xxuW / Histidine kinase homolog
2210	1922612	1923430	[+2 L= 819]	xxuX / Polysaccharide deacetylase homolog
2211	1923448	1924101	[+1 L= 654]	xxuY / Hypothetical protein
2212	1924264	1924941	[+1 L= 678]	mgtC / Magnesium (Mg2+) transporter
2213	1925014	1925559	[+1 L= 546]	xxuZ / Acetyltransferase homolog
2214	1925860	1927665	[+1 L=1806]	xxvA / Hypothetical protein
2215	1927699	1929564	[+1 L=1866]	xxvB / Hypothetical protein
2216	1929554	1930789	[+2 L=1236]	xxvC / AMP-binding protein homolog
2217	1930789	1931061	[+1 L= 273]	xxvD / Hypothetical protein
2218	1931076	1932068	[+3 L= 993]	xxvE / Hypothetical protein
2219	1932109	1932948	[+1 L= 840]	xxvF / Endonuclease homolog
2220	1933068	1933277	[+3 L= 210]	sspA / Small acid-soluble spore protein (major alpha-type SASP)
2221	1933492	1934253	[+1 L= 762]	xxvG / Multidrug resistance protein homolog
2222	1934228	1934743	[+2 L= 516]	ymfE / Phage protein
2224	1935417	1934803	[-1 L= 615]	yisU / Hypothetical protein
2225	1935533	1936972	[+2 L=1440]	ydfD / Transcriptional regulator, GntR family
2227	1938233	1937271	[-3 L= 963]	xxvH / Hypothetical protein
2230	1938681	1939430	[+3 L= 750]	xxvI / Hypothetical protein
2231	1939584	1940741	[+3 L=1158]	xxvJ / Transglutaminase homolog
2233	1941021	1941539	[+3 L= 519]	xxvK / Hypothetical protein
2234	1942410	1941595	[-1 L= 816]	nadE / NH(3)-dependent NAD(+) synthetase (Spore outgrowth factor b)
2235	1942681	1944558	[+1 L=1878]	yxdM / ABC transporter permease homolog
2236	1944642	1944962	[+3 L= 321]	xxvL / Transcriptional pleiotropic regulator of transitiion state genes
2237	1945241	1946185	[+2 L= 945]	ispQ / Intracellular serine protease, subtilase family
2238	1946538	1946233	[-1 L= 306]	yczG / Transcriptional regulator
2239	1946645	1947577	[+2 L= 933]	iolS / myo-Inositol metabolism protein
2240	1947628	1947834	[+1 L= 207]	yceJ / Multidrug efflux transporter homolog
2241	1947834	1948799	[+3 L= 966]	yceJ / Multidrug efflux transporter homolog
2244	1949201	1949560	[+2 L= 360]	xxvM / Hypothetical protein

2245	1950041	1949766	[-3 L= 276]	xxvN / Hypothetical protein
2246	1950428	1950075	[-3 L= 354]	ytvB / Hypothetical protein
2247	1950595	1951140	[+1 L= 546]	xxvO / Hypothetical protein
2248	1951278	1952372	[+3 L=1095]	xxvP / GTPase homolog
2249	1952576	1954555	[+2 L=1980]	mcpA / Methyl-accepting chemotaxis protein
2251	1955383	1955745	[+1 L= 363]	xxvQ / Hypothetical protein
2252	1956823	1955786	[-2 L=1038]	ykvI / Hypothetical protein
2253	1957064	1957504	[+2 L= 441]	dlpB / Miniferritin Dlp2
2254	1957611	1958063	[+3 L= 453]	xxvR / Hypothetical protein
2255	1958106	1959221	[+3 L=1116]	xxvS / Hypothetical protein
2256	1960270	1959272	[-2 L= 999]	ywcH / Monooxygenase homolog
2258	1960566	1960378	[-1 L= 189]	xxvT / Hypothetical protein
2259	1960745	1962205	[+2 L=1461]	oxlA / Flavin-containing amine oxidase
2260	1962284	1962874	[+2 L= 591]	xxvU / Acetyltransferase homolog
2262	1963804	1962905	[-2 L= 900]	ycsN / Aryl-alcohol dehydrogenase
2263	1963960	1964916	[+1 L= 957]	xxvV / Cobalamin synthesis protein homolog
2264	1965502	1965035	[-2 L= 468]	bltD / Spermine/spermidine acetyltransferase
2265	1966591	1965644	[-2 L= 948]	adcA / Zinc-binding lipoprotein
2268	1967122	1967778	[+1 L= 657]	xxvW / Semialdehyde dehydrogenase
2269	1968851	1967814	[-3 L=1038]	yqjM / NADH-dependent flavin oxidoreductase
2270	1968982	1969353	[+1 L= 372]	ogtA / Methylated-DNA--protein-cysteine methyltransferase (6-O-methylguanine-DNA methyltransferase)
2271	1969442	1970443	[+2 L=1002]	xxvX / Hypothetical protein
2272	1970516	1972189	[+2 L=1674]	xxvY / Extracellular solute-binding protein homolog
2273	1972252	1972665	[+1 L= 414]	fofB / Fosfomycin resistance protein
2274	1972682	1973224	[+2 L= 543]	xxvZ / Short-chain dehydrogenase
2275	1973241	1973849	[+3 L= 609]	gpmB / phosphoglycerate mutase (Phosphoglyceromutase)
2276	1974494	1973901	[-3 L= 594]	xxwA / Hypothetical protein
2277	1974658	1975731	[+1 L=1074]	cotH / Inner spore coat protein H
2278	1975839	1976453	[+3 L= 615]	xxwB / Mutator protein, MutT family
2279	1976561	1977160	[+2 L= 600]	yngC / Alkaline phosphatase homolog
2280	1977258	1978637	[+3 L=1380]	xxwC / Spore cortex protein
2281	1978973	1979911	[+2 L= 939]	corA / Magnesium and cobalt transport protein
2282	1980083	1981006	[+2 L= 924]	ycgR / Hypothetical protein
2283	1981013	1981879	[+2 L= 867]	ycgQ / Hypothetical protein
2284	1981993	1982505	[+1 L= 513]	ykhA / Acyl-CoA thioester hydrolase
2285	1982882	1984063	[+2 L=1182]	xxwD / Phospholipase D
2286	1984098	1984553	[+3 L= 456]	xxwE / Hypothetical protein
2288	1985063	1985683	[+2 L= 621]	yheG / Isoflavone reductase, clacium-binding protein
2289	1986193	1985714	[-2 L= 480]	yqgC / Hypothetical protein
2290	1987550	1986198	[-3 L=1353]	yhdP / Hypothetical protein
2291	1988580	1987714	[-1 L= 867]	xxwF / Hypothetical protein
2292	1988837	1989481	[+2 L= 645]	xxwG / Cystathione beta-synthase domain homolog
2293	1989926	1991275	[+2 L=1350]	brnQ / Branched-chain amino acid transport system carrier protein
2294	1991344	1991670	[+1 L= 327]	csaA / Protein secretion chaperonin
2295	1991654	1992217	[+2 L= 564]	xxwH / Hypothetical protein
2297	1992888	1994039	[+3 L=1152]	spbP / Stage II sporulation protein P
2298	1994134	1994805	[+1 L= 672]	xxwI / Acetyltransferase homolog
2299	1994820	1995557	[+3 L= 738]	vanY / D-Alanyl-D-alanine carboxypeptidase
2300	1995584	1996027	[+2 L= 444]	xxwJ / MutT family protein
2301	1996212	1997684	[+3 L=1473]	xxwK / Amidase
2303	1998966	1997740	[-1 L=1227]	yfmI / Hypothetical protein
2304	1999223	1999654	[+2 L= 432]	xxwL / Hypothetical protein
2305	1999660	2000625	[+1 L= 966]	xxwM / Hypothetical protein
2307	2000631	2001923	[+3 L=1293]	xxwN / Hypothetical protein
2308	2001943	2002530	[+1 L= 588]	xxwO / Phosphoglycerate mutase homolog
2309	2002540	2003313	[+1 L= 774]	xxwP / Haloacid dehalogenase homolog
2310	2003335	2003724	[+1 L= 390]	xxwQ / Hypothetical protein
2311	2004204	2003746	[-1 L= 459]	xxwR / Hypothetical protein
2312	2004325	2005548	[+1 L=1224]	alrB / Alanine racemase 2
2313	2006757	2005840	[-1 L= 918]	xxwS / Acetyltransferase homolog

2314	2007608	2006733	[-3 L= 876]	xxwT / Hypothetical protein
2315	2008017	2009222	[+3 L=1206]	udpT / UDP-glucuronosyl and UDP-glucosyl transferase
2316	2009406	2010248	[+3 L= 843]	xxwU / Hypothetical protein
2318	2011756	2010344	[-2 L=1413]	yhdI / Transcriptional regulator, GntR family
2319	2011886	2012305	[+2 L= 420]	xxwV / Acetyltransferase homolog
2320	2012433	2013605	[+3 L=1173]	xxwW / Hypothetical protein
2321	2014255	2013641	[-2 L= 615]	yvaZ / Hypothetical protein
2322	2014377	2014955	[+3 L= 579]	xxwX / Acetyltransferase homolog
2324	2015522	2016004	[+2 L= 483]	xxwZ / Acetyltransferase homolog
2325	2016020	2016382	[+2 L= 363]	xaxA / Hypothetical protein
2326	2016389	2016814	[+2 L= 426]	xaxB / Acetyltransferase homolog
2327	2017124	2017417	[+2 L= 294]	xaxC / Hypothetical protein
2328	2017547	2021275	[+2 L=3729]	yueB / Hypothetical protein
2329	2021250	2021750	[+3 L= 501]	xaxD / Hypothetical protein
2330	2021758	2022006	[+1 L= 249]	yukD / Hypothetical protein
2331	2022083	2023279	[+2 L=1197]	yukC / Hypothetical protein
2332	2023322	2027824	[+2 L=4503]	yukA / Hypothetical protein
2336	2030522	2030869	[+2 L= 348]	xaxE / Hypothetical protein
2350	2039662	2038880	[-2 L= 783]	xaxF / Hypothetical protein
2351	2039794	2040219	[+1 L= 426]	ytfJ / Hypothetical protein
2352	2040311	2041156	[+2 L= 846]	xaxG / Hypothetical protein
2353	2041166	2041528	[+2 L= 363]	xaxH / Hypothetical protein
2355	2042187	2041846	[-1 L= 342]	xaxI / Hypothetical protein
2356	2042369	2043064	[+2 L= 696]	xaxJ / Methyltransferase homolog
2357	2043099	2044847	[+3 L=1749]	fthS / Formate-tetrahydrofolate ligase (formyltetrahydrofolate synthetase)
2358	2044929	2045465	[+3 L= 537]	xaxK / Hypothetical protein
2360	2045488	2046654	[+1 L=1167]	yfmL / RNA helicase homolog
2362	2046876	2047682	[+3 L= 807]	xaxL / Hypothetical protein
2363	2047741	2048121	[+1 L= 381]	xaxM / Glyoxalase/bleomycin resistance protein homolog
2364	2048817	2048173	[-1 L= 645]	xaxN / Hypothetical protein
2365	2049824	2048841	[-3 L= 984]	qorA / Quinone oxidoreductase (NADPH:quinone reductase)
2366	2050033	2050608	[+1 L= 576]	sigY / RNA polymerase sigma factor
2367	2050608	2051285	[+3 L= 678]	xaxO / Hypothetical protein
2368	2053452	2051395	[-1 L=2058]	xaxP / Hypothetical protein
2369	2053937	2053452	[-3 L= 486]	xaxQ / Outer membrane protein
2370	2054172	2053972	[-1 L= 201]	xaxR / Metallo-beta-lactamase homolog
2371	2054317	2054150	[-2 L= 168]	xaxR / Metallo-beta-lactamase homolog
2372	2054510	2054307	[-3 L= 204]	xaxR / Metallo-beta-lactamase homolog
2373	2054952	2054482	[-1 L= 471]	xaxR / Metallo-beta-lactamase homolog
2375	2055446	2055952	[+2 L= 507]	bsaA / Glutathione peroxidase homolog
2377	2058267	2056042	[-1 L=2226]	xaxS / Transglutaminase homolog
2378	2059482	2058499	[-1 L= 984]	xaxT / Hypothetical protein
2379	2060441	2059482	[-3 L= 960]	yeaC / Methanol dehydrogenase regulation homolog
2380	2060937	2064626	[+3 L=3690]	narG / Nitrate reductase alpha chain
2381	2064619	2066091	[+1 L=1473]	narH / Nitrate reductase beta chain
2382	2066114	2066641	[+2 L= 528]	narJ / Nitrate reductase delta chain
2383	2066623	2067348	[+1 L= 726]	narI / Nitrate reductase gamma chain
2384	2068164	2067448	[-1 L= 717]	fnrA / Anaerobic regulatory protein
2385	2068416	2069426	[+3 L=1011]	moaA / Molybdenum cofactor biosynthesis protein A (narA protein)
2386	2069429	2070457	[+2 L=1029]	thiF / Adenylyltransferase
2387	2070502	2071788	[+1 L=1287]	mocF / Molybdopterin biosynthesis protein
2388	2071836	2072303	[+3 L= 468]	moaE / Molybdopterin converting factor subunit 2 (MPT synthase subunit 2)
2389	2072303	2072533	[+2 L= 231]	moaD / Molybdopterin converting factor subunit 1 (MPT synthase subunit 1)
2390	2072617	2073783	[+1 L=1167]	narK / Nitrite extrusion protein (Nitrite facilitator)
2392	2074490	2075404	[+2 L= 915]	xaxU / Hypothetical protein
2393	2075559	2076050	[+3 L= 492]	xaxV / Hypothetical protein
2395	2076713	2076243	[-3 L= 471]	xaxW / Uroporphyrin-III C-methyltransferase homolog
2396	2077416	2076709	[-1 L= 708]	xaxX / Hypothetical protein
2397	2078837	2077416	[-3 L=1422]	nasF / Uroporphyrin-III C-methyltransferase (Urogen III methylase)

2398	2079213	2078899	[-1 L= 315]	nasE / Assimilatory nitrite reductase [NAD(P)H] small subunit
2399	2081583	2079232	[-1 L=2352]	nasD / Nitrite reductase [NAD(P)H] large subunit
2401	2082550	2081846	[-2 L= 705]	xaxY / Hypothetical protein
2403	2083654	2083391	[-2 L= 264]	xaxZ / Hypothetical protein
2406	2085415	2084537	[-2 L= 879]	xbxA / N-acetyltransferase homolog
2407	2085927	2087525	[+3 L=1599]	lacT / Lecithin:cholesterol acyltransferase
2409	2088806	2089078	[+2 L= 273]	xbxB / Stage V sporulation protein S
2411	2089391	2089675	[+2 L= 285]	xbxC / Hypothetical protein
2413	2090148	2090537	[+3 L= 390]	xbxD / 5-Methylcytosine-specific restriction enzyme A
2414	2091241	2090882	[-2 L= 360]	xbxE / Hypothetical protein
2415	2091417	2092487	[+3 L=1071]	xbxF / Response regulator
2419	2093847	2094491	[+3 L= 645]	xbxG / Hypothetical protein
2420	2094476	2096383	[+2 L=1908]	yfmR / ABC transporter ATP-binding protein homolog
2421	2096462	2097190	[+2 L= 729]	xbxH / Hypothetical protein
2423	2097715	2098047	[+1 L= 333]	ssbA / Single-strand binding protein (Helix-destabilizing protein)
2424	2098299	2099423	[+3 L=1125]	ypgR / Hypothetical protein
2425	2099430	2099810	[+3 L= 381]	xbxI / Hypothetical protein
2426	2099897	2100328	[+2 L= 432]	yphP / Hypothetical protein
2428	2100381	2101154	[+3 L= 774]	pcmT / Protein-L-isoD-O-methyltransferase
2429	2101458	2102078	[+3 L= 621]	syrA / Arginyl-tRNA synthetase (Arginine--tRNA ligase)
2430	2102247	2103134	[+3 L= 888]	syrA / Arginyl-tRNA synthetase (Arginine--tRNA ligase)
2431	2103260	2103586	[+2 L= 327]	xbxJ / Hypothetical protein
2433	2103971	2104849	[+2 L= 879]	xbxK / Hypothetical protein
2435	2105373	2109572	[+3 L=4200]	xbxL / Hypothetical protein
2436	2109955	2113059	[+1 L=3105]	syiP / Isoleucyl-tRNA synthetase (Isoleucine--tRNA ligase) (Mupirocin resistance protein)
2437	2114218	2113118	[-2 L=1101]	yrkO / Hypothetical protein
2438	2114786	2114205	[-3 L= 582]	xbxM / Transcriptional regulator TetR family
2439	2115065	2116627	[+2 L=1563]	nprE / Bacillolysin precursor (Extracellular neutral metalloprotease)
2440	2117222	2116740	[-3 L= 483]	xbxN / Hypothetical protein
2442	2117922	2119052	[+3 L=1131]	syiD / Aspartyl-tRNA synthetase (Aspartate--tRNA ligase)
2443	2119625	2120962	[+2 L=1338]	xbxO / Sodium-dependent transporter
2444	2121000	2121914	[+3 L= 915]	pipA / Proline iminopeptidase (Prolyl aminopeptidase)
2445	2122541	2121957	[-3 L= 585]	xbxP / Hypothetical protein
2446	2123360	2122557	[-3 L= 804]	ydaH / Hypothetical protein
2447	2123542	2124261	[+1 L= 720]	xbxQ / Haloacid dehalogenase homolog
2448	2124415	2125851	[+1 L=1437]	yxjC / Hypothetical protein
2449	2125925	2127133	[+2 L=1209]	xbxR / Alcohol dehydrogenase homolog
2450	2127317	2128006	[+2 L= 690]	xbxS / Amino acid racemase
2451	2128099	2128575	[+1 L= 477]	xbxT / Hypothetical protein
2452	2128554	2129012	[+3 L= 459]	yhfO / Acetyltransferase homolog
2453	2129191	2129673	[+1 L= 483]	yoaS / Hypothetical protein
2454	2129678	2129902	[+2 L= 225]	yozG / Transcriptional regulator
2455	2130673	2130149	[-2 L= 525]	xbxU / Haloacid dehalogenase homolog
2456	2131135	2130707	[-2 L= 429]	xbxV / Acetyltransferase homolog
2457	2131259	2131996	[+2 L= 738]	ythP / ABC transporter ATP-binding protein
2458	2131983	2133203	[+3 L=1221]	xbxW / Hypothetical protein
2459	2133477	2134061	[+3 L= 585]	ypjP / Hypothetical protein
2460	2134120	2134803	[+1 L= 684]	xbxX / Haloacid dehalogenase homolog
2461	2134808	2135191	[+2 L= 384]	xbxY / Hypothetical protein
2462	2135206	2136135	[+1 L= 930]	xbxZ / Hypothetical protein
2463	2137661	2136192	[-3 L=1470]	xcxA / Hypothetical protein
2464	2137845	2138798	[+3 L= 954]	tysY / Thymidylate synthase (TS)
2466	2138752	2139306	[+1 L= 555]	dhfR / Dihydrofolate reductaser
2467	2139465	2141447	[+3 L=1983]	pbpC / Penicillin-binding protein 3 (PBP 3)
2468	2141692	2142324	[+1 L= 633]	yvaB / Acyl carrier protein phosphodiesterase 2
2469	2142438	2143154	[+3 L= 717]	plsC / 1-acyl-sn-glycerol-3-phosphate acyltransferase (Lysophosphatidic acid acyltransferase)
2470	2143915	2143202	[-2 L= 714]	hlyC / Hemolysin III
2471	2144069	2144251	[+2 L= 183]	xcxB / Hypothetical protein
2473	2144285	2145034	[+2 L= 750]	ycbT / Hypothetical protein

2474	2145346	2145615	[+1 L= 270]	ypmP / Hypothetical protein
2475	2145773	2146612	[+2 L= 840]	degV / DegV protein
2478	2147928	2146948	[-1 L= 981]	xcxC / Hypothetical protein
2479	2148255	2148839	[+3 L= 585]	ypmQ / Hypothetical protein
2480	2149341	2148880	[-1 L= 462]	xcxD / Heat shock protein
2481	2149559	2151457	[+2 L=1899]	asnB / Asparagine synthetase [glutamine-hydrolyzing] 1
2482	2151554	2151910	[+2 L= 357]	xcxE / Acetyltransferase homolog
2485	2152397	2153380	[+2 L= 984]	cwlC / Sporulation-specific N-acetylmuramoyl-L-alanine amidase (Cell wall hydrolase)
2486	2153622	2154581	[+3 L= 960]	yfiY / Iron(III) dicitrate transport permease
2488	2154669	2155583	[+3 L= 915]	daaA / D-alanine aminotransferase (D-amino acid aminotransferase)
2489	2155685	2156329	[+2 L= 645]	xcxF / Nitroreductase homolog
2490	2156591	2157076	[+2 L= 486]	xcxG / Hypothetical protein
2491	2157508	2158059	[+1 L= 552]	yueJ / Pyrazinamidase/nicotinamidase homolog
2493	2158399	2158833	[+1 L= 435]	xcxH / Heat shock protein
2494	2159137	2160027	[+1 L= 891]	xcxI / Mechanosensitive ion channel protein
2496	2160177	2161304	[+3 L=1128]	yhcZ / Two-component sensor histidine kinase
2497	2161304	2161960	[+2 L= 657]	xcxJ / Two-component response regulator
2498	2162168	2163019	[+2 L= 852]	xcxK / Transcritpional regulator, RpiR family
2499	2163187	2164047	[+1 L= 861]	xcxL / Phenazine biosynthesis protein homolog
2500	2164344	2165378	[+3 L=1035]	xcxM / Alcohol dehydrogenase
2501	2166581	2165535	[-3 L=1047]	xcxN / Hypothetical protein
2503	2167486	2166551	[-2 L= 936]	xcxO / Hypothetical protein
2504	2168011	2169546	[+1 L=1536]	gntK / Gluconokinase (Gluconate kinase)
2506	2169555	2170910	[+3 L=1356]	gnuT / Gluconate permease
2508	2170923	2171825	[+3 L= 903]	yqeC / 6-Phosphogluconate dehydrogenase homolog
2509	2172574	2171900	[-2 L= 675]	ywbB / Hypothetical protein
2510	2172800	2174017	[+2 L=1218]	xcxP / Glycosyltransferase homolog
2511	2174055	2175206	[+3 L=1152]	xcxQ / Hypothetical protein
2512	2175354	2175887	[+3 L= 534]	xcxR / Azoreductase
2513	2175892	2177118	[+1 L=1227]	xcxS / Hypothetical protein
2514	2177185	2177739	[+1 L= 555]	xcxT / Hypothetical protein
2515	2177789	2178787	[+2 L= 999]	opbA / Glycine/betaine/carnitine/choline transport ATP-binding protein
2516	2178794	2180302	[+2 L=1509]	opcB / Glycine/betaine/carnitine/choline transport system permease protein
2518	2180519	2181943	[+2 L=1425]	arcD / Arginine/ornithine antiporter
2519	2182018	2182281	[+1 L= 264]	xcxU / Hypothetical protein
2523	2182644	2184203	[+3 L=1560]	xcxV / Hypothetical protein
2524	2184190	2186043	[+1 L=1854]	xcxW / Hypothetical protein
2525	2186275	2186919	[+1 L= 645]	xcxX / Hypothetical protein
2526	2187669	2187022	[-1 L= 648]	xcxY / Hemagglutinin
2527	2187916	2189268	[+1 L=1353]	yrkA / Hemolysin homolog
2529	2189554	2190825	[+1 L=1272]	xcxZ / NADP-dependent glyceraldehyde-3-phosphate dehydrogenase
2530	2191341	2190934	[-1 L= 408]	yueI / Hypothetical protein
2531	2191560	2192690	[+3 L=1131]	xdxA / Histidine kinase homolog
2532	2193482	2192730	[-3 L= 753]	xdxB / Hypothetical protein
2535	2194365	2195732	[+3 L=1368]	yodT / Adenosylmethionine-8-amino-7-oxononanoate aminotransferase homolog
2536	2195732	2196427	[+2 L= 696]	yodS / 3-Oxoadipate CoA-transferase
2537	2196415	2197074	[+1 L= 660]	yodR / Butyrate-acetoactetate CoA-transferase
2538	2197093	2198358	[+1 L=1266]	argE / Acetylornithine deacetylase
2539	2198358	2199254	[+3 L= 897]	yodP / Hypothetical protein
2540	2199374	2200804	[+2 L=1431]	ntrC / Transcriptional regulator, NifA family
2541	2201018	2202436	[+2 L=1419]	yodO / Hypothetical protein
2542	2202436	2202705	[+1 L= 270]	yokU / Hypothetical protein
2543	2202781	2202993	[+1 L= 213]	yozE / Hypothetical protein
2544	2203247	2203906	[+2 L= 660]	yodN / Hypothetical protein
2545	2204069	2203917	[-3 L= 153]	xdxC / Hypothetical protein
2546	2204210	2204395	[+2 L= 186]	yozD / Hypothetical protein
2549	2204691	2205509	[+3 L= 819]	ybdM / Serine/threonine protein kinase
2550	2205494	2206246	[+2 L= 753]	xdxD / Hypothetical protein

2551	2206306	2206959	[+1 L= 654]	yodM / Acid phosphatase homolog
2552	2207842	2206955	[-2 L= 888]	yeaB / Cation efflux system membrane protein homolog
2553	2208525	2208190	[-1 L= 336]	ydbP / Thioredoxin
2554	2209297	2208770	[-2 L= 528]	xdxE / Hypothetical protein
2555	2209919	2210209	[+2 L= 291]	xdxF / Hypothetical protein
2557	2210746	2211279	[+1 L= 534]	xdxG / Hypothetical protein
2558	2211436	2212008	[+1 L= 573]	xdxH / Hypothetical protein
2562	2214228	2215223	[+3 L= 996]	xdxI / Phage endolysin
2563	2215399	2216277	[+1 L= 879]	lipA / Rotamase
2564	2216626	2216898	[+1 L= 273]	xdxJ / Hypothetical protein
2568	2217879	2218211	[+3 L= 333]	xdxK / Hypothetical protein
2569	2218647	2218426	[-1 L= 222]	gepF / Spore germination protein gerPF
2572	2219560	2220273	[+1 L= 714]	xdxL / Hypothetical protein
2573	2220406	2221086	[+1 L= 681]	xdxM / Hypothetical protein
2574	2221204	2221413	[+1 L= 210]	xdxN / Hypothetical protein
2576	2222161	2224650	[+1 L=2490]	pbpA / Penicillin-binding protein 1A/1B (PBP1)
2578	2225257	2226417	[+1 L=1161]	xdxO / Hypothetical protein
2579	2226436	2226723	[+1 L= 288]	yneR / Hypothetical protein
2580	2227089	2228240	[+3 L=1152]	cisW / Citrate synthase III
2581	2228258	2229775	[+2 L=1518]	yqiP / Hypothetical protein
2582	2229799	2230704	[+1 L= 906]	cppM / Carboxyvinyl-carboxyphosphonate phosphorylmutase (Carboxyphosphonoenolpyruvate phosphonomutase)
2583	2230860	2232566	[+3 L=1707]	xdxP / Butyryl-CoA dehydrogenase
2584	2232586	2233473	[+1 L= 888]	xdxQ / 3-Hydroxybutyrate dehydrogenase
2585	2233499	2234956	[+2 L=1458]	mmsA / Methylmalonate-semialdehyde dehydrogenase [acylating] (MMSDH)
2586	2235668	2235033	[-3 L= 636]	yrhP / Dihydropicolinate reductase homolog
2587	2236970	2235918	[-3 L=1053]	echA / Enoyl-CoA hydratase
2589	2237742	2237978	[+3 L= 237]	ytmB / Hypothetical protein
2591	2237997	2239151	[+3 L=1155]	sbcD / Exonuclease homolog
2592	2239151	2242237	[+2 L=3087]	xdxR / Exonuclease
2594	2242882	2243307	[+1 L= 426]	xdxS / Arsenical resistance operon repressor homolog
2595	2243554	2243372	[-2 L= 183]	xdxT / Hypothetical protein
2599	2244910	2246109	[+1 L=1200]	xdxU / Hypothetical protein
2600	2246741	2247523	[+2 L= 783]	dhbA / 2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase (Cold shock protein CSI14)
2601	2247552	2248748	[+3 L=1197]	dhbC / Isochorismate synthase (Isochorismate mutase)
2602	2248764	2250377	[+3 L=1614]	dhbE / 2,3-dihydroxybenzoate-AMP ligase (Dihydroxybenzoic acid-activating enzyme)
2603	2250405	2251295	[+3 L= 891]	dhbB / Isochorismatase (2,3 dihydro-2,3 dihydroxybenzoate synthase) (Superoxide-inducible protein 1)
2604	2251332	2255279	[+3 L=3948]	dhbF / Serine activating enzyme
2606	2255376	2257988	[+3 L=2613]	dhbF / Serine activating enzyme
2607	2258018	2258488	[+2 L= 471]	dhbF / Serine activating enzyme
2608	2258488	2258709	[+1 L= 222]	xdxV / Hypothetical protein
2609	2258712	2260139	[+3 L=1428]	yhcA / Multidrug resistance protein homolog
2610	2260200	2260946	[+3 L= 747]	hetI / 4'-phosphopantetheinyl transferase
2611	2260966	2261514	[+1 L= 549]	xdxW / Hypothetical protein
2612	2261828	2261559	[-3 L= 270]	dbhA / DNA-binding protein HU 1 (DNA-binding protein II)
2613	2262033	2262797	[+3 L= 765]	xdxX / Hypothetical protein
2614	2262815	2263336	[+2 L= 522]	dinB / Nuclease inhibitor protein
2615	2264624	2263434	[-3 L=1191]	xdxY / Cysteine-dependent serine protease
2616	2266224	2264860	[-1 L=1365]	xdxZ / Sodium:alanine symporter homolog
2617	2267235	2266663	[-1 L= 573]	xexA / Hypothetical protein
2618	2267368	2267727	[+1 L= 360]	xexB / Hypothetical protein
2619	2267913	2268551	[+3 L= 639]	ydbC / Hypothetical protein
2620	2268731	2269444	[+2 L= 714]	xexC / 16S rRNA uridine--pseudouridylate synthase
2622	2270095	2272014	[+1 L=1920]	syiT / Threonyl-tRNA synthetase 2 (Threonine--tRNA ligase)
2624	2272258	2273031	[+1 L= 774]	xexD / ABC transporter homolog
2625	2273046	2274923	[+3 L=1878]	xexE / Permease homolog
2626	2275112	2275798	[+2 L= 687]	ykuC / Hypothetical protein

2627	2275920	2276783	[+3 L= 864]	xexF / Hypothetical protein
2628	2276779	2277786	[+1 L=1008]	xexG / Hypothetical protein
2630	2279534	2277837	[-3 L=1698]	ydaP / Pyruvate oxidase homolog
2631	2280432	2279674	[-1 L= 759]	xexH / Zinc transporter protein homolog
2632	2280557	2281426	[+2 L= 870]	xexI / Metallo-beta-lactamase homolog
2633	2282547	2281597	[-1 L= 951]	xexJ / Inosine/adenosine/guanosine-nucleosidase hydrolase
2634	2283201	2282572	[-1 L= 630]	xexK / Hypothetical protein
2635	2283384	2283866	[+3 L= 483]	yybC / Hypothetical protein
2636	2284038	2284460	[+3 L= 423]	xexL / Hypothetical protein
2637	2284477	2285175	[+1 L= 699]	xexM / Transcriptional regulator
2638	2285168	2285662	[+2 L= 495]	xexN / Hypothetical protein
2639	2285747	2286664	[+2 L= 918]	pipD / Proline iminopeptidase (Prolyl aminopeptidase)
2640	2287253	2287657	[+2 L= 405]	xexO / Acetyltransferase homolog
2641	2287778	2288428	[+2 L= 651]	xexP / Metallo-beta-lactamase homolog
2642	2289158	2288532	[-3 L= 627]	xexQ / Transcriptional regulator, TetR family
2643	2289274	2289429	[+1 L= 156]	xexR / Hypothetical protein
2644	2289440	2291503	[+2 L=2064]	xexS / Transport protein homolog
2645	2292372	2291566	[-1 L= 807]	xexT / Transposase
2646	2292998	2292402	[-3 L= 597]	xexU / Insertion element DNA-binding protein
2648	2293426	2293830	[+1 L= 405]	xexV / Transposase-related protein
2649	2293830	2294915	[+3 L=1086]	xexW / Transposase
2650	2295442	2295963	[+1 L= 522]	xexX / Acetyltransferase homolog
2651	2296004	2296945	[+2 L= 942]	xexY / Acetyltransferase homolog
2652	2297053	2297619	[+1 L= 567]	xexZ / Acetyltransferase homolog
2653	2298454	2297648	[-2 L= 807]	xfxA / Hypothetical protein
2655	2298685	2299260	[+1 L= 576]	xfxB / Transcriptional regulator, MerR family
2656	2299297	2300238	[+1 L= 942]	xfxC / Hypothetical protein
2658	2300739	2302127	[+3 L=1389]	ppoX / Protoporphyrinogen oxidase (PPO)
2659	2302653	2302189	[-1 L= 465]	xfxD / Hypothetical protein
2661	2303043	2303591	[+3 L= 549]	yoaA / Acetyltransferase homolog
2662	2303823	2303641	[-1 L= 183]	ydjO / Hypothetical protein
2663	2304182	2303913	[-3 L= 270]	cspA / Major cold shock protein
2664	2304506	2305399	[+2 L= 894]	xfxE / Hypothetical protein
2666	2305402	2306058	[+1 L= 657]	xfxG / Hypothetical protein
2668	2306319	2306921	[+3 L= 603]	xfxH / Hypothetical protein
2669	2307885	2306998	[-1 L= 888]	xfxI / Transcriptional regulator, LysR family
2670	2307991	2309031	[+1 L=1041]	dhaS / Aspartate-semialdehyde dehydrogenase (ASADH)
2673	2309906	2310952	[+2 L=1047]	xfxJ / Hypothetical protein
2674	2311058	2311267	[+2 L= 210]	xfxK / Hypothetical protein
2675	2312269	2311370	[-2 L= 900]	xfxL / Transcriptional regulator, LysR family
2676	2312426	2313112	[+2 L= 687]	yflK / Hypothetical protein
2677	2313296	2314258	[+2 L= 963]	xfxM / Acetyltransferase homolog
2678	2314274	2314888	[+2 L= 615]	xfxN / Hypothetical protein
2679	2315113	2316864	[+1 L=1752]	yfiB / ABC transporter ATP-binding protein
2680	2316794	2318653	[+2 L=1860]	yfiC / ABC transporter ATP-binding protein
2681	2319526	2319323	[-2 L= 204]	xfxO / Hypothetical protein
2685	2320998	2320729	[-1 L= 270]	xfxP / Hypothetical protein
2687	2322932	2322351	[-3 L= 582]	xfxQ / Transport protein
2688	2322988	2323599	[+1 L= 612]	xfxR / Hypothetical protein
2690	2324567	2323965	[-3 L= 603]	xfxS / Hypothetical protein
2693	2326182	2327384	[+3 L=1203]	xfxT / Hypothetical protein
2694	2328151	2327954	[-2 L= 198]	xfxU / Hypothetcial protein
2696	2328803	2329111	[+2 L= 309]	xfxV / Hypothetical protein
2697	2329176	2330516	[+3 L=1341]	xfxW / Phytoene dehydrogenase homolog
2698	2330476	2331363	[+1 L= 888]	ecfA / RNA polymerase sigma factor, ECF subfamily
2699	2331593	2331402	[-3 L= 192]	xfxX / Hypothetical protein
2700	2331847	2332452	[+1 L= 606]	xfxY / O-Methyltransferase
2701	2332716	2333879	[+3 L=1164]	xfxZ / Hypothetical protein
2702	2333907	2334737	[+3 L= 831]	xgxA / Hypothetical protein
2704	2337617	2336103	[-3 L=1515]	yngK / Hypothetical protein
2707	2337887	2338189	[+2 L= 303]	ptcB / PTS system, cellobiose-specific IIB component (Cellobiose-

				permease IIB component)
2708	2338204	2339484	[+1 L=1281]	ywbA / PTS system IIBC component
2709	2339566	2339829	[+1 L= 264]	xgxB / Hypothetical protein
2711	2339846	2341024	[+2 L=1179]	xgxC / Hypothetical protein
2712	2341024	2341914	[+1 L= 891]	xgxD / N-Acetylglucosamine kinase homolog
2713	2342043	2342600	[+3 L= 558]	xgxE / Hypothetical protein
2715	2342674	2344254	[+1 L=1581]	xgxF / Aminotransferase homolog
2716	2344332	2345330	[+3 L= 999]	thdB / Threonine dehydratase homolog (Threonine deaminase)
2718	2345565	2346032	[+3 L= 468]	xgxG / Transcriptional regulator, MarR family
2719	2346242	2347474	[+2 L=1233]	tcrC / Tetracycline resistance protein, class C homolog
2720	2348079	2347705	[-1 L= 375]	xgxH / Hypothetical protein
2722	2348629	2348892	[+1 L= 264]	xgxI / Hypothetical protein
2724	2349068	2349751	[+2 L= 684]	xgxJ / Metallo-beta-lactamase homolog
2725	2349888	2350181	[+3 L= 294]	xgxK / Hypothetical protein
2727	2350258	2351631	[+1 L=1374]	xgxL / ATP-dependent RNA helicase homolog
2731	2353498	2354130	[+1 L= 633]	xgxM / Transcriptional regulator, TetR family
2732	2354180	2355439	[+2 L=1260]	xgxN / Hypothetical protein
2734	2355784	2356095	[+1 L= 312]	xgxO / Permease homolog
2735	2356256	2356480	[+2 L= 225]	xgxP / Hypothetical protein
2740	2360250	2359789	[-1 L= 462]	xgxQ / Hypothetical protein
2743	2362184	2362663	[+2 L= 480]	xgxR / Phage-related protein homolog
2744	2362666	2363205	[+1 L= 540]	xgxS / Phage integrase
2745	2363535	2365502	[+3 L=1968]	xgxT / Hypothetical protein
2750	2367518	2369308	[+2 L=1791]	xgxU / Hypothetical protein
2751	2370382	2371080	[+1 L= 699]	xgxV / Hypothetical protein
2754	2373496	2373588	[+1 L= 93]	xgxW / ABC transporter ATP-binding protein
2756	2373846	2374553	[+3 L= 708]	xgxX / Hypothetical protein
2757	2374629	2375078	[+3 L= 450]	xgxY / Hypothetical protein
2758	2375105	2375482	[+2 L= 378]	ybaJ / Hypothetical protein
2759	2377328	2375646	[-3 L=1683]	pyrD / Pyruvate decarboxylase
2760	2377436	2377915	[+2 L= 480]	xgxZ / Transcriptional regulator, MarR family
2761	2378085	2378819	[+3 L= 735]	gpmA / 2,3-bisphosphoglycerate-dependent phosphoglycerate mutase (Phosphoglyceromutase)
2762	2379061	2379795	[+1 L= 735]	ykaC / Stage II sporulation protein SA (Killer protein spoIISA)
2765	2380592	2380311	[-3 L= 282]	xhxA / Hypothetical protein
2767	2380909	2382375	[+1 L=1467]	pepD / Aminoacyl-histidine dipeptidase (X-His dipeptidase)
2770	2384556	2384308	[-1 L= 249]	xhxB / Hypothetical protein
2771	2384931	2385806	[+3 L= 876]	xhxC / Hypothetical protein
2772	2385890	2386225	[+2 L= 336]	xhxD / Transition state regulatory protein, AbrB family
2773	2386843	2388090	[+1 L=1248]	xhxE / Hypothetical protein
2774	2388161	2388916	[+2 L= 756]	xhxF / Hypothetical protein
2775	2389173	2389829	[+3 L= 657]	xhxG / Chloramphenicol acetyltransferase homolog
2777	2389991	2391472	[+2 L=1482]	dacA / D-alanyl-D-alanine carboxypeptidase precursor (DD-carboxypeptidase)
2778	2391854	2392483	[+2 L= 630]	xhxH / Hypothetical protein
2779	2393545	2394795	[+1 L=1251]	yfiS / Multidrug resistance protein homolog
2780	2394812	2395384	[+2 L= 573]	ppsA / Peptide synthetase 1
2781	2395430	2399368	[+2 L=3939]	ppsB / Peptide synthetase 2
2782	2399374	2405841	[+1 L=6468]	grsB / Gramicidin S synthetase II (ATP-dependent proline/valine/ornithine/leucine adenylase)
2783	2405841	2406536	[+3 L= 696]	bacB / Bacitracin synthetase II (ATP-dependent lysine/ornithine adenylase)
2784	2406529	2408076	[+1 L=1548]	tycC / Tyrocidine synthetase III (ATP-dependent asparagineglutamine/tyrosine/valine/ornithine/leucine adenylase)
2785	2407988	2420722	[+2 L=12735]	bacB / Bacitracin synthetase II (ATP-dependent lysine/ornithine adenylase)
2786	2421047	2421748	[+2 L= 702]	gspA / 4'-phosphopantetheinyl transferase (Gramicidin synthetase-activating enzyme)
2787	2421717	2422457	[+3 L= 741]	grsT / Gramicidin S biosynthesis protein
2792	2424755	2424168	[-3 L= 588]	ybfO / Erythromycin esterase homolog
2793	2425252	2425896	[+1 L= 645]	yocA / Transposon-related protein
2794	2426217	2426720	[+3 L= 504]	ynaD / Acetyltransferase homolog

2796	2428116	2429624	[+3 L=1509]	xhxI / N-Acetylmuramoyl-L-alnine amidase homolog
2797	2430608	2430937	[+2 L= 330]	xhxJ / Hypothetical protein
2799	2432078	2433793	[+2 L=1716]	colA / Microbial collagenase precursor (120 kDa collagenase)
2800	2434448	2435491	[+2 L=1044]	pbpE / Penicillin-binding protein 4* (PBP 4*)
2801	2435744	2437708	[+2 L=1965]	pbpC / Penicillin-binding protein 3 (PBP 3)
2802	2438142	2438678	[+3 L= 537]	sigZ / RNA polymerase sigma factor sigZ
2803	2438668	2439495	[+1 L= 828]	xhxK / Hypothetical protein
2805	2441270	2439513	[-3 L=1758]	xhxL / Penicillin binding protein homolog
2807	2441636	2442955	[+2 L=1320]	xhxM / Penicillin binding protein homolog
2808	2443002	2443766	[+3 L= 765]	xhxM / Penicillin binding protein homolog
2809	2443978	2444913	[+1 L= 936]	blaC / Beta-lactamase, type I precursor (penicillinase)
2810	2445073	2445630	[+1 L= 558]	xhxN / Acetyltransferase homolog
2811	2445652	2445750	[+1 L= 99]	xhxO / Hypothetical protein
2812	2446105	2446989	[+1 L= 885]	xhxP / Phosphoesterase homolog
2815	2447705	2448370	[+2 L= 666]	xhxQ / ABC transporter ATP-binding protein
2816	2448370	2449380	[+1 L=1011]	xhxR / Hypothetical protein
2817	2449408	2450058	[+1 L= 651]	xhxS / Transcriptional regulator, TetR family
2819	2450716	2451681	[+1 L= 966]	xhxT / Hypothetical protein
2820	2451889	2452752	[+1 L= 864]	yngJ / Butyryl-CoA dehydrogenase homolog
2821	2452765	2453043	[+1 L= 279]	xhxU / Butyryl-CoA dehydrogenase homolog
2822	2453061	2454395	[+3 L=1335]	yngH / Biotin carboxylase
2823	2454425	2454637	[+2 L= 213]	yngX / Biotin-requiring protein
2824	2454662	2455570	[+2 L= 909]	yngG / Hydroxymethylglutaryl-CoA lyase homolog
2826	2455578	2456363	[+3 L= 786]	yngF / Hydroxybutyryl dehydratase (enoyl-CoA dehydratase)
2827	2456369	2457907	[+2 L=1539]	yngE / Propionyl-CoA carboxylase homolog
2828	2457960	2459897	[+3 L=1938]	acsA / Acetyl-coenzyme A synthetase (Acetate--CoA ligase)
2829	2460037	2460729	[+1 L= 693]	xhxV / Insertion element DNA-binding protein
2830	2460759	2461565	[+3 L= 807]	xhxW / Transposase
2831	2462100	2461666	[-1 L= 435]	xhxX / Hypothetical protein
2833	2462664	2463017	[+3 L= 354]	xhxY / Hypothetical protein
2836	2463126	2463656	[+3 L= 531]	xhxZ / Acetyltransferase homolog
2837	2464556	2463930	[-3 L= 627]	xixA / Hypothetical protein
2839	2465562	2465654	[+3 L= 93]	xixB / Hypothetical protein
2840	2466736	2465723	[-2 L=1014]	dacF / Penicillin-binding protein dacF precursor (D-alanyl-D-alanine carboxypeptidase)
2841	2468114	2466915	[-3 L=1200]	xixC / Two-component sensor hostidine kinase
2842	2468805	2468062	[-1 L= 744]	xixD / Two component response regulator
2843	2468947	2469552	[+1 L= 606]	xixE / Hypothetical protein
2844	2469545	2469730	[+2 L= 186]	ynaE / Hypothetical protein
2845	2470139	2470270	[+2 L= 132]	xixF / Hypothetical protein
2846	2470270	2471004	[+1 L= 735]	xixG / Hypothetical protein
2847	2471050	2471895	[+1 L= 846]	xixH / Hypothetical protein
2848	2472039	2472461	[+3 L= 423]	xixI / Hypothetical protein
2849	2472639	2475317	[+3 L=2679]	xixJ / Thermolysin metallopeptidase homolog
2850	2476843	2475656	[-2 L=1188]	trrA / Transcriptional regulator
2851	2477443	2479131	[+1 L=1689]	xixK / Hypothetical protein
2853	2479177	2480019	[+1 L= 843]	xixL / Hypothetical protein
2854	2480164	2482416	[+1 L=2253]	xixM / Hypothetical protein
2855	2482570	2483136	[+1 L= 567]	xixN / Hypothetical protein
2856	2483343	2483855	[+3 L= 513]	xixO / Hypothetical protein
2857	2483938	2487105	[+1 L=3168]	xixP / ABC transporter protein
2858	2487282	2488091	[+3 L= 810]	xixQ / Transcriptional regulator, MerR family
2859	2489443	2488169	[-2 L=1275]	xixR / Hypothetical protein
2860	2490449	2489736	[-3 L= 714]	xixS / Acyl-carrier protein reductase homolog
2861	2490794	2491138	[+2 L= 345]	yckH / Hypothetical protein
2862	2491275	2492024	[+3 L= 750]	xixT / Methyltransferase homolog
2864	2492164	2492994	[+1 L= 831]	xixU / Hypothetical protein
2865	2493115	2493906	[+1 L= 792]	xixV / Hypothetical protein
2866	2494026	2494775	[+3 L= 750]	xixW / Hypothetical protein
2867	2495183	2494860	[-3 L= 324]	yerI / Hypothetical protein
2868	2495174	2495983	[+2 L= 810]	araC / Arabinose operon control protein

2870	2497692	2496004	[-1 L=1689]	xixX / Peptidase homolog
2871	2497848	2498453	[+3 L= 606]	xixY / Hypothetical protein
2872	2498527	2499894	[+1 L=1368]	ycxD / Transcriptional regulator, GntR family
2874	2501138	2500485	[-3 L= 654]	xixZ / Hypothetical protein
2878	2502044	2502967	[+2 L= 924]	xjxA / Zinc-binding dehydrogenase homolog
2880	2503052	2503906	[+2 L= 855]	xjxB / Hypothetical protein
2882	2503965	2504462	[+3 L= 498]	ydfR / Membrane protein homolog
2883	2504722	2505348	[+1 L= 627]	xjxC / Methyltransferase homolog
2884	2506305	2505607	[-1 L= 699]	xjxD / Hypothetical protein
2885	2507213	2506305	[-3 L= 909]	yvrE / RNA polymerase homolog
2887	2507925	2509475	[+3 L=1551]	syiK / Lysyl-tRNA synthetase (Lysine--tRNA ligase)
2888	2509965	2509516	[-1 L= 450]	cwlJ / Cell wall hydrolase protein
2889	2510116	2511027	[+1 L= 912]	amdA / Acetamidase
2890	2511158	2511862	[+2 L= 705]	xjxE / Two-component response regulator
2891	2511862	2512842	[+1 L= 981]	yxdK / Two-component sensor hostidine kinase
2892	2513759	2513085	[-3 L= 675]	xjxF / Hypothetical protein
2893	2514266	2515891	[+2 L=1626]	expZ / ATP-binding transport protein
2894	2515915	2516496	[+1 L= 582]	xjxG / Acetyltransferase homolog
2895	2516623	2517525	[+1 L= 903]	yxdL / ABC transporter ATP-binding protein
2896	2517503	2519434	[+2 L=1932]	yxdM / ABC transporter permease
2897	2519492	2520175	[+2 L= 684]	xjxH / Hypothetical protein
2898	2520585	2520247	[-1 L= 339]	xjxI / Hypothetical protein
2899	2520865	2521110	[+1 L= 246]	xjxJ / Lipase homolog
2900	2521097	2522104	[+2 L=1008]	lipA / Lipase precursor (Triacylglycerol lipase)
2901	2522156	2523217	[+2 L=1062]	dhoM / Homoserine dehydrogenase (HDH)
2902	2523289	2524755	[+1 L=1467]	xjxK / Transcriptional regulator, MocR family
2903	2524773	2525675	[+3 L= 903]	ddlL / D-alanine--D-alanine ligase (D-alanylalanine synthetase)
2904	2525985	2526671	[+3 L= 687]	tenA / Transcriptional activator of extracellular enzyme genes
2909	2529308	2530006	[+2 L= 699]	xjxL / Hypothetical protein
2910	2531157	2530051	[-1 L=1107]	xjxM / Phage integrase
2912	2531772	2533010	[+3 L=1239]	xjxN / Hypothetical protein
2915	2533806	2533459	[-1 L= 348]	xjxO / Transcriptional regulator
2919	2535143	2535886	[+2 L= 744]	xjxP / Phage protein
2921	2535828	2536700	[+3 L= 873]	xjxQ / Phage protein
2922	2536719	2536910	[+3 L= 192]	xjxR / Hypothetical protein
2923	2536939	2537109	[+1 L= 171]	xjxS / Hypothetical protein
2924	2537127	2537378	[+3 L= 252]	xjxT / Hypothetical protein
2925	2537396	2537605	[+2 L= 210]	xjxU / Hypothetical protein
2934	2542956	2543435	[+3 L= 480]	xjxV / Phage protein
2935	2543438	2543977	[+2 L= 540]	xjxW / Phage integrase
2936	2544278	2544619	[+2 L= 342]	xjxX / Hypothetical protein
2938	2545585	2545986	[+1 L= 402]	xjxY / Hypothetical protein
2939	2546116	2546751	[+1 L= 636]	xjxZ / Hypothetical protein
2940	2546837	2547121	[+2 L= 285]	xkxA / Phage protein
2943	2548020	2549741	[+3 L=1722]	xkxB / Phage protein
2944	2549811	2550314	[+3 L= 504]	xkxC / Hypothetical protein
2945	2550334	2551515	[+1 L=1182]	xkxD / Phage protein
2946	2551481	2552086	[+2 L= 606]	xkxE / Phage protein
2947	2552091	2553392	[+3 L=1302]	xkxF / Phage protein
2955	2555952	2559473	[+3 L=3522]	xkxG / Phage protein
2957	2559477	2560157	[+3 L= 681]	xkxH / Phage protein
2958	2560157	2561665	[+2 L=1509]	xkxI / Phage protein
2960	2562595	2563797	[+1 L=1203]	xkxJ / Phage protein
2961	2563850	2564272	[+2 L= 423]	xkxK / Phage protein
2962	2564275	2565090	[+1 L= 816]	xkxL / Phage endolysin
2965	2566577	2568175	[+2 L=1599]	xkxM / Hypothetical protein
2967	2568385	2569146	[+1 L= 762]	xkxN / Hypothetical protein
2971	2570765	2571784	[+2 L=1020]	xkxO / Hypothetical protein
2972	2571933	2572334	[+3 L= 402]	xkxP / Hypothetical protein
2974	2572719	2573729	[+3 L=1011]	cpxY / Cytochrome P450
2975	2573952	2575280	[+3 L=1329]	ykuC / Hypothetical protein

2976	2575249	2575902	[+1 L= 654]	xkxQ / Streptogramin A acetyltransferase
2977	2575913	2576128	[+2 L= 216]	xkxR / Hypothetical protein
2979	2576300	2576566	[+2 L= 267]	yjiB / Cytochrome P450 homolog
2980	2576681	2577085	[+2 L= 405]	xkxS / Transposase
2981	2577085	2578170	[+1 L=1086]	xkxT / Transposase
2982	2578357	2578656	[+1 L= 300]	cpxM / Cytochrome P450 (Steroid 15-beta-monooxygenase)
2983	2578769	2579344	[+2 L= 576]	xkxU / Hypothetical protein
2984	2579523	2580371	[+3 L= 849]	xkxV / Haloacid dehalogenase homolog
2985	2580826	2582610	[+1 L=1785]	ykrQ / Two-component sensor histidine kinase
2986	2582848	2584971	[+1 L=2124]	yqgF / Transpeptidase homolog
2987	2585051	2585578	[+2 L= 528]	lepQ / Signal peptidase I P (Leader peptidase I)
2988	2585840	2586118	[+2 L= 279]	ydhE / Macrolide glycosyltransferase homolog
2989	2586204	2587025	[+3 L= 822]	ydhE / Macrolide glycosyltransferase homolog
2991	2587859	2587122	[-3 L= 738]	xkxW / Aspartate/glutamate racemase homolog
2992	2588209	2588469	[+1 L= 261]	xkxX / Hypothetical protein
2993	2588560	2589954	[+1 L=1395]	xkxY / Transposase
2994	2589954	2592320	[+3 L=2367]	xkxZ / Hypothetical protein
2997	2595714	2594767	[-1 L= 948]	xlxA / Hypothetical protein
2998	2596607	2595714	[-3 L= 894]	xlxB / Hypothetical protein
2999	2596719	2597693	[+3 L= 975]	xlxC / Transcriptional regulator
3000	2598154	2599014	[+1 L= 861]	xlxD / Transcriptional regulator, Arac/XylS family
3004	2600334	2600603	[+3 L= 270]	xlxE / Cytochrome P450 homolog
3005	2600635	2601204	[+1 L= 570]	bioI / Biotin biosynthesis; cytochrome P450-like enzyme
3010	2603611	2604777	[+1 L=1167]	grbC / Spore germination protein B3 precursor
3012	2608140	2608418	[+3 L= 279]	xlxF / Hypothetical protein
3017	2620141	2605112	[-2 L=15030]	xlxG / Hypothetical protein
3018	2621120	2620620	[-3 L= 501]	xlxH / Isochorismatase homolog
3023	2623206	2623475	[+3 L= 270]	xlxI / Hypothetical protein
3025	2624480	2623740	[-3 L= 741]	xlxJ / Transposase
3026	2625183	2624227	[-1 L= 957]	xlxK / Transposase
3027	2625413	2626177	[+2 L= 765]	xlxL / L-2-haloalkanoic acid dehydrogenase homolog
3029	2626822	2627355	[+1 L= 534]	xlxM / Acetyltransferase homolog
3030	2629410	2627767	[-1 L=1644]	xlxN / Phage reverse transcriptase homolg
3031	2630535	2630098	[-1 L= 438]	xlxO / Hypothetical protein
3032	2630776	2631879	[+1 L=1104]	xlxP / myo-Inositol phosphate synthase homolog
3034	2632536	2632171	[-1 L= 366]	xlxQ / Transcriptional regulator, Cro family
3036	2633842	2633423	[-2 L= 420]	xlxR / Hypothetical protein
3038	2634324	2635022	[+3 L= 699]	xlxS / Hypothetical protein
3040	2636175	2636495	[+3 L= 321]	xlxT / Hypothetical protein
3042	2636488	2638206	[+1 L=1719]	xlxU / ABC transporter homolog
3043	2638202	2638999	[+2 L= 798]	cbiQ / ABC-type cobalt transport system permease protein
3045	2640085	2639342	[-2 L= 744]	kinB / Sporulation kinase B
3048	2640657	2640139	[-1 L= 519]	xlxV / ATPase homolog
3049	2641580	2640702	[-3 L= 879]	xlxW / Protein kinase domain
3050	2641678	2642211	[+1 L= 534]	xlxX / Hypothetical protein
3051	2642380	2643366	[+1 L= 987]	yogA / Alcohol dehydrogenase homolog
3053	2643617	2644213	[+2 L= 597]	ywoA / Bacitracin transport permease homolog
3054	2644505	2646640	[+2 L=2136]	pbpB / Penicillin-binding protein 2B (PBP-2B)
3055	2647128	2647910	[+3 L= 783]	xlxY / Hypothetical protein
3056	2647891	2648358	[+1 L= 468]	xlxZ / Hypothetical protein
3057	2648520	2649551	[+3 L=1032]	xmxA / Penicillin-binding protein homolog
3058	2649759	2650409	[+3 L= 651]	xmxB / Hypothetical protein
3060	2650815	2651318	[+3 L= 504]	xmxC / Hypothetical protein
3061	2651521	2652324	[+1 L= 804]	yviA / Hypothetical protein
3062	2653073	2652684	[-3 L= 390]	xmxD / Hypothetical protein
3063	2653797	2654756	[+3 L= 960]	xmxE / Hypothetical protein
3064	2654859	2655464	[+3 L= 606]	yoaZ / Hypothetical protein
3065	2655791	2657089	[+2 L=1299]	xmxF / Transcriptional activator of multidrug-efflux transporter genes
3066	2657037	2658497	[+3 L=1461]	xmxG / Hypothetical protein
3067	2659256	2658543	[-3 L= 714]	xmxH / Hypothetical protein
3069	2659753	2660553	[+1 L= 801]	xmxI / Hypothetical protein

3070	2660602	2661477	[+1 L= 876]	gdpD / Glycerophosphoryl diester phosphodiesterase
3072	2661766	2662608	[+1 L= 843]	aepE / Phage L-alanyl-D-glutamate peptidase
3073	2663206	2662748	[-2 L= 459]	xmxJ / Hypothetical protein
3074	2663340	2663900	[+3 L= 561]	xmxK / Hypothetical protein
3075	2665381	2663951	[-2 L=1431]	xmxL / Transcriptional activator, GntR family
3076	2665534	2666445	[+1 L= 912]	ydfC / Transport protein homolog
3077	2666536	2667945	[+1 L=1410]	xmxM / Chitosanase
3078	2668093	2669031	[+1 L= 939]	iunH / Inosine-uridine preferring nucleoside hydrolase (Purine nucleosidase)
3079	2669111	2669566	[+2 L= 456]	xmxN / Acetyltransferase homolog
3080	2669600	2669944	[+2 L= 345]	xmxO / Hypothetical protein
3081	2669964	2670407	[+3 L= 444]	xmxP / MutT-like protein
3085	2670978	2671991	[+3 L=1014]	ygrA / Hypothetical protein
3087	2672449	2673654	[+1 L=1206]	xmxQ / Hypothetical protein
3088	2673908	2674531	[+2 L= 624]	xmxR / Hypothetical protein
3089	2674743	2675207	[+3 L= 465]	xmxS / Acetyltransferase homolog
3090	2675490	2676044	[+3 L= 555]	xmxT / MutT-like protein
3091	2676233	2677096	[+2 L= 864]	dpcB / DNA polymerase III, beta chain
3092	2677314	2678183	[+3 L= 870]	xmxU / Hypothetical protein
3093	2679273	2678314	[-1 L= 960]	xmxV / Metallo-beta=lactamase homolog
3094	2679570	2680562	[+3 L= 993]	xmxW / Hypothetical protein
3095	2680655	2681110	[+2 L= 456]	yabJ / Putative regulator of purine biosynthesis
3096	2682654	2681842	[-1 L= 813]	ywqG / Hypothetical protein
3097	2684301	2682736	[-1 L=1566]	xmxY / Esterase homolog
3098	2684807	2684445	[-3 L= 363]	xmxZ / Hypothetical protein
3099	2685460	2685092	[-2 L= 369]	xnxA / Hypothetical protein
3100	2686324	2685476	[-2 L= 849]	xnxB / Hypothetical protein
3101	2686504	2686878	[+1 L= 375]	xnxC / Hypothetical protein
3102	2687228	2686947	[-3 L= 282]	xnxD / Acetyltransferase homolog
3104	2688047	2687475	[-3 L= 573]	xnxE / Hypothetical protein
3105	2688537	2688013	[-1 L= 525]	xnxF / Acetyltransferase homolog
3106	2689923	2688607	[-1 L=1317]	xnxG / Monooxygenase homolog
3107	2690874	2690005	[-1 L= 870]	bacA / Putative undecaprenol kinase (Bacitracin resistance protein)
3108	2690914	2691117	[+1 L= 204]	xnxH / Hypothetical protein
3109	2691559	2691227	[-2 L= 333]	yurQ / Excinuclease homolog
3112	2692215	2691640	[-1 L= 576]	xnxI / Acetyltransferase homolog
3113	2692808	2692236	[-3 L= 573]	xnxJ / Hypothetical protein
3114	2694418	2692991	[-2 L=1428]	xnxK / Hypothetical protein
3115	2694554	2694808	[+2 L= 255]	xnxL / Hypothetical protein
3118	2695571	2696527	[+2 L= 957]	yhcH / ABC transporter ATP-binding protein
3119	2696532	2697275	[+3 L= 744]	xnxM / Hypothetical protein
3121	2698346	2697651	[-3 L= 696]	xnxN / Protein kinase homolog
3122	2699106	2698669	[-1 L= 438]	xnxO / MutT-like protein
3123	2700447	2699326	[-1 L=1122]	yurR / Opine catabolism protein, oxidoreductase homolog
3124	2701218	2700568	[-1 L= 651]	xnxP / Hypothetical protein
3126	2702341	2701568	[-2 L= 774]	xnxQ / Acetyltransferase homolog
3127	2702714	2702568	[-3 L= 147]	xnxR / Hypothetical protein
3128	2703036	2702710	[-1 L= 327]	xnxS / Hypothetical protein
3129	2703492	2703127	[-1 L= 366]	xnxT / Hypothetical protein
3131	2705172	2704135	[-1 L=1038]	xnxU / Hypothetical protein
3132	2706366	2705674	[-1 L= 693]	xnxV / Haloacid dehalogenase homolog
3133	2706619	2707161	[+1 L= 543]	xnxW / Hypothetical protein
3135	2708230	2709243	[+1 L=1014]	ydjC / Hypothetical protein
3136	2712131	2709567	[-3 L=2565]	pulA / Pullulanase precursor (Alpha-dextrin endo-1,6-alpha-glucosidase)
3137	2714351	2712609	[-3 L=1743]	xnxX / Thermolysin metallopeptidase homolog
3138	2716071	2714653	[-1 L=1419]	xnxY / 2',3'-cyclic-nucleotide 2'-phosphodiesterase precursor
3139	2716483	2716190	[-2 L= 294]	xnxY / 2',3'-cyclic-nucleotide 2'-phosphodiesterase precursor
3142	2717657	2717145	[-3 L= 513]	xnxZ / Hypothetical protein
3143	2718263	2717790	[-3 L= 474]	xoxA / Hypothetical protein
3144	2718515	2718979	[+2 L= 465]	xoxB / Glyoxalase/bleomycin resistance protein homolog
3146	2719250	2720638	[+2 L=1389]	secY / Preprotein translocase

3147	2721644	2720730 [-3 L= 915]	xoxC / Hypothetical protein
3148	2721736	2723223 [+1 L=1488]	xoxD / Transcriptional regulator, GntR family
3150	2723652	2724503 [+3 L= 852]	xoxE / Streptothricin acetyltransferase homolog
3151	2724953	2724621 [-3 L= 333]	xoxF / Hypothetical protein
3152	2726134	2724968 [-2 L=1167]	xoxG / Hypothetical protein
3154	2727379	2726795 [-2 L= 585]	xoxH / Hypothetical protein
3156	2728413	2727361 [-1 L=1053]	xoxI / Hypothetical protein
3157	2729030	2728521 [-3 L= 510]	xoxJ / Acetyltransferase homolog
3158	2729416	2729045 [-2 L= 372]	xoxK / Hypothetical protein
3159	2730114	2729524 [-1 L= 591]	ylaJ / Hypothetical protein
3160	2731469	2730132 [-3 L=1338]	ypeB / Sporulation protein joeB
3161	2732264	2731488 [-3 L= 777]	sleB / Spore cortex-lytic enzyme precursor (Germination-specific amidase)
3162	2732410	2732739 [+1 L= 330]	xoxL / Hypothetical protein
3163	2733564	2732893 [-1 L= 672]	xoxM / Hypothetical protein
3164	2734462	2733533 [-2 L= 930]	xoxN / 6-Aminohexanoate-dimer hydrolase homolog
3165	2735415	2734570 [-1 L= 846]	wdiX / Tryptophan 2,3-dioxygenase (Tryptophan pyrrolase)
3166	2736068	2735442 [-3 L= 627]	xoxO / Hypothetical protein
3167	2737357	2736074 [-2 L=1284]	kynU / Kynureninase (L-kynurenine hydrolase)
3168	2737517	2738125 [+2 L= 609]	xoxP / Transcriptional regulator, TetR family
3169	2738616	2738167 [-1 L= 450]	xoxQ / MutT-like protein
3171	2738989	2739498 [+1 L= 510]	xoxR / Hypothetical protein
3172	2740017	2739532 [-1 L= 486]	xoxS / Hypothetical protein
3173	2740480	2740139 [-2 L= 342]	xoxT / Hypothetical protein
3175	2742732	2740885 [-1 L=1848]	acoR / Transcriptional activator of acetoin/lipoamide dehydrogenase operon
3179	2743384	2743049 [-2 L= 336]	xoxU / Hypothetical protein
3180	2743953	2743360 [-1 L= 594]	xoxV / Acetyltransferase homolog
3181	2744735	2743953 [-3 L= 783]	yulB / Transcriptional regulator, deoR family
3182	2744953	2745474 [+1 L= 522]	xoxW / Hypothetical protein
3183	2746141	2745545 [-2 L= 597]	xoxX / Short-chain dehydrogenase homolog
3184	2746632	2746234 [-1 L= 399]	xoxY / Hypothetical protein
3185	2747527	2746721 [-2 L= 807]	xoxZ / Hypothetical protein
3186	2747562	2748152 [+3 L= 591]	xpxA / Hypothetical protein
3187	2749620	2748244 [-1 L=1377]	acoD / Dihydrolipoamide dehydrogenase (E3 component of acetoin cleaving system)
3188	2750835	2749639 [-1 L=1197]	acoC / Dihydrolipoamide acetyltransferase component of acetoin cleaving system (Acetoin dehydrogenase E2 component)
3189	2751897	2750866 [-1 L=1032]	acoB / Acetoin:2,6-dichlorophenolindophenol oxidoreductase beta subunit (TPP-dependent acetoin dehydrogenase E1 beta-subunit)
3190	2752913	2751918 [-3 L= 996]	acoA / Acetoin:2,6-dichlorophenolindophenol oxidoreductase alpha subunit (Acetoin:DCPIP oxidoreductase-alpha)
3192	2753561	2753085 [-3 L= 477]	xpxB / Hypothetical protein
3193	2753697	2754569 [+3 L= 873]	yusZ / Oxidoreductase homolog
3194	2754613	2755119 [+1 L= 507]	yqkA / Hypothetical protein
3195	2755588	2755202 [-2 L= 387]	ywrE / Hypothetical protein
3196	2756067	2755609 [-1 L= 459]	xpxC / MutT-like protein
3197	2756383	2756084 [-2 L= 300]	xpxD / Hypothetical protein
3198	2757294	2756467 [-1 L= 828]	xpxE / Serine/threonine phosphatase homolog
3199	2757823	2757275 [-2 L= 549]	xpxF / Hypothetical protein
3203	2759375	2758542 [-3 L= 834]	opaB / Glycine betaine transport system permease protein
3204	2760573	2759371 [-1 L=1203]	opaA / Glycine betaine transport ATP-binding protein (Quaternary-amine-transporting ATPase)
3205	2760745	2761599 [+1 L= 855]	opaC / Glycine betaine-binding protein precursor
3206	2762242	2761649 [-2 L= 594]	clpP / ATP-dependent Clp protease proteolytic subunit (Endopeptidase Clp)
3207	2762944	2762252 [-2 L= 693]	xpxG / RNA polymerase sigma factor, ECF-type
3208	2763078	2763395 [+3 L= 318]	xpxH / Hypothetical protein
3210	2763370	2764062 [+1 L= 693]	rpiA / Ribose 5-phosphate isomerase A (Phosphoriboisomerase A)
3211	2764180	2764611 [+1 L= 432]	yybD / Acetyltransferase homolog
3212	2766115	2764745 [-2 L=1371]	chiA / Chitinase A1 precursor
3213	2767753	2766554 [-2 L=1200]	xpxI / UDP-glucuronyltransferase homolog

3214	2768517	2767840	[-1 L= 678]	xpxJ / Hypothetical protein
3215	2769182	2768682	[-3 L= 501]	xpxK / Hypothetical protein
3216	2769592	2769209	[-2 L= 384]	yjgA / Hypothetical protein
3217	2770374	2769661	[-1 L= 714]	xpxL / Hypothetical protein
3218	2770752	2770390	[-1 L= 363]	xpxM / Hypothetical protein
3222	2771617	2771198	[-2 L= 420]	xpxN / Acetyltransferase homolog
3224	2772011	2771643	[-3 L= 369]	xpxO / Hypothetical protein
3225	2772790	2772011	[-2 L= 780]	xpxP / Hypothetical protein
3226	2773424	2772915	[-3 L= 510]	xpxQ / N-acetyltransferase homolog
3227	2774506	2773508	[-2 L= 999]	xpxR / Hypothetical protein
3228	2774840	2774496	[-3 L= 345]	xpxS / Hypothetical protein
3230	2775824	2776489	[+2 L= 666]	xpxT / Hypothetical protein
3231	2778423	2776612	[-1 L=1812]	xpxU / DNA helicase
3232	2778684	2778430	[-1 L= 255]	xpxU / DNA helicase
3233	2779005	2779847	[+3 L= 843]	xpxV / Hypothetical protein
3234	2780285	2779908	[-3 L= 378]	xpxW / Hypothetical protein
3235	2782428	2780314	[-1 L=2115]	recQ / ATP-dependent DNA helicase
3238	2783342	2784127	[+2 L= 786]	xpxX / Hypothetical protein
3240	2784800	2785249	[+2 L= 450]	xpxY / Hypothetical protein
3241	2785311	2785844	[+3 L= 534]	xpxZ / Hypothetical protein
3242	2785874	2786680	[+2 L= 807]	xqxA / Transposase
3243	2786874	2786701	[-1 L= 174]	xqxB / Hypothetical protein
3245	2787922	2787095	[-2 L= 828]	xqxC / Phage endolysin
3246	2789086	2788355	[-2 L= 732]	xqxD / Phage N-acetylmuramoyl-L-alanine amidase
3247	2789825	2789379	[-3 L= 447]	yfjM / Hypothetical protein
3249	2791519	2790584	[-2 L= 936]	ppaC / Manganese-dependent inorganic pyrophosphatase (Pyrophosphate phospho-hydrolase)
3251	2792336	2791674	[-3 L= 663]	xqxE / Chitin-binding protein homolog
3252	2793086	2792586	[-3 L= 501]	xqxF / Acetyltransferase homolog
3253	2793192	2793830	[+3 L= 639]	xqxG / Hypothetical protein
3254	2794290	2793901	[-1 L= 390]	cmdA / Carboxymuconolactone decarboxylase
3255	2795910	2794366	[-1 L=1545]	alcP / Sodium/proton-dependent alanine carrier protein
3256	2797468	2795987	[-2 L=1482]	dhaL / Aldehyde dehydrogenase (ALDDH)
3257	2798382	2797489	[-1 L= 894]	dapA / Dihydrodipicolinate synthase (DHDPS)
3258	2799346	2798408	[-2 L= 939]	dapF / Diaminopimelate epimerase (DAP epimerase)
3259	2800416	2799346	[-1 L=1071]	xqxH / Proline racemase homolog
3260	2801552	2800380	[-3 L=1173]	xqxI / Oxidoreductase homolog
3261	2801733	2803391	[+3 L=1659]	xqxJ / Transcriptional regulator
3262	2803452	2803772	[+3 L= 321]	xqxK / Hypothetical protein
3263	2803772	2804101	[+2 L= 330]	xqxL / Hypothetical protein
3264	2804101	2805333	[+1 L=1233]	xqxM / Hypothetical protein
3265	2805669	2805364	[-1 L= 306]	xqxN / Hypothetical protein
3266	2806106	2805660	[-3 L= 447]	xqxO / Hypothetical protein
3268	2806365	2807126	[+3 L= 762]	ykrK / Hypothetical protein
3269	2807364	2807633	[+3 L= 270]	yngC / Hypothetical protein
3270	2807716	2807967	[+1 L= 252]	yngC / Hypothetical protein
3271	2808139	2808360	[+1 L= 222]	xqxP / Hypothetical protein
3272	2809586	2808408	[-3 L=1179]	dltD / undecaprenol-phosphate-poly(glycerophosphate chain) D-alanine transfer protein
3273	2810390	2809857	[-3 L= 534]	xqxQ / Acetyltransferase homolog
3274	2812124	2810505	[-3 L=1620]	xqxR / Extracellular solute-binding protein, family 5
3275	2813146	2812148	[-2 L= 999]	ykfC / Polysugar degrading enzyme homolog
3276	2814262	2813189	[-2 L=1074]	xqxS / Muconate cycloisomerase
3277	2814760	2814437	[-2 L= 324]	xqxT / Hypothetical protein
3278	2815415	2815062	[-3 L= 354]	xqxU / Hypothetical protein
3280	2815679	2816356	[+2 L= 678]	xqxV / Oxidoreductase homolog
3281	2816448	2816624	[+3 L= 177]	xqxV / Oxidoreductase homolog
3282	2817243	2816650	[-1 L= 594]	xqxW / Hypothetical protein
3283	2817764	2817243	[-3 L= 522]	xqxX / Hypothetical protein
3284	2818494	2818267	[-1 L= 228]	xqxY / Hypothetical protein
3286	2819127	2818867	[-1 L= 261]	xqxZ / Hypothetical protein

3287	2819828	2819271	[-3 L= 558]	xrxA / Hypothetical protein
3288	2820691	2819933	[-2 L= 759]	xrxB / Methyltransferase homolog
3290	2822703	2820922	[-1 L=1782]	pepX / Xaa-Pro dipeptidyl-peptidase (X-prolyl-dipeptidyl aminopeptidase)
3291	2823895	2822987	[-2 L= 909]	xrxC / Rotamase homolog
3292	2825449	2824019	[-2 L=1431]	xrxD / Two component histidine kinase sensor protein
3293	2826059	2825388	[-3 L= 672]	xrxE / Two-component response regulator
3294	2826046	2826567	[+1 L= 522]	xrxF / Hypothetical protein
3295	2827261	2826770	[-2 L= 492]	xrxG / Hypothetical protein
3296	2828301	2827552	[-1 L= 750]	xrxH / Hypothetical protein
3297	2828968	2828312	[-2 L= 657]	xrxI / Nucleoside phosphorylase homolog
3298	2829684	2828974	[-1 L= 711]	mtnA / MTA/SAH nucleosidase (5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase)
3299	2830451	2829705	[-3 L= 747]	tagA / Teichoic acid biosynthesis protein A
3300	2832059	2830467	[-3 L=1593]	xrxJ / Peptidase homolog
3302	2833198	2832341	[-2 L= 858]	yitS / Hypothetical protein
3304	2834146	2833679	[-2 L= 468]	xrxK / Spore coat protein X homolog
3305	2834343	2834146	[-1 L= 198]	xrxL / Spore coat protein W homolog
3306	2835276	2834710	[-1 L= 567]	xrxM / Spore coat protein X homolog
3307	2836080	2836556	[+3 L= 477]	xrxN / Acetyltransferase homolog
3308	2837644	2836877	[-2 L= 768]	xrxO / Hypothetical protein
3311	2838987	2839304	[+3 L= 318]	xrxP / Hypothetical protein
3312	2840897	2839365	[-3 L=1533]	yhcA / Multidrug-efflux transporter homolog
3313	2841629	2840925	[-3 L= 705]	yhbF / Hypothetical protein
3314	2842358	2841651	[-3 L= 708]	yhbE / Hypothetical protein
3315	2843022	2842375	[-1 L= 648]	yhbD / Hypothetical protein
3316	2844893	2843157	[-3 L=1737]	yhjP / Transporter binding protein homolog
3317	2844908	2846203	[+2 L=1296]	yhjO / Multidrug-efflux transporter homolog
3319	2847048	2846380	[-1 L= 669]	xrxQ / Hypothetical protein
3321	2848267	2847794	[-2 L= 474]	xrxR / Hypothetical protein
3322	2848533	2848267	[-1 L= 267]	xrxS / Hypothetical protein
3323	2849715	2848690	[-1 L=1026]	iunH / Inosine-uridine preferring nucleoside hydrolase (Purine nucleosidase)
3325	2850773	2849991	[-3 L= 783]	xrxT / Methyltransferase homolog
3326	2851337	2850972	[-3 L= 366]	xrxU / Hypothetical protein
3329	2852105	2852554	[+2 L= 450]	xrxV / Hypothetical protein
3331	2852851	2854050	[+1 L=1200]	xrxW / Hypothetical protein
3333	2854676	2855035	[+2 L= 360]	xrxX / Hypothetical protein
3335	2855344	2856576	[+1 L=1233]	xrxY / Aspartate aminotransferase homolog
3336	2856636	2857031	[+3 L= 396]	ywpB / (3R)-hydroxymyristoyl-[acyl carrier protein] dehydratase
3337	2857119	2857937	[+3 L= 819]	xrxZ / Hypothetical protein
3338	2858464	2857958	[-2 L= 507]	xsxA / Hypothetical protein
3339	2859061	2858585	[-2 L= 477]	yneJ / Hypothetical protein
3340	2859772	2859104	[-2 L= 669]	xsxB / Hypothetical protein
3341	2860641	2859772	[-1 L= 870]	yhcG / ABC transporter ATP-binding protein
3342	2860841	2860641	[-3 L= 201]	xsxC / Transcriptional regulator GntR family
3343	2861019	2860825	[-1 L= 195]	xsxC / Transcriptional regulator GntR family
3344	2861632	2861147	[-2 L= 486]	xsxD / Hypothetical protein
3345	2862239	2861649	[-3 L= 591]	xsxE / Hypothetical protein
3352	2865054	2863936	[-1 L=1119]	yueF / Hypothetical protein
3353	2865054	2865986	[+3 L= 933]	xsxG / Hypothetical protein
3354	2867630	2866509	[-3 L=1122]	ssuD / Alkanesulfonate monooxygenase (FMNH2-dependent aliphatic sulfonate monooxygenase)
3355	2868543	2867698	[-1 L= 846]	ssuC / Aliphatic sulfonates transport permease protein
3357	2869546	2868563	[-2 L= 984]	ssuA / Aliphatic sulfonates binding protein precursor
3358	2870319	2869567	[-1 L= 753]	ssuB / Aliphatic sulfonates transport ATP-binding protein
3359	2871288	2870563	[-1 L= 726]	xsxH / Hypothetical protein
3360	2871875	2871288	[-3 L= 588]	xsxI / Transcriptional regulator, TetR family
3361	2872624	2872118	[-2 L= 507]	xsxJ / Hypothetical protein
3363	2873885	2872833	[-3 L=1053]	xsxK / Hypothetical protein
3364	2874380	2873901	[-3 L= 480]	xsxL / Hypothetical protein
3365	2875212	2874517	[-1 L= 696]	xsxM / Hypothetical protein

3366	2876043	2875222	[-1 L= 822]	xsxN / Aminoglycoside acetyltransferase
3367	2876655	2876257	[-1 L= 399]	xsxO / Acetyltransferase homolog
3368	2877650	2876715	[-3 L= 936]	yjlA / Hypothetical protein
3371	2878696	2878199	[-2 L= 498]	xsxP / Acetyltransferase homolog
3372	2879275	2878733	[-2 L= 543]	xsxQ / Acetyltransferase homolog
3373	2879992	2879294	[-2 L= 699]	xsxR / Hypothetical protein
3374	2880692	2880012	[-3 L= 681]	xsxS / Hypothetical protein
3375	2881587	2881129	[-1 L= 459]	yycE / Hypothetical protein
3376	2882597	2881707	[-3 L= 891]	ymaE / Metallo-beta-lactamase homolog
3377	2882818	2883642	[+1 L= 825]	xsxT / Polysaccharide deacteylase homolog
3379	2884570	2884968	[+1 L= 399]	xsxU / Hypothetical protein
3380	2884949	2885248	[+2 L= 300]	xsxV / Hypothetical protein
3381	2887302	2885311	[-1 L=1992]	xsxW / Sulfatase homolog
3382	2889434	2887812	[-3 L=1623]	ykpA / ABC transporter ATP-binding protein homolog
3383	2890660	2889815	[-2 L= 846]	xsxX / Hypothetical protein
3384	2891863	2891135	[-2 L= 729]	xsxY / Hypothetical protein
3386	2894259	2891920	[-1 L=2340]	ydgH / Membrane protein
3387	2895036	2894464	[-1 L= 573]	yrhl / Transcriptional regulator, TetR family
3388	2896303	2895260	[-2 L=1044]	xsxZ / Acetyltransferase homolog
3389	2897837	2896542	[-3 L=1296]	aroA / 3-phosphoshikimate 1-carboxyvinyltransferase (EPSPS)
3391	2898982	2897849	[-2 L=1134]	tyrA / Prephenate dehydrogenase (PDH)
3392	2900039	2898942	[-3 L=1098]	hisC / Histidinol-phosphate aminotransferase (Imidazole acetol-phosphate transaminase)
3393	2901230	2900061	[-3 L=1170]	aroC / Chorismate synthase (5-enolpyruvylshikimate-3-phosphate phospholyase)
3394	2902589	2901516	[-3 L=1074]	aroG / Phospho-2-dehydro-3-deoxyheptonate aldolase / Chorismate mutase
3395	2904243	2903419	[-1 L= 825]	xtxA / Hypothetical protein
3397	2906929	2904428	[-2 L=2502]	xtxB / Hypothetical protein
3398	2907081	2907515	[+3 L= 435]	xtxC / NADH dehydrogenase homolog
3399	2908208	2907672	[-3 L= 537]	xtxD / Isochorismatase homolog
3400	2908770	2908237	[-1 L= 534]	xtxE / Acetyltransferase homolog
3401	2908995	2908786	[-1 L= 210]	xtxF / Hypothetical protein
3403	2909343	2909864	[+3 L= 522]	xtxG / Hypothetical protein
3405	2911819	2910335	[-2 L=1485]	yabE / Hypothetical protein
3407	2912666	2913070	[+2 L= 405]	yyaH / Glyoxalase/Bleomycin resistance protein homolog
3409	2913258	2913419	[+3 L= 162]	yvdP / Reticuline oxidase homolog
3410	2913737	2914018	[+2 L= 282]	xtxH / Hypothetical protein
3411	2914363	2914716	[+1 L= 354]	xtxI / Hypothetical protein
3412	2915899	2914856	[-2 L=1044]	xtxJ / Hypothetical protein
3413	2916166	2917779	[+1 L=1614]	mqoA / Malate:quinone oxidoreductase (Malate dehydrogenase [acceptor]) (MQO)
3414	2918873	2917833	[-3 L=1041]	xtxK / Hypothetical protein
3416	2919886	2918873	[-2 L=1014]	xtxL / Branched-chain amino acid transporter permease component
3417	2920809	2919859	[-1 L= 951]	xtxM / Branched-chain amino acid transporter permease componenet
3418	2922143	2920809	[-3 L=1335]	xtxN / ABC transporter ATP-binding protein
3420	2922466	2923416	[+1 L= 951]	xtxO / Hypothetical protein
3421	2923413	2924978	[+3 L=1566]	xtxP / Sugar kinase homolog
3422	2924971	2925366	[+1 L= 396]	xtxQ / Hypothetical protein
3423	2925376	2926155	[+1 L= 780]	xtxR / Deoxyribose-phosphate aldolase homolog
3425	2927257	2926925	[-2 L= 333]	yetG / Hypothetical protein
3426	2928565	2927348	[-2 L=1218]	xtxS / Multidrug-efflux transporter homolog
3428	2929660	2928620	[-2 L=1041]	xtxT / Transcriptional regulator, ArsR family
3429	2929964	2930452	[+2 L= 489]	xtxU / Hypothetical protein
3430	2930788	2931978	[+1 L=1191]	yxjA / Pyrimidine nucleoside transporter homolog
3432	2932420	2932034	[-2 L= 387]	proA / Gamma-glutamyl phosphate reductase (Glutamate-5-semialdehyde dehydrogenase)
3434	2933333	2932416	[-3 L= 918]	proA / Gamma-glutamyl phosphate reductase (Glutamate-5-semialdehyde dehydrogenase)
3435	2934426	2933299	[-1 L=1128]	proB / Glutamate 5-kinase 1 (Gamma-glutamyl kinase 1)
3436	2935096	2935911	[+1 L= 816]	proC / Pyrroline-5-carboxylate reductase (P5C reductase)
3437	2937757	2936096	[-2 L=1662]	yqjN / Peptidase homolog
3438	2938571	2937813	[-3 L= 759]	ycsO / Transcriptional regulator, IclR family
3440	2938815	2940248	[+3 L=1434]	rocC / Amino-acid permease

3441	2940552	2941016	[+3 L= 465]	xtxV / Glyoxalase/Bleomycin resistance protein homolog
3442	2942304	2941276	[-1 L=1029]	yocE / Fatty acid desaturase (Delta 12 desaturase)
3443	2944999	2942615	[-2 L=2385]	inhA / Immune inhibitor A precursor
3445	2946087	2945236	[-1 L= 852]	xtxW / Hypothetical protein
3446	2948248	2946539	[-2 L=1710]	ppbC / Alkaline phosphatase III precursor (APASE III)
3447	2948498	2948986	[+2 L= 489]	yoaS / Hypothetical protein
3448	2948991	2949212	[+3 L= 222]	yozG / Transcriptional regulator
3450	2950506	2949922	[-1 L= 585]	xtxX / Hypothetical protein
3452	2951114	2950524	[-3 L= 591]	xtxY / Hypothetical protein
3454	2951677	2951105	[-2 L= 573]	yoaA / Acetyltransferase homolog
3455	2952042	2951662	[-1 L= 381]	ysfE / Glyoxalase/Bleomycin resistance protein homolog
3458	2953659	2953126	[-1 L= 534]	xtxZ / Hypothetical protein
3459	2953984	2953670	[-2 L= 315]	xuxA / Hypothetical protein
3460	2954140	2955117	[+1 L= 978]	xuxB / Magnesium chelatase
3461	2955117	2956280	[+3 L=1164]	xuxC / Hypothetical protein
3462	2956177	2957361	[+1 L=1185]	xuxD / Hypothetical protein
3463	2958920	2957424	[-3 L=1497]	xuxE / Proline/betaine transporter (Proline porter II)
3464	2959625	2961118	[+2 L=1494]	xuxF / Glycosyltransferase homolog
3468	2964514	2962127	[-2 L=2388]	xuxG / Glycosyltransferase homolog
3469	2966015	2964501	[-3 L=1515]	xuxH / Glycosyltransferase homolog
3470	2967259	2966240	[-2 L=1020]	xuxI / Hypothetical protein
3472	2968748	2967534	[-3 L=1215]	atgD / Acetylornithine aminotransferase (ACOAT)
3473	2968975	2970426	[+1 L=1452]	catE / Catalase 2
3474	2972085	2970649	[-1 L=1437]	colA / Microbial collagenase precursor
3475	2973283	2971958	[-2 L=1326]	colA / Microbial collagenase precursor
3476	2974285	2973776	[-2 L= 510]	xuxJ / Hypothetical protein
3477	2976168	2974402	[-1 L=1767]	yeaR / Adenine deaminase
3478	2977676	2976513	[-3 L=1164]	dacP / D-alanyl-D-alanine carboxypeptidase precursor (DD-peptidase)
3479	2978441	2977938	[-3 L= 504]	xuxK / Hypothetical protein
3480	2979060	2978629	[-1 L= 432]	xuxL / Hypothetical protein
3481	2979371	2979105	[-3 L= 267]	xuxM / Hypothetical protein
3482	2980496	2979390	[-3 L=1107]	xuxN / Hypothetical protein
3483	2981272	2980496	[-2 L= 777]	xuxO / Magnesium chelatase
3484	2982983	2981730	[-3 L=1254]	xuxP / Hypothetical protein
3485	2984769	2983006	[-1 L=1764]	xuxQ / Hypothetical protein
3488	2985974	2985660	[-3 L= 315]	ycnE / Hypothetical protein
3489	2986635	2986000	[-1 L= 636]	ydgI / NAD(P)H nitroreductase
3491	2987082	2986657	[-1 L= 426]	ydgJ / Transcriptional regulator, MarR family
3493	2987348	2989288	[+2 L=1941]	tetP / Tetracycline resistance protein
3494	2990002	2989340	[-2 L= 663]	xuxR / Hypothetical protein
3495	2990470	2990006	[-2 L= 465]	xuxS / MutT-like protein
3497	2990619	2991452	[+3 L= 834]	xuxT / Hypothetical protein
3498	2991978	2991523	[-1 L= 456]	xuxU / Hypothetical protein
3500	2993029	2992007	[-2 L=1023]	xuxV / Isoflavone reductase homolog
3501	2994065	2993133	[-3 L= 933]	xuxW / Hypothetical protein
3502	2994980	2994093	[-3 L= 888]	xuxX / Transcriptional regulator, AraC family
3503	2995655	2995149	[-3 L= 507]	xuxY / Cytosine deaminase homolog
3504	2996302	2995814	[-2 L= 489]	yqjY / Acetyltransferase homolog
3505	2996706	2996302	[-1 L= 405]	xuxZ / Hypothetical protein
3506	2996791	2997267	[+1 L= 477]	xvxA / MutT-like protein
3507	2998251	2997292	[-1 L= 960]	yyaM / Transport protein homolog
3508	2998284	2999765	[+3 L=1482]	xvxB / Transcriptional regulator, GntR family
3509	2999790	3000287	[+3 L= 498]	xvxC / Hypothetical protein
3510	3000709	3000380	[-2 L= 330]	ywsA / Hypothetical protein
3511	3001750	3000758	[-2 L= 993]	ybdK / Two-component sensor histidine kinase
3512	3002418	3001750	[-1 L= 669]	ybdJ / Two-component response regulator
3513	3003439	3002456	[-2 L= 984]	ybdG / Hypothetical protein
3514	3004369	3003548	[-2 L= 822]	xvxD / Hypothetical protein
3515	3005206	3004490	[-2 L= 717]	xvxE / Uridine kinase homolog
3516	3006080	3005271	[-3 L= 810]	xvxF / Protein phosphatase 2A homolog
3517	3006963	3006028	[-1 L= 936]	aphD / Aminoglycoside 3'-phosphotransferase (Neomycin-kanamycin

			phosphotransferase, type IV)
3518	3007766	3006972 [-3 L= 795]	xvxG / Hypothetical protein
3519	3007846	3008871 [+1 L=1026]	ytnM / Hypothetical protein
3520	3009360	3008914 [-1 L= 447]	xvxH / Acetyltransferase homolog
3521	3009978	3011450 [+3 L=1473]	lysP / Lysine-specific permease
3523	3011474	3011869 [+2 L= 396]	xvxI / Hypothetical protein
3524	3011876	3012673 [+2 L= 798]	xvxJ / DNA alkylation repair enzyme homolog
3529	3014574	3015332 [+3 L= 759]	xvxK / Methyltransferase homolog
3530	3016067	3015519 [-3 L= 549]	xvxL / MutT-like protein
3532	3016247	3016819 [+2 L= 573]	xvxM / Hypothetical protein
3533	3017391	3016849 [-1 L= 543]	lepP / Signal peptidase I P (Leader peptidase I)
3534	3019659	3017464 [-1 L=2196]	yqgF / Penicillin binding protein transpeptidase homolog
3535	3020676	3019942 [-1 L= 735]	yhdZ / Transcriptional regulator, Sir2 family
3536	3021390	3020746 [-1 L= 645]	pcpA / Pyrrolidone-carboxylate peptidase (Pyroglutamyl-peptidase I)
3537	3022369	3021410 [-2 L= 960]	xvxN / Hypothetical protein
3538	3023075	3022374 [-3 L= 702]	xvxO / Hypothetical protein
3540	3023850	3023092 [-1 L= 759]	xvxP / Lactam utilization protein
3541	3024858	3023872 [-1 L= 987]	xvxQ / Hypothetical protein
3542	3025562	3024852 [-3 L= 711]	ycsJ / Allophanate hydrolase homolog
3543	3026383	3025580 [-2 L= 804]	xvxR / Transcriptional regulator, IclR family
3544	3027036	3026488 [-1 L= 549]	lepL / Signal peptidase I (Leader peptidase I)
3545	3027737	3027063 [-3 L= 675]	xvxS / Hypothetical protein
3546	3028643	3027939 [-3 L= 705]	ydfF / Transcriptional regulator, ArsR family
3547	3028713	3029180 [+3 L= 468]	xvxT / Hypothetical protein
3548	3029674	3029402 [-2 L= 273]	ydbM / Butyryl-CoA dehydrogenase homolog
3549	3030548	3029745 [-3 L= 804]	ydbM / Butyryl-CoA dehydrogenase homolog
3550	3031362	3030706 [-1 L= 657]	xvxU / Hypothetical protein
3552	3032252	3031668 [-3 L= 585]	xvxV / Hypothetical protein
3555	3033972	3032647 [-1 L=1326]	xvxW / Na+ dependent nucleoside transporter homolog
3556	3034962	3034087 [-1 L= 876]	kkaH / Aminoglycoside 3'-phosphotransferase (Neomycin-kanamycin phosphotransferase)
3557	3035478	3034966 [-1 L= 513]	yesJ / Hypothetical protein
3558	3035966	3035505 [-3 L= 462]	yncE / Hypothetical protein
3559	3036620	3036186 [-3 L= 435]	yhjR / Hypothetical protein
3560	3036927	3037430 [+3 L= 504]	xvxX / Hypothetical protein
3561	3038762	3037542 [-3 L=1221]	xvxY / Hypothetical protein
3562	3038742	3039506 [+3 L= 765]	xvxZ / Transcriptional regulator, TetR family
3564	3039888	3039616 [-1 L= 273]	inhA / Immune inhibitor A precursor
3565	3042001	3040073 [-2 L=1929]	inhA / Immune inhibitor A precursor
3566	3044874	3042247 [-1 L=2628]	ppsA / Phosphoenolpyruvate synthase (PEP synthase)
3568	3045340	3046194 [+1 L= 855]	yflN / Metallo-beta-lactamase homolog
3569	3046463	3046981 [+2 L= 519]	ycbP / Hypothetical protein
3570	3047649	3047023 [-1 L= 627]	yvdQ / Hypothetical protein
3571	3048042	3047833 [-1 L= 210]	sasP / Small, acid soluble spore protein 1
3572	3048308	3049438 [+2 L=1131]	adhB / Alcohol dehydrogenase, NAD dependent
3573	3051242	3049815 [-3 L=1428]	aspA / Aspartate ammonia-lyase (Aspartase)
3574	3052315	3051299 [-2 L=1017]	ansA / L-asparaginase (L-asparagine amidohydrolase)
3575	3052476	3052859 [+3 L= 384]	ansR / Ans operon repressor protein
3577	3053220	3053321 [+3 L= 102]	xwxA / Hypothetical protein
3578	3054901	3053732 [-2 L=1170]	graC / Spore germination protein A3 precursor
3579	3055917	3054814 [-1 L=1104]	graB / Spore germination protein A2
3580	3057413	3055917 [-3 L=1497]	griA / Spore germination protein
3581	3060179	3057777 [-3 L=2403]	kinA / Sporulation kinase A (Stage II sporulation protein J)
3582	3062258	3060861 [-3 L=1398]	hblA / Hemolysin BL binding component precursor
3583	3063776	3062637 [-3 L=1140]	hblB / Hemolysin BL binding component precursor
3584	3065018	3063801 [-3 L=1218]	hblC / Hemolysin L1 lytic component
3585	3066408	3065083 [-1 L=1326]	hblC / Hemolysin L2 lytic component
3587	3068808	3067582 [-1 L=1227]	trrA / Transcriptional regulator
3589	3070346	3070119 [-3 L= 228]	sasE / Small acid-soluble spore protein C5
3590	3071154	3070516 [-1 L= 639]	xwxB / Endo/exinuclease homolog
3591	3072736	3071324 [-2 L=1413]	ctrA / High-affinity cationic amino acid transporter-1 (CAT-1)

3593	3073688	3072873	[-3 L= 816]	proC / Pyrroline-5-carboxylate reductase (P5C reductase)
3594	3075206	3074016	[-3 L=1191]	grbC / Spore germination protein B3 precursor
3595	3076294	3075206	[-2 L=1089]	graB / Spore germination protein A2
3596	3077442	3076324	[-1 L=1119]	yndD / Spore germination protein homolog
3598	3078151	3077399	[-2 L= 753]	yndD / Spore germination protein homolog
3600	3079522	3078581	[-2 L= 942]	ycbB / Two-component response protein
3601	3080843	3079530	[-3 L=1314]	ycbA / Two-component histidine kinase
3602	3082057	3081080	[-2 L= 978]	ybgJ / Glutaminase homolog
3604	3083624	3082185	[-3 L=1440]	ybgH / Sodium/proton-dependent alanine transporter homolog
3606	3084483	3085709	[+3 L=1227]	xwxC / Hypothetical protein
3607	3086137	3085880	[-2 L= 258]	cypX / Cytochrome P450 homolog
3608	3087779	3086484	[-3 L=1296]	xwxD / Alkaline D-peptidase homolog
3609	3089473	3088145	[-2 L=1329]	xwxE / Hypothetical protein
3610	3091583	3089997	[-3 L=1587]	yhcR / 5'-Nucleotidase homolog
3611	3092874	3091996	[-1 L= 879]	prxC / Non-heme chloroperoxidase homolog (Chloride peroxidase)
3613	3093333	3093974	[+3 L= 642]	xwxF / Isochorismatase homolog
3614	3094121	3094783	[+2 L= 663]	xwxG / Isochorismatase homolog
3615	3094783	3095373	[+1 L= 591]	xwxH / Hypothetical protein
3617	3095499	3096689	[+3 L=1191]	xwxI / Hypothetical protein
3618	3096658	3097224	[+1 L= 567]	xwxJ / Hypothetical protein
3619	3098408	3097533	[-3 L= 876]	ywbI / Transcriptional regulator, LysR family
3620	3099113	3098631	[-3 L= 483]	ykvE / Transcriptional regulator, MarR family
3621	3100465	3099518	[-2 L= 948]	yqxL / Hypothetical protein
3622	3101796	3100774	[-1 L=1023]	xwxK / Hypothetical protein
3623	3102242	3101835	[-3 L= 408]	xwxL / Hypothetical protein
3624	3102705	3102322	[-1 L= 384]	yflT / General stress protein 17M (GSP17M)
3625	3104592	3103036	[-1 L=1557]	xwxM / Hypothetical protein
3626	3105127	3105489	[+1 L= 363]	yxeA / Hypothetical protein
3627	3106290	3105583	[-1 L= 708]	xwxN / Hypothetical protein
3628	3106854	3106396	[-1 L= 459]	ytaB / TspO/MBR family protein
3629	3108390	3106963	[-1 L=1428]	xwxO / DNA photolyase
3631	3110528	3109314	[-3 L=1215]	xwxP / Oxidoreductase homolog
3632	3111359	3110832	[-3 L= 528]	ybcF / Hypothetical protein
3633	3114039	3111433	[-1 L=2607]	ybcD / Hypothetical protein
3634	3115568	3114039	[-3 L=1530]	ndhF / NADH-quinone oxidoreductase subunit 5 (NADH dehydrogenase subunit 5)
3635	3116374	3116198	[-2 L= 177]	ybcI / Hypothetical protein
3636	3117767	3116928	[-3 L= 840]	xwxQ / Polysaccharide deacetylase
3637	3118161	3118718	[+3 L= 558]	yyaR / Acetyltransferase homolog
3638	3119719	3118811	[-2 L= 909]	menA / 1,4-dihydroxy-2-naphthoate octaprenyltransferase (DHNA-octaprenyltransferase)
3639	3120626	3120015	[-3 L= 612]	xwxR / ThiJ/PfpI family protein
3640	3121533	3120706	[-1 L= 828]	xwxS / Hypothetical protein
3641	3122115	3121702	[-1 L= 414]	arsC / Arsenate reductase (Arsenical pump modifier)
3643	3123182	3122133	[-3 L=1050]	arsB / Heavy metal membrane efflux protein
3644	3123626	3123192	[-3 L= 435]	yqcK / Glyoxalase/Bleomycin resistance protein homolog
3645	3123992	3123690	[-3 L= 303]	arsR / Arsenical resistance operon repressor
3647	3124959	3124453	[-1 L= 507]	xwxT / Hypothetical protein
3648	3125259	3125849	[+3 L= 591]	xwxU / Hypothetical protein
3649	3127937	3126084	[-3 L=1854]	xwxV / Hypothetical protein
3650	3128580	3127999	[-1 L= 582]	xwxW / Transcriptional regulator, TetR family
3651	3131843	3128922	[-3 L=2922]	colA / Microbial collagenase precursor (120 kDa collagenase)
3652	3133907	3132720	[-3 L=1188]	ydeR / Antibiotic (chloramphenicol) resistance protein homolog
3653	3134255	3134848	[+2 L= 594]	ydeS / Transcriptional regulator, TetR family
3655	3135902	3135306	[-3 L= 597]	pucB / Purine catabolism protein
3656	3136860	3135865	[-1 L= 996]	xdhA / Xanthine dehydrogenase subunit A (XDHase subunit a)
3657	3137324	3136878	[-3 L= 447]	dcmS / Carbon monoxide dehydrogenase small chain (CO dehydrogenase subunit S)
3658	3138196	3137324	[-2 L= 873]	dcmM / Carbon monoxide dehydrogenase middle subunit
3659	3140394	3138160	[-1 L=2235]	dcmL / Carbon monoxide dehydrogenase large subunit
3661	3141535	3141377	[-2 L= 159]	xwxX / Transposase
3662	3142654	3141824	[-2 L= 831]	xwxY / Hypothetical protein

3663	3143937	3143494	[-1 L= 444]	xwxZ / Hypothetical protein
3664	3145035	3144265	[-1 L= 771]	fabG / 3-oxoacyl-[acyl-carrier protein] reductase (3-ketoacyl-acyl carrier protein reductase)
3665	3145196	3145633	[+2 L= 438]	xxaA / Transcriptional regulator
3667	3147112	3145808	[-2 L=1305]	xxaB / Peptidase homolog
3668	3149586	3147280	[-1 L=2307]	xxaC / Hypothetical protein
3669	3149698	3150087	[+1 L= 390]	ywbC / Glyoxalase/Bleomycin resistance protein homolog
3672	3151062	3152150	[+3 L=1089]	xxaD / Low temperature requirement protein A homolog
3673	3153118	3152978	[-2 L= 141]	xxaE / Hypothetical protein
3674	3153337	3153158	[-2 L= 180]	xxaF / Hypothetical protein
3676	3154630	3153602	[-2 L=1029]	xxaG / Hypothetical protein
3678	3158254	3157556	[-2 L= 699]	yrrS / Hypothetical protein
3680	3161528	3159444	[-3 L=2085]	xxaH / Beta-lactamase
3681	3162788	3161622	[-3 L=1167]	xxaI / Alkaline D-peptidase homolog
3683	3163950	3165266	[+3 L=1317]	sdaC / Serine transporter
3685	3166550	3165681	[-3 L= 870]	yvbU / Transcriptional regulator, LysR family
3686	3166671	3167537	[+3 L= 867]	xxaJ / Transporter homolog
3687	3168093	3167785	[-1 L= 309]	xxaK / Hypothetical protein
3688	3168637	3168287	[-2 L= 351]	xxaL / Hypothetical protein
3689	3169382	3168966	[-3 L= 417]	xxaM / Transcriptional regulator, MarR family
3690	3170368	3169889	[-2 L= 480]	xxaN / Hypothetical protein
3692	3172274	3171006	[-3 L=1269]	ywfE / Hypothetical protein
3693	3173524	3172283	[-2 L=1242]	ywfF / Hypothetical protein
3694	3174567	3174241	[-1 L= 327]	xxaO / Hypothetical protein
3695	3175052	3174585	[-3 L= 468]	xxaP / Hypothetical protein
3696	3175284	3175991	[+3 L= 708]	xxaQ / Two-component response regulator
3697	3175991	3177361	[+2 L=1371]	xxaR / Two-component histidine kinase
3698	3177771	3177559	[-1 L= 213]	xxaS / Hypothetical protein
3700	3179614	3178121	[-2 L=1494]	xxaT / Hypothetical protein
3702	3180966	3180208	[-1 L= 759]	xxaU / Hypothetical protein
3703	3181387	3182778	[+1 L=1392]	xxaV / Hypothetical protein
3705	3183822	3185606	[+3 L=1785]	xxaW / Two-component response regulator
3706	3186355	3185933	[-2 L= 423]	xxaX / Hypothetical protein
3707	3186906	3187787	[+3 L= 882]	xxaY / Hypothetical protein
3708	3187708	3189015	[+1 L=1308]	xxaZ / Hypothetical protein
3709	3192436	3189233	[-2 L=3204]	cypD / Bifunctional P-450:NADPH-P450 reductase 1 (Cytochrome P450 102 ; NADPH-cytochrome P450 reductase)
3710	3194538	3193000	[-1 L=1539]	yhcA / Multidrug-efflux transporter homolog
3712	3194902	3195495	[+1 L= 594]	xxbA / Hypothetical protein
3715	3197433	3196441	[-1 L= 993]	xxbB / 1-Aminocyclopropane-1-carboxylate deaminase/Cysteine desulfhydrase homolog
3717	3199090	3197792	[-2 L=1299]	xxbC / Hypothetical protein
3718	3200758	3199259	[-2 L=1500]	xxbD / Hypothetical protein
3719	3201889	3200972	[-2 L= 918]	yktD / Hypothetical protein
3720	3202093	3202692	[+1 L= 600]	xxbE / Hypothetical protein
3721	3202806	3203945	[+3 L=1140]	xxbF / V-type ATPase subunit A
3722	3204669	3204001	[-1 L= 669]	xxbG / ABC transporter ATP-binding protein
3723	3205766	3204672	[-3 L=1095]	xxbH / ABC transporter permease protein
3724	3205910	3206539	[+2 L= 630]	xxbI / Transcriptional regulator, ArsR family
3725	3206612	3207868	[+2 L=1257]	xxbJ / Hypothetical protein
3726	3208451	3207984	[-3 L= 468]	xxbK / Hypothetical protein
3727	3210029	3208656	[-3 L=1374]	xxbL / Two-component sensor histidine kinase
3728	3210708	3210034	[-1 L= 675]	xxbM / Two-component response regulator
3729	3211712	3210864	[-3 L= 849]	yxkD / Hypothetical protein
3731	3212688	3212035	[-1 L= 654]	xxbN / Hypothetical protein
3733	3212982	3214010	[+3 L=1029]	xxbO / Microcin immunity protein homolog
3734	3214632	3214420	[-1 L= 213]	xxbP / Hypothetical protein
3737	3216770	3216498	[-3 L= 273]	xxbQ / Hypothetical protein
3738	3217445	3217035	[-3 L= 411]	xxbR / Hypothetical protein
3741	3218781	3218326	[-1 L= 456]	subT / Subtilisin-like protease (Alkaline mesentericopeptidase)
3742	3220942	3218765	[-2 L=2178]	xxbS / Hypothetical protein

3743	3221930	3220905	[-3 L=1026]	hupE / Hydrogenase expression/formation protein homolog
3744	3222594	3222016	[-1 L= 579]	xxbT / Isochorismatase homolog
3745	3223238	3222801	[-3 L= 438]	xxbU / Transcriptional regulator
3746	3223389	3224681	[+3 L=1293]	yecA / Amino acid permease homolog
3748	3226127	3225552	[-3 L= 576]	xxbV / Hypothetical protein
3749	3226673	3226206	[-3 L= 468]	xxbW / Hypothetical protein
3750	3227473	3226673	[-2 L= 801]	xxbX / Hypothetical protein
3751	3228638	3227469	[-3 L=1170]	serA / D-3-phosphoglycerate dehydrogenase homolog
3752	3229967	3228654	[-3 L=1314]	serC / Phosphoserine aminotransferase (PSAT)
3753	3230133	3229945	[-1 L= 189]	xxbY / Hypothetical protein
3754	3231395	3230226	[-3 L=1170]	xxbZ / Hypothetical protein
3755	3231743	3231495	[-3 L= 249]	xxcA / Hypothetical protein
3756	3232852	3232028	[-2 L= 825]	xxcB / Transcriptional regulator, AraC/XylS family
3758	3235619	3233409	[-3 L=2211]	pacB / Penicillin acylase II precursor (Penicillin amidase II)
3760	3239403	3235903	[-1 L=3501]	molR / Molybdate metabolism regulator
3761	3240471	3239428	[-1 L=1044]	xxcC / Hypothetical protein
3762	3242551	3240707	[-2 L=1845]	xlyA / N-acetylmuramoyl-L-alanine amidase precursor (Cell wall hydrolase)
3765	3244798	3244472	[-2 L= 327]	xxcD / Hypothetical protein
3768	3246347	3245829	[-3 L= 519]	yeeE / Hypothetical protein
3769	3246440	3247222	[+2 L= 783]	xxcE / Hypothetical protein
3770	3247780	3247316	[-2 L= 465]	xxcF / Hypothetical protein
3772	3248762	3248343	[-3 L= 420]	xxcG / Hypothetical protein
3775	3250458	3249574	[-1 L= 885]	xxcH / Hypothetical protein
3776	3250803	3250486	[-1 L= 318]	xxcI / Hypothetical protein
3778	3251443	3252057	[+1 L= 615]	xxcJ / Hypothetical protein
3781	3252904	3252491	[-2 L= 414]	xxcK / Hypothetical protein
3783	3253525	3253064	[-2 L= 462]	ywqK / Hypothetical protein
3785	3255385	3254201	[-2 L=1185]	xxcL / Hypothetical protein
3787	3255784	3256266	[+1 L= 483]	xxcM / Hypothetical protein
3788	3256876	3256523	[-2 L= 354]	yxaF / Hypothetical protein
3789	3257307	3256978	[-1 L= 330]	xxcN / Hypothetical protein
3791	3257615	3257866	[+2 L= 252]	ynzG / Hypothetical protein
3798	3261130	3260666	[-2 L= 465]	xxcO / Hypothetical protein
3799	3261856	3261206	[-2 L= 651]	xxcP / Hypothetical protein
3804	3263680	3263201	[-2 L= 480]	yeeF / Hypothetical protein
3805	3263984	3263676	[-3 L= 309]	xxcQ / Transposase
3807	3265203	3264739	[-1 L= 465]	xxcR / Hypothetical protein
3808	3265965	3265222	[-1 L= 744]	xxcS / Hypothetical protein
3811	3268397	3267876	[-3 L= 522]	xxcT / Hypothetical protein
3813	3271047	3269242	[-1 L=1806]	xxcU / Hypothetical protein
3815	3272126	3271410	[-3 L= 717]	xxcV / Hypothetical protein
3818	3274280	3273552	[-3 L= 729]	vanY / D-alanyl-D-alanine carboxypeptidase (DD-carboxypeptidase)
3819	3275564	3274332	[-3 L=1233]	xxcW / Hypothetical protein
3820	3276364	3276167	[-2 L= 198]	yebG / Hypothetical protein
3821	3277544	3276351	[-3 L=1194]	yfkF / Multidrug-efflux transporter homolog
3823	3278869	3277955	[-2 L= 915]	xxcX / Hypothetical protein
3824	3279026	3279457	[+2 L= 432]	xxcY / Transcriptional regulator, MarR family
3825	3279470	3280672	[+2 L=1203]	ywoG / Antibiotic (quinolone) resistance protein homolog
3826	3280776	3281534	[+3 L= 759]	xxcZ / Hypothetical protein
3828	3282752	3282279	[-3 L= 474]	yjdI / Transcriptional regulator
3829	3283084	3284367	[+1 L=1284]	syiH / Histidyl-tRNA synthetase (histidine-tRNA ligase)
3830	3284531	3284839	[+2 L= 309]	xxdA / Hypothetical protein
3832	3285064	3285660	[+1 L= 597]	xxdB / Hypothetical protein
3833	3286114	3285737	[-2 L= 378]	yybR / Hypothetical protein
3834	3286226	3286924	[+2 L= 699]	yfkO / Nitroreductase homolog
3835	3287046	3287360	[+3 L= 315]	xxdC / Hypothetical protein
3836	3288538	3287417	[-2 L=1122]	kpyK / Pyruvate kinase (PK)
3837	3288743	3289228	[+2 L= 486]	xxdD / Hypothetical protein
3839	3289294	3290238	[+1 L= 945]	xxdE / Phage protein
3840	3291158	3290307	[-3 L= 852]	ywbM / Hypothetical protein
3842	3292132	3291362	[-2 L= 771]	xxdF / 3-oxoacyl-[acyl-carrier protein] reductase homolog

3843	3293833	3292178	[-2 L=1656]	xxdG / Hypothetical protein
3844	3294560	3293829	[-3 L= 732]	xxdH / ABC transporter ATP-binding protein
3846	3295014	3295370	[+3 L= 357]	xxdI / Hypothetical protein
3847	3295361	3295558	[+2 L= 198]	xxdJ / Transcriptional regulator
3848	3296605	3295643	[-2 L= 963]	xxdK / Hypothetical protein
3849	3297628	3296921	[-2 L= 708]	xxdL / Haloacid dehalogenase homolog
3850	3298736	3297720	[-3 L=1017]	xxdM / Hypothetical protein
3852	3300439	3299720	[-2 L= 720]	xxdN / Acetyltransferase homolog
3853	3300563	3301399	[+2 L= 837]	xxdO / Hypothetical protein
3854	3301420	3301863	[+1 L= 444]	xxdP / MutT-like protein
3855	3302912	3301878	[-3 L=1035]	syiW / Tryptophanyl-tRNA synthetase (Tryptophan--tRNA ligase)
3856	3303264	3304418	[+3 L=1155]	dxpR / 1-deoxy-D-xylulose 5-phosphate reductoisomerase (1-deoxyxylulose-5-phosphate reductoisomerase)
3857	3305581	3304454	[-2 L=1128]	yubA / Hypothetical protein
3859	3306088	3306552	[+1 L= 465]	yqkA / Acetyltransferase homolog
3861	3309563	3307053	[-3 L=2511]	xxdQ / Hypothetical protein
3862	3312093	3309589	[-1 L=2505]	xxdR / Collagen-like glycine-rich protein
3863	3312959	3312243	[-3 L= 717]	xxdS / Hypothetical protein
3864	3313578	3313039	[-1 L= 540]	xxdT / Hypothetical protein
3865	3313691	3314881	[+2 L=1191]	xxdU / Hypothetical protein
3866	3315839	3314928	[-3 L= 912]	xxdV / Hypothetical protein
3867	3316139	3316513	[+2 L= 375]	xxdW / Hypothetical protein
3868	3316593	3316829	[+3 L= 237]	xxdX / Hypothetical protein
3869	3317503	3316958	[-2 L= 546]	xxdY / Hypothetical protein
3870	3318115	3317705	[-2 L= 411]	xxdZ / Hypothetical protein
3872	3319496	3318171	[-3 L=1326]	yrkA / Hemolysin-like protein
3873	3320023	3319619	[-2 L= 405]	yhdQ / Transcriptional regulator, MerR family
3875	3321174	3321938	[+3 L= 765]	rfbF / Glucose-1-phosphate cytidylyltransferase (CDP-glucose pyrophosphorylase)
3876	3321943	3322995	[+1 L=1053]	rfbG / CDP-glucose 4,6-dehydratase
3877	3323011	3324231	[+1 L=1221]	xxeA / Methyltransferase homolog
3878	3324231	3325136	[+3 L= 906]	xxeB / Hypothetical protein
3880	3326348	3325989	[-3 L= 360]	xxeC / Hypothetical protein
3881	3326537	3327418	[+2 L= 882]	yetK / Transport protein homolog
3883	3328816	3327998	[-2 L= 819]	yybG / Hypothetical protein
3884	3329013	3329186	[+3 L= 174]	xxeD / Hypothetical protein
3885	3330300	3329236	[-1 L=1065]	ykgB / Hypothetical protein
3886	3331962	3330424	[-1 L=1539]	gntK / Gluconokinase (Gluconate kinase)
3887	3333418	3332096	[-2 L=1323]	gnuT / Gluconate permease
3888	3334489	3333818	[-2 L= 672]	talA / Transaldolase (20 kDa phosphoprotein orfU)
3889	3335504	3334596	[-3 L= 909]	yqeC / 6-Phosphogluconate dehydrogenase homolog
3890	3336358	3335603	[-2 L= 756]	tktA / Transketolase (TK)
3891	3337620	3336409	[-1 L=1212]	tktA / Transketolase (TK)
3892	3339117	3337636	[-1 L=1482]	yqjJ / Glucose-6-phosphate 1-dehydrogenase
3893	3339880	3339473	[-2 L= 408]	yqjJ / Glucose-6-phosphate 1-dehydrogenase
3894	3341219	3340260	[-3 L= 960]	xxeE / Zinc-binding oxidoreductase homolog
3895	3342186	3341227	[-1 L= 960]	xxeF / Monooxygenase homolog
3897	3342597	3343589	[+3 L= 993]	xxeG / Zinc-binding dehydrogenase homolog
3899	3344638	3343847	[-2 L= 792]	yvaG / 3-oxoacyl-[acyl-carrier-protein] reductase homolog
3900	3347023	3345329	[-2 L=1695]	xxeH / Thermolysin metallopeptidase homolog
3901	3349420	3347195	[-2 L=2226]	xxeI / Hypothetical protein
3902	3351434	3349722	[-3 L=1713]	xxeJ / Methyl-accepting chemotaxis protein homolog
3903	3352457	3351891	[-3 L= 567]	xxeK / Hypothetical protein
3905	3352738	3352520	[-2 L= 219]	ribD / Riboflavin biosynthesis protein (diaminohydroxyphosphoribosylaminopyrimidine deaminase/5-amino-6-(5-phosphoribosylamino)uracil reductase)
3906	3353675	3352710	[-3 L= 966]	ribD / Riboflavin biosynthesis protein (diaminohydroxyphosphoribosylaminopyrimidine deaminase/5-amino-6-(5-phosphoribosylamino)uracil reductase)
3907	3354420	3353611	[-1 L= 810]	ribA / Riboflavin biosynthesis protein (GTP cyclohydrolase II/3,4-dihydroxy-2-butanone 4-phosphate synthase)
3909	3354649	3354963	[+1 L= 315]	yvaP / Hypothetical protein

3910	3355904	3355308	[-3 L= 597]	xxeL / Nitroreductase homolog
3912	3357367	3356297	[-2 L=1071]	xxeM / Hypothetical protein
3913	3358612	3357776	[-2 L= 837]	ytbE / Dehydrogenase homolog
3915	3359843	3358632	[-3 L=1212]	ytbD / Antibiotic (chloramphenicol) resistance protein homolog
3916	3360898	3360428	[-2 L= 471]	xxeN / Tautomerase homolog
3917	3361495	3360944	[-2 L= 552]	xxeO / Hypothetical protein
3918	3362360	3361992	[-3 L= 369]	xxeP / Hypothetical protein
3921	3364499	3363132	[-3 L=1368]	sdaC / Serine transporter
3922	3365882	3365550	[-3 L= 333]	xxeR / Hypothetical protein
3923	3366456	3366010	[-1 L= 447]	xxeS / Hypothetical protein
3924	3366780	3366613	[-1 L= 168]	xxeT / Hypothetical protein
3925	3367187	3366795	[-3 L= 393]	yjbD / Hypothetical protein
3926	3367766	3368110	[+2 L= 345]	ytcD / Hypothetical protein
3927	3368690	3368175	[-3 L= 516]	xxeU / Transcriptional regulator, GntR family
3929	3370004	3368937	[-3 L=1068]	xxeV / Oxidoreductase homolog
3930	3371410	3370211	[-2 L=1200]	cmaS / Cyclopropane-fatty-acyl-phospholipid synthase
3931	3371999	3371697	[-3 L= 303]	ytcD / Hypothetical protein
3932	3372567	3372193	[-1 L= 375]	xxeW / Hypothetical protein
3933	3372948	3373928	[+3 L= 981]	xxeX / Aldo-keto reductase homolog
3934	3373999	3374451	[+1 L= 453]	xxeY / Hypothetical protein
3935	3375992	3374619	[-3 L=1374]	xxeZ / Subtilase family serine protease
3937	3377017	3376454	[-2 L= 564]	xxfA / Hypothetical protein
3938	3377908	3377036	[-2 L= 873]	ymaE / Metallo-beta-lactamase homolog
3939	3378917	3378027	[-3 L= 891]	xxfB / Hypothetical protein
3942	3379809	3379063	[-1 L= 747]	xxfC / Hypothetical protein
3944	3379893	3380099	[+3 L= 207]	xxfD / Hypothetical protein
3945	3381034	3380138	[-2 L= 897]	yfhB / Hypothetical protein
3948	3382820	3381321	[-3 L=1500]	lcfA / Long-chain-fatty-acid--CoA ligase (Long-chain acyl-CoA synthetase)
3950	3383491	3382958	[-2 L= 534]	yrkL / Oxidoreductase homolog
3951	3383535	3383933	[+3 L= 399]	ytcD / Hypothetical protein
3953	3384656	3384384	[-3 L= 273]	xxfE / Transcriptional regulator, ArsR family
3954	3386373	3384910	[-1 L=1464]	xxfF / Polysaccharide deacetylase homolog
3955	3388267	3386354	[-2 L=1914]	xxfF / Polysaccharide deacetylase homolog
3957	3389751	3388465	[-1 L=1287]	ykrI / Hypothetical protein
3958	3390280	3389744	[-2 L= 537]	ykoZ / RNA polymerase sigma factor
3960	3391850	3391050	[-3 L= 801]	xxfG / Glycosyltransferase homolog
3961	3392538	3391909	[-1 L= 630]	xxfH / Hypothetical protein
3962	3394437	3392956	[-1 L=1482]	xxfI / Hypothetical protein
3964	3395813	3395331	[-3 L= 483]	xxfJ / Hypothetical protein
3965	3395917	3396876	[+1 L= 960]	xxfK / Transcriptional regulator, DeoR family
3966	3397792	3397046	[-2 L= 747]	xxfL / ABC transporter permease protein
3967	3398554	3397796	[-2 L= 759]	xxfM / ABC transporter ATP-binding protein
3968	3399099	3398728	[-1 L= 372]	xxfN / Hypothetical protein
3969	3399462	3399145	[-1 L= 318]	xxfO / Hypothetical protein
3970	3401262	3399955	[-1 L=1308]	priS / Prismane protein homolog (Hybrid-cluster protein)
3972	3402732	3401941	[-1 L= 792]	blaB / Beta-lactamase II precursor (Penicillinase) (Cephalosporinase)
3973	3403586	3402852	[-3 L= 735]	xxfP / Glycosyltransferase homolog
3974	3403956	3403624	[-1 L= 333]	xxfQ / Hypothetical protein
3975	3404018	3404314	[+2 L= 297]	xxfR / Hypothetical protein
3977	3404670	3404350	[-1 L= 321]	xxfS / Hypothetical protein
3978	3404764	3404955	[+1 L= 192]	xxfT / Hypothetical protein
3979	3405361	3405050	[-2 L= 312]	xxfU / Hypothetical protein
3980	3406619	3405579	[-3 L=1041]	trkA / Potassium uptake protein
3981	3407123	3406773	[-3 L= 351]	xxfV / Glyoxalase/Bleomycin resistance protein homolog
3982	3407829	3407140	[-1 L= 690]	xxfW / Transcriptional regulator
3983	3407938	3408381	[+1 L= 444]	xxfX / Hypothetical protein
3984	3408398	3408859	[+2 L= 462]	xxfY / Hypothetical protein
3985	3408952	3409443	[+1 L= 492]	xxfZ / Hypothetical protein
3986	3410239	3409490	[-2 L= 750]	xxgA / Acetyl-homocysteine-lactone lactonase
3987	3412059	3410644	[-1 L=1416]	ybxG / Amino acid permease protein
3989	3413769	3412573	[-1 L=1197]	xxgB / Multidrug-efflux protein homolog

3990	3414132	3414695	[+3 L= 564]	xxgC / Hypothetical protein
3995	3416135	3416893	[+2 L= 759]	xxgD / Glucose 1-dehydrogenase homolog
3996	3417671	3417012	[-3 L= 660]	xxgE / Hypothetical protein
3997	3418037	3417690	[-3 L= 348]	xxgF / Hypothetical protein
3998	3418300	3419622	[+1 L=1323]	arsB / Aresenical pump membrane protein
3999	3419924	3419700	[-3 L= 225]	xxgG / Hypothetical protein
4000	3420617	3420027	[-3 L= 591]	xxgH / Acetyltransferase homolog
4001	3421701	3420796	[-1 L= 906]	feuA / Iron-uptake system binding protein precursor
4002	3422739	3421726	[-1 L=1014]	fhuG / Ferrichrome transport system permease protein
4003	3423774	3422743	[-1 L=1032]	fhuB / Ferrichrome transport system permease protein
4004	3424052	3424813	[+2 L= 762]	yoaT / Hypothetical protein
4005	3425982	3424948	[-1 L=1035]	yeaA / Hypothetical protein
4006	3426623	3426144	[-3 L= 480]	xxgI / Hypothetical protein
4007	3426762	3427274	[+3 L= 513]	xxgJ / Hypothetical protein
4009	3427505	3428038	[+2 L= 534]	xxgK / Hypothetical protein
4010	3428630	3428157	[-3 L= 474]	yjfA / Hypothetical protein
4011	3429160	3428651	[-2 L= 510]	xxgL / Hypothetical protein
4012	3430345	3429455	[-2 L= 891]	ywqM / Transcriptional regulator, LysR family
4013	3430454	3431431	[+2 L= 978]	xxgM / Oxidoreductase homolog
4014	3432210	3431503	[-1 L= 708]	xxgN / Phosphoglycerate mutase homolog
4016	3432895	3432374	[-2 L= 522]	xxgO / Acetyltransferase homolog
4017	3434818	3432905	[-2 L=1914]	mutS / DNA mismatch repair protein
4020	3437956	3436325	[-2 L=1632]	amyA / Alpha-amylase precursor (1,4-alpha-D-glucan glucanohydrolase)
4021	3438067	3438855	[+1 L= 789]	yvcN / N-acetyltransferase homolog
4022	3438955	3440760	[+1 L=1806]	pepF / Oligoendopeptidase F homolog
4023	3441122	3440814	[-3 L= 309]	xxgP / Hypothetical protein
4024	3442119	3441301	[-1 L= 819]	xxgQ / Transcriptional regulator, MerR family
4025	3443139	3442165	[-1 L= 975]	xxgR / Hypothetical protein
4027	3444195	3443776	[-1 L= 420]	xxgS / Hypothetical protein
4028	3445570	3444356	[-2 L=1215]	xxgT / Hypothetical protein
4029	3447031	3445907	[-2 L=1125]	pbpX / Penicillin-binding protein homolog
4030	3447289	3447516	[+1 L= 228]	xxgU / Hypothetical protein
4032	3448858	3447632	[-2 L=1227]	xxgV / Transporter homolog
4033	3448945	3449793	[+1 L= 849]	yusT / Transcriptional regulator, LysR family
4034	3449789	3450295	[+2 L= 507]	xxgW / Hypothetical protein
4035	3451281	3450340	[-1 L= 942]	glpQ / Glycerophosphoryl diester phosphodiesterase (Glycerophosphodiester phosphodiesterase)
4036	3451993	3451676	[-2 L= 318]	xxgX / Monooxygenase (polyketide hydroxylase) homolog
4037	3453308	3451956	[-3 L=1353]	xxgX / Monooxygenase (polyketide hydroxylase) homolog
4039	3453804	3454145	[+3 L= 342]	xxgY / Transcriptional regulator, ArsR
4040	3454167	3455162	[+3 L= 996]	xxgZ / Oxidoreductase homolog
4041	3455344	3456807	[+1 L=1464]	xxhA / Hypothetical protein
4043	3458344	3457154	[-2 L=1191]	xxhB / Response regulator homolog
4044	3458748	3458404	[-1 L= 345]	xxhC / Hypothetical protein
4046	3460361	3458967	[-3 L=1395]	dldH / D-lactate dehydrogenase
4047	3460916	3460485	[-3 L= 432]	xxhD / Hypothetical protein
4048	3461136	3461636	[+3 L= 501]	xxhE / Acetyltransferase homolog
4049	3461842	3462021	[+1 L= 180]	xxhF / Hypothetical protein
4053	3462913	3463401	[+1 L= 489]	pssP / CDP-diacylglycerol--serine O-phosphatidyltransferase (Phosphatidylserine synthase)
4056	3465474	3464026	[-1 L=1449]	xxhG / Metallo-beta-lactamase homolog
4057	3466725	3465529	[-1 L=1197]	xxhH / Hypothetical protein
4059	3467779	3468459	[+1 L= 681]	xxhI / Hypothetical protein
4061	3469131	3469877	[+3 L= 747]	yfnH / Glucose-1-phosphate cytidyltransferase homolog
4062	3469901	3471967	[+2 L=2067]	yfnD / Glucosyltransferase homolog
4063	3472053	3473009	[+3 L= 957]	xxhJ / Hypothetical protein
4064	3473041	3474126	[+1 L=1086]	rfbG / CDP-glucose 4,6-dehydratase
4067	3475260	3476387	[+3 L=1128]	xxhK / Response regulator homolog
4069	3478695	3476716	[-1 L=1980]	xxhL / Methyl-accepting chemotaxis protein homolog
4073	3483620	3482988	[-3 L= 633]	yttP / Transcriptional regulator, TetR family
4074	3485218	3483971	[-2 L=1248]	hlaB / Hemolysin II

4075	3486733	3485504	[-2 L=1230]	xxhM / N-acetylmuramoyl-L-alanine amidase (cell wall amidase) homolog
4076	3487670	3487939	[+2 L= 270]	xxhN / Hypothetical protein
4077	3491347	3488024	[-2 L=3324]	xxhO / Collagen adhesin protein homolog
4080	3493712	3495013	[+2 L=1302]	kinB / Sporulation kinase B
4081	3498310	3495398	[-2 L=2913]	xxhP / Collagenase homolog
4082	3499196	3498516	[-3 L= 681]	xxhQ / Hypothetical protein
4083	3499481	3499996	[+2 L= 516]	xxhR / Acetyltransferase homolog
4085	3500967	3500050	[-1 L= 918]	yfiE / Glyoxalase/Bleomycin resistance protein homolog
4086	3502041	3501133	[-1 L= 909]	yoaR / Hypothetical protein
4087	3502453	3502851	[+1 L= 399]	xxhS / Hypothetical protein
4088	3502962	3504059	[+3 L=1098]	yetN / Hypothetical protein
4089	3504767	3504402	[-3 L= 366]	xxhT / Hypothetical protein
4092	3505956	3505114	[-1 L= 843]	xxhU / DNA polymerase homolog
4093	3506345	3506148	[-3 L= 198]	cspD / Cold shock protein
4094	3507523	3506564	[-2 L= 960]	ykuO / Hypothetical protein
4095	3507941	3507480	[-3 L= 462]	flaV / Flavodoxin 1
4097	3508870	3508253	[-2 L= 618]	xxhV / Hypothetical protein
4098	3509352	3508960	[-1 L= 393]	xxhW / Hypothetical protein
4099	3509699	3509352	[-3 L= 348]	xxhX / Hypothetical protein
4100	3509801	3510355	[+2 L= 555]	xxhY / Hypothetical protein
4102	3515108	3510411	[-3 L=4698]	xxhZ / Hypothetical protein
4104	3517881	3515059	[-1 L=2823]	xxiA / Hypothetical protein
4106	3517947	3518744	[+3 L= 798]	xxiB / Benzil reductase
4107	3519622	3518786	[-2 L= 837]	xxiC / Acetyltransferase homolog
4108	3521209	3519686	[-2 L=1524]	arlY / Argininosuccinate lyase (Arginosuccinase)
4109	3522402	3521296	[-1 L=1107]	xxiD / D-alanyl-D-alanine carboxypeptidase homolog
4110	3523467	3522523	[-1 L= 945]	iunH / Inosine-uridine preferring nucleoside hydrolase (Purine nucleosidase)
4111	3525009	3523579	[-1 L=1431]	panF / Sodium/pantothenate symporter (Pantothenate permease)
4112	3525309	3525016	[-1 L= 294]	xxiE / Hypothetical protein
4113	3525565	3527046	[+1 L=1482]	dhaS / Aldehyde dehydrogenase
4114	3527840	3527103	[-3 L= 738]	xxiF / 3-ketoacyl-[acyl-carrier-protein] reductase homolog
4116	3530091	3528199	[-1 L=1893]	sqhC / Squalene--hopene cyclase
4117	3530574	3530152	[-1 L= 423]	xxiG / Hypothetical protein
4118	3531595	3530657	[-2 L= 939]	xxiH / Hypothetical protein
4119	3531936	3531691	[-1 L= 246]	xxiI / Hypothetical protein
4120	3532527	3532123	[-1 L= 405]	xxiJ / Hypothetical protein
4121	3532786	3532547	[-2 L= 240]	xxiK / Hypothetical protein
4122	3533860	3532805	[-2 L=1056]	xxiL / ATP-binding Mrp protein homolog
4123	3534160	3533927	[-2 L= 234]	xxiM / Hypothetical protein
4124	3534638	3534168	[-3 L= 471]	moaE / Molybdopterin converting factor subunit 2 (Molybdopterin synthase subunit 2)
4125	3535926	3534613	[-1 L=1314]	moeA / Molybdopterin converting factor subunit 1 (Molybdopterin synthase subunit 1)
4126	3536552	3535938	[-3 L= 615]	xxiN / Hypothetical protein
4128	3537771	3536980	[-1 L= 792]	yrhG / Formate/nitrate transport protein
4130	3538970	3537951	[-3 L=1020]	moaA / Molybdenum cofactor biosynthesis protein A
4131	3539778	3538984	[-1 L= 795]	fdhD / Protein required for formate dehydrogenase activity
4132	3540139	3539798	[-2 L= 342]	yrhF / Hypothetical protein
4133	3540737	3540258	[-3 L= 480]	yrhD / Hypothetical protein
4134	3543848	3540753	[-3 L=3096]	yrhE / Formate dehydrogenase homolog
4135	3544056	3545591	[+3 L=1536]	yfkQ / Spore germination response protein homolog
4136	3545591	3546685	[+2 L=1095]	xxiO / Hypothetical protein
4137	3546689	3547822	[+2 L=1134]	xxiP / Spore germination protein homolog
4138	3549234	3547903	[-1 L=1332]	yfnA / Amino acid permease
4142	3553312	3549944	[-2 L=3369]	xxiQ / Hypothetical protein
4143	3555542	3553386	[-3 L=2157]	xxiR / Hypothetical protein
4144	3556077	3555742	[-1 L= 336]	xxiS / Hypothetical protein
4145	3556484	3556140	[-3 L= 345]	xxiT / Hypothetical protein
4146	3556619	3557011	[+2 L= 393]	xxiU / Hypothetical protein
4147	3557774	3557058	[-3 L= 717]	xxiV / Methyltransferase homolog
4148	3559551	3557860	[-1 L=1692]	xxiW / Extracellular solute-binding protein homolog

4149	3561708	3559996	[-1 L=1713]	xxiX / Extracellular solute-binding protein homolog
4150	3563710	3562010	[-2 L=1701]	xxiY / Extracellular solute-binding protein homolog
4151	3565094	3564060	[-3 L=1035]	xxiZ / Hypothetical protein
4152	3566110	3565115	[-2 L= 996]	xxjA / Hypothetical protein
4153	3566656	3566126	[-2 L= 531]	xxjB / RNA polymerase Sigma factor
4154	3567615	3566863	[-1 L= 753]	xxjC / ABC transporter permease protein homolog
4155	3568551	3567661	[-1 L= 891]	xxjD / ABC transporter ATP-binding protein homolog
4156	3568584	3569306	[+3 L= 723]	xxjE / Transcriptional regulator, TetR family
4157	3570372	3569407	[-1 L= 966]	xxjF / Hypothetical protein
4158	3570432	3570872	[+3 L= 441]	xxjG / Hypothetical protein
4159	3571962	3570934	[-1 L=1029]	yvaA / Oxidoreductase homolog
4160	3574609	3572189	[-2 L=2421]	parC / Topoisomerase IV subunit A
4161	3576575	3574614	[-3 L=1962]	parE / Topoisomerase IV subunit B
4162	3577364	3576954	[-3 L= 411]	yneT / Hypothetical protein
4163	3578685	3577447	[-1 L=1239]	yyxA / Serine protease
4164	3579566	3578892	[-3 L= 675]	xxjH / Two-component response regulator
4165	3580037	3579588	[-3 L= 450]	nrdG / Ribonucleoside-triphosphate reductase activating protein
4166	3581890	3580037	[-2 L=1854]	nrdD / Anaerobic ribonucleoside-triphosphate reductase
4168	3582116	3582709	[+2 L= 594]	yneS / Hypothetical protein
4169	3582806	3583108	[+2 L= 303]	yneR / Hypothetical protein
4170	3583605	3583141	[-1 L= 465]	hbcT / 4-Hydroxybenzoyl-CoA thioesterase
4171	3583667	3584956	[+2 L=1290]	yaaH / Cortical fragment-lytic enzyme
4172	3585185	3584991	[-3 L= 195]	xxjI / Thioredoxin-like protein
4175	3586702	3585749	[-2 L= 954]	xxjJ / DNA polymerase III alphas subunit
4176	3587384	3586812	[-3 L= 573]	yneN / Thiol:disulfide interchange protein homolog
4177	3587565	3587792	[+3 L= 228]	xxjK / Hypothetical protein
4178	3589401	3588220	[-1 L=1182]	xxjL / ABC transporter, ATP-binding protein
4179	3589876	3589568	[-2 L= 309]	xxjM / ABC transporter ATP-binding protein
4181	3592718	3589998	[-3 L=2721]	acoN / Aconitate hydratase (Citrate hydro-lyase) (Aconitase)
4183	3593926	3593204	[-2 L= 723]	xxjN / Polysaccharide deacetylase homolog
4184	3594236	3593976	[-3 L= 261]	xxjO / Hypothetical protein
4186	3594596	3594982	[+2 L= 387]	xxjP / Hypothetical protein
4187	3596314	3595037	[-2 L=1278]	yqjV / Multidrug resistance protein homolog
4188	3596752	3596342	[-2 L= 411]	xxjQ / Hypothetical protein
4189	3596851	3597576	[+1 L= 726]	syiA / Alanyl-tRNA synthetase (Alanine--tRNA ligase)
4190	3597605	3598084	[+2 L= 480]	syiA / Alanyl-tRNA synthetase (Alanine--tRNA ligase)
4191	3598619	3598134	[-3 L= 486]	xxjR / MutT-like protein
4192	3598679	3599257	[+2 L= 579]	xxjS / Hypothetical protein
4193	3600381	3599272	[-1 L=1110]	thlA / Acetyl-CoA acetyltransferase (Acetoacetyl-CoA thiolase)
4194	3601603	3600356	[-2 L=1248]	lcfA / Long-chain-fatty-acid--CoA ligase (Long-chain acyl-CoA synthetase)
4196	3602458	3601886	[-2 L= 573]	bioY / Biotin biosynthesis protein homolog
4197	3603223	3602585	[-2 L= 639]	alkK / Medium-chain-fatty-acid--CoA ligase (Medium-chain acyl-CoA synthetase)
4198	3604194	3603223	[-1 L= 972]	alkK / Medium-chain-fatty-acid--CoA ligase (Medium-chain acyl-CoA synthetase)
4200	3605072	3604515	[-3 L= 558]	xxjT / N-acetyltransferase homolog
4201	3605323	3605072	[-2 L= 252]	xxjU / Hypothetical protein
4202	3605425	3606231	[+1 L= 807]	xxjV / Hypothetical protein
4203	3606406	3606615	[+1 L= 210]	xxjW / Hypothetical protein
4205	3606891	3606646	[-1 L= 246]	xxjX / Hypothetical protein
4206	3607363	3606914	[-2 L= 450]	xxjY / N-acetylmuramoyl-L-alanine amidase homolog
4207	3608200	3607382	[-2 L= 819]	xxjZ / Serine/threonine phosphatase homolog
4208	3608297	3609133	[+2 L= 837]	yitT / Hypothetical protein
4209	3609527	3609159	[-3 L= 369]	xxkA / Glyoxalase/Bleomycin resistance protein homolog
4211	3609746	3611293	[+2 L=1548]	ykrQ / Two-component sensor histidine-kinase
4212	3611949	3611344	[-1 L= 606]	yodD / Hypothetical protein
4213	3612921	3611977	[-1 L= 945]	ydfO / ABC transporter ATP-binding protein homolog
4214	3614746	3613268	[-2 L=1479]	opuE / Osmoregulated proline transporter (Sodium/proline symporter)
4217	3617216	3615645	[-3 L=1572]	glxD / Glutamate synthase large subunit-like protein
4218	3618411	3617287	[-1 L=1125]	nemA / N-ethylmaleimide reductase (N-ethylmaleimide reducing enzyme)
4219	3619501	3619001	[-2 L= 501]	ydeB / Transcriptional regulator, CarD family
4220	3620502	3619723	[-1 L= 780]	hutG / Formimidoylglutamase (Formiminoglutamate hydrolase)
4221	3620692	3620489	[-2 L= 204]	hutG / Formimidoylglutamase (Formiminoglutamate hydrolase)

4222	3621942	3620674	[-1 L=1269]	hutI / Imidazolonepropionase (Imidazolone-5-propionate hydrolase)
4223	3623613	3621958	[-1 L=1656]	hutU / Urocanate hydratase (Imidazolonepropionate hydrolase)
4224	3625157	3623640	[-3 L=1518]	hutH / Histidine ammonia-lyase (Histidase)
4225	3625698	3625261	[-1 L= 438]	hutP / Hut operon positive regulatory protein
4226	3625874	3626137	[+2 L= 264]	xxkB / Methyltransferase homolog
4227	3626385	3626843	[+3 L= 459]	xxkB / Methyltransferase homolog
4228	3627422	3626853	[-3 L= 570]	xxkC / Hypothetical protein
4229	3627868	3627422	[-2 L= 447]	xxkD / Thymidylate kinase homolog
4230	3628251	3628544	[+3 L= 294]	xxkE / Hypothetical protein
4231	3628651	3629079	[+1 L= 429]	yneK / Hypothetical protein
4232	3629659	3629156	[-2 L= 504]	ccdC / CcdC protein
4233	3630514	3629753	[-2 L= 762]	ccdA / Cytochrome c-type biogenesis protein ccdA
4235	3630946	3631851	[+1 L= 906]	xxkF / Hypothetical protein
4236	3631994	3633136	[+2 L=1143]	yxeP / Aminoacylase/hippurate hydrolase homolog
4237	3634130	3633189	[-3 L= 942]	yhcI / Hypothetical protein
4238	3635043	3634126	[-1 L= 918]	yhcH / ABC transporter ATP-binding protein
4240	3635700	3635128	[-1 L= 573]	xxkG / ABC transporter permease protein
4242	3637462	3636566	[-2 L= 897]	alsR / Als operon regulatory protein
4244	3637562	3637978	[+2 L= 417]	ywbH / Hypothetical protein
4245	3637978	3638514	[+1 L= 537]	ywbG / Hypothetical protein
4247	3639157	3638711	[-2 L= 447]	xxkH / MutT-like protein
4249	3640569	3639796	[-1 L= 774]	ydbH / Hypothetical protein
4251	3641581	3641036	[-2 L= 546]	xxkI / Hypothetical protein
4252	3642624	3641608	[-1 L=1017]	xxkJ / Hypothetical protein
4253	3643811	3642768	[-3 L=1044]	xxkK / Probable autolytic lysozyme (1,4-beta-N-acetylmuramidase) (Autolysin)
4254	3645708	3643945	[-1 L=1764]	xxkL / ABC transporter ATP-binding protein
4255	3647456	3645708	[-3 L=1749]	xxkM / ABC transporter ATP-binding protein
4257	3648319	3647882	[-2 L= 438]	xxkN / Hypothetical protein
4259	3650518	3648479	[-2 L=2040]	tktA / Transketolase (TK)
4260	3651576	3650776	[-1 L= 801]	ptxC / Phosphonates transport system permease protein
4261	3652370	3651579	[-3 L= 792]	xxkO / Hypothetical protein
4262	3653140	3652370	[-2 L= 771]	ptxA / Phosphonates transport ATP-binding protein
4263	3654225	3653227	[-1 L= 999]	xxkP / Periplasmic substrate-binding protein
4265	3654348	3655928	[+3 L=1581]	xxkQ / 5'-Nucleotide/2',3'-cyclic phosphodiesterase homolog
4266	3656210	3655974	[-3 L= 237]	xxkR / Hypothetical protein
4267	3656912	3656259	[-3 L= 654]	yneB / Transposon resolvase
4268	3656991	3657671	[+3 L= 681]	lexA / Transcriptional repressor of the SOS regulon
4269	3658568	3657768	[-3 L= 801]	xxkS / Hypothetical protein
4270	3659129	3658572	[-3 L= 558]	xxkT / Hypothetical protein
4271	3659427	3659107	[-1 L= 321]	xxkU / Hypothetical protein
4276	3661521	3660469	[-1 L=1053]	alyS / Endolysin (N-acetylmuramoyl-L-alanine amidase)
4280	3663447	3662629	[-1 L= 819]	xxkV / Peptidase homolog
4281	3664777	3663800	[-2 L= 978]	xxkW / Homolog of protein on pXO2
4284	3666414	3665521	[-1 L= 894]	xxkX / Phage protein
4286	3667513	3666752	[-2 L= 762]	xxkY / Hypothetical protein
4289	3668106	3668822	[+3 L= 717]	xxkZ / Hypothetical protein
4290	3669373	3669164	[-2 L= 210]	glnA / Glutamine synthetase (glutamate ammonia-ligase)
4291	3670497	3669376	[-1 L=1122]	glnA / Glutamine synthetase (glutamate ammonia-ligase)
4292	3670935	3670549	[-1 L= 387]	glnR / Glutamine synthetase transcription repressor
4293	3672381	3671113	[-1 L=1269]	ynbB / Cysteine/methionine metabolism enzyme homolog
4294	3673651	3672377	[-2 L=1275]	feoB / Ferrous iron transport protein
4295	3673741	3674361	[+1 L= 621]	yvgT / Hypothetical protein
4297	3675075	3674635	[-1 L= 441]	spvK / Stage V sporulation protein K
4298	3675268	3675059	[-2 L= 210]	spvK / Stage V sporulation protein K
4299	3675590	3675273	[-3 L= 318]	spvK / Stage V sporulation protein K
4300	3675704	3676666	[+2 L= 963]	xxlA / Phage integrase
4301	3676783	3679236	[+1 L=2454]	xxlB / Hypothetical protein
4302	3679545	3679324	[-1 L= 222]	ymaH / Host factor-1 protein homolog
4303	3680529	3679570	[-1 L= 960]	miaA / tRNA delta(2)-isopentenylpyrophosphate transferase (IPP transferase)
4304	3680701	3680943	[+1 L= 243]	xxlC / Hypothetical protein
4305	3681623	3681012	[-3 L= 612]	xxlD / Hypothetical protein

4306	3681996	3681661	[-1 L= 336]	xxlD / Hypothetical protein
4307	3684166	3682313	[-2 L=1854]	ptfB / PTS system, fructose-specific IIBC component (Fructose-permease IIBC component)
4308	3685091	3684183	[-3 L= 909]	kapF / 1-phosphofructokinase (Fructose 1-phosphate kinase)
4309	3685933	3685091	[-2 L= 843]	xxlE / Transcriptional regulator, DeoR family
4310	3687163	3686003	[-2 L=1161]	adhA / NADH-dependent butanol dehydrogenase 1
4311	3687859	3687284	[-2 L= 576]	xxlF / Hypothetical protein
4313	3688456	3688145	[-2 L= 312]	xxlG / Hypothetical protein
4316	3690030	3688618	[-1 L=1413]	gabP / GABA permease (4-amino butyrate transport carrier) (Gamma-aminobutyrate permease)
4317	3690262	3691359	[+1 L=1098]	chiD / Chitinase precursor
4318	3692455	3691565	[-2 L= 891]	ykuE / Phosphodiesterase homolog
4319	3692648	3693460	[+2 L= 813]	yrhG / Formate/nitrate transport protein
4320	3693594	3693872	[+3 L= 279]	dbhU / DNA-binding protein HU (DNA-binding protein II)
4321	3694373	3693894	[-3 L= 480]	xxlH / Hypothetical protein
4322	3696959	3694533	[-3 L=2427]	atcU / Copper-transporting ATPase
4323	3697252	3697049	[-2 L= 204]	yvgY / Mercuric ion-binding protein homolog
4324	3697758	3697459	[-1 L= 300]	yvgZ / Hypothetical protein
4327	3699380	3698565	[-3 L= 816]	lacT / Lecithin/cholesterol acyltransferase
4328	3700217	3699399	[-3 L= 819]	fhuC / Ferrichrome transport ATP-binding protein
4329	3701254	3700235	[-2 L=1020]	feuC / Iron-uptake system permease protein
4330	3702263	3701250	[-3 L=1014]	feuB / Iron-uptake system permease protein
4332	3703247	3702285	[-3 L= 963]	feuA / Iron-uptake system binding protein precursor
4334	3704308	3703553	[-2 L= 756]	exoA / Exodeoxyribonuclease
4335	3704462	3705055	[+2 L= 594]	adaA / Methylphosphotriester-DNA alkyltransferase
4336	3705039	3705566	[+3 L= 528]	adaB / Methylated-DNA--protein-cysteine methyltransferase (O-6-methylguanine-DNA alkyltransferase)
4337	3705566	3706474	[+2 L= 909]	dmgA / DNA-3-methyladenine glycosylase (3-methyladenine-DNA glycosidase)
4338	3707754	3706519	[-1 L=1236]	pepT / Peptidase T (Tripeptide aminopeptidase) (Aminotripeptidase) (Tripeptidase)
4339	3708338	3707988	[-3 L= 351]	xxlI / Hypothetical protein
4340	3709199	3708627	[-3 L= 573]	xxlM / Phosphoglycerate mutase homolog
4341	3710154	3709342	[-1 L= 813]	xxlN / Hydrolase homolog
4342	3710553	3713279	[+3 L=2727]	xxlO / Hypothetical protein
4343	3714426	3713365	[-1 L=1062]	murG / UDP-N-acetylglucosamine–N-acetylmuramyl-(pentapeptide) pyrophosphoryl-undecaprenol N-acetylglucosamine transferase
4345	3715733	3714825	[-3 L= 909]	xxlP / Hypothetical protein
4347	3716743	3715733	[-2 L=1011]	xxlQ / Nucleoside-diphosphate sugar epimerase homolog
4348	3716986	3718194	[+1 L=1209]	yppC / Hypothetical protein
4350	3719036	3718599	[-3 L= 438]	yfmQ / Hypothetical protein
4351	3719713	3719045	[-2 L= 669]	xxlR / Hypothetical protein
4352	3720093	3719740	[-1 L= 354]	xxlS / Hypothetical protein
4353	3721560	3720130	[-1 L=1431]	xxlT / Transcriptional regulator, GntR family
4356	3722769	3722161	[-1 L= 609]	yydK / Transcriptional regulator, GntR family
4357	3723043	3722900	[-2 L= 144]	bglB / Beta-glucosidase (Gentiobiase) (Cellobiase)
4358	3724346	3723039	[-3 L=1308]	bglB / Beta-glucosidase (Gentiobiase) (Cellobiase)
4359	3725489	3724503	[-3 L= 987]	pplC / 1-phosphatidylinositol phosphodiesterase precursor (Phosphatidylinositol-specific phospholipase C)
4361	3727510	3725672	[-2 L=1839]	xxlU / Subtilase-like serine protease
4362	3727803	3728042	[+3 L= 240]	xxlV / Cell wall hydrolase
4363	3728032	3728598	[+1 L= 567]	xxlV / Cell wall hydrolase
4364	3728813	3730201	[+2 L=1389]	xxlW / Hypothetical protein
4365	3730707	3732623	[+3 L=1917]	yqgS / Sulfatase
4367	3735488	3732678	[-3 L=2811]	xxlX / Hypothetical protein
4368	3738356	3736416	[-3 L=1941]	mutL / DNA mismatch repair protein
4370	3741037	3738368	[-2 L=2670]	mutS / DNA mismatch repair protein
4371	3741760	3741221	[-2 L= 540]	cotE / Spore coat protein E
4373	3742317	3741889	[-1 L= 429]	ymcA / Hypothetical protein
4374	3743895	3742324	[-1 L=1572]	ymcB / Hypothetical protein
4375	3745147	3744284	[-2 L= 864]	korB / 2-oxoglutarate synthase subunit (2-ketoglutarate oxidoreductase beta chain)
4376	3746891	3745137	[-3 L=1755]	korA / 2-oxoglutarate synthase subunit korA (2-ketoglutarate oxidoreductase alpha chain)

4377	3748075	3747119	[-2 L= 957]	xxlY / Dipeptidase
4378	3748398	3748102	[-1 L= 297]	spvS / Stage V sporulation protein S
4379	3749330	3748512	[-3 L= 819]	ymdB / Hypothetical protein
4380	3751028	3749469	[-3 L=1560]	ymdA / Hypothetical protein
4381	3752542	3751514	[-2 L=1029]	recA / RecA protein (Recombinase A)
4382	3753924	3752689	[-1 L=1236]	cinA / Competence-damaged inducible protein
4383	3754523	3753948	[-3 L= 576]	pgsA / CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase (Phosphatidylglycerophosphate synthase)
4385	3755508	3754591	[-1 L= 918]	xxlZ / Hypothetical protein
4386	3756306	3755524	[-1 L= 783]	xxmA / Hypothetical protein
4387	3756709	3756452	[-2 L= 258]	xxmB / Hypothetical protein
4388	3757483	3756773	[-2 L= 711]	xxmC / 3-oxoacyl-[acyl-carrier-protein] reductase homolog
4389	3758870	3757587	[-3 L=1284]	ymfH / Processing protease homolog
4390	3760145	3758874	[-3 L=1272]	xxmD / Hypothetical protein
4391	3761314	3760358	[-2 L= 957]	xxmE / Branched-chain amino acid transport system permease component
4392	3761668	3761318	[-2 L= 351]	xxmF / Hypothetical protein
4393	3762374	3761697	[-3 L= 678]	yufP / ABC transporter permease protein
4394	3763926	3762370	[-1 L=1557]	xxmG / ABC transporter ATP-binding protein
4395	3765102	3764020	[-1 L=1083]	yufN / ABC transporter homolog
4396	3765935	3765198	[-3 L= 738]	ymcF / Transcriptional regulator, GntR family
4397	3768881	3766461	[-3 L=2421]	spcE / Stage III sporulation protein E / Translocase
4398	3769255	3769055	[-2 L= 201]	xxmH / Hypothetical protein
4399	3770001	3769255	[-1 L= 747]	xxmI / Hypothetical protein
4400	3771773	3770106	[-3 L=1668]	ykqC / Hypothetical protein
4402	3773388	3772513	[-1 L= 876]	dapA / Dihydrodipicolinate synthase (Vegetative protein 81)
4403	3774641	3773403	[-3 L=1239]	aspK / Aspartokinase 1 (Aspartate kinase 1)
4405	3775705	3774659	[-2 L=1047]	dhaS / Aspartate-semialdehyde dehydrogenase (ASA dehydrogenase)
4406	3776452	3775856	[-2 L= 597]	svfB / Dipicolinate synthase, B chain
4407	3777351	3776452	[-1 L= 900]	svfA / Dipicolinate synthase, A chain
4408	3777779	3777525	[-3 L= 255]	ymxH / Hypothetical protein
4409	3779205	3777910	[-1 L=1296]	ymxG / Zinc protease homolog
4410	3780134	3779238	[-3 L= 897]	ylxY / Deacetylase homolog
4411	3782424	3780289	[-1 L=2136]	pnpA / Polyribonucleotide nucleotidyltransferase (Polynucleotide phosphorylase) (Vegetative protein 15)
4412	3782854	3782588	[-2 L= 267]	rpsO / 30S ribosomal protein S15
4413	3783962	3782958	[-3 L=1005]	ribC / Riboflavin biosynthesis protein (riboflavin kinase / FMN adenylyltransferase)
4414	3784818	3783973	[-1 L= 846]	truB / tRNA pseudouridine synthase B (tRNA pseudouridine 55 synthase) (Uracil hydrolyase)
4415	3785336	3784983	[-3 L= 354]	rbfA / Ribosome-binding factor A (P15B protein)
4416	3785633	3785355	[-3 L= 279]	ylxP / Hypothetical protein
4417	3787690	3785633	[-2 L=2058]	eftU / Translation initiation factor IF-2
4418	3788006	3787698	[-3 L= 309]	ylxQ / Ribosomal protein L7AE family homolog
4419	3788288	3788010	[-3 L= 279]	ylxR / Hypothetical protein
4420	3789397	3788294	[-2 L=1104]	nusA / N utilization substance protein A homolog
4421	3789939	3789418	[-1 L= 522]	ylxS / Hypothetical protein
4422	3794529	3790225	[-1 L=4305]	polC / DNA polymerase III (PolIII)
4423	3796348	3794651	[-2 L=1698]	syiP / Prolyl-tRNA synthetase (Proline--tRNA ligase)
4424	3797516	3796461	[-3 L=1056]	yluC / Zinc metalloprotease homolog
4425	3797725	3797522	[-2 L= 204]	yluC / Zinc metalloprotease homolog
4426	3798945	3797734	[-1 L=1212]	dxrI / 1-deoxy-D-xylulose 5-phosphate reductoisomerase (DXP reductoisomerase)
4427	3799694	3798900	[-3 L= 795]	cdsA / Phosphatidate cytidylyltransferase (CDP-diglyceride synthetase)
4429	3800482	3799709	[-2 L= 774]	uppS / Undecaprenyl pyrophosphate synthetase (Undecaprenyl diphosphate synthase)
4431	3801125	3800571	[-3 L= 555]	rrfA / Ribosome recycling factor (Ribosome releasing factor) (Vegetative protein 12B)
4432	3801850	3801131	[-2 L= 720]	pyrH / Uridylate kinase (Uridine monophosphate kinase)
4433	3802813	3801920	[-2 L= 894]	eftS / Elongation factor Ts (EF-Ts)
4434	3803609	3802911	[-3 L= 699]	rpsB / 30S ribosomal protein S2 (Vegetative protein 209)
4435	3804736	3803960	[-2 L= 777]	codY / Transcriptional regulator
4436	3806244	3804817	[-1 L=1428]	hslU / ATP-dependent hsl protease ATP-binding subunit
4437	3806770	3806231	[-2 L= 540]	hslV / ATP-dependent protease
4438	3807721	3806816	[-2 L= 906]	codV / Integrase/Recombinase homolog
4439	3809082	3807781	[-1 L=1302]	gidA / Glucose-inhibited division protein

4440	3811119	3809134	[-1 L=1986]	topA / DNA topoisomerase I (Relaxing enzyme)
4441	3812224	3811358	[-2 L= 867]	smfA / DNA processing protein
4442	3813215	3812316	[-3 L= 900]	sucD / Succinyl-CoA synthetase alpha chain (Vegetative protein 239)
4443	3814395	3813238	[-1 L=1158]	sucC / Succinyl-CoA synthetase beta chain (SCS-beta)
4444	3815363	3814593	[-3 L= 771]	mhB / Ribonuclease HII (RNase HII)
4445	3816364	3815423	[-2 L= 942]	ylqF / Hypothetical protein
4446	3816897	3816334	[-1 L= 564]	lepA / Signal peptidase I (Leader peptidase I)
4447	3817328	3816987	[-3 L= 342]	rplS / 50S ribosomal protein L19
4448	3818209	3817478	[-2 L= 732]	trmD / tRNA (Guanine-N(1)-)-methyltransferase (M1G-methyltransferase)
4449	3818790	3818212	[-1 L= 579]	rimM / 16S rRNA processing protein
4450	3819079	3818849	[-2 L= 231]	xxmJ / Hypothetical protein
4451	3819360	3819091	[-1 L= 270]	rpsP / 30S ribosomal protein S16
4452	3820811	3819465	[-3 L=1347]	ffhA / Signal recognition particle protein (Fifty-four homolog)
4453	3821156	3820827	[-3 L= 330]	ylxM / Hypothetical protein
4454	3822279	3821293	[-1 L= 987]	ftsY / Signal recognition particle (docking protein)
4455	3825864	3822298	[-1 L=3567]	smcA / Chromosome partition protein
4457	3826799	3826014	[-3 L= 786]	mcC / Ribonuclease III (RNase III)
4458	3827049	3826810	[-1 L= 240]	accP / Acyl carrier protein (ACP)
4460	3827850	3827113	[-1 L= 738]	fabG / 3-oxoacyl-[acyl-carrier protein] reductase (3-ketoacyl-acyl carrier protein reductase)
4461	3828794	3827853	[-3 L= 942]	fabD / Malonyl CoA-acyl carrier protein transacylase (MCT)
4462	3829801	3828812	[-2 L= 990]	plsX / Fatty acid/phospholipid synthesis protein
4463	3830550	3829801	[-1 L= 750]	ylpC / Hypothetical protein
4464	3832537	3830483	[-2 L=2055]	recG / ATP-dependent DNA helicase
4465	3834495	3832822	[-1 L=1674]	yloV / Hypothetical protein
4466	3834880	3834521	[-2 L= 360]	yloU / Hypothetical protein
4467	3835257	3835442	[+3 L= 186]	rpmB / 50S ribosomal protein L28
4468	3835620	3835522	[-1 L= 99]	spfM / Stage V sporulation protein M
4470	3836232	3835669	[-1 L= 564]	yloS / Hypothetical protein
4471	3837060	3836419	[-1 L= 642]	yloR / Ribulose-phosphate 3-epimerase (Pentose-5-phosphate 3-epimerase)
4472	3837944	3837066	[-3 L= 879]	yloQ / Hypothetical protein
4473	3840176	3838194	[-3 L=1983]	yloP / Serine/threonine kinase homolog
4474	3841003	3840176	[-2 L= 828]	yloO / Hypothetical protein
4475	3842018	3840933	[-3 L=1086]	yloN / Hypothetical protein
4477	3843357	3842026	[-1 L=1332]	yloM / RNA-binding SUN protein homolog
4479	3844298	3843357	[-3 L= 942]	fmtA / Methionyl-tRNA formyltransferase
4480	3844792	3844325	[-2 L= 468]	defA / Peptide deformylase 1 (Polypeptide deformylase 1)
4481	3847209	3844807	[-1 L=2403]	priA / Primosomal protein N' (Replication factor Y)
4482	3848411	3847209	[-3 L=1203]	yloI / DNA/pantothenate metabolism flavoprotein homolog
4483	3848796	3848587	[-1 L= 210]	yloH / DNA-directed RNA polymerase omega chain (RNA polymerase omega subunit)
4484	3849416	3848802	[-3 L= 615]	kguA / Guanylate kinase (GMP kinase)
4485	3849693	3849409	[-1 L= 285]	xxmK / Hypothetical protein
4486	3850651	3849764	[-2 L= 888]	xxmL / Hypothetical protein
4487	3852706	3850739	[-2 L=1968]	yloB / Calcium-transporting ATPase homolog
4488	3853541	3852666	[-3 L= 876]	yloB / Calcium-transporting ATPase homolog
4489	3853566	3855272	[+3 L=1707]	yloA / Fibronectin-binding protein homolog
4492	3856814	3857881	[+2 L=1068]	yghT / Xaa-Proline dipeptidase homolog
4494	3857965	3858486	[+1 L= 522]	xxmM / Hypothetical protein
4495	3858779	3858525	[-3 L= 255]	xxmN / Hypothetical protein
4497	3859335	3858820	[-1 L= 516]	xxmO / Hypothetical protein
4498	3859427	3860818	[+2 L=1392]	yhfA / Hypothetical protein
4500	3860989	3861240	[+1 L= 252]	xxmP / Hypothetical protein
4501	3861266	3861358	[+2 L= 93]	xxmQ / Hypothetical protein
4502	3861429	3861584	[+3 L= 156]	xxmR / Hypothetical protein
4503	3862275	3861628	[-1 L= 648]	pyrE / Orotate phosphoribosyltransferase (OPRTase)
4504	3862997	3862257	[-3 L= 741]	pyrF / Orotidine 5'-phosphate decarboxylase (OMP decarboxylase)
4505	3863884	3862958	[-2 L= 927]	pyrD / Dihydroorotate dehydrogenase, catalytic subunit (Dihydroorotate oxidase)
4506	3864660	3863884	[-1 L= 777]	pyrK / Dihydroorotate dehydrogenase electron transfer subunit
4507	3867875	3864660	[-3 L=3216]	carB / Carbamoyl-phosphate synthase, pyrimidine-specific, large chain (Carbamoyl-phosphate synthetase ammonia chain)
4508	3868981	3867863	[-2 L=1119]	carA / Carbamoyl-phosphate synthase, pyrimidine-specific, small chain (Carbamoyl-phosphate synthetase glutamine chain)
4509	3870240	3868957	[-1 L=1284]	pyrC / Dihydroorotase (DHOase)
4510	3871144	3870227	[-2 L= 918]	pyrB / Aspartate carbamoyltransferase (Aspartate transcarbamylase)

				(ATCase)
4511	3872633	3871290	[-3 L=1344]	pyrP / Uracil permease (uracil transporter)
4512	3873261	3872722	[-1 L= 540]	pyrR / PyrR bifunctional protein (Pyrimidine operon regulatory protein / Uracil phosphoribosyltransferase (UPRTase))
4513	3874373	3873468	[-3 L= 906]	ylyB / Hypothetical protein
4514	3874869	3874381	[-1 L= 489]	lspA / Lipoprotein signal peptidase (Prolipoprotein signal peptidase) (Signal peptidase II)
4515	3875290	3874964	[-2 L= 327]	xxmS / Hypothetical protein
4516	3878219	3875451	[-3 L=2769]	syiI / Isoleucyl-tRNA synthetase (Isoleucine--tRNA ligase)
4517	3879066	3878563	[-1 L= 504]	divI / Cell-division initiation protein (septum placement)
4518	3879923	3879159	[-3 L= 765]	ylmH / Cell-division protein homolog
4519	3880202	3879942	[-3 L= 261]	xxmT / Hypothetical protein
4521	3880679	3880212	[-3 L= 468]	ylmF / Hypothetical protein
4522	3881373	3880702	[-1 L= 672]	ylmE / Hypothetical protein
4523	3882230	3881373	[-3 L= 858]	ylmD / Hypothetical protein
4526	3882650	3882312	[-3 L= 339]	ylmC / Hypothetical protein
4527	3883533	3882757	[-1 L= 777]	rpsG / RNA polymerase sigma-G factor (Stage III sporulation protein G)
4528	3884482	3883694	[-2 L= 789]	sigE / RNA polymerase sigma-35 factor precursor
4529	3885396	3884434	[-1 L= 963]	murC / UDP-N-acetylmuramate--alanine ligase (UDP-N-acetylmuramoyl-L-alanine synthetase)
4530	3886760	3885609	[-3 L=1152]	ftsZ / Cell division protein, tubulin family
4531	3888107	3886803	[-3 L=1305]	ftsA / Cell division protein
4533	3889277	3888510	[-3 L= 768]	ftsQ / Division initiation protein (Cell division and sporulation protein)
4534	3890281	3889379	[-2 L= 903]	murB / UDP-N-acetylenolpyruvoylglucosamine reductase (UDP-N-acetylmuramate dehydrogenase)
4536	3891663	3890497	[-1 L=1167]	murG / UDP-N-acetylglucosamine--N-acetylmuramyl-(pentapeptide) pyrophosphoryl-undecaprenol N-acetylglucosamine transferase (Undecaprenyl-PP-MurNAc-pentapeptide-UDPGlcNAc GlcNAc transferase)
4537	3892792	3891695	[-2 L=1098]	speE / Stage V sporulation protein E
4538	3894226	3892877	[-2 L=1350]	murD / UDP-N-acetylmuramoylalanine--D-glutamate ligase (UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase)
4539	3895219	3894230	[-2 L= 990]	mraY / Phospho-N-acetylmuramoyl-pentapeptide-transferase (UDP-MurNAc-pentapeptide phosphotransferase)
4540	3896699	3895227	[-3 L=1473]	murE / uDP-N-acetylmuramoylalanyl-D-glutamate--2,6-diaminopimelate ligase (UDP-N-acetylmuramyl-tripeptide synthetase)
4541	3898801	3896888	[-2 L=1914]	speD / Stage V sporulation protein D (Sporulation specific penicillin-binding protein)
4542	3901033	3898886	[-2 L=2148]	pbpB / Penicillin-binding protein 2B (PBP-2B)
4543	3901417	3901058	[-2 L= 360]	ftsL / Cell division protein homolog
4544	3902365	3901436	[-2 L= 930]	mraW / S-adenosyl-methyltransferase
4545	3904421	3902739	[-3 L=1683]	yllA / Hypothetical protein
4546	3905322	3904435	[-1 L= 888]	ylbQ / 2-Dehydropantoate 2-reductase (Ketopantoate reductase) homolog
4547	3905613	3906083	[+3 L= 471]	ylbP / Hypothetical protein
4548	3906662	3906123	[-3 L= 540]	ylbO / Hypothetical protein
4549	3906852	3906760	[-1 L= 93]	rlmF/ 50S ribosomal protein L32 (Ribosomal protein I)
4550	3907493	3907026	[-3 L= 468]	ylbN / Hypothetical protein
4551	3907707	3908408	[+3 L= 702]	ylbM / Hypothetical protein
4552	3908421	3908885	[+3 L= 465]	ylbM / Hypothetical protein
4553	3909959	3908901	[-3 L=1059]	ylbL / Hypothetical protein
4554	3910728	3909931	[-1 L= 798]	ylbK / Hypothetical protein
4555	3910797	3912059	[+3 L=1263]	ylbJ / Hypothetical protein
4556	3912545	3912057	[-3 L= 489]	coaD / Phosphopantetheine adenylyltransferase (Pantetheine-phosphate adenylyltransferase)
4557	3913108	3912545	[-2 L= 564]	xxmU / RNA methylase homolog
4558	3913607	3913993	[+2 L= 387]	xxmV / Hypothetical protein
4559	3914191	3914054	[-2 L= 138]	ylbG / Hypothetical protein
4561	3914929	3914447	[-2 L= 483]	ylbF / Hypothetical protein
4562	3915583	3915014	[-2 L= 570]	yhfR / Phosphoglycerate mutase homolog
4563	3915908	3915663	[-3 L= 246]	ylbE / Hypothetical protein
4564	3916363	3915920	[-2 L= 444]	xxmW / Hypothetical protein
4565	3917660	3916545	[-3 L=1116]	ylbC / Hypothetical protein
4566	3917781	3918143	[+3 L= 363]	ylbA / Hypothetical protein
4567	3919191	3918196	[-1 L= 996]	aimE / Aliphatic amidase
4568	3920336	3919428	[-3 L= 909]	ctaG / Unknown function CtaG protein
4569	3920742	3920413	[-1 L= 330]	coxD / Cytochrome c oxidase polypeptide IVB (cytochrome AA3 subunit 4B)
4570	3921369	3920749	[-1 L= 621]	coxC / Cytochrome c oxidase polypeptide III (cytochrome AA3 subunit 3)

4571	3923231	3921372	[-3 L=1860]	coxA / Cytochrome c oxidase polypeptide I (Cytochrome AA3 subunit 1)
4572	3924329	3923268	[-3 L=1062]	coxB / Cytochrome c oxidase polypeptide II precursor (cytochrome AA3 subunit 2)
4573	3925334	3924411	[-3 L= 924]	coxX / Cytochrome AA3 oxidase assembly factor / Protoheme IX farnesyltransferase
4576	3925830	3926762	[+3 L= 933]	ctaA / Cytochrome AA3 controlling protein
4578	3930297	3926854	[-1 L=3444]	pycA / Pyruvate carboxylase
4579	3931807	3930632	[-2 L=1176]	ylaO / Cell-division protein homolog
4580	3932376	3931936	[-1 L= 441]	ylaN / Hypotheical protein
4581	3932376	3932870	[+3 L= 495]	ylaL / Hypothetical protein
4582	3934254	3932908	[-1 L=1347]	ylaK / Phosphate starvation inducible protein homolog
4583	3935013	3934483	[-1 L= 531]	xxmX / Hypothetical protein
4584	3935081	3935278	[+2 L= 198]	ylaI / Hypothetical protein
4585	3935612	3935340	[-3 L= 273]	xxmY / Hypothetical protein
4586	3935930	3935631	[-3 L= 300]	ylaH / Hypothetical protein
4587	3937940	3936093	[-3 L=1848]	typA / GTP-binding translation elongation factor homolog
4590	3939090	3938308	[-1 L= 783]	suhB / Inositol-1-monophosphatase (IMPase)
4591	3939367	3939182	[-2 L= 186]	xxmZ / Hypothetical protein
4592	3939574	3940197	[+1 L= 624]	yktB / Hypothetical protein
4593	3940563	3940285	[-1 L= 279]	xxnA / Hypothetical protein
4595	3940940	3942298	[+2 L=1359]	dclY / Lysine decarboxylase (LDC)
4596	3942219	3942389	[+3 L= 171]	dclY / Lysine decarboxylase (LDC)
4597	3942468	3943295	[+3 L= 828]	tglA / Transglutaminase
4602	3944363	3944022	[-3 L= 342]	xxnB / Hypothetical protein
4603	3944446	3944835	[+1 L= 390]	xxnC / Hypothetical protein
4604	3946712	3945303	[-3 L=1410]	dldA / Dihydrolipoamide dehydrogenase (E3 component of pyruvate complex)
4605	3948007	3946721	[-2 L=1287]	odpL / Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase complex (E2)
4606	3949078	3948104	[-2 L= 975]	odpB / Pyruvate dehydrogenase E1 component, beta subunit
4607	3950272	3949085	[-2 L=1188]	odpA / Pyruvate dehydrogenase E1 component, alpha subunit
4610	3951028	3951579	[+1 L= 552]	defB / Peptide deformylase 2 (Polypeptide deformylase 2)
4611	3952416	3951646	[-1 L= 771]	ykrA / Haloacid dehalogenase homolog
4612	3952964	3953173	[+2 L= 210]	ykzG / Hypothetical protein
4614	3953181	3954845	[+3 L=1665]	ykqC / Hypothetical protein
4615	3955557	3954895	[-1 L= 663]	ykqB / Hypothetical protein
4616	3956518	3955643	[-2 L= 876]	xxnD / Hypothetical protein
4617	3957883	3956756	[-2 L=1128]	ykuR / Hippurate hydrolase homolog
4618	3958669	3957950	[-2 L= 720]	ykuQ / 2,3,4,5-tetrahydropyridine-2,6-dicarboxylate n-succinyltransferase (Tetrahydrodipicolinate n-succinyltransferase)
4619	3959625	3958744	[-1 L= 882]	ykuM / Transcriptional regulator, LysR family
4620	3960248	3959808	[-3 L= 441]	ykuL / Hypothetical protein
4622	3961265	3960732	[-3 L= 534]	ykuK / Hypothetical protein
4624	3962111	3961716	[-3 L= 396]	ykuJ / Hypothetical protein
4625	3962183	3962416	[+2 L= 234]	xxnE / Hypothetical protein
4626	3962989	3962504	[-2 L= 486]	xxnF / Hypothetical protein
4628	3964389	3963175	[-1 L=1215]	ykuI / Hypothetical protein
4629	3965424	3964648	[-1 L= 777]	ykuF / 2,4-dienoyl-CoA reductase (NADPH)
4630	3965621	3966496	[+2 L= 876]	ykuE / Phosphodiesterase homolog
4631	3966411	3966830	[+3 L= 420]	xxnG / Hypothetical protein
4632	3969112	3966998	[-2 L=2115]	ppkA / Polyphosphate kinase (ATP-polyphosphate phosphotransferase)
4633	3970787	3969216	[-3 L=1572]	ppxA / Exopolyphosphatase (Metaphosphatase)
4634	3970929	3971384	[+3 L= 456]	ykyB / Hypothetical protein
4635	3972081	3971422	[-1 L= 660]	xxnH / Hypothetical protein
4638	3973349	3972699	[-3 L= 651]	xxnI / Hypothetical protein
4639	3973513	3973743	[+1 L= 231]	xxnJ / Hypothetical protein
4640	3974278	3973781	[-2 L= 498]	xxnK / Hypothetical protein
4641	3974690	3976228	[+2 L=1539]	xxnL / Multidrug-efflux transporter homolog
4642	3976321	3976875	[+1 L= 555]	xxnM / Hypothetical protein
4643	3977392	3979677	[+1 L=2286]	metE / 5-methyltetrahydropteroyltriglutamate–homocysteine methyltransferase (Methionine synthase, vitamin-B12 independent isozyme)
4645	3980108	3979722	[-3 L= 387]	comJ / DNA-entry nuclease inhibitor (Competence protein J)
4646	3980591	3980148	[-3 L= 444]	nucA / DNA-entry nuclease (Competence-specific nuclease)
4647	3980803	3981552	[+1 L= 750]	xxnN / Hypothetical protein
4648	3982868	3981597	[-3 L=1272]	kinB / Sporulation-specific ATP-dependent protein kinase
4651	3983502	3984662	[+3 L=1161]	patA / Aspartate aminotransferase homolog

4652	3985755	3984682	[-1 L=1074]	xxnO / Transcriptional regulator involved in crabon catabolite control
4653	3986813	3985974	[-3 L= 840]	malD / Maltose/maltodextrin transport system permease protein
4654	3988115	3986817	[-3 L=1299]	malC / Maltose/maltodextrin transport system permease protein
4656	3988421	3988254	[-3 L= 168]	malX / Maltose/maltodextrin-binding protein precursor
4657	3989509	3988433	[-2 L=1077]	malX / Maltose/maltodextrin-binding protein precursor
4658	3989779	3991536	[+1 L=1758]	nepU / Neopullulanase
4660	3993280	3991589	[-2 L=1692]	oguC / Oligo-1,6-glucosidase (Oligosaccharide alpha-1,6-glucosidase) (Sucrase-isomaltase)
4661	3993525	3994622	[+3 L=1098]	msmX / Multiple sugar-binding transport ATP-binding protein
4663	3995199	3994693	[-1 L= 507]	xxnP / Hypothetical protein
4664	3996032	3995580	[-3 L= 453]	xxnQ / Hypothetical protein
4665	3996164	3996592	[+2 L= 429]	xxnR / Hypothetical protein
4666	3997413	3996628	[-1 L= 786]	xxnS / Hypothetical protein
4667	3998152	3997427	[-2 L= 726]	xxnT / Hypothetical protein
4668	3998368	3999117	[+1 L= 750]	xxnU / ABC transporter homolog
4669	4000325	3999153	[-3 L=1173]	thlA / Acetyl-CoA acetyltransferase (Acetoacetyl-CoA thiolase)
4670	4000914	4000468	[-1 L= 447]	xxnV / MutT-like protein
4671	4001315	4001025	[-3 L= 291]	xxnW / Hypothetical protein
4672	4001350	4002105	[+1 L= 756]	xxnX / Hypothetical protein
4673	4003166	4002408	[-3 L= 759]	xxnY / Hypothetical protein
4674	4003947	4003186	[-1 L= 762]	xxnZ / Hypothetical protein
4675	4004280	4004026	[-1 L= 255]	xxoA / Hypothetical protein
4676	4004535	4005251	[+3 L= 717]	yxjF / Oxidoreductase homolog
4677	4005445	4005287	[-2 L= 159]	xxoB / Hypothetical protein
4678	4006574	4005516	[-3 L=1059]	ykrS / Putative translation initiation factor eIF-2B (eIF-2B gDP-GTP exchange factor)
4679	4007752	4006574	[-2 L=1179]	ykrT / 5-Methylthioribose kinase
4680	4009002	4008058	[-1 L= 945]	ykrU / Carbon-nitrogen hydrolase homolog
4681	4008924	4010108	[+3 L=1185]	ykrV / Aspartate aminotransferase homolog
4684	4010346	4011587	[+3 L=1242]	ykrW / Ribulose bisphosphate carboxylase homolog
4685	4011587	4012243	[+2 L= 657]	ykrX / Hypothetical protein
4686	4012243	4012878	[+1 L= 636]	ykrY / Class II aldolase homolog
4687	4012859	4013368	[+2 L= 510]	ykrZ / Possible methionine salvage enzyme
4688	4013658	4013930	[+3 L= 273]	xxoC / Hypothetical protein
4689	4014317	4013988	[-3 L= 330]	xxoD / Hypothetical protein
4690	4015201	4014326	[-2 L= 876]	ykwC / 3-Hydroxybutyrate dehydrogenase homolog
4692	4016399	4015209	[-3 L=1191]	pbpX / Penicillin-binding protein
4693	4017728	4016436	[-3 L=1293]	xxoE / Hypothetical protein
4694	4018053	4018667	[+3 L= 615]	yodC / Putative NAD(P)H nitroreductase 12C (Vegetative protein 12C) (VEG12C)
4698	4021492	4019783	[-2 L=1710]	pppT / Phosphoenolpyruvate-protein phosphotransferase (Phosphotransferase system, enzyme I)
4699	4021755	4021495	[-1 L= 261]	pthP / Phosphocarrier protein HPr of phosphotransferase system (Histidine-containing protein)
4700	4024011	4021894	[-1 L=2118]	ptgA / PTS system, glucose-specific IIABC component (Glucose-permease IIABC component) (Phosphotransferase enzyme II)
4701	4025142	4024297	[-1 L= 846]	glcT / Transcription antiterminator
4702	4025308	4026111	[+1 L= 804]	xxoF / Hydrolase homolog
4703	4026919	4026191	[-2 L= 729]	xxoG / Transcriptional regulator, GntR family
4704	4027637	4026852	[-3 L= 786]	nagB / Glucosamine-6-phosphate isomerase (Glucosamine-6-phosphate deaminase)
4705	4028790	4027645	[-1 L=1146]	nagA / N-acetylglucosamine-6-phosphate deacetylase (GlcNAc 6-P deacetylase)
4707	4029964	4028999	[-2 L= 966]	comE / Late competence protein
4709	4030549	4029980	[-2 L= 570]	ypuH / Hypothetical protein
4710	4031466	4030711	[-1 L= 756]	ypuG / Hypothetical protein
4712	4031816	4032331	[+2 L= 516]	ypuF / Hypothetical protein
4713	4032723	4032358	[-1 L= 366]	ribT / Reductase homolog
4714	4033621	4033187	[-2 L= 435]	ppiB / Peptidyl-prolyl cis-trans isomerase B (Rotamase B)
4716	4033809	4034672	[+3 L= 864]	ypuA / Hypothetical protein
4717	4035516	4034710	[-1 L= 807]	xxoH / Hypothetical protein
4718	4037089	4035611	[-2 L=1479]	spaF / Stage V sporulation protein AF
4719	4037636	4037070	[-3 L= 567]	spaE / Stage V sporulation protein AE
4721	4037992	4037645	[-2 L= 348]	spaE / Stage V sporulation protein AE
4722	4039012	4037999	[-2 L=1014]	spaD / Stage V sporulation protein AD
4723	4039483	4039028	[-2 L= 456]	spaC / Stage V sporulation protein AC

4724	4039920	4039501	[-1 L= 420]	spaB / Stage V sporulation protein AB
4725	4040527	4039910	[-2 L= 618]	spaA / Stage V sporulation protein AA
4727	4042267	4040744	[-2 L=1524]	xxoI / Sodium-dependent transporter
4729	4043161	4042406	[-2 L= 756]	rpsF / RNA polymerase sigma-F factor (stage II sporulation protein AC)
4730	4043614	4043177	[-2 L= 438]	spbB / Anti-sigma F factor (stage II sporulation protein AB)
4731	4043965	4043618	[-2 L= 348]	spbA / Anti-sigma F factor antagonist (stage II sporulation protein AA)
4732	4045325	4044138	[-3 L=1188]	dacF / Penicillin-binding protein precursor (D-alanyl-D-alanine carboxypeptidase)
4733	4045291	4045908	[+1 L= 618]	ytrA / Transcriptional regulator, GntR family
4734	4045862	4046755	[+2 L= 894]	xxoJ / ABC transporter ATP-binding protein
4735	4046709	4047812	[+3 L=1104]	xxoK / Hypothetical protein
4736	4047828	4048910	[+3 L=1083]	xxoL / Hypothetical protein
4737	4049478	4048936	[-1 L= 543]	xxoM / Hypothetical protein
4738	4050030	4049581	[-1 L= 450]	ypoP / Transcriptional regulator, MarR family
4740	4050157	4050825	[+1 L= 669]	xxoN / Hypothetical protein
4742	4050963	4052249	[+3 L=1287]	xxoO / Xanthine/uracil permease
4743	4053262	4052288	[-2 L= 975]	yfjQ / Divalent cation transport protein
4744	4054612	4053311	[-2 L=1302]	pynP / Pyrimidine-nucleoside phosphorylase
4745	4055213	4054623	[-3 L= 591]	punA / Purine nucleoside phosphorylase I (Inosine phosphorylase)
4746	4056639	4055458	[-1 L=1182]	deoB / Phosphopentomutase (Phosphodeoxyribomutase)
4747	4057740	4056997	[-1 L= 744]	xxoP / Hypothetical protein
4748	4058772	4057885	[-1 L= 888]	ripX / Integrase/recombinase
4749	4059051	4058782	[-1 L= 270]	xxoQ / Hypothetical protein
4750	4059568	4059116	[-2 L= 453]	furP / Ferric uptake regulation protein (Ferric uptake regulator)
4751	4060293	4059679	[-1 L= 615]	spbM / Stage II sporulation protein M
4753	4060449	4060997	[+3 L= 549]	xxoR / Acetyltransferase homolog
4754	4061564	4061028	[-3 L= 537]	adpP / ADP-ribose pyrophosphatase (Adenosine diphosphoribose pyrophosphatase)
4756	4061866	4062777	[+1 L= 912]	yqkF / Oxidoreductase homolog
4757	4063705	4062842	[-2 L= 864]	yvsB / Plant-metabolite dehydrogenase homolog
4758	4064318	4063797	[-3 L= 522]	ykqA / Hypothetical protein
4761	4064851	4066437	[+1 L=1587]	yhcR / 5'-Nucleotidase homolog
4762	4067071	4066568	[-2 L= 504]	xxoS / Hypothetical protein
4763	4067163	4068158	[+3 L= 996]	ybaC / Hypothetical protein
4764	4068293	4069609	[+2 L=1317]	yuiF / Hypothetical protein
4765	4070500	4069640	[-2 L= 861]	rbsR / Ribose operon transcriptional repressor
4766	4071082	4070603	[-2 L= 480]	yxbD / Acetyltransferase homolog
4767	4071164	4072087	[+2 L= 924]	yqkD / Hypothetical protein
4769	4072314	4072688	[+3 L= 375]	xxoT / Hypothetical protein
4772	4073175	4074440	[+3 L=1266]	ribD / Riboflavin biosynthesis protein (diaminohydroxyphosphoribosylaminopyrimidine deaminase / 5-amino-6-(5-phosphoribosylamino)uracil reductase)
4773	4074425	4075066	[+2 L= 642]	ribB / Riboflavin synthase alpha chain
4774	4075082	4076272	[+2 L=1191]	ribA / Riboflavin biosynthesis protein (GTP cyclohydrolase II / 3,4-dihydroxy-2-butanone 4-phosphate synthase)
4775	4076294	4076752	[+2 L= 459]	risB / 6,7-dimethyl-8-ribityllumazine synthase (DMRL synthase) (Lumazine synthase) (Riboflavin synthase beta chain)
4776	4077098	4076781	[-3 L= 318]	xxoU / Hypothetical protein
4777	4078279	4077284	[-2 L= 996]	bioB / Biotin synthase (Biotin synthetase)
4778	4079090	4078284	[-3 L= 807]	bioC / Biotin synthesis protein
4779	4079796	4079059	[-1 L= 738]	xxoV / Hypothetical protein
4780	4080980	4079796	[-3 L=1185]	bioF / 8-amino-7-oxononanoate synthase (8-amino-7-ketopelargonate synthase)
4781	4081674	4080949	[-1 L= 726]	bioD / Dethiobiotin synthetase (Dethiobiotin synthase)
4782	4083107	4081677	[-3 L=1431]	bioA / Adenosylmethionine-8-amino-7-oxononanoate aminotransferase (7,8-diamino-pelargonic acid aminotransferase)
4783	4083577	4083188	[-2 L= 390]	xxoW / Hypothetical protein
4784	4084181	4085551	[+2 L=1371]	nhaC / Na(+)/H(+) antiporter (Sodium/proton antiporter)
4786	4087576	4085606	[-2 L=1971]	yfkN / 2',3'-cyclic-nucleotide 2'-phosphodiesterase precursor
4787	4087961	4087569	[-3 L= 393]	yfkN / 2',3'-cyclic-nucleotide 2'-phosphodiesterase precursor
4788	4088327	4089103	[+2 L= 777]	xxoX / Hypothetical protein
4789	4089155	4089622	[+2 L= 468]	xxoY / Transcriptional regulator, MarR family
4792	4090483	4089926	[-2 L= 558]	xxoZ / Hypothetical protein
4793	4091572	4090625	[-2 L= 948]	otcA / Ornithine carbamoyltransferase, anabolic (OTCase)
4795	4092784	4091588	[-2 L=1197]	argD / Acetylornithine aminotransferase (ACOAT)
4796	4093536	4092745	[-1 L= 792]	argB / Acetylglutamate kinase (N-acetyl-L-glutamate 5-phosphotransferase)

4797	4094747	4093524	[-3 L=1224]	argJ / Arginine biosynthesis bifunctional protein (Glutamate N-acetyltransferase / Amino-acid acetyltransferase)
4798	4095009	4094758	[-1 L= 252]	argC / N-acetyl-gamma-glutamyl-phosphate reductase (N-acetyl-glutamate semialdehyde dehydrogenase)
4799	4095793	4094918	[-2 L= 876]	argC / N-acetyl-gamma-glutamyl-phosphate reductase (N-acetyl-glutamate semialdehyde dehydrogenase)
4801	4097040	4096339	[-1 L= 702]	yqjQ / Ketoacyl reductase homolog
4804	4098171	4097044	[-1 L=1128]	yqjP / Metallo-beta-lactamase homolog
4805	4098160	4098996	[+1 L= 837]	proI / Pyrroline-5-carboxylate reductase 2 (P5C reductase 2)
4806	4099942	4099049	[-2 L= 894]	sdhA / L-serine dehydratase, alpha chain (L-serine deaminase)
4807	4100605	4099946	[-2 L= 660]	sdhB / L-serine dehydratase, beta chain (L-serine deaminase)
4810	4102406	4101486	[-3 L= 921]	yqjK / Metallo-beta-lactamase homolog
4812	4102596	4102844	[+3 L= 249]	xxpA / Hypothetical protein
4814	4104068	4106791	[+2 L=2724]	mgtB / Mg(2+) transport ATPase, P-type 1
4815	4106852	4107565	[+2 L= 714]	mgtC / Mg(2+) transporter
4816	4108856	4107612	[-3 L=1245]	yqjH / DNA polymerase IV 1 (Pol IV 1)
4818	4110413	4109298	[-3 L=1116]	yqjE / Tripeptidase homolog
4819	4111113	4110544	[-1 L= 570]	yjcK / Ribosomal-protein alanine N-acetyltransferase
4821	4111680	4111444	[-1 L= 237]	xxpB / Hypothetical protein
4822	4112307	4111750	[-1 L= 558]	yqjB / Hypothetical protein
4823	4113349	4112327	[-2 L=1023]	yqjA / Hypothetical protein
4825	4114115	4113396	[-3 L= 720]	yqiZ / Amino-acid ABC transporter ATP-binding protein
4826	4114785	4114111	[-1 L= 675]	yqiY / Amino-acid ABC transporter permease protein
4827	4115583	4114807	[-1 L= 777]	yqiX / Amino-acid ABC transporter extracellular binding protein
4829	4116270	4115839	[-1 L= 432]	yqiW / Hypothetical protein
4830	4116889	4116383	[-2 L= 507]	yjdF / Hypothetical protein
4831	4117415	4116927	[-3 L= 489]	xxpC / MutT-like protein
4832	4118166	4117462	[-1 L= 705]	xxpD / Hypothetical protein
4833	4119509	4118274	[-3 L=1236]	speE / Stage V sporulation protein E
4834	4121111	4119795	[-3 L=1317]	odbC / Lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex (E2)
4835	4122110	4121130	[-3 L= 981]	odbB / 2-oxoisovalerate dehydrogenase beta subunit (Branched-chain alpha-keto acid dehydrogenase E1 component beta chain)
4836	4123125	4122127	[-1 L= 999]	odbA / 2-oxoisovalerate dehydrogenase alpha subunit (Branched-chain alpha-keto acid dehydrogenase E1 component alpha chain)
4837	4124574	4123156	[-1 L=1419]	dldB / Dihydrolipoamide dehydrogenase (E3 component of branched-chain alpha-keto acid dehydrogenase complex)
4839	4125709	4124582	[-2 L=1128]	bukA / Butyrate kinase (Branched-chain carboxylic acid kinase)
4840	4126870	4125773	[-2 L=1098]	dhlE / Leucine dehydrogenase (LeuDH)
4842	4127804	4126908	[-3 L= 897]	yqiS / Phosphate butyryltransferase (Phosphotransbutyrylase)
4843	4130114	4128003	[-3 L=2112]	yqiR / Sigma L-dependent transcriptional regulator
4844	4130210	4130440	[+2 L= 231]	xxpE / Hypothetical protein
4845	4131227	4130496	[-3 L= 732]	gdpD / Glycerophosphoryl diester phosphodiesterase
4846	4131272	4131415	[+2 L= 144]	yycC / Hypothetical protein
4847	4132223	4131663	[-3 L= 561]	xxpF / Hypothetical protein
4848	4133306	4132479	[-3 L= 828]	spzA / Stage 0 sporulation protein A
4849	4134859	4133564	[-2 L=1296]	spdB / Stage IV sporulation protein B
4850	4136444	4134981	[-3 L=1464]	recN / DNA repair protein (Recombination protein N)
4851	4136779	4136648	[-2 L= 132]	recN / DNA repair protein (Recombination protein N)
4852	4137460	4136984	[-2 L= 477]	argR / Arginine repressor
4853	4138412	4137576	[-3 L= 837]	yqxC / Hypothetical protein
4854	4140317	4138419	[-3 L=1899]	dxpS / 1-deoxy-D-xylulose 5-phosphate synthase (1-deoxyxylulose-5-phosphate synthase)
4855	4141500	4140613	[-1 L= 888]	ispA / Geranyltranstransferase (Farnesyl-diphosphate synthase)
4856	4141730	4141503	[-3 L= 228]	exgS / Exodeoxyribonuclease VII small subunit (Exonuclease VII small subunit)
4857	4143078	4141723	[-1 L=1356]	exgL / Probable exodeoxyribonuclease VII large subunit (Exonuclease VII large subunit)
4858	4143965	4143108	[-3 L= 858]	folD / FolD bifunctional protein (methylenetetrahydrofolate dehydrogenase / Methenyltetrahydrofolate cyclohydrolase)
4859	4144381	4143992	[-2 L= 390]	nusB / N utilization substance protein B homolog (NusB protein)
4860	4145120	4144731	[-3 L= 390]	xxpG / Hypothetical protein
4861	4146465	4145146	[-1 L=1320]	accA / Biotin carboxylase (A subunit of acetyl-CoA carboxylase)
4862	4146998	4146513	[-3 L= 486]	accB / Biotin carboxyl carrier protein of acetyl-CoA carboxylase (BCCP)
4863	4148418	4147777	[-1 L= 642]	spcH / Stage III sporulation protein AH
4864	4149096	4148437	[-1 L= 660]	spcG / Stage III sporulation protein AG

4865	4149727	4149089	[-2 L= 639]	spcF / Stage III sporulation protein AF
4866	4150903	4149734	[-2 L=1170]	spcE / Stage III sporulation protein AE
4867	4151249	4150917	[-3 L= 333]	spcD / Stage III sporulation protein AD
4868	4151524	4151324	[-2 L= 201]	spcC / Stage III sporulation protein AC
4869	4152045	4151542	[-1 L= 504]	spcB / Stage III sporulation protein AB
4870	4152979	4152032	[-2 L= 948]	spcA / Stage III sporulation protein AA
4871	4153288	4153010	[-2 L= 279]	yqhV / Hypothetical protein
4872	4153480	4154055	[+1 L= 576]	xxpH / Acetyltransferase homolog
4873	4154024	4154356	[+2 L= 333]	xxpI / Hypothetical protein
4875	4154953	4154399	[-2 L= 555]	efpA / Elongation factor P (EF-P)
4876	4156036	4154978	[-2 L=1059]	yqhT / Xaa-proline dipeptidase homolog
4877	4156517	4156044	[-3 L= 474]	aroQ / 3-dehydroquinate dehydratase (3-dehydroquinase)
4878	4157040	4156537	[-1 L= 504]	yqhR / Hypothetical protein
4879	4157177	4158184	[+2 L=1008]	yqhQ / Hypothetical protein
4880	4158258	4158665	[+3 L= 408]	xxpJ / Hypothetical protein
4881	4159372	4158668	[-2 L= 705]	yhcW / Phosphoglycolate phosphatase homolog
4882	4159873	4159385	[-2 L= 489]	mntR / Transcriptional regulator (Manganese transport regulator)
4883	4160980	4159958	[-2 L=1023]	splB / Spore photoproduct lyase
4884	4161138	4161452	[+3 L= 315]	xxpK / Hypothetical protein
4885	4161452	4162129	[+2 L= 678]	xxpL / Hypothetical protein
4887	4162334	4163173	[+2 L= 840]	xxpM / Hypothetical protein
4888	4164053	4163208	[-3 L= 846]	yqhM / Lipoate protein ligase
4889	4164212	4164592	[+2 L= 381]	yqhL / Hypothetical protein
4891	4165478	4166461	[+2 L= 984]	xxpN / Periplasmic binding protein homolog
4892	4166561	4167139	[+2 L= 579]	xxpO / Transcriptional regulator, TetR family
4893	4167214	4167543	[+1 L= 330]	ykkC / Chaperonin homolog
4895	4167548	4167859	[+2 L= 312]	ykkD / Chaperonin homolog
4899	4169212	4168589	[-2 L= 624]	xxpP / Hypothetical protein
4900	4169819	4169199	[-3 L= 621]	xxpQ / Hypothetical protein
4901	4170522	4169893	[-1 L= 630]	xxpR / Hypothetical protein
4902	4171241	4170540	[-3 L= 702]	xxpS / Hypothetical protein
4903	4172055	4171186	[-1 L= 870]	xxpT / ABC transporter ATP-binding protein
4904	4172433	4172062	[-1 L= 372]	xxpU / Transcriptional regulator, GntR family
4906	4173038	4172817	[-3 L= 222]	xxpV / Hypothetical protein
4907	4174936	4173335	[-2 L=1602]	gcsB / Glycine dehydrogenase [decarboxylating] subunit 2 (Glycine cleavage system P-protein)
4908	4176276	4174936	[-1 L=1341]	gcsA / Glycine dehydrogenase [decarboxylating] subunit 1 (Glycine cleavage system P-protein)
4909	4177397	4176300	[-3 L=1098]	gcsT / Aminomethyltransferase (Glycine cleavage system T protein)
4910	4177788	4179467	[+3 L=1680]	yqhH / Helicase homolog
4911	4179424	4180251	[+1 L= 828]	yqhG / Hypothetical protein
4913	4180755	4180522	[-1 L= 234]	xxpW / Hypothetical protein
4915	4181054	4181707	[+2 L= 654]	xxpX / Hypothetical protein
4916	4181976	4181779	[-1 L= 198]	xxpY / Hypothetical protein
4917	4182527	4182018	[-3 L= 510]	shiK / Shikimate kinase
4918	4183374	4182631	[-1 L= 744]	pdhA / Prolyl 4-hydroxylase alpha-1 subunit precursor (4-PH alpha-1)
4920	4184291	4183824	[-3 L= 468]	cmgF / ComG operon protein 6 (late competence protein)
4921	4184587	4184264	[-2 L= 324]	xxpZ / Hypothetical protein
4922	4185011	4184559	[-3 L= 453]	cmgD / ComG operon protein 4 precursor (DNA transport machinery protein)
4923	4185307	4185011	[-2 L= 297]	cmgC / ComG operon protein 3 precursor
4924	4186356	4185322	[-1 L=1035]	cmgB / ComG operon protein 2 (DNA transport machinery protein)
4925	4187458	4186346	[-2 L=1113]	cmgA / ComG operon protein 1 (late competence protein)
4926	4187511	4188284	[+3 L= 774]	xxqA / Hypothetical protein
4927	4188413	4188652	[+2 L= 240]	yqgY / Hypothetical protein
4928	4188742	4190154	[+1 L=1413]	yhcL / Sodium-glutamate symporter homolog
4929	4190646	4190239	[-1 L= 408]	xxqB / Hypothetical protein
4930	4190958	4190719	[-1 L= 240]	xxqC / Hypothetical protein
4931	4191184	4191492	[+1 L= 309]	xxqD / Hypothetical protein
4932	4192063	4191533	[-2 L= 531]	xxqE / Hypothetical protein
4933	4192472	4192101	[-3 L= 372]	xxqF / Hypothetical protein
4934	4192828	4192571	[-2 L= 258]	xxqG / Hypothetical protein
4935	4194081	4193026	[-1 L=1056]	murG / UDP-N-acetylglucosamine--N-acetylmuramyl-(pentapeptide) pyrophosphoryl-undecaprenol N-acetylglucosamine transferase (Undecaprenyl-PP-MurNAc-pentapeptide-UDPGlcNAc GlcNAc transferase)
4936	4197501	4194103	[-1 L=3399]	metH / 5-methyltetrahydrofolate--homocysteine methyltransferase (Methionine synthase, vitamin-B12 dependent isozyme)

4937	4199330	4197501	[-3 L=1830]	yitJ / 5-methyltetrahydrofolate--homocysteine methyltransferase (Methionine synthase, vitamin-B12 dependent isozyme)
4938	4199919	4201028	[+3 L=1110]	metB / Cystathionine gamma-synthase (O-succinylhomoserine (Thiol)-lyase)
4939	4201028	4202188	[+2 L=1161]	metC / Cystathionine beta-lyase (Beta-cystathionase) (Cysteine lyase)
4940	4202350	4202868	[+1 L= 519]	xxqH / Isochorismatase homolog
4941	4203293	4203592	[+2 L= 300]	xxqI / Transcriptional regulator, ArsR family
4942	4204850	4203741	[-3 L=1110]	xxqJ / Hypothetical protein
4944	4205579	4204863	[-3 L= 717]	yqgX / Metallo-beta-lactamase homolog
4946	4206897	4205917	[-1 L= 981]	glcK / Glucokinase (Glucose kinase)
4947	4207138	4206920	[-2 L= 219]	xxqK / Hypothetical protein
4948	4207859	4207224	[-3 L= 636]	yqgN / 5-Formyltetrahydrofolate cyclo-ligase homolog
4949	4208054	4207908	[-3 L= 147]	rpmF / 50S ribosomal protein L33 type 1
4950	4210478	4208127	[-3 L=2352]	mpgA / Mannose-1-phosphate guanyltransferase (ATP-mannose-1-phosphate guanylyltransferase)
4951	4211475	4210822	[-1 L= 654]	xxqL / Transcriptional regulator involved in phosphate transport system
4952	4212639	4211770	[-1 L= 870]	xxqM / Phosphate ABC transporter ATP-binding protein
4953	4213477	4212614	[-2 L= 864]	xxqN / Hypothetical protein
4954	4214429	4213482	[-3 L= 948]	xxqO / Hypothetical protein
4955	4215374	4214460	[-3 L= 915]	xxqP / Phosphate ABC transporter, periplasmic phosphate-binding protein
4956	4217851	4215710	[-2 L=2142]	xxqQ / Transpeptidase homolog
4957	4219226	4217946	[-3 L=1281]	yqgE / Hypothetical protein
4958	4219993	4219340	[-2 L= 654]	sodM / Superoxide dismutase [Mn]
4960	4220454	4221242	[+3 L= 789]	yqgB / Hypothetical protein
4961	4221311	4221682	[+2 L= 372]	yqfZ / Hypothetical protein
4962	4221841	4222950	[+1 L=1110]	ispG / 1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate synthase
4965	4223494	4223036	[-2 L= 459]	yqfV / Zinc-specific metalloregulatory protein
4966	4224293	4223463	[-3 L= 831]	xxqR / Zinc transport protein, ABC transporter permease protein
4967	4225063	4224296	[-2 L= 768]	xxqS / ABC transporter ATP-binding protein
4968	4226122	4225247	[-2 L= 876]	yqfU / Hypothetical protein
4969	4226253	4226522	[+3 L= 270]	yqfT / Hypothetical protein
4970	4227441	4226548	[-1 L= 894]	endD / Endonuclease IV (Endodeoxyribonuclease IV)
4971	4228920	4227613	[-1 L=1308]	yqfR / ATP-dependent RNA helicase homolog
4973	4229063	4229833	[+2 L= 771]	xxqT / Hypothetical protein
4974	4229926	4230321	[+1 L= 396]	ispH / Penicillin tolerance protein homolog
4975	4230439	4230873	[+1 L= 435]	ispH / Penicillin tolerance protein homolog
4977	4232038	4230920	[-2 L=1119]	yqfO / Hypothetical protein
4978	4232742	4232038	[-1 L= 705]	yqfN / Hypothetical protein
4979	4233264	4232911	[-1 L= 354]	cccA / Cytochrome c-550
4981	4234778	4233654	[-3 L=1125]	rpsA / RNA polymerase sigma factor (Sigma-A) (Sigma-43)
4982	4236634	4234841	[-2 L=1794]	priM / DNA primase
4985	4238307	4237498	[-1 L= 810]	yqfL / Hypothetical protein
4986	4238972	4238340	[-3 L= 633]	yqzB / Hypothetical protein
4987	4239850	4239080	[-2 L= 771]	recO / DNA repair protein (Recombination protein O)
4989	4241082	4240180	[-1 L= 903]	yqfH / GTP-binding protein era homolog (Bex protein)
4990	4241473	4241078	[-2 L= 396]	cddA / Cytidine deaminase (Cytidine aminohydrolase)
4991	4241927	4241577	[-3 L= 351]	kdgL / Diacylglycerol kinase (Diglyceride kinase)
4992	4242394	4241927	[-2 L= 468]	yqfG / Hypothetical protein
4993	4244535	4242394	[-1 L=2142]	yqfF / Hypothetical protein
4994	4245689	4244733	[-3 L= 957]	phoL / Phosphate starvation-induced protein homolog
4995	4246892	4245696	[-3 L=1197]	yqfD / Hypothetical protein
4996	4247347	4247057	[-2 L= 291]	xxqU / Hypothetical protein
4997	4247773	4248396	[+1 L= 624]	xxqV / Hypothetical protein
4998	4248978	4248538	[-1 L= 441]	yqeY / Hypothetical protein
4999	4249128	4248997	[-1 L= 132]	rpsU / 30S ribosomal protein S21
5001	4250844	4249495	[-1 L=1350]	yqeV / Hypothetical protein
5002	4251601	4250867	[-2 L= 735]	yqeU / Hypothetical protein
5003	4252684	4251749	[-2 L= 936]	yqeT / Ribosomal protein L11 methyltransferase
5004	4253873	4252716	[-3 L=1158]	dnaJ / Chaperone protein
5005	4255868	4254036	[-3 L=1833]	dnaK / Chaperone protein (Heat shock 70 kDa protein)
5006	4256470	4255898	[-2 L= 573]	grpE / Heat shock GrpE protein (HSP-70 cofactor)
5007	4257592	4256579	[-2 L=1014]	hrcA / Heat-inducible transcription repressor
5008	4258865	4257729	[-3 L=1137]	hemN / Oxygen-independent coproporphyrinogen III oxidase (Coproporphyrinogenase)
5009	4259333	4258920	[-3 L= 414]	yckH / Hypothetical protein
5010	4261245	4259425	[-1 L=1821]	lepA / GTP-binding protein
5011	4261821	4261459	[-1 L= 363]	xxqW / Hypothetical protein

5012	4262966	4261821	[-3 L=1146]	gprA / SASP degradation spore protease
5013	4263036	4263356	[+3 L= 321]	rpsT / 30S ribosomal protein S20
5014	4264453	4263446	[-2 L=1008]	yqeN / Hypothetical protein
5018	4267287	4264969	[-1 L=2319]	cmeC / ComE operon protein 3 (late competence protein)
5019	4267867	4267313	[-2 L= 555]	cmeB / ComE operon protein 2 (late competence protein required for DNA binding and uptake)
5020	4268521	4267925	[-2 L= 597]	cmeA / ComE operon protein 1 (late competence protein required for DNA binding and uptake)
5021	4268560	4269423	[+1 L= 864]	cmeD / ComE operon protein 4 (non-essential gene for competence, pyrroline-5-carboxylate reductase homolog)
5022	4270347	4269601	[-1 L= 747]	yqeM / Hypothetical protein
5023	4270700	4270347	[-3 L= 354]	yqeL / Hypothetical protein
5024	4271275	4270700	[-2 L= 576]	yqeK / Hypothetical protein
5025	4271825	4271259	[-3 L= 567]	nadD / Nicotinate-nucleotide adenylyltransferase (Deamido-NAD(+) diphosphorylase) (Nicotinate mononucleotide adenylyltransferase)
5026	4272226	4271966	[-2 L= 261]	yqeI / Dihydropicolinate reductase homolog
5027	4273096	4272266	[-2 L= 831]	aroE / Shikimate 5-dehydrogenase
5028	4274217	4273144	[-1 L=1074]	yqeH / Hypothetical protein
5029	4274733	4274224	[-1 L= 510]	yqeG / Haloacid dehlaogenase homolog
5031	4276109	4275324	[-3 L= 786]	dpsD / Phosphatidylserine decarboxylase proenzyme
5033	4277214	4276402	[-1 L= 813]	rpsK / RNA polymerase sigma-K factor
5034	4277265	4278182	[+3 L= 918]	xxqX / Hypothetical protein
5035	4279773	4278232	[-1 L=1542]	xxqY / Hypothetical protein
5036	4279961	4279815	[-3 L= 147]	rpmG / 50S ribosomal protein L33 type 1
5037	4280784	4280161	[-1 L= 624]	ydfN / Nitroreductase homolog
5039	4281134	4281781	[+2 L= 648]	xxqZ / Hypothetical protein
5040	4282371	4281865	[-1 L= 507]	xxrA / Hypothetical protein
5041	4283769	4282387	[-1 L=1383]	ppbC / Alkaline phosphatase III precursor (APASE III)
5042	4284030	4284860	[+3 L= 831]	xxrB / Acetyltransferase homolog
5043	4284879	4285760	[+3 L= 882]	xxrC / Hydrolase homolog
5044	4286305	4285808	[-2 L= 498]	xxrD / Hypothetical protein
5045	4287106	4286573	[-2 L= 534]	xxrE / Hypothetical protein
5046	4287727	4287128	[-2 L= 600]	xxrF / Phosphoglycerate mutase homolog
5047	4288036	4288338	[+1 L= 303]	xxrG / Hypothetical protein
5049	4289811	4288576	[-1 L=1236]	xxrH / Hypothetical protein
5050	4290012	4292789	[+3 L=2778]	subV / Minor extracellular serine protease vpr precursor
5052	4293683	4295434	[+2 L=1752]	xxrI / Hypothetical protein
5053	4295418	4295729	[+3 L= 312]	pacD / Pterin-4-alpha-carbinolamine dehydratase (4-alpha-hydroxy-tetrahydropterin dehydratase)
5054	4296604	4295750	[-2 L= 855]	xxrJ / Hypothetical protein
5055	4297031	4296630	[-3 L= 402]	xxrK / Hypothetical protein
5056	4297020	4297730	[+3 L= 711]	xxrL / Transcriptional regulator
5057	4298146	4297772	[-2 L= 375]	xxrM / Hypothetical protein
5058	4298756	4298271	[-3 L= 486]	xxrN / Acetyltransferase homolog
5059	4299336	4298800	[-1 L= 537]	xxrO / Acetyltransferase homolog
5060	4300160	4299768	[-3 L= 393]	xxrP / Hypothetical protein
5061	4300945	4300130	[-2 L= 816]	fhuC / Ferrichrome transport ATP-binding protein
5062	4301969	4300935	[-3 L=1035]	fhuG / Ferrichrome ABC transporter permease protein
5063	4302913	4301969	[-2 L= 945]	fhuD / Ferrichrome ABC transporter protein
5064	4303385	4303074	[-3 L= 312]	xxrQ / Hypothetical protein
5065	4306028	4303428	[-3 L=2601]	xxrR / Iron-containing alcohol dehydrogenase homolog
5067	4307426	4306296	[-3 L=1131]	yrhB / Cystathionine beta-lyase (Cysteine lyase) homolog
5068	4308377	4307433	[-3 L= 945]	cysM / Cysteine synthase (O-acetylserine sulfhydrylase)
5069	4309131	4308439	[-1 L= 693]	mtnA / MTA/SAH nucleosidase (5'-methylthioadenosine nucleosidase / S-adenosylhomocysteine nucleosidase)
5071	4309848	4309222	[-1 L= 627]	yrrT / Hypothetical protein
5072	4309922	4310134	[+2 L= 213]	yrzA / Hypothetical protein
5073	4310900	4310175	[-3 L= 726]	yrrS / Hypothetical protein
5074	4312714	4310954	[-2 L=1761]	yrrR / Penicillin-binding protein homolog
5075	4313530	4312796	[-2 L= 735]	yxiP / Hypothetical protein
5076	4314300	4313776	[-1 L= 525]	greA / Transcription elongation factor (Transcript cleavage factor) (General stress protein 20M)
5077	4315166	4314531	[-3 L= 636]	urkA / Uridine kinase (Uridine monophosphokinase) (Cytidine monophosphokinase)
5078	4316464	4315187	[-2 L=1278]	yrrO / Protease homolog
5079	4317412	4316486	[-2 L= 927]	yrrN / Protease homolog

5081	4318061	4317423	[-3 L= 639]	camT / Caffeoyl-CoA O-methyltransferase (Trans-caffeoyl-CoA 3-O-methyltransferase)
5082	4319336	4318218	[-3 L=1119]	yrrL / Folate metabolism protein homolog
5083	4319847	4319563	[-1 L= 285]	yrzB / Hypothetical protein
5084	4320264	4319854	[-1 L= 411]	yrrK / Hypothetical protein
5085	4320645	4320271	[-1 L= 375]	xxrS / Hypothetical protein
5087	4323253	4320614	[-2 L=2640]	syiA / Alanyl-tRNA synthetase (Alanine--tRNA ligase)
5088	4323755	4324096	[+2 L= 342]	xxrT / Hypothetical protein
5089	4325229	4324147	[-1 L=1083]	yrrI / Hypothetical protein
5090	4325388	4325597	[+3 L= 210]	xxrU / Hypothetical protein
5092	4325981	4325796	[-3 L= 186]	xxrV / Hypothetical protein
5093	4328523	4326112	[-1 L=2412]	yrrC / Conjugation transfer protein homolog
5094	4329209	4328544	[-3 L= 666]	yrrB / Hypothetical protein
5095	4330440	4329313	[-1 L=1128]	trmU / tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase
5097	4331588	4330530	[-3 L=1059]	yrvO / Cysteine desulfurase (NifS homolog)
5098	4332040	4331627	[-2 L= 414]	xxrW / Hypothetical protein
5099	4332190	4333617	[+1 L=1428]	yrvN / Hypothetical protein
5100	4333553	4334296	[+2 L= 744]	rsfA / Prespore specific transcriptional activator rsfA
5101	4335641	4334877	[-3 L= 765]	xxrX / Hypothetical protein
5102	4337914	4336142	[-2 L=1773]	syiD / Aspartyl-tRNA synthetase (Aspartate--tRNA ligase)
5103	4339198	4337930	[-2 L=1269]	syiH / Histidyl-tRNA synthetase (Histidine--tRNA ligase)
5105	4339750	4339556	[-2 L= 195]	xxrY / Hypothetical protein
5106	4340335	4339898	[-2 L= 438]	dtdA / D-tyrosyl-tRNA(Tyr) deacylase
5107	4342535	4340355	[-3 L=2181]	relA / GTP pyrophosphokinase (ATP:GTP 3'-pyrophosphotransferase) (PPGPP synthetase I)
5108	4343258	4342749	[-3 L= 510]	aprT / Adenine phosphoribosyltransferase
5109	4345696	4343309	[-2 L=2388]	ykrvE / Single-strand DNA-specific exonuclease
5110	4346640	4345750	[-1 L= 891]	xxrZ / Zinc/cadmium cation efflux system protein
5111	4349112	4346800	[-1 L=2313]	secD / Preprotein translocase
5112	4349615	4349334	[-3 L= 282]	xxsA / Hypothetical protein
5113	4349802	4351358	[+3 L=1557]	spoB / Stage V sporulation protein B
5114	4352089	4351445	[-2 L= 645]	yrbG / Hypothetical protein
5116	4352193	4352573	[+3 L= 381]	xxsB / Hypothetical protein
5117	4352873	4352616	[-3 L= 258]	yrbF / Hypothetical protein
5118	4354040	4352904	[-3 L=1137]	tgtA / Queuine tRNA-ribosyltransferase (tRNA-guanine transglycosylase) (Guanine insertion enzyme)
5119	4355117	4354056	[-3 L=1062]	queA / S-adenosylmethionine:tRNA ribosyltransferase-isomerase (Queuosine biosynthesis protein)
5120	4355325	4355128	[-1 L= 198]	xxsC / Hypothetical protein
5121	4356182	4355325	[-3 L= 858]	ruvB / Holliday junction DNA helicase
5122	4356946	4356332	[-2 L= 615]	ruvA / Holliday junction DNA helicase
5123	4357135	4358076	[+1 L= 942]	xxsD / Hypothetical protein
5125	4358623	4358096	[-2 L= 528]	bofC / Forespore sigma-K checkpoint regulator protein
5128	4359048	4359488	[+3 L= 441]	xxsE / Hypothetical protein
5129	4360169	4359528	[-3 L= 642]	xxsF / Hypothetical protein
5131	4362090	4360351	[-1 L=1740]	yrbA / Spore coat protein homolog
5132	4363446	4362319	[-1 L=1128]	nadA / Quinolinate synthetase A
5133	4364312	4363455	[-3 L= 858]	nadC / Nicotinate-nucleotide pyrophosphorylase [carboxylating] (Quinolinate phosphoribosyltransferase [decarboxylating])
5134	4365834	4364308	[-1 L=1527]	nadB / L-aspartate oxidase (Quinolinate synthetase B)
5135	4365987	4367126	[+3 L=1140]	iscS / Cysteine desulfurase (NifS protein homolog)
5136	4367129	4367668	[+2 L= 540]	xxsG / Transcriptional regulator
5137	4367751	4368395	[+3 L= 645]	xxsH / Hypothetical protein
5138	4369410	4368562	[-1 L= 849]	pheA / Prephenate dehydratase (PDT)
5139	4370547	4369510	[-1 L=1038]	xxsI / ABC transporter permease homolog
5140	4371423	4370563	[-1 L= 861]	xxsI / ABC transporter permease homolog
5142	4373395	4371476	[-2 L=1920]	xxsJ / ABC transporter permease homolog
5143	4374146	4373373	[-3 L= 774]	yvcR / ABC transporter ATP-binding protein
5144	4375364	4374243	[-3 L=1122]	yxdK / Two-component sensor histidine kinase
5145	4376058	4375315	[-1 L= 744]	yxdJ / Two-component response regulator
5146	4377445	4376162	[-2 L=1284]	obgA / Spo0B-associated GTP-binding protein
5147	4377993	4377448	[-1 L= 546]	spaB / Sporulation initiation phosphotransferase B (Stage 0 sporulation protein B)
5148	4378347	4378060	[-1 L= 288]	rpmA / 50S ribosomal protein L27
5149	4378695	4378354	[-1 L= 342]	ysxB / Hypothetical protein
5150	4379015	4378710	[-3 L= 306]	rplU / 50S ribosomal protein L21

5151	4380573	4379188	[-1 L=1386]	rnuG / Ribonuclease G (RNase G) (Cytoplasmic axial filament protein)
5152	4381501	4380644	[-2 L= 858]	spdG / Stage IV sporulation protein FB
5153	4382240	4381497	[-3 L= 744]	spdF / Stage IV sporulation protein FA
5154	4383171	4382377	[-1 L= 795]	minD / Septum site-determining protein (Cell division inhibitor)
5155	4383860	4383177	[-3 L= 684]	minC / Septum site-determining protein
5156	4384441	4383899	[-2 L= 543]	mreD / Rod shape-determining protein
5157	4385313	4384459	[-1 L= 855]	mreC / Rod shape-determining protein
5159	4386368	4385352	[-3 L=1017]	mreB / Rod shape-determining protein mreB
5160	4386711	4386529	[-1 L= 183]	radC / DNA repair protein homolog
5169	4398131	4396632	[-3 L=1500]	xxsK / Hypothetical protein
5171	4399594	4398212	[-2 L=1383]	xxsL / Hypothetical protein
5172	4401368	4399737	[-3 L=1632]	xxsM / Hypothetical protein
5173	4402636	4401395	[-2 L=1242]	xxsN / Hypothetical protein
5176	4404219	4402816	[-1 L=1404]	xxsO / Type I restriction enzyme
5177	4404808	4404245	[-2 L= 564]	xxsP / Hypothetical protein
5179	4405914	4405366	[-1 L= 549]	radC / DNA repair protein homolog
5180	4406557	4405964	[-2 L= 594]	mafA / Septum formation protein
5182	4407734	4406772	[-3 L= 963]	spbB / Stage II sporulation protein B
5183	4409213	4407888	[-3 L=1326]	folC / Folylpolyglutamate synthase (Folylpoly-gamma-glutamate synthetase)
5184	4411925	4409283	[-3 L=2643]	syiV / Valyl-tRNA synthetase (Valine-tRNA ligase)
5186	4413470	4412448	[-3 L=1023]	ysxE / Hypothetical protein
5187	4414547	4413540	[-3 L=1008]	spgD / Stage VI sporulation protein D
5188	4415916	4414630	[-1 L=1287]	hemL / Glutamate-1-semialdehyde 2,1-aminomutase (Glutamate-1-semialdehyde aminotransferase)
5189	4416905	4415919	[-3 L= 987]	hemB / Delta-aminolevulinic acid dehydratase (Porphobilinogen synthase)
5190	4417678	4416929	[-2 L= 750]	hemD / Uroporphyrinogen-III synthase (Uroporphyrinogen-III cosynthetase)
5191	4418610	4417684	[-1 L= 927]	hemC / Porphobilinogen deaminase (Pre-uroporphyrinogen synthase)
5192	4419504	4418629	[-1 L= 876]	hemX / HemX protein
5194	4420811	4419480	[-3 L=1332]	hemA / Glutamyl-tRNA reductase (GluTR)
5195	4421199	4421678	[+3 L= 480]	ohrR / Organic hydroperoxide resistance transcriptional regulator
5197	4421684	4422097	[+2 L= 414]	ohrA / Organic hydroperoxide resistance protein
5198	4422730	4422137	[-2 L= 594]	engB / GTP-binding protein
5200	4425090	4422730	[-1 L=2361]	lonA / ATP-dependent protease La 1
5201	4426910	4425243	[-3 L=1668]	lonB / ATP-dependent protease La homolog
5202	4428351	4427020	[-1 L=1332]	clpX / ATP-dependent Clp protease ATP-binding subunit (class III heat shock protein)
5204	4429818	4428544	[-1 L=1275]	tigA / Trigger factor (TF) (Vegetative protein 2)
5205	4431126	4430131	[-1 L= 996]	xxsQ / Hypothetical protein
5210	4432092	4432703	[+3 L= 612]	yvbH / Hypothetical protein
5212	4434506	4434033	[-3 L= 474]	xxsR / Hypothetical protein
5214	4436626	4435211	[-2 L=1416]	xxsS / Hypothetical protein
5218	4439119	4438616	[-2 L= 504]	ysnB / Phosphoesterase homolog
5219	4439747	4439133	[-3 L= 615]	hamA / HAM1 protein homolog
5220	4440487	4439753	[-2 L= 735]	rnpH / Ribonuclease PH (RNase PH) (tRNA nucleotidyltransferase)
5221	4441668	4440622	[-1 L=1047]	gerM / Cortex hydrolysis and sporulation (stage II, multiple polar septa) protein
5222	4442674	4441853	[-2 L= 822]	murI / Glutamate racemase
5223	4444207	4442876	[-2 L=1332]	xxsT / Tetracycline efflux-like protein
5224	4444741	4445424	[+1 L= 684]	xxsU / Hypothetical protein
5225	4446114	4445479	[-1 L= 636]	xxsV / Transcriptional regulator, TetR family
5226	4447097	4446438	[-3 L= 660]	xxsW / Hypothetical protein
5227	4447428	4447207	[-1 L= 222]	gerE / Germination protein, transcriptional regulator
5229	4448889	4447597	[-1 L=1293]	ywdJ / Purine permease
5230	4450228	4448990	[-2 L=1239]	xxsX / Deaminase homolog
5231	4450413	4450595	[+3 L= 183]	yvlC / Hypothetical protein
5232	4451244	4450663	[-1 L= 582]	xxsY / Hypothetical protein
5233	4451276	4451737	[+2 L= 462]	yjlA / Hypothetical protein
5235	4451712	4452296	[+3 L= 585]	yjlA / Hypothetical protein
5238	4452443	4453105	[+2 L= 663]	aqpZ / Aquaporin Z (Aquaporin X)
5239	4453624	4453172	[-2 L= 453]	xxsZ / Hypothetical protein
5240	4454945	4453722	[-3 L=1224]	yhaP / Hypothetical protein
5241	4455874	4454951	[-2 L= 924]	xxtA / ABC transporter ATP-binding protein
5242	4456175	4456999	[+2 L= 825]	xxtB / Hypothetical protein
5243	4457817	4457032	[-1 L= 786]	motB / Chemotaxis protein (Motility protein B)
5244	4458607	4457810	[-2 L= 798]	motA / Chemotaxis protein (Motility protein A)
5245	4458868	4459644	[+1 L= 777]	vanY / D-Alanyl-D-Alanine carboxypeptidase (DD-peptidase)

5246	4460130	4459687	[-1 L= 444]	ysmA / Hypothetical protein
5247	4461008	4460226	[-3 L= 783]	dhsB / Succinate dehydrogenase iron-sulfur protein
5248	4462770	4460980	[-1 L=1791]	dhsA / Succinate dehydrogenase flavoprotein subunit
5249	4463410	4462787	[-2 L= 624]	dhsC / Succinate dehydrogenase cytochrome B-558 subunit
5250	4463711	4464157	[+2 L= 447]	yslB / Hypothetical protein
5251	4466060	4464279	[-3 L=1782]	uvrC / Excinuclease ABC subunit C
5252	4466524	4466213	[-2 L= 312]	thiO / Thioredoxin (TRX)
5253	4467005	4466739	[-3 L= 267]	etfA / Electron transfer flavoprotein alpha-subunit (Electron transfer flavoprotein large subunit)
5254	4467732	4466980	[-1 L= 753]	etfA / Electron transfer flavoprotein alpha-subunit (Electron transfer flavoprotein large subunit)
5255	4468524	4467754	[-1 L= 771]	etfB / Electron transfer flavoprotein beta-subunit (Electron transfer flavoprotein small subunit)
5256	4469409	4468606	[-1 L= 804]	ysiB / Enoyl-CoA hydratase homolog
5257	4470023	4469394	[-3 L= 630]	ysiA / Transcriptional regulator, TetR family
5258	4471602	4470088	[-1 L=1515]	lcfA / Long-chain-fatty-acid--CoA ligase (Long-chain acyl-CoA synthetase)
5259	4471833	4471663	[-1 L= 171]	xxtC / Hypothetical protein
5260	4472910	4471963	[-1 L= 948]	xxtD / Hypothetical protein
5261	4473245	4474276	[+2 L=1032]	xxtE / Iron (III) dicitrate transport permease protein
5262	4474287	4474928	[+3 L= 642]	xxtE / Iron (III) dicitrate transport permease protein
5263	4474876	4476321	[+1 L=1446]	xxtE / Iron (III) dicitrate transport permease protein
5265	4477576	4478076	[+1 L= 501]	yrdA / Hypothetical protein
5266	4478216	4478545	[+2 L= 330]	xxtF / Hypothetical protein
5268	4479307	4478615	[-2 L= 693]	xxtG / Hypothetical protein
5269	4480203	4479337	[-1 L= 867]	xxtH / Hypothetical protein
5270	4480945	4480244	[-2 L= 702]	xxtI / Hypothetical protein
5271	4481156	4480983	[-3 L= 174]	xxtJ / Hypothetical protein
5272	4482057	4481137	[-1 L= 921]	ycbN / Bacitracin ABC transporter ATP-binding protein
5273	4483118	4482186	[-3 L= 933]	ycbM / Two-component sensor histidine kinase
5274	4483812	4483123	[-1 L= 690]	ycbL / Two-component response regulator
5276	4484155	4484346	[+1 L= 192]	ywbE / Hypothetical protein
5277	4485668	4484391	[-3 L=1278]	ywbD / Hypothetical protein
5278	4485883	4486203	[+1 L= 321]	xxtK / Hypothetical protein
5279	4487043	4486282	[-1 L= 762]	xxtL / Hypothetical protein
5280	4487858	4487079	[-3 L= 780]	xxtM / Ferrichrome ABC transporter ATP-binding protein
5281	4488819	4487839	[-1 L= 981]	xxtN / Ferrichrome ABC transporter permease protein
5282	4489728	4488850	[-1 L= 879]	xxtO / Ferrichrome ABC transporter ferrichrome-binding protein
5284	4492512	4489801	[-1 L=2712]	xxtP / Hypothetical protein
5285	4493013	4492540	[-1 L= 474]	xxtQ / Hypothetical protein
5287	4493732	4493022	[-3 L= 711]	xxtR / Hypothetical protein
5289	4495581	4494226	[-1 L=1356]	braB / Branched-chain amino acid transport system carrier protein (Branched-chain amino acid uptake carrier)
5290	4496717	4496031	[-3 L= 687]	xxtS / tRNA pseudouridine synthase homolog
5292	4497110	4496916	[-3 L= 195]	yshD / DNA mismatch repair protein homolog
5293	4499274	4497169	[-1 L=2106]	yshD / DNA mismatch repair protein homolog
5294	4501015	4499297	[-2 L=1719]	yshC / DNA-dependent DNA polymerase beta chain
5296	4501607	4501071	[-3 L= 537]	xxtT / Colicin V production protein homolog
5297	4501893	4501612	[-1 L= 282]	yshA / Hypothetical protein
5298	4501925	4502935	[+2 L=1011]	rnhC / Ribonuclease HIII (RNase HIII)
5302	4505233	4503845	[-2 L=1389]	syiN / Asparaginyl-tRNA synthetase (Asparagine--tRNA ligase)
5303	4508112	4505695	[-1 L=2418]	syfB / Phenylalanyl-tRNA synthetase beta chain (Phenylalanine--tRNA ligase beta chain)
5304	4509165	4508134	[-1 L=1032]	syfA / Phenylalanyl-tRNA synthetase alpha chain (Phenylalanine--tRNA ligase alpha chain)
5305	4510284	4509490	[-1 L= 795]	ysgA / rRNA methylase homolog
5306	4510358	4510573	[+2 L= 216]	ysfA / Hypothetical protein
5307	4510754	4511308	[+2 L= 555]	yueE / Hypothetical protein
5308	4511536	4512357	[+1 L= 822]	xxtU / Hypothetical protein
5309	4512504	4512872	[+3 L= 369]	xxtV / Hypothetical protein
5310	4512914	4513267	[+2 L= 354]	xxtW / Hypothetical protein
5311	4515091	4513295	[-2 L=1797]	xxtX / Transporter homolog
5313	4515781	4515107	[-2 L= 675]	yhbJ / Hypothetical protein
5314	4516055	4516669	[+2 L= 615]	xxtY / Transcriptional regulator, TetR family
5315	4517807	4516716	[-3 L=1092]	ysdC / Endo-1,4-glucanase homolog
5316	4518381	4517872	[-1 L= 510]	xxtZ / Hypothetical protein
5317	4519158	4518805	[-1 L= 354]	rplT / 50S ribosomal protein L20

5318	4519396	4519199	[-2 L= 198]	rpml / 50S ribosomal protein L35
5319	4520017	4519421	[-2 L= 597]	infC / Translation initiation factor IF-3
5320	4522256	4520319	[-3 L=1938]	syiT / Threonyl-tRNA synthetase 1 (Threonine--tRNA ligase)
5323	4523328	4522564	[-1 L= 765]	ytxC / Hypothetical protein
5326	4524845	4523910	[-3 L= 936]	dnal / Primosomal protein (helicase loader)
5328	4526288	4524882	[-3 L=1407]	dnaB / Replication initiation and membrane attachment protein
5329	4526911	4526444	[-2 L= 468]	ytcG / Hypothetical protein
5330	4527578	4527189	[-3 L= 390]	speH / S-adenosylmethionine decarboxylase proenzyme (AdoMetDC) (SamDC)
5331	4528988	4527963	[-3 L=1026]	gapB / Glyceraldehyde 3-phosphate dehydrogenase 2 (GAPDH) (NAD(P)-dependent glyceraldehyde-3-phosphate dehydrogenase)
5332	4529715	4529101	[-1 L= 615]	ytaG / Dephospho-CoA kinase
5334	4530384	4529755	[-1 L= 630]	xxuA / Hypothetical protein
5335	4531287	4530460	[-1 L= 828]	fpgA / Formamidopyrimidine-DNA glycosylase (FAPY-DNA glycosylase)
5336	4533975	4531303	[-1 L=2673]	dpoA / DNA polymerase I (POL I)
5338	4535982	4534222	[-1 L=1761]	phoR / Alkaline phosphatase synthesis sensor protein
5339	4536694	4535978	[-2 L= 717]	phoP / Alkaline phosphatase synthesis transcriptional regulatory protein
5340	4537093	4536860	[-2 L= 234]	xxuB / Hypothetical protein
5341	4537845	4537375	[-1 L= 471]	xxuC / Hypothetical protein
5342	4538999	4538064	[-3 L= 936]	mdhA / Malate dehydrogenase
5343	4540326	4539022	[-1 L=1305]	idhA / Isocitrate dehydrogenase [NADP] (Oxalosuccinate decarboxylase)
5344	4541620	4540475	[-2 L=1146]	cisZ / Citrate synthase II
5345	4542469	4542011	[-2 L= 459]	ytwl / Hypothetical protein
5347	4542889	4544004	[+1 L=1116]	ytvl / Hypothetical protein
5348	4545029	4544643	[-3 L= 387]	ytzA / Hypothetical protein
5349	4547028	4545229	[-1 L=1800]	kpyK / Pyruvate kinase (Vegetative protein 17)
5350	4547996	4547040	[-3 L= 957]	kfpF / 6-phosphofructokinase (Phosphohexokinase)
5351	4549099	4548128	[-2 L= 972]	accA / Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha
5352	4549956	4549090	[-1 L= 867]	accB / Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta
5353	4550786	4550145	[-3 L= 642]	xxuD / Transcriptional regulator, GntR family
5354	4552105	4550804	[-2 L=1302]	ytsJ / Malate dehydrogenase (malic enzyme) homolog
5355	4555469	4552146	[-3 L=3324]	dpcA / DNA polymerase III alpha subunit
5356	4555512	4555922	[+3 L= 411]	xxuE / Hypothetical protein
5357	4555901	4556422	[+2 L= 522]	xxuF / Hypothetical protein
5358	4557547	4556480	[-2 L=1068]	ytql / Hypothetical protein
5359	4557554	4557871	[+2 L= 318]	xxuG / Hypothetical protein
5360	4558172	4557885	[-3 L= 288]	xxuH / Hypothetical protein
5361	4559670	4558363	[-1 L=1308]	ytol / Hypothetical protein
5362	4559870	4560073	[+2 L= 204]	xxul / Hypothetical protein
5363	4560800	4560120	[-3 L= 681]	xxuJ / Metallo-beta-lactamase homolog
5364	4560950	4562044	[+2 L=1095]	xxuK / Xaa-proline dipeptidase homolog
5365	4562444	4562082	[-3 L= 363]	xxuL / Hypothetical protein
5366	4562842	4562468	[-2 L= 375]	xxuM / Hypothetical protein
5367	4562933	4563757	[+2 L= 825]	xxuN / Hypothetical protein
5370	4564758	4564417	[-1 L= 342]	xxuO / Hypothetical protein
5371	4565549	4564758	[-3 L= 792]	ydfB / Antibiotic resistance protein homolog
5372	4565890	4565549	[-2 L= 342]	ydbB / Hypothetical protein
5375	4567621	4566491	[-2 L=1131]	alaD / Alanine dehydrogenase
5376	4568717	4567839	[-3 L= 879]	ytkK / 3-Oxoacyl-[acyl-carrier-protein] reductase homolog
5377	4568775	4569230	[+3 L= 456]	xxuP / Hypothetical protein
5378	4569970	4569278	[-2 L= 693]	xxuQ / Hypothetical protein
5379	4570042	4570242	[+1 L= 201]	xxuR / Hypothetical protein
5380	4570642	4570292	[-2 L= 351]	xxuS / Hypothetical protein
5381	4572129	4570744	[-1 L=1386]	arlY / Argininosuccinate lyase (Arginosuccinase)
5382	4573361	4572129	[-3 L=1233]	assY / Argininosuccinate synthase (Citrulline--aspartate ligase)
5383	4573402	4573812	[+1 L= 411]	xxuT / Hypothetical protein
5384	4574039	4573833	[-3 L= 207]	xxuU / Hypothetical protein
5386	4574893	4575552	[+1 L= 660]	xxuV / Hypothetical protein
5387	4576432	4575590	[-2 L= 843]	xxuW / ABC transporter substrate-binding protein
5388	4576558	4577190	[+1 L= 633]	xxuX / Hypothetical protein
5389	4577264	4577695	[+2 L= 432]	xxuY / MutT-like protein
5390	4578915	4577725	[-1 L=1191]	ackA / Acetate kinase (Acetokinase)
5391	4580207	4579218	[-3 L= 990]	ytxK / Hypothetical protein
5392	4580900	4580403	[-3 L= 498]	tpxA / Thioredoxin peroxidase
5393	4581430	4581038	[-2 L= 393]	xxuZ / Hypothetical protein
5394	4582081	4581446	[-2 L= 636]	xxvA / Hypothetical protein

5395	4582272	4583087	[+3 L= 816]	ppnB / Inorganic polyphosphate/ATP-NAD kinase 2 (Poly(P)/ATP NAD kinase 2)
5396	4584821	4583247	[-3 L=1575]	ytcJ / Hypothetical protein
5397	4585315	4584887	[-2 L= 429]	xxvB / Hypothetical protein
5399	4587004	4585421	[-2 L=1584]	yctI / Acetate-CoA ligase homolog
5400	4587399	4587205	[-1 L= 195]	sasB / Small acid-soluble spore protein A
5401	4588694	4587483	[-3 L=1212]	thiL / Thiamine biosynthesis protein
5402	4589928	4588705	[-1 L=1224]	nifZ / L-cysteine sulfurtransferase (iron-sulfur cofactor synthesis)
5403	4591935	4590226	[-1 L=1710]	ezrA / Septation ring formation regulator
5404	4593003	4592146	[-1 L= 858]	xxvC / Transcriptional regulator, LysR family
5405	4593110	4594051	[+2 L= 942]	yrdR / Transporter homolog
5406	4594722	4594069	[-1 L= 654]	yttP / Transcriptional regulator, TetR family
5407	4594852	4595328	[+1 L= 477]	xxvD / Hypothetical protein
5408	4596569	4595397	[-3 L=1173]	megL / Methionine gamma-lyase
5409	4596969	4597568	[+3 L= 600]	rpsD / 30S ribosomal protein S4
5411	4597818	4598204	[+3 L= 387]	xxvE / Hypothetical protein
5412	4599541	4598288	[-2 L=1254]	syiY / Tyrosyl-tRNA synthetase 1 (Tyrosine--tRNA ligase)
5413	4600578	4600021	[-1 L= 558]	maaT / Maltose O-acetyltransferase (Maltose transacetylase)
5414	4602381	4600666	[-1 L=1716]	acsA / Acetyl-coenzyme A synthetase (Acetate--CoA ligase)
5415	4602543	4603187	[+3 L= 645]	acuA / Acetoin dehydrogenase
5416	4603208	4603849	[+2 L= 642]	acuB / Acetoin dehydrogenase
5417	4603822	4605012	[+1 L=1191]	acuC / Acetoin dehydrogenase
5418	4605158	4606042	[+2 L= 885]	xxvF / Hypothetical protein
5420	4607197	4606499	[-2 L= 699]	xxvG / Two-component response regulator
5421	4608641	4607190	[-3 L=1452]	xxvH / Two-component sensor histidine kinase
5422	4608791	4609468	[+2 L= 678]	xxvI / Hypothetical protein
5423	4609503	4610474	[+3 L= 972]	xxvJ / Oxidoreductase homolog
5424	4610606	4611001	[+2 L= 396]	mscL / Large-conductance mechanosensitive channel
5426	4611326	4611057	[-3 L= 270]	xxvK / Hypothetical protein
5428	4612721	4611714	[-3 L=1008]	ccpA / Catabolite control protein A (Glucose-resistance amylase regulator)
5430	4614275	4613205	[-3 L=1071]	aroG / Phospho-2-dehydro-3-deoxyheptonate aldolase / Chorismate mutase
5431	4615464	4614445	[-1 L=1020]	xxvL / Hypothetical protein
5432	4615911	4615585	[-1 L= 327]	ytxJ / Hypothetical protein
5433	4616465	4615911	[-3 L= 555]	xxvM / Hypothetical protien
5434	4616608	4617720	[+1 L=1113]	xxvN / Aminopeptidase homolog
5436	4618796	4618395	[-3 L= 402]	xxvO / Hypothetical protein
5437	4619379	4618876	[-1 L= 504]	xxvP / Hypothetical protein
5438	4619909	4619364	[-3 L= 546]	xxvQ / Acetyltransferase homolog
5439	4621402	4620095	[-2 L=1308]	murC / UDP-N-acetylmuramate--alanine ligase (UDP-N-acetylmuramoyl-L-alanine synthetase)
5440	4622775	4621660	[-1 L=1116]	xxvR / Hypothetical protein
5441	4627012	4622840	[-2 L=4173]	spcE / Stage III sporulation protein E
5442	4628112	4627162	[-1 L= 951]	amiC / N-acetylmuramoyl-L-alanine amidase precursor
5444	4628497	4628156	[-2 L= 342]	xxvS / Hypothetical protein
5445	4629382	4628771	[-2 L= 612]	syfB / Phenylalanyl-tRNA synthetase beta chain (Phenylalanine--tRNA ligase beta chain)
5446	4630257	4629382	[-1 L= 876]	ytpQ / Hypothetical protein
5447	4630585	4630274	[-2 L= 312]	xxvT / Thioredoxin
5448	4631132	4630671	[-3 L= 462]	xxvU / Hypothetical protein
5449	4632704	4631616	[-3 L=1089]	xxvV / Endo-1,4-beta-glucanase
5450	4632835	4633143	[+1 L= 309]	xxvW / Hypothetical protein
5451	4634156	4633305	[-3 L= 852]	xxvX / Metallo-beta-lactamase homolog
5452	4634880	4634230	[-1 L= 651]	xxvY / Methyltransferase homolog
5453	4635109	4635384	[+1 L= 276]	ytzH / Hypothetical protein
5455	4636188	4635394	[-1 L= 795]	ytmP / Hypothetical protein
5456	4638029	4636419	[-3 L=1611]	xxvZ / Pullulanase
5457	4638559	4638086	[-2 L= 474]	xxvZ / Pullulanase
5458	4639322	4638774	[-3 L= 549]	xxwA / Hypothetical protein
5459	4640845	4639424	[-2 L=1422]	ytjP / Xaa-proline dipeptidase homolog
5460	4641185	4641403	[+2 L= 219]	ytzE / Transcriptional regulator, DeoR family
5461	4642224	4641490	[-1 L= 735]	xxwB / 16S pseudouridylate synthase
5462	4643909	4642260	[-3 L=1650]	ytgP / Spore cortex protein homolog
5463	4644204	4645472	[+3 L=1269]	ytfP / Hypothetical protein
5464	4645372	4647114	[+1 L=1743]	xxwC / Transporter homolog
5466	4647468	4647148	[-1 L= 321]	xxwD / Transcriptional regulator, ArsR family

5467	4647906	4647472	[-1 L= 435]	yndB / Hypothetical protein
5469	4648770	4648591	[-1 L= 180]	yteV / Hypothetical protein
5470	4649008	4648775	[-2 L= 234]	xxwE / Hypothetical protein
5471	4649264	4649755	[+2 L= 492]	xxwF / Transcriptional regulator, CarD-like
5472	4650622	4649834	[-2 L= 789]	dhgA / Glucose 1-dehydrogenase
5473	4651490	4650633	[-3 L= 858]	ycxE / Hypothetical protein
5474	4651942	4651526	[-2 L= 417]	xxwG / Hypothetical protein
5475	4652269	4652039	[-2 L= 231]	xxwH / Molybdopterin converting factor subunit 1
5476	4652367	4652275	[-1 L= 93]	moaE / Molybdopterin converting factor subunit 2 (Molybdopterin synthase subunit 2)
5477	4652735	4652319	[-3 L= 417]	moaE / Molybdopterin converting factor subunit 2 (Molybdopterin synthase subunit 2)
5478	4653253	4652735	[-2 L= 519]	mobB / Molybdopterin-guanine dinucleotide biosynthesis protein B
5479	4654506	4653220	[-1 L=1287]	mocF / Molybdenum cofactor biosynthesis protein
5480	4654485	4655072	[+3 L= 588]	moaC / Molybdenum cofactor biosynthesis protein C
5481	4656126	4655116	[-1 L=1011]	thiF / Adenylyltransferase
5482	4657162	4656146	[-2 L=1017]	moaA / Molybdenum cofactor biosynthesis protein A
5483	4661285	4657359	[-3 L=3927]	xxwI / Hypothetical protein
5486	4662443	4662051	[-3 L= 393]	ytwF / Hypothetical protein
5488	4663907	4662786	[-3 L=1122]	metX / Homoserine O-acetyltransferase (Homoserine o-trans-acetylase)
5489	4664060	4666243	[+2 L=2184]	griA / Spore germination protein
5490	4666260	4667360	[+3 L=1101]	griB / Spore germination protein A2
5491	4667276	4668415	[+2 L=1140]	griC / Spore germination protein A3 precursor
5492	4668500	4668694	[+2 L= 195]	xxwJ / Hypothetical protein
5493	4668795	4669214	[+3 L= 420]	xxwK / Hypothetical protein
5496	4670158	4669265	[-2 L= 894]	xxwL / Hypothetical protein
5497	4672761	4670356	[-1 L=2406]	syiL / Leucyl-tRNA synthetase (Leucine--tRNA ligase)
5498	4674460	4673237	[-2 L=1224]	yttB / Multidrug resistance protein homolog
5499	4675898	4674678	[-3 L=1221]	yhaU / Sodium/proton antiporter homolog
5501	4676399	4675905	[-3 L= 495]	yhaT / Hypothetical protein
5502	4677000	4676437	[-1 L= 564]	xxwM / Phage integrase
5503	4679206	4677350	[-2 L=1857]	xxwN / Permease homolog
5504	4679986	4679228	[-2 L= 759]	xxwO / ABC transporter ATP-binding protein homolog
5505	4681254	4680235	[-1 L=1020]	yamY / Hypothetical protein
5507	4681840	4681559	[-2 L= 282]	xxwP / Hypothetical protein
5508	4681931	4682887	[+2 L= 957]	ytqA / Hypothetical protein
5509	4682887	4683456	[+1 L= 570]	ytqB / Hypothetical protein
5510	4683821	4684651	[+2 L= 831]	xxwQ / ABC transporter ATP-binding protein homolog
5511	4684673	4685350	[+2 L= 678]	xxwR / Hypothetical protein
5512	4685378	4686049	[+2 L= 672]	racX / Amino acid racemase
5514	4686295	4687509	[+1 L=1215]	xxwS / Hypothetical protein
5516	4688626	4687553	[-2 L=1074]	ytpB / Hypothetical protein
5517	4689500	4688658	[-3 L= 843]	ytpA / Lysophospholipase homolog
5518	4689533	4690042	[+2 L= 510]	ytoA / Hypothetical protein
5519	4690189	4690719	[+1 L= 531]	xxwT / Hypothetical protein
5520	4690732	4691874	[+1 L=1143]	xxwU / Alpha-D-mannose-alpha(1-6)phosphatidyl-myo-inositol monomannoside transferase
5521	4692760	4692161	[-2 L= 600]	mobA / Molybdopterin-guanine dinucleotide biosynthesis protein A
5522	4693266	4692760	[-1 L= 507]	moaB / Molybdenum cofactor biosynthesis protein B
5523	4693503	4693679	[+3 L= 177]	xxwV / Hypothetical protein
5524	4693754	4694275	[+2 L= 522]	xxwW / Hypothetical protein
5525	4695519	4694323	[-1 L=1197]	metK / S-adenosylmethionine synthetase (Methionine adenosyltransferase)
5527	4696039	4697622	[+1 L=1584]	ppcK / Phosphoenolpyruvate carboxykinase [ATP] (PEP carboxykinase)
5529	4698359	4697979	[-3 L= 381]	xxwX / Hypothetical protein
5532	4699794	4698892	[-1 L= 903]	xxwY / Hypothetical protein
5533	4700341	4700021	[-2 L= 321]	xxwZ / Hypothetical protein
5535	4700716	4701633	[+1 L= 918]	zazA / Hypothetical protein
5538	4704288	4703071	[-1 L=1218]	zazB / Histidine-kinase homolog
5539	4705538	4704288	[-3 L=1251]	zazC / Histidine-kinase homolog
5540	4705712	4705906	[+2 L= 195]	catE / Catalase
5541	4705968	4706183	[+3 L= 216]	catE / Catalase
5542	4706202	4707008	[+3 L= 807]	zazD / Non-heme chloroperoxidase
5543	4709291	4707225	[-3 L=2067]	zazE / Hypothetical protein
5546	4710210	4709917	[-1 L= 294]	zazF / Hypothetical protein
5547	4710307	4711335	[+1 L=1029]	zazG / ABC transporter substrate-binding protein

5549	4711350	4712111	[+3 L= 762]	ytlC / ABC transporter ATP-binding protein
5550	4712107	4712910	[+1 L= 804]	ytlD / ABC transporter permease protein
5552	4714529	4713408	[-3 L=1122]	zazH / Hypothetical protein
5553	4714610	4715284	[+2 L= 675]	zazI / Haloacid dehalogenase homolog
5554	4715918	4715385	[-3 L= 534]	zazJ / Hypothetical protein
5555	4716510	4716034	[-1 L= 477]	ytkD / MutT-like protein
5556	4716957	4716598	[-1 L= 360]	zazK / Hypothetical protein
5557	4717147	4717374	[+1 L= 228]	zazL / Hypothetical protein
5560	4718713	4718243	[-2 L= 471]	luxS / Autoinducer-2 production protein luxS (AI-2 synthesis protein) / S-ribosylhomocysteine cleavage enzyme
5561	4718842	4719075	[+1 L= 234]	ytjA / Hypothetical protein
5562	4719638	4719078	[-3 L= 561]	ytiB / Carbonic anhydrase homolog
5563	4719863	4721209	[+2 L=1347]	cydA / Cytochrome D ubiquinol oxidase subunit I
5564	4721193	4722227	[+3 L=1035]	cydB / Cytochrome oxidase subunit II
5565	4722629	4722399	[-3 L= 231]	gepF / Spore germination protein
5568	4723286	4724338	[+2 L=1053]	zazM / Hypothetical protein
5569	4724511	4725398	[+3 L= 888]	ydeO / Hypothetical protein
5570	4725727	4725512	[-2 L= 216]	zazN / Hypothetical protein
5571	4726642	4725830	[-2 L= 813]	zazO / Hypothetical protein
5572	4727161	4726658	[-2 L= 504]	zazP / Hypothetical protein
5573	4727587	4727186	[-2 L= 402]	zazQ / Hypothetical protein
5574	4728481	4727819	[-2 L= 663]	zazR / Hypothetical protein
5576	4728884	4729459	[+2 L= 576]	zazS / Hypothetical protein
5577	4729607	4730011	[+2 L= 405]	zazT / Transposase
5578	4730278	4730072	[-2 L= 207]	zazU / Hypothetical protein
5579	4730666	4730259	[-3 L= 408]	feoB / Ferrous iron transport protein B
5580	4732245	4730641	[-1 L=1605]	feoB / Ferrous iron transport protein B
5581	4732523	4732245	[-3 L= 279]	zazV / Hypothetical protein
5583	4732750	4733517	[+1 L= 768]	zazW / Hypothetical protein
5584	4735581	4733731	[-1 L=1851]	zazX / Two-component histidine kinase
5585	4736267	4735581	[-3 L= 687]	zazY / Two-component response protein
5586	4736927	4736310	[-3 L= 618]	zazZ / Hypothetical protein
5590	4738016	4737687	[-3 L= 330]	zbzA / Hypothetical protein
5592	4738577	4739101	[+2 L= 525]	hprT / Hypoxanthine-guanine phosphoribosyltransferase (HGPRT)
5593	4739187	4740086	[+3 L= 900]	bmrU / Multidrug resistance protein
5595	4741351	4740668	[-2 L= 684]	zbzB / Hypothetical protein
5596	4741527	4742471	[+3 L= 945]	zbzC / Hypothetical protein
5597	4743273	4742518	[-1 L= 756]	zbzD / Hypothetical protein
5598	4744058	4743261	[-3 L= 798]	zbzE / Hypothetical protein
5602	4747162	4745252	[-2 L=1911]	yxdM / ABC transporter permease protein
5603	4747565	4747143	[-3 L= 423]	yxdL / ABC transporter ATP-binding protein
5604	4747911	4747537	[-1 L= 375]	yxdL / ABC transporter ATP-binding protein
5605	4748669	4748325	[-3 L= 345]	zbzF / Hypothetical protein
5606	4749472	4748843	[-2 L= 630]	zbzG / Hypothetical protein
5607	4750017	4749442	[-1 L= 576]	zbzH / Ribosomal RNA adenine dimethylase
5608	4752110	4750164	[-3 L=1947]	zbzI / ABC transporter permease protein
5609	4752882	4752100	[-1 L= 783]	zbzJ / ABC transporter ATP-binding protein
5611	4753108	4754043	[+1 L= 936]	ydeE / Transcriptional regulator, AraC/XylS family
5612	4754728	4754096	[-2 L= 633]	zbzK / Hypothetical protein
5613	4754997	4754728	[-1 L= 270]	yvbA / Transcriptional regulator, ArsR family
5614	4755189	4755899	[+3 L= 711]	yxdJ / Two-component response regulator
5615	4755905	4756924	[+2 L=1020]	yxdK / Two-component sensor histidine kinase
5616	4757022	4758998	[+3 L=1977]	yxdM / ABC transporter permease protein
5617	4759070	4761022	[+2 L=1953]	yxdM / ABC transporter permease protein
5618	4761037	4761795	[+1 L= 759]	yxdL / ABC transporter ATP-binding protein
5619	4761795	4763768	[+3 L=1974]	yxdM / ABC transporter permease protein
5623	4765511	4764189	[-3 L=1323]	zbzL / Permease, GntP family
5624	4766285	4765563	[-3 L= 723]	zbzM / Transcriptional regulator, GntR family
5625	4767310	4766288	[-2 L=1023]	kdgK 2-dehydro-3-deoxygluconokinase (2-keto-3-deoxygluconokinase)
5626	4768049	4767297	[-3 L= 753]	zbzN / Hypothetical protein
5627	4769154	4768054	[-1 L=1101]	zbzO / Selenocysteine synthase homolog
5628	4770232	4769135	[-2 L=1098]	zbzP / Adenine deaminase homolog
5629	4771454	4770597	[-3 L= 858]	vanY / D-Alanyl-D-Alanine carboxypeptidase (DD-peptidase)
5630	4772643	4771540	[-1 L=1104]	vanS / Sensor protein (Vancomycin histidine protein kinase)
5631	4773334	4772639	[-2 L= 696]	vanR / Two-component response regulator
5632	4774054	4773578	[-2 L= 477]	ytfD / N-acylamino acid racemase homolog

5633	4774682	4774068	[-3 L= 615]	ytfD / N-acylamino acid racemase homolog
5634	4776132	4774687	[-1 L=1446]	menE / O-succinylbenzoic acid--CoA ligase (O-succinylbenzoate-CoA synthase)
5635	4777392	4776577	[-1 L= 816]	menB / Naphthoate synthase (Dihydroxynaphthoic acid synthetase)
5636	4778274	4777465	[-1 L= 810]	ytxM / Prolyl aminopeptidase homolog
5637	4780025	4778274	[-3 L=1752]	menD / Menaquinone biosynthesis protein (2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase / 2-oxoglutarate decarboxylase)
5639	4781416	4780025	[-2 L=1392]	menF / Menaquinone-specific isochorismate synthase (Isochorismate mutase)
5641	4781545	4782561	[+1 L=1017]	menA / 1,4-dihydroxy-2-naphthoate octaprenyltransferase (DHNA-octaprenyltransferase)
5642	4782674	4783402	[+2 L= 729]	yteA / Hypothetical protein
5643	4783650	4783453	[-1 L= 198]	cspD / Cold shock protein
5644	4784034	4784822	[+3 L= 789]	zbzQ / Hypothetical protein
5645	4785032	4785187	[+2 L= 156]	zbzR / Hypothetical protein
5646	4785528	4786247	[+3 L= 720]	zbzS / Lipase homolog
5648	4788973	4786568	[-2 L=2406]	phsG / Glycogen phosphorylase
5649	4790488	4788995	[-2 L=1494]	glgA / Glycogen synthase (Starch [bacterial glycogen] synthase)
5650	4791063	4790539	[-1 L= 525]	glgD / Glycogen biosynthesis protein
5651	4791571	4791053	[-2 L= 519]	glgD / Glycogen biosynthesis protein
5652	4792720	4791593	[-2 L=1128]	glgC / Glucose-1-phosphate adenylyltransferase (ADP-glucose synthase)
5654	4794614	4792671	[-3 L=1944]	glgB / 1,4-alpha-glucan branching enzyme (Glycogen branching enzyme)
5655	4795076	4795678	[+2 L= 603]	cotN / Spore coat-associated protein N
5657	4795715	4799935	[+2 L=4221]	subV / Minor extracellular serine protease
5658	4801106	4800165	[-3 L= 942]	ldhX / L-lactate dehydrogenase X
5659	4806482	4806910	[+2 L= 429]	zbzT / Hypothetical protein
5662	4809052	4809729	[+1 L= 678]	sapB / Mg2+ transporter homolog
5664	4809825	4810067	[+3 L= 243]	zbzU / Hypothetical protein
5665	4810092	4810817	[+3 L= 726]	zbzV / Calcium-gated potassium channel
5666	4811226	4810810	[-1 L= 417]	yugN / Hypothetical protein
5667	4812680	4811331	[-3 L=1350]	ppgI / Glucose-6-phosphate isomerase A (Phosphoglucose isomerase A)
5668	4812955	4813185	[+1 L= 231]	yuzA / Hypothetical protein
5669	4813657	4813301	[-2 L= 357]	gspM / General stress protein 13 (GSP13)
5670	4815086	4813899	[-3 L=1188]	yugH / Aspartate aminotransferase homolog
5671	4815589	4815086	[-2 L= 504]	yugG / Transcriptional regulator, Lrp/AsnC family
5672	4815699	4816688	[+3 L= 990]	tkrA / 2-ketogluconate reductase (2KR)
5673	4816801	4817637	[+1 L= 837]	yugF / Dihydrolipoamide S-acetyltransferase homolog
5674	4818012	4817764	[-1 L= 249]	yugE / Hypothetical protein
5675	4818130	4819278	[+1 L=1149]	patB / Aspartate aminotransferase homolog
5676	4820090	4819485	[-3 L= 606]	sodB / Superoxide dismutase [Cu-Zn]
5678	4820422	4820811	[+1 L= 390]	kapB / Kinase-associated lipoprotein B
5680	4821478	4820858	[-2 L= 621]	yugB / Sporulation inhibitor
5681	4821759	4823090	[+3 L=1332]	zbzW / Arsenical pump membrane protein homolog
5682	4823640	4823176	[-1 L= 465]	zbzX / Hypothetical protein
5683	4823758	4824468	[+1 L= 711]	zbzY / DNA alkylation repair protein
5686	4824731	4825942	[+2 L=1212]	syiG / Glycyl-tRNA synthetase (Glycine--tRNA ligase)
5688	4825994	4826191	[+2 L= 198]	syiG / Glycyl-tRNA synthetase (Glycine--tRNA ligase)
5689	4826617	4826237	[-2 L= 381]	yuxO / Hypothetical protein
5690	4826713	4827453	[+1 L= 741]	zbzZ / Hypothetical protein
5692	4827553	4828098	[+1 L= 546]	bioY / Biotin synthesis protein
5693	4829036	4828149	[-3 L= 888]	gtaB / UTP--glucose-1-phosphate uridylyltransferase (UDP-glucose pyrophosphorylase) (General stress protein 33)
5695	4830865	4829144	[-2 L=1722]	yhxB / Phosphomannomutase (PMM) homolog
5696	4830964	4831611	[+1 L= 648]	yojJ / Hypothetical protein
5697	4833272	4831791	[-3 L=1482]	ampA / Cytosol aminopeptidase (Leucine aminopeptidase)
5698	4834077	4833421	[-1 L= 657]	yuiC / Hypothetical protein
5700	4834448	4834134	[-3 L= 315]	yuiB / Hypothetical protein
5701	4834951	4834448	[-2 L= 504]	zczA / MutT-like protein
5702	4836370	4835075	[-2 L=1296]	yumB / NADH dehydrogenase-like protein
5703	4836736	4837728	[+1 L= 993]	yumC / Thioredoxin reductase (TRXR) homolog
5704	4847967	4837849	[-1 L=10119]	zczB / Hypothetical protein
5705	4848405	4848881	[+3 L= 477]	zczC / Hypothetical protein
5707	4849102	4850346	[+1 L=1245]	zczD / Hypothetical protein
5708	4851256	4850363	[-2 L= 894]	zczE / Hypothetical protein
5709	4851328	4851786	[+1 L= 459]	ybbK / Hypothetical protein
5711	4852182	4851823	[-1 L= 360]	zczF / Hypothetical protein

5714	4854486	4854097	[-1 L= 390]	yutM / Hypothetical protein
5715	4855355	4854492	[-3 L= 864]	dapF / Diaminopimelate epimerase (DAP epimerase)
5716	4855890	4855627	[-1 L= 264]	yuzB / Hypothetical protein
5717	4856215	4857282	[+1 L=1068]	yutJ / NADH dehydrogenase-like protein
5718	4857747	4858403	[+3 L= 657]	zczG / ABC transporter ATP-binding protein
5719	4858342	4859184	[+1 L= 843]	zczH / Hypothetical protein
5720	4859749	4859390	[-2 L= 360]	zczI / Hypothetical protein
5722	4861036	4860242	[-2 L= 795]	zczJ / Hypothetical protein
5723	4862469	4861339	[-1 L=1131]	zczK / Hypothetical protein
5724	4862995	4862435	[-2 L= 561]	zczL / Hypothetical protein
5725	4863082	4863549	[+1 L= 468]	zczM / Hypothetical protein
5726	4863533	4864174	[+2 L= 642]	zczN / Hypothetical protein
5727	4864983	4864183	[-1 L= 801]	zczO / Hypothetical protein
5729	4865664	4864996	[-1 L= 669]	zczP / Hypothetical protein
5731	4866618	4865788	[-1 L= 831]	zczQ / Hypothetical protein
5732	4867002	4866634	[-1 L= 369]	yuzD / Hypothetical protein
5733	4867135	4867368	[+1 L= 234]	nifU / Nitrogen fixation protein homolog
5735	4868857	4867847	[-2 L=1011]	yutH / Hypothetical protein
5737	4869089	4869454	[+2 L= 366]	yutG / Low temperature requirement C protein
5738	4869969	4869484	[-1 L= 486]	zczR / Hypothetical protein
5739	4870583	4871161	[+2 L= 579]	yabF / NADPH-quinone reductase homolog
5740	4872074	4871313	[-3 L= 762]	yutF / N-acetyl-glucosamine catabolism protein homolog
5741	4872816	4872187	[-1 L= 630]	zczS / Transcriptional regulator, deoR family
5742	4873346	4872900	[-3 L= 447]	yutE / Hypothetical protein
5744	4873485	4874453	[+3 L= 969]	zczT / Glycerol-inducible protein
5746	4874467	4874736	[+1 L= 270]	zczU / Hypothetical protein
5748	4875112	4875606	[+1 L= 495]	zczV / Hypothetical protein
5749	4875927	4875658	[-1 L= 270]	yutD / Hypothetical protein
5751	4876076	4876651	[+2 L= 576]	yutC / Hypothetical protein
5752	4877477	4876692	[-3 L= 786]	zczW / Transcriptional activator of multidrug efflux genes
5753	4877524	4878336	[+1 L= 813]	yhfC / Hypothetical protein
5754	4878796	4878368	[-2 L= 429]	zczX / Hypothetical protein
5755	4878930	4879481	[+3 L= 552]	zczY / Hypothetical protein
5756	4879559	4880035	[+2 L= 477]	zczZ / Hypothetical protein
5757	4880966	4880067	[-3 L= 900]	lipA / Lipoic acid synthetase (Lipoate synthase)
5758	4881051	4882127	[+3 L=1077]	yutA / Hypothetical protein
5759	4882935	4882207	[-1 L= 729]	yunB / Hypothetical protein
5761	4883292	4882993	[-1 L= 300]	yunC / Hypothetical protein
5762	4884638	4883361	[-3 L=1278]	yunD / Hypothetical protein
5763	4886871	4885477	[-1 L=1395]	yurU / Hypothetical protein
5764	4887351	4886923	[-1 L= 429]	yurV / Iron-sulfur cofactor synthesis protein homolog
5765	4888561	4887344	[-2 L=1218]	yurW / Cysteine desulfurase homolog
5766	4889853	4888564	[-1 L=1290]	yurX / Hypothetical protein
5767	4890654	4889872	[-1 L= 783]	yurY / ABC transporter ATP-binding protein
5768	4891720	4890896	[-2 L= 825]	yusA / Hypothetical protein
5770	4892607	4891774	[-1 L= 834]	zdzA / Hypothetical protein
5771	4893278	4892610	[-3 L= 669]	yusB / Hypothetical protein
5772	4894290	4893268	[-1 L=1023]	yusC / ABC transporter ATP-binding protein
5773	4895178	4894837	[-1 L= 342]	zdzB / Hypothetical protein
5775	4895639	4895334	[-3 L= 306]	yusE / thioredoxin homolog
5776	4895987	4895646	[-3 L= 342]	yusF / Hypothetical protein
5778	4896687	4896247	[-1 L= 441]	gcsH / Glycine cleavage system H protein
5779	4897073	4896672	[-3 L= 402]	yusI / Arsenate reductase homolog
5780	4898053	4897529	[-2 L= 525]	zdzC / Hypothetical protein
5781	4898197	4898841	[+1 L= 645]	zdzD / Hypothetical protein
5782	4899926	4898907	[-3 L=1020]	zdzE / Hypothetical protein
5784	4901043	4899943	[-1 L=1101]	ldhB / L-lactate dehydrogenase 2 (L-LDH 2)
5785	4901384	4901139	[-3 L= 246]	zdzF / Hypothetical protein
5786	4901610	4901401	[-1 L= 210]	zdzG / Hypothetical protein
5787	4902440	4901730	[-3 L= 711]	zdzH / Amino terminal protease homolog
5788	4903456	4902908	[-2 L= 549]	yobS / Transcriptional regulator
5789	4904179	4903460	[-2 L= 720]	yobT / Metallo-beta-lactamase homolog
5790	4906117	4904318	[-2 L=1800]	acdS / Acyl-CoA dehydrogenase, short-chain specific (SCAD) (Butyryl-CoA dehydrogenase)
5792	4907532	4906363	[-1 L=1170]	yusK / Acetyl-CoA C-acyltransferase homolog
5793	4909935	4907557	[-1 L=2379]	yusL / s-Hydroxyacyl-CoA dehydrogenase homolog

5797	4910407	4911243	[+1 L= 837]	zdzI / D-Alanyl-D-alanine carboxypeptidase homolog
5798	4912195	4911272	[-2 L= 924]	proD / Proline dehydrogenase
5799	4912743	4912501	[-1 L= 243]	yusU / Hypothetical protein
5800	4913094	4912795	[-1 L= 300]	zdzJ / Hypothetical protein
5801	4915181	4913175	[-3 L=2007]	mcpC / Methyl-accepting chemotaxis protein
5802	4915359	4916114	[+3 L= 756]	zdzK / Hypothetical protein
5804	4917640	4916405	[-2 L=1236]	ydhL / Chloramphenicol resistance protein homolog
5805	4919127	4917697	[-1 L=1431]	ykbA / Amino acid permeased homolog
5807	4920066	4919782	[-1 L= 285]	zdzL / Hypothetical protein
5808	4920595	4920050	[-2 L= 546]	zdzM / Hypothetical protein
5809	4921513	4920728	[-2 L= 786]	spcJ / Stage III sporulation protein J precursor
5810	4921820	4921539	[-3 L= 282]	zdzN / Hypothetical protein
5811	4922075	4922989	[+2 L= 915]	yitT / Hypothetical protein
5813	4923623	4923105	[-3 L= 519]	zdzO / Hypothetical protein
5814	4924084	4924467	[+1 L= 384]	zdzP / Hypothetical protein
5816	4926038	4924959	[-3 L=1080]	zdzQ / Hypothetical protein
5818	4926758	4926054	[-3 L= 705]	zdzR / Hypothetical protein
5819	4926987	4926751	[-1 L= 237]	zdzS / Hypothetical protein
5820	4927881	4927198	[-1 L= 684]	ybfM / Hypothetical protein
5822	4928210	4928650	[+2 L= 441]	zdzT / Hypothetical protein
5823	4928684	4929142	[+2 L= 459]	zdzU / Hypothetical protein
5824	4929510	4930172	[+3 L= 663]	zdzV / Two-component response regulator
5825	4930153	4931592	[+1 L=1440]	zdzW / Two-component sensor histidine kinase
5826	4931565	4932635	[+3 L=1071]	zdzX / Proline dehydrogenase homolog
5828	4934636	4933005	[-3 L=1632]	syiM / Methionyl-tRNA synthetase (Methionine--tRNA ligase)
5829	4934970	4935887	[+3 L= 918]	zdzY / Short-chain dehydrogenase homolog
5831	4936287	4937315	[+3 L=1029]	mcpC / Methyl-accepting chemotaxis protein
5832	4937364	4937996	[+3 L= 633]	mcpA / Methyl-accepting chemotaxis protein
5833	4938213	4939901	[+3 L=1689]	tlpB / Methyl-accepting chemotaxis protein
5834	4940025	4940339	[+3 L= 315]	yitW / Hypothetical protein
5835	4942105	4940423	[-2 L=1683]	nprB / Neutral metalloprotease B precursor
5836	4942933	4942229	[-2 L= 705]	zdzZ / Hypothetical protein
5837	4943386	4942979	[-2 L= 408]	zezA / Transcriptional regulator, MarR family
5838	4943930	4943481	[-3 L= 450]	zezB / Hypothetical protein
5839	4944706	4944071	[-2 L= 636]	yngC / Alkaline phosphatase homolog
5840	4945945	4944749	[-2 L=1197]	yhaU / Sodium/proton antiporter homolog
5842	4946459	4945953	[-3 L= 507]	yhaT / Hypothetical protein
5844	4946845	4948284	[+1 L=1440]	alsT / Amino acid carrier protein (sodium/alanine symporter)
5846	4948736	4949182	[+2 L= 447]	gspU / General stress protein 20U (DPS protein homolog)
5849	4950936	4950361	[-1 L= 576]	yvdD / Hypothetical protein
5850	4951010	4951330	[+2 L= 321]	yvdE / Hypothetical protein
5851	4951387	4951890	[+1 L= 504]	ftnA / Ferritin
5852	4951924	4953210	[+1 L=1287]	yxaH / Hypothetical protein
5853	4954439	4953261	[-3 L=1179]	nupC / Pyrimidine nucleoside transport protein
5854	4956204	4954738	[-1 L=1467]	alsT / Amino acid carrier protein
5855	4957793	4956513	[-3 L=1281]	ybgH / Sodium/proton-dependent alanine transporter
5856	4957939	4957793	[-2 L= 147]	ybgH / Sodium/proton-dependent alanine transporter
5857	4958229	4958879	[+3 L= 651]	ywnB / Hypothetical protein
5858	4962841	4958930	[-2 L=3912]	zezC / Hypothetical protein
5859	4964232	4963306	[-1 L= 927]	zezD / Hypothetical protein
5860	4965180	4964344	[-1 L= 837]	ytbE / Plant metabolite dehydrogenase homolog
5862	4966411	4965200	[-2 L=1212]	ytbD / Chloramphenicol resistance protein homolog
5864	4966734	4967075	[+3 L= 342]	zezE / Hypothetical protein
5865	4967505	4967948	[+3 L= 444]	yjlC / Hypothetical protein
5866	4967996	4969171	[+2 L=1176]	yjlD / NADH dehydrogenase homolog (Glucose starvation-inducible protein)
5867	4970627	4969368	[-3 L=1260]	syiY / Tyrosyl-tRNA synthetase (Tyrosine--tRNA ligase)
5868	4971909	4970995	[-1 L= 915]	murB / UDP-N-acetylenolpyruvoylglucosamine reductase (UDP-N-acetylmuramate dehydrogenase)
5870	4972697	4972296	[-3 L= 402]	zezF / Hypothetical protein
5871	4974369	4972858	[-1 L=1512]	tlpC / Methyl-accepting chemotaxis protein
5872	4975448	4974393	[-3 L=1056]	zezG / Hypothetical protein
5873	4975767	4976198	[+3 L= 432]	zezH / Hypothetical protein
5875	4976198	4976551	[+2 L= 354]	zezI / Hypothetical protein
5877	4977137	4976907	[-3 L= 231]	zezJ / Hypothetical protein
5878	4978499	4977300	[-3 L=1200]	zezK / Hypothetical protein

5879	4980043	4978499	[-2 L=1545]	ydiF / ABC transporter ATP-binding protein
5880	4980915	4980484	[-1 L= 432]	atdA / Spermidine N(1)-acetyltransferase (Diamine acetyltransferase)
5883	4982855	4982433	[-3 L= 423]	rplK / 50S Ribosomal protein L11
5884	4983900	4983115	[-1 L= 786]	zezL / Hypothetical protein
5886	4984834	4984412	[-2 L= 423]	rplK / 50S Ribosomal protein L11
5887	4985697	4984930	[-1 L= 768]	zezM / Hypothetical protein
5888	4986513	4985719	[-1 L= 795]	zezN / Hypothetical protein
5889	4988095	4986509	[-2 L=1587]	zezO / Hypothetical protein
5893	4992633	4990021	[-1 L=2613]	zezP / Hypothetical protein
5894	4994643	4992664	[-1 L=1980]	zezQ / Hypothetical protein
5901	4997392	4998132	[+1 L= 741]	zezR / Hypothetical protein
5906	5000115	4999771	[-1 L= 345]	lrpB / Transcriptional regulator, Lrp/AsnC family
5908	5000472	5001434	[+3 L= 963]	zezS / Hypothetical protein
5911	5004319	5002784	[-2 L=1536]	tacY / Hemolysin precursor / Cereolysin O
5912	5005507	5004758	[-2 L= 750]	zezT / ABC transporter ATP-binding protein / Fe3+ siderophore transport system
5913	5006568	5005507	[-1 L=1062]	fatC / Fe3+ siderophore transport system permease protein
5914	5007581	5006568	[-3 L=1014]	fatD / Fe3+ siderophore transport system permease protein
5915	5008695	5007604	[-1 L=1092]	fatB / Fe3+ siderphore transport system, periplasmic component
5916	5009771	5009097	[-3 L= 675]	zezU / Transcriptional regulator
5920	5012529	5011381	[-1 L=1149]	zezV / Hypothetical protein
5921	5015071	5012504	[-2 L=2568]	zezW / Hypothetical protein
5924	5016702	5015731	[-1 L= 972]	zezY / Hypothetical protein
5926	5018285	5017896	[-3 L= 390]	zezZ / Insertion sequence protein
5932	5020844	5020119	[-3 L= 726]	zfzA / ABC transporter ATP-binding protein
5936	5024908	5023658	[-2 L=1251]	zfzB / Hypothetical protein
5938	5027774	5025636	[-3 L=2139]	zfzC / Hypothetical protein
5941	5029548	5029970	[+3 L= 423]	zfzD / Insertion sequence protein
5942	5031251	5030787	[-3 L= 465]	ssrP / SsrA-binding protein
5945	5033927	5031504	[-3 L=2424]	rnrA / Ribonuclease R (RNase R) (VacB protein homolog)
5946	5034813	5034073	[-1 L= 741]	yvaK / Carboxylesterase homolog
5947	5035203	5034973	[-1 L= 231]	yvaL / Protein-export membrane protein
5948	5035990	5035301	[-2 L= 690]	zfzE / Hypothetical protein
5950	5036364	5035990	[-1 L= 375]	zfzF / Hypothetical protein
5951	5036627	5037655	[+2 L=1029]	iunH / Inosine-uridine preferring nucleoside hydrolase (Purine nucleosidase)
5952	5039005	5037713	[-2 L=1293]	enoA / Enolase (2-phosphoglycerate dehydratase)
5953	5040565	5039039	[-2 L=1527]	gpmI / 2,3-bisphosphoglycerate-independent phosphoglycerate mutase (Phosphoglyceromutase)
5954	5040879	5040565	[-1 L= 315]	tpiS / Triosephosphate isomerase (TIM)
5955	5041326	5040925	[-1 L= 402]	tpiS / Triosephosphate isomerase (TIM)
5957	5042024	5041353	[-3 L= 672]	pgkA / Phosphoglycerate kinase
5958	5042535	5042122	[-1 L= 414]	pgkA / Phosphoglycerate kinase
5960	5043670	5042678	[-2 L= 993]	gcpA / Glyceraldehyde 3-phosphate dehydrogenase 1 (GAPDH) (NAD-dependent glyceraldehyde-3-phosphate dehydrogenase)
5961	5044750	5043710	[-2 L=1041]	cggR / Central glycolytic genes regulator
5962	5045126	5044875	[-3 L= 252]	zfzG / Hypothetical protein
5963	5046503	5045130	[-3 L=1374]	sigL / RNA polymerase sigma-54 factor
5965	5047216	5047755	[+1 L= 540]	zfzH / Hypothetical protein
5966	5047788	5048261	[+3 L= 474]	spaC / Stage V sporulation protein AC
5967	5048265	5049278	[+3 L=1014]	spaD / Stage V sporulation protein AD
5968	5049278	5049625	[+2 L= 348]	spaE / Stage V sporulation protein AE
5970	5049640	5049843	[+1 L= 204]	zfzI / Hypothetical protein
5971	5049867	5050733	[+3 L= 867]	zfzJ / Hypothetical protein
5972	5050977	5051555	[+3 L= 579]	clpP / ATP-dependent Clp protease proteolytic subunit (Caseinolytic protease) (Stress protein G7)
5973	5052201	5051956	[-1 L= 246]	crhA / Phosphocarrier HPr-like protein (Catabolite repression HPr)
5974	5053184	5052228	[-3 L= 957]	yvcL / Hypothetical protein
5975	5054217	5053267	[-1 L= 951]	yvcK / Hypothetical protein
5976	5055102	5054224	[-1 L= 879]	yvcJ / Hypothetical protein
5977	5055581	5055126	[-3 L= 456]	yvcI / MutT-like protein
5978	5056635	5055814	[-1 L= 822]	zfzL / Hypothetical protein
5979	5057748	5056786	[-1 L= 963]	trxB / Thioredoxin reductase (TRXR) (General stress protein 35)
5980	5059411	5057828	[-2 L=1584]	yvcD / Hypothetical protein
5981	5059988	5059479	[-3 L= 510]	yvoF / O-Acetyltransferase homolog
5982	5060672	5060025	[-3 L= 648]	hprP / HPr(Ser) phosphatase (P-Ser-HPr phosphatase) (phosphoglycolate

				phosphatase)
5984	5061552	5060743	[-1 L= 810]	lgtA / Prolipoprotein diacylglyceryl transferase (Spore germination protein gerF)
5985	5062637	5061582	[-3 L=1056]	hprK / HPr(Ser) kinase/phosphatase
5987	5063117	5062668	[-3 L= 450]	yvlD / Hypothetical protein
5988	5063610	5063164	[-1 L= 447]	zfzM / Hypothetical protein
5990	5066555	5063673	[-3 L=2883]	uvrA / Excinuclease ABC subunit A (DNA repair protein ABC)
5992	5068528	5066555	[-2 L=1974]	uvrB / Excinuclease ABC subunit B
5993	5069110	5068682	[-2 L= 429]	zfzN / Hypothetical protein
5995	5069776	5069159	[-2 L= 618]	zfzO / Hypothetical protein
5996	5070537	5069776	[-1 L= 762]	zfzP / Transcriptional regulator, MerR family
5998	5071222	5071013	[-2 L= 210]	zfzQ / Hypothetical protein
6000	5072583	5071528	[-1 L=1056]	zfzR / Hypothetical protein
6001	5072694	5073590	[+3 L= 897]	ywfK / Transcriptional regulator, LysR family
6002	5073645	5074010	[+3 L= 366]	zfzS / Transcriptional regulator, MerR family
6004	5074018	5074560	[+1 L= 543]	ywqN / Hypothetical protein
6005	5074829	5076460	[+2 L=1632]	zfzT / ABC transporter ATP-binding protein
6006	5076546	5077121	[+3 L= 576]	zfzU / Insertion sequence protein
6007	5077151	5077957	[+2 L= 807]	zfzV / Transposase
6008	5078373	5078020	[-1 L= 354]	zfzW / Hypothetical protein
6009	5080109	5078397	[-3 L=1713]	ywjA / ABC transporter ATP-binding protein
6010	5081583	5080384	[-1 L=1200]	yvjD / Hypothetical protein
6011	5083162	5081678	[-2 L=1485]	yvjB / Carboxy-terminal processing protease
6012	5084171	5083233	[-3 L= 939]	zfzX / Hypothetical protein
6013	5084799	5084116	[-1 L= 684]	zfzY / ABC transporter ATP-binding protein
6014	5085408	5085088	[-1 L= 321]	cytH / Cytochrome c-551 precursor (C551)
6017	5086828	5085851	[-2 L= 978]	pcrF / Peptide chain release factor 2 (RF-2)
6019	5089599	5087095	[-1 L=2505]	secA / Preprotein translocase binding subunit
6020	5090416	5089877	[-2 L= 540]	yvyD / S30EA ribosomal protein homolog
6023	5090943	5090743	[-1 L= 201]	cspC / Cold-shock protein
6024	5091768	5091067	[-1 L= 702]	cmfC /Late competence gene
6025	5092991	5091771	[-3 L=1221]	cmfA / Late competence protein required for DNA uptake
6028	5094444	5093359	[-1 L=1086]	zfzZ / Transposase
6029	5094848	5094444	[-3 L= 405]	zgzA / Transposase-related protein
6030	5096357	5095053	[-3 L=1305]	zgzB / Hypothetical protein
6032	5096934	5096614	[-1 L= 321]	zgzC / Hypothetical protein
6033	5098012	5097101	[-2 L= 912]	yviA / Hypothetical protein
6035	5098177	5098809	[+1 L= 633]	yvyE / Hypothetical protein
6036	5098895	5100016	[+2 L=1122]	yvhJ / Transcriptional regulator homolog
6037	5101174	5100062	[-2 L=1113]	yvyH / UDP-N-acetylglucosamine 2-epimerase homolog
6038	5102574	5101252	[-1 L=1323]	ywqF / UDP-glucose 6-dehydrogenase (UDP-Glc dehydrogenase)
6039	5103109	5104179	[+1 L=1071]	yvhI / Undecaprenyl-phosphate alpha-N-acetylglucosaminyltransferase (UDP-GlcNAc:undecaprenyl-phosphate GlcNAc-1-phosphate transferase)
6041	5104355	5105116	[+2 L= 762]	zgzD / Polysaccharide deacetylase
6042	5105224	5107896	[+1 L=2673]	celR / Transcriptional regulatory protein
6043	5108457	5108047	[-1 L= 411]	zgzE / Hypothetical protein
6044	5108646	5109824	[+3 L=1179]	zgzF / Chromate transport protein homolog
6046	5110574	5109870	[-3 L= 705]	ydjC / Hypothetical protein
6047	5111946	5110624	[-1 L=1323]	licH / 6-phospho-beta-glucosidase
6048	5112330	5111953	[-1 L= 378]	ptcA / PTS system, cellobiose-specific IIA component (Phosphotransferase enzyme II, A component)
6049	5113763	5112459	[-3 L=1305]	ptcC / PTS system, cellobiose-specific IIC component (Cellobiose-permease IIC component) (Phosphotransferase enzyme II, c component)
6050	5113893	5113783	[-1 L= 111]	ptcB / PTS system, cellobiose-specific IIB component (Cellobiose-permease IIB component) (Phosphotransferase enzyme II, b component)
6051	5114083	5113880	[-2 L= 204]	ptcB / PTS system, cellobiose-specific IIB component (Cellobiose-permease IIB component) (Phosphotransferase enzyme II, b component)
6052	5114494	5115591	[+1 L=1098]	speE / Spermidine synthase
6053	5115622	5115990	[+1 L= 369]	speH / S-adenosylmethionine decarboxylase proenzyme 1 (SamDC 1)
6054	5116471	5116157	[-2 L= 315]	ptcA / PTS system, cellobiose-specific IIA component (Phosphotransferase enzyme II, A component)
6055	5117614	5116484	[-2 L=1131]	ptcC / PTS system, cellobiose-specific IIC component (Cellobiose-permease IIC component) (Phosphotransferase enzyme II, c component)
6056	5117783	5117649	[-3 L= 135]	ptcC / PTS system, cellobiose-specific IIC component (Cellobiose-permease IIC component) (Phosphotransferase enzyme II, c component)
6057	5118100	5117801	[-2 L= 300]	ptcB / PTS system, cellobiose-specific IIB component (Cellobiose-

				permease IIB component) (Phosphotransferase enzyme II, b component)
6058	5118325	5119539	[+1 L=1215]	gltT / Proton/sodium-glutamate symport protein (Glutamate-aspartate carrier protein)
6059	5119689	5120864	[+3 L=1176]	zgzG / Hypothetical protein
6060	5120907	5121284	[+3 L= 378]	zgzH / Glyoxalase/Belomycin resistance protein homolog
6061	5123328	5121331	[-1 L=1998]	yhgE / Hypothetical protein
6062	5123464	5124345	[+1 L= 882]	yybE / Transcriptional regulator, LysR family
6063	5125490	5124399	[-3 L=1092]	ydaJ / Hypothetical protein
6065	5125951	5127330	[+1 L=1380]	ythA / Cytochrome D ubiquinol oxidase subunit I
6066	5127296	5128348	[+2 L=1053]	ythB / Cytochrome D ubiquinol oxidase subunit II
6067	5128743	5130098	[+3 L=1356]	ywrK / Arsenical pump membrane protein homolog
6069	5132014	5130206	[-2 L=1809]	thiC / Thiamine biosynthesis protein
6070	5133924	5132266	[-1 L=1659]	zgzI / L-Lactate permease
6072	5134161	5134535	[+3 L= 375]	zgzJ / Hypothetical protein
6073	5135100	5134612	[-1 L= 489]	zgzK / Hypothetical protein
6074	5135591	5135154	[-3 L= 438]	zgzL / Hypothetical protein
6076	5136063	5137988	[+3 L=1926]	zgzM / Sulfatase
6077	5138586	5139503	[+3 L= 918]	daaA / D-alanine aminotransferase (D-amino acid aminotransferase) (DAAT)
6080	5139716	5141446	[+2 L=1731]	zgzN / Peptidase homolog
6082	5141817	5143025	[+3 L=1209]	yutK / Sodium/nucleoside cotransporter homolog
6083	5143290	5144042	[+3 L= 753]	zgzO / Viral capsid protein
6084	5144042	5145340	[+2 L=1299]	ydaM / Cellulose synthase homolog
6086	5147519	5145969	[-3 L=1551]	opuD / Glycine betaine transporter
6087	5148070	5149020	[+1 L= 951]	zgzP / Hypothetical protein
6088	5149109	5149408	[+2 L= 300]	zgzQ / Hypothetical protein
6089	5150921	5149545	[-3 L=1377]	zgzR / Hypothetical protein
6091	5152484	5150937	[-3 L=1548]	zgzS / Hypothetical protein
6092	5153002	5152493	[-2 L= 510]	zgzT / Hypothetical protein
6093	5153140	5154756	[+1 L=1617]	ywqB / Hypothetical protein
6094	5154743	5157496	[+2 L=2754]	ywqA / SNF2 helicase homolog
6095	5158048	5157566	[-2 L= 483]	zgzU / Hypothetical protein
6096	5158151	5158381	[+2 L= 231]	zgzV / Hypothetical protein
6097	5158501	5158713	[+1 L= 213]	zgzW / Hypothetical protein
6099	5159136	5158741	[-1 L= 396]	zgzY / Hypothetical protein
6100	5159329	5159802	[+1 L= 474]	zgzZ / Hypothetical protein
6101	5160335	5159868	[-3 L= 468]	zhzA / Sigma-70 factor
6102	5161222	5160557	[-2 L= 666]	zhzB / Hypothetical protein
6103	5162547	5161339	[-1 L=1209]	yknZ / Hypothetical protein
6104	5163215	5162538	[-3 L= 678]	zhzC / ABC transporter ATP-binding protein
6105	5164405	5163215	[-2 L=1191]	zhzD / ABC transporter exported solute-binding protein
6106	5164775	5164978	[+2 L= 204]	zhzE / Hypothetical protein
6108	5166938	5165607	[-3 L=1332]	zhzF / Sugar transporter homolog
6109	5167992	5166961	[-1 L=1032]	zhzG / Extracelllular solute-binding protein
6110	5168771	5167992	[-3 L= 780]	zhzH / Hypothetical protein
6111	5170286	5168841	[-3 L=1446]	zhzI / Two-component sensor histidine-kinase
6112	5171062	5170283	[-2 L= 780]	zhzJ / Two-component response regulator
6113	5172064	5171075	[-2 L= 990]	galE / UDP-glucose 4-epimerase (Galactowaldenase) (UDP-galactose 4-epimerase)
6114	5172979	5172152	[-2 L= 828]	zhzK / Hypothetical protein
6115	5173992	5173081	[-1 L= 912]	lytR / Membrane-bound attenuator protein for lytABC expression
6116	5175554	5174136	[-3 L=1419]	zhzL / Hypothetical protein
6117	5176782	5175709	[-1 L=1074]	ggaB / Minor teichoic acids biosynthesis protein
6118	5178155	5176716	[-3 L=1440]	zhzM / Hypothetical protein
6119	5179476	5178208	[-1 L=1269]	zhzN / Hypothetical protein
6120	5180093	5179479	[-3 L= 615]	zhzO / Hypothetical protein
6121	5180976	5180074	[-1 L= 903]	zhzP / Hypothetical protein
6122	5182163	5181051	[-3 L=1113]	zhzQ / Hypothetical protein
6123	5183397	5182183	[-1 L=1215]	zhzR / Capsular polysaccharide biosynthesis protein
6124	5185305	5183500	[-1 L=1806]	yveM / Capsular polysaccharide biosynthesis protein
6125	5186248	5185370	[-2 L= 879]	gtaB / UTP--glucose-1-phosphate uridylyltransferase (UDP-glucose pyrophosphorylase) (General stress protein 33)
6126	5187273	5186500	[-1 L= 774]	ywqE / Capsular polysaccharide biosynthesis protein / tyrosine phosphatase homolog
6127	5188077	5187379	[-1 L= 699]	ywqD / Capsular polysaccharide biosynthesis protein / tyrosine-protein kinase homolog

6128	5188822	5188070	[-2 L= 753]	ywqC / Capsular polysaccharide biosnthesis protein
6129	5189847	5189077	[-1 L= 771]	yveL / Capsular polysaccharide biosynthesis protein / tyrosine-protein kinase homolog
6130	5190530	5190099	[-3 L= 432]	fabZ / (3R)-hydroxymyristoyl-[acyl carrier protein] dehydratase ((3R)-hydroxymyristoyl ACP dehydrase)
6131	5191988	5190963	[-3 L=1026]	mblA / MreB-like protein / Cell shape determining protein
6132	5192520	5192125	[-1 L= 396]	spcD / Stage III sporulation protein D (14 kDa transcription factor)
6134	5193884	5192982	[-3 L= 903]	spbQ / Stage II sporulation protein Q (required for completion of engulfment)
6135	5194751	5194050	[-3 L= 702]	zhzS / Hypothetical protein
6136	5195593	5194754	[-2 L= 840]	zhzT / ABC transporter ATP-binding protein
6138	5196782	5195778	[-3 L=1005]	zhzU / ABC transporter ATP-binding protein
6139	5197953	5196886	[-1 L=1068]	spbD / Stage II sporulation protein D
6141	5199414	5198113	[-1 L=1302]	muaA / UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1 (Enoylpyruvate transferase 1)
6142	5200164	5199457	[-1 L= 708]	ywmB / Hypothetical protein
6143	5200446	5200213	[-1 L= 234]	ywzB / Hypothetical protein
6144	5202169	5200652	[-2 L=1518]	nunB / NADH-quinone oxidoreductase chain N 2 (NADH dehydrogenase i, chain N 2)
6145	5203673	5202174	[-3 L=1500]	nuoM / NADH-quinone oxidoreductase chain M (NADH dehydrogenase i, chain M)
6146	5205532	5203673	[-2 L=1860]	nueC / NAD(P)H-quinone oxidoreductase chain 5 (NAD(P)H dehydrogenase I, chain 5)
6147	5205877	5205566	[-2 L= 312]	nulC / NAD(P)H-quinone oxidoreductase chain 4L, (NAD(P)H dehydrogenase, chain 4L)
6148	5206394	5205873	[-3 L= 522]	nufC / NAD(P)H-quinone oxidoreductase chain 6 (NAD(P)H dehydrogenase I, chain 6
6149	5206810	5206394	[-2 L= 417]	nuiM / NADH-ubiquinone oxidoreductase 23 kDa subunit (Complex I-23KD)
6150	5207837	5206839	[-3 L= 999]	nuaM / NADH-ubiquinone oxidoreductase chain 1
6152	5208937	5207840	[-2 L=1098]	nudB / NADH-quinone oxidoreductase chain D 2 (NADH dehydrogenase i, chain D 2)
6153	5210181	5208943	[-1 L=1239]	zhzV / NADH-quinone oxidoreductase 30 Kd subunit (Complex I-30KD)
6154	5210717	5210181	[-3 L= 537]	nuoB / NADH-quinone oxidoreductase chain B (NADH dehydrogenase i, chain B)
6155	5211055	5210690	[-2 L= 366]	nucC / NAD(P)H-quinone oxidoreductase chain 3 (NAD(P)H dehydrogenase, chain 3)
6156	5211310	5214036	[+1 L=2727]	zhzW / Hypothetical protein
6157	5214707	5214066	[-3 L= 642]	zhzX / Hypothetical protein
6158	5214942	5214760	[-1 L= 183]	zhzX / Hypothetical protein
6159	5215643	5214942	[-3 L= 702]	zhzX / Hypothetical protein
6160	5216088	5215690	[-1 L= 399]	atpE / ATP synthase epsilon chain (ATP synthase F1 sector epsilon subunit)
6161	5217515	5216112	[-3 L=1404]	atpB / ATP synthase beta chain
6163	5218616	5217759	[-3 L= 858]	atpG / ATP synthase gamma chain
6164	5220471	5218957	[-1 L=1515]	atpA / ATP synthase alpha chain
6165	5221016	5220477	[-3 L= 540]	atpD / ATP synthase delta chain
6166	5221519	5221016	[-2 L= 504]	atpF / ATP synthase B chain
6168	5221867	5221652	[-2 L= 216]	atpL / ATP synthase C chain (Lipid-binding protein)
6169	5222643	5221927	[-1 L= 717]	atpG / ATP synthase A chain (Protein 6)
6170	5223046	5222654	[-2 L= 393]	atpZ / ATP SYNTHASE PROTEIN I
6174	5224416	5223790	[-1 L= 627]	uppA / Uracil phosphoribosyltransferase (UMP pyrophosphorylase)
6175	5225933	5224692	[-3 L=1242]	glyA / Serine hydroxymethyltransferase (Serine methylase)
6176	5226801	5226187	[-1 L= 615]	ywlG / Hypothetical protein
6177	5227266	5226826	[-1 L= 441]	ywlF / Ribose-5-phosphate epimerase homolog
6178	5227804	5227367	[-2 L= 438]	ywlE / Low molecular weight protein-tyrosine-phosphatase
6179	5228544	5228050	[-1 L= 495]	ypqE / PTS system IIA component (phosphotransferase system glucose-specific enzyme II)
6180	5228931	5229314	[+3 L= 384]	zhzY / Hypothetical protein
6181	5229476	5230084	[+2 L= 609]	ywrF / Hypothetical protein
6182	5230559	5230284	[-3 L= 276]	zhzZ / Hypothetical protein
6183	5231338	5230793	[-2 L= 546]	ywlD / Hypothetical protein
6184	5232456	5231419	[-1 L=1038]	ywlC / Hypothetical protein
6185	5233023	5232568	[-1 L= 456]	ywlB / Hypothetical protein
6186	5233948	5233076	[-2 L= 873]	spbR / Stage II sporulation protein R
6187	5234903	5234055	[-3 L= 849]	ywkE / Protoporphyrinogen oxidase homolog
6188	5235979	5234906	[-2 L=1074]	prfA / Peptide chain release factor 1 (RF-1)

6189	5237071	5236487	[-2 L= 585]	kitH / Thymidine kinase
6190	5237512	5237183	[-2 L= 330]	rpmE / 50S ribosomal protein L31 type B
6192	5239425	5238157	[-1 L=1269]	rhoA / Transcription termination factor rho
6193	5240785	5239823	[-2 L= 963]	ywjI / Glycerol-inducible protein
6195	5242191	5240905	[-1 L=1287]	muaB / UDP-N-acetylglucosamine 1-carboxyvinyltransferase 2 (Enoylpyruvate transferase 2) (UDP-N-acetylglucosamine enolpyruvyl transferase 2)
6196	5243381	5242527	[-3 L= 855]	alfA / Fructose-bisphosphate aldolase
6197	5243969	5243595	[-3 L= 375]	spaF / Sporulation initiation phosphotransferase F (Stage 0 sporulation protein F)
6198	5244162	5244683	[+3 L= 522]	ywjG / Hypothetical protein
6199	5246325	5244721	[-1 L=1605]	pyrG / CTP synthase (UTP--ammonia ligase)
6201	5247116	5246586	[-3 L= 531]	rpoE / DNA-directed RNA polymerase delta subunit (RNAP delta factor)
6202	5247909	5247274	[-1 L= 636]	zizA / Transcriptional regulator, TetR/AcrR family
6203	5249106	5247970	[-1 L=1137]	acdA / Acyl-CoA dehydrogenase
6204	5250273	5249131	[-1 L=1143]	acdB / Acyl-CoA dehydrogenase
6205	5251184	5250366	[-3 L= 819]	hbdA / 3-hydroxybutyryl-CoA dehydrogenase (Beta-hydroxybutyryl-CoA dehydrogenase)
6206	5252516	5251236	[-3 L=1281]	thlA / Acetyl-CoA acetyltransferase (Acetoacetyl-CoA thiolase)
6208	5254688	5252529	[-3 L=2160]	ywjF / Iron-sulfur-binding reductase homolog
6210	5255084	5256274	[+2 L=1191]	ywjE / Cardiolipin synthetase homolog
6211	5256244	5257260	[+1 L=1017]	uvsE / UV DNA damage endonuclease (UV-endonuclease)
6212	5257273	5259669	[+1 L=2397]	ykoW / Hypothetical protein
6213	5259923	5260063	[+2 L= 141]	ykoW / Hypothetical protein
6214	5260229	5260086	[-3 L= 144]	zizB / Hypothetical protein
6215	5261174	5260320	[-3 L= 855]	plcR / Transcriptional activator
6216	5261343	5263091	[+3 L=1749]	nprM / Bacillolysin precursor (neutral metalloprotease)
6217	5263614	5263192	[-1 L= 423]	yvfU / Two-component response regulator
6218	5264886	5263759	[-1 L=1128]	zizC / Two-component sensor histidine kinase
6219	5265621	5264890	[-1 L= 732]	yvfS / Hypothetical protein
6220	5266520	5265621	[-3 L= 900]	yvfR / ABC transporter ATP-binding protein
6221	5266678	5267469	[+1 L= 792]	yflG / Methionine aminopeptidase homolog
6222	5268226	5269269	[+1 L=1044]	zizD / Hypothetical protein
6224	5269419	5277644	[+3 L=8226]	zizE / Hypothetical protein
6225	5278098	5279534	[+3 L=1437]	ywaD / Leucine aminopeptidase homolog
6227	5280757	5280089	[-2 L= 669]	syiS / Seryl-tRNA synthetase (Serine--tRNA ligase)
6228	5281055	5280753	[-3 L= 303]	zizF / Hypothetical protein
6229	5281665	5281045	[-1 L= 621]	sigW / RNA polymerase sigma factor
6230	5283515	5281848	[-3 L=1668]	syiR / Arginyl-tRNA synthetase (Arginine--tRNA ligase)
6231	5283970	5283518	[-2 L= 453]	zizG / Hypothetical protein
6233	5284101	5285138	[+3 L=1038]	yocD / Hypothetical protein
6234	5285550	5285170	[-1 L= 381]	zizH / Hypothetical protein
6235	5285718	5286797	[+3 L=1080]	zizI / Hypothetical protein
6236	5288100	5287231	[-1 L= 870]	ywhG / Agmatinase homolog
6237	5289145	5288321	[-2 L= 825]	speE / Spermidine synthase (Putrescine aminopropyltransferase)
6238	5290495	5289335	[-2 L=1161]	zizJ / Multidrug-efflux transporter homolog
6239	5290926	5290504	[-1 L= 423]	yfmP / Transcriptional regulator, MerR family
6241	5291121	5291783	[+3 L= 663]	zizK / Glyerophosphoryl diester phosphodiesterase
6242	5291887	5293935	[+1 L=2049]	ywhE / Penicillin-binding protein homolog
6243	5294500	5293976	[-2 L= 525]	ywhD / Hypothetical protein
6244	5295182	5294511	[-3 L= 672]	ywhC / Hypothetical protein
6246	5295295	5295477	[+1 L= 183]	ywhB / 4-Oxocrotonate tautomerase homolog
6247	5296824	5295523	[-1 L=1302]	ywfO / Hypothetical protein
6248	5297146	5296973	[-2 L= 174]	zizL / ABC transporter protein
6249	5297909	5297032	[-3 L= 828]	zizL / ABC transporter protein
6250	5298911	5298102	[-3 L= 810]	fhuC / Ferrichrome transport ATP-binding protein
6251	5299943	5298930	[-3 L=1014]	fhuG / Ferrichrome transport system permease protein
6252	5300995	5299943	[-2 L=1053]	fhuB / Ferrichrome transport system permease protein
6253	5301532	5301311	[-2 L= 222]	ywzC / Hypothetical protein
6254	5301817	5302506	[+1 L= 690]	rsfA / Prespore specific transcriptional activator
6256	5302638	5303480	[+3 L= 843]	ywfL / Hypothetical protein
6257	5304503	5303535	[-3 L= 969]	ptaA / Phosphate acetyltransferase (Phosphotransacetylase) (Vegetative protein 43)
6258	5304750	5305499	[+3 L= 750]	ywfI / Hypothetical protein
6259	5305669	5306970	[+1 L=1302]	dacA / D-alanyl-D-alanine carboxypeptidase precursor (DD-carboxypeptidase)
6260	5307293	5307712	[+2 L= 420]	cwlJ / Cell wall hydrolase (sporulation)
6262	5307743	5308168	[+2 L= 426]	ywdL / Hypothetical protein

6264	5308570	5308205	[-2 L= 366]	ywdK / Hypothetical protein
6265	5308922	5308638	[-3 L= 285]	ywdI / Hypothetical protein
6266	5309933	5308932	[-3 L=1002]	zizM / Hypothetical protein
6267	5309999	5311105	[+2 L=1107]	ywdJ / Purine permease
6269	5311529	5312347	[+2 L= 819]	zizN / Haloacid dehalogenase homolog
6270	5312560	5312850	[+1 L= 291]	ydzA / Hypothetical protein
6271	5313572	5312898	[-3 L= 675]	ungA / Uracil-DNA glycosylase (UDG)
6272	5314608	5313595	[-1 L=1014]	zizO / Hypothetical protein
6273	5315494	5314580	[-2 L= 915]	yhcH / ABC transporter ATP-binding protein
6274	5316372	5315494	[-1 L= 879]	zizP / Hypothetical protein
6275	5317360	5316386	[-2 L= 975]	zizQ / Hypothetical protein
6276	5317458	5318081	[+3 L= 624]	zizR / Hypothetical protein
6277	5319422	5318118	[-3 L=1305]	dhoM / Homoserine dehydrogenase (HDH)
6278	5320472	5319555	[-3 L= 918]	metA / Homoserine O-succinyltransferase (Homoserine o-transsuccinylase)
6279	5321739	5320444	[-1 L=1296]	cysD / O-acetylhomoserine (Thiol)-lyase (O-acetylhomoserine sulfhydrylase) (Homocysteine synthase)
6281	5322258	5323484	[+3 L=1227]	zizS / Hypothetical protein
6282	5324228	5323536	[-3 L= 693]	yfnB / Hypothetical protein
6283	5324336	5325004	[+2 L= 669]	zizT / Hypothetical protein
6284	5325695	5325072	[-3 L= 624]	acdA / Acyl carrier protein phosphodiesterase 1 (ACP phosphodiesterase 1)
6285	5326534	5325890	[-2 L= 645]	zizU / Two-component response regulator
6286	5328132	5326558	[-1 L=1575]	zizV / Two-component sensor histidine kinase
6288	5328261	5329082	[+3 L= 822]	thiD / Phosphomethylpyrimidine kinase (HMP-phosphate kinase)
6289	5330229	5329174	[-1 L=1056]	zizW / Hypothetical protein
6290	5330599	5330378	[-2 L= 222]	zizX / Hypothetical protein
6291	5332661	5330574	[-3 L=2088]	cstA / Carbon starvation protein A
6292	5333497	5332772	[-2 L= 726]	zizY / Two-component response regulator
6294	5334903	5333707	[-1 L=1197]	yceI / Hypothetical metabolite transport protein
6295	5335858	5335121	[-2 L= 738]	tagA / Teichoic acid biosynthesis protein A
6296	5336989	5335883	[-2 L=1107]	zizZ / Glycosyltransferase homolog
6298	5338576	5337245	[-2 L=1332]	zjzA / Hypothetical protein
6299	5339021	5339650	[+2 L= 630]	zjzB / Hypothetical protein
6300	5339785	5341086	[+1 L=1302]	hmaT / Heme-based aerotactic transducer
6301	5342613	5341303	[-1 L=1311]	zjzC / Hypothetical protein
6302	5342912	5343421	[+2 L= 510]	ykhA / Acyl-CoA thioester hydrolase
6303	5343583	5344359	[+1 L= 777]	zjzD / Hypothetical protein
6305	5346117	5344810	[-1 L=1308]	zjzE / Hypothetical protein
6306	5346310	5347287	[+1 L= 978]	zjzF / Hypothetical protein
6307	5347388	5348800	[+2 L=1413]	zjzG / Hypothetical protein
6309	5349125	5351827	[+2 L=2703]	yfhO / Hypothetical protein
6310	5351914	5352849	[+1 L= 936]	ccsB / Stress response protein
6311	5352952	5354559	[+1 L=1608]	zjzH / ABC transporter ATP-binding protein
6312	5355489	5354617	[-1 L= 873]	yuxN / Transcriptional regulator, TetR family
6313	5355630	5358743	[+3 L=3114]	yerP / Acriflavin resistance protein homolog
6314	5359729	5358767	[-2 L= 963]	msaB / Peptide methionine sulfoxide reductase
6315	5360864	5359824	[-3 L=1041]	zjzI / Hypothetical protein
6316	5361879	5361190	[-1 L= 690]	ysbB / Hypothetical protein
6318	5362427	5361918	[-3 L= 510]	ysbA / Hypothetical protein
6319	5363219	5362482	[-3 L= 738]	lytR / Two-component response regulator
6320	5364966	5363200	[-1 L=1767]	lytS / Two-component sensor histidine kinase
6321	5365293	5366588	[+3 L=1296]	zjzJ / Sugar transporter homolog
6322	5368212	5366647	[-1 L=1566]	opuD / Glycine betaine transporter
6323	5369650	5368577	[-2 L=1074]	nosO / Nitric oxide synthase oxygenase (NOSoxy-like protein)
6324	5369862	5370485	[+3 L= 624]	sodM / Superoxide dismutase [Mn]
6325	5370924	5370580	[-1 L= 345]	zjzK / Isoflavone reductase homolog
6326	5371463	5371131	[-3 L= 333]	zjzK / Isoflavone reductase homolog
6328	5372153	5371566	[-3 L= 588]	zjzL / Hypothetical protein
6329	5373666	5372602	[-1 L=1065]	galE / UDP-glucose 4-epimerase (Galactowaldenase) (UDP-galactose 4-epimerase)
6330	5374461	5373802	[-1 L= 660]	zjzM / Hypothetical protein
6331	5374611	5375168	[+3 L= 558]	zjzN / Hypothetical protein
6332	5376657	5375215	[-1 L=1443]	dbpA / ATP-dependent RNA helicase
6333	5377130	5378113	[+2 L= 984]	yumD / GMP reductase homolog
6334	5378253	5380067	[+3 L=1815]	pepF / Oligoendopeptidase F homolog
6336	5380988	5380113	[-3 L= 876]	zjzO / Hypothetical protein
6337	5383226	5381211	[-3 L=2016]	zjzP / Hypothetical protein

6338	5383843	5383298	[-2 L= 546]	yydA / Hypothetical protein
6340	5384028	5383837	[-1 L= 192]	zjzQ / Hypothetical protein
6341	5385248	5384076	[-3 L=1173]	yyxA / Serine protease homolog
6342	5385542	5385315	[-3 L= 228]	yycJ / Metallo-beta-lactamase homolog
6343	5386107	5385523	[-1 L= 585]	yycJ / Metallo-beta-lactamase homolog
6344	5386933	5386094	[-2 L= 840]	yycI / Hypothetical protein
6345	5388236	5386917	[-3 L=1320]	yycH / Hypothetical protein
6347	5390068	5388230	[-2 L=1839]	yycG / Two-component sensor histidine kinase
6348	5390779	5390075	[-2 L= 705]	yycF / Two-component response regulator
6349	5392974	5391580	[-1 L=1395]	purA / Adenylosuccinate synthetase (IMP--aspartate ligase)
6350	5393318	5393085	[-3 L= 234]	dnaC / Replicative DNA helicase
6351	5394448	5393318	[-2 L=1131]	dnaC / Replicative DNA helicase
6352	5394916	5394473	[-2 L= 444]	rplI / 50S ribosomal protein L9 (BL17)
6353	5396886	5394916	[-1 L=1971]	yybT / Hypothetical protein
6354	5397900	5396968	[-1 L= 933]	yybS / Hypothetical protein
6355	5398213	5397983	[-2 L= 231]	rpsR / 30S ribosomal protein S18 (BS21)
6356	5398780	5398262	[-2 L= 519]	ssbA / Single-strand binding protein (SSB) (Helix-destabilizing protein)
6357	5399139	5398801	[-1 L= 339]	rpsF / 30S ribosomal protein S6 (BS9)
6358	5400389	5399283	[-3 L=1107]	yyaF / GTP-binding protein homolog
6359	5400693	5400499	[-1 L= 195]	zjzR / Hypothetical protein
6360	5401595	5400717	[-3 L= 879]	zjzS / Hypothetical protein
6361	5401855	5402448	[+1 L= 594]	yyaC / Hypothetical protein
6362	5403329	5402475	[-3 L= 855]	spaJ / Stage 0 sporulation protein J
6363	5404095	5403319	[-1 L= 777]	spoJ / Sporulation initiation inhibitor protein
6364	5405140	5404271	[-2 L= 870]	yyaA / DNA-binding protein homolog
6365	5405965	5405249	[-2 L= 717]	gidB / Methyltransferase (Glucose inhibited division protein B)
6366	5407876	5405990	[-2 L=1887]	gidA / Glucose inhibited division protein A
6367	5409299	5407926	[-3 L=1374]	trmE / tRNA modification GTPase
6368	5410143	5409529	[-1 L= 615]	jagA / Jag protein (SpoIIIJ associated protein)
6369	5410916	5410143	[-3 L= 774]	spcJ / Stage III sporulation protein J precursor
6370	5411328	5410972	[-1 L= 357]	rnpA / Ribonuclease P protein component (RNaseP protein)
6371	5411527	5411396	[-2 L= 132]	rpmH / 50S ribosomal protein L34
6372	5412092	5412415	[+2 L= 324]	dnaA / Chromosomal replication initiator protein

***Table 4**. The enzymes of the methylthioadenosine cycle in B. cereus 14579 and B. subtilis 168. The location and identification of the genes involved in polyamine synthesis and the subsequent recycling of methionine and adenine are shown for both organisms. The enzymes are listed in order of their functionality in the cycle (see Figure 1 in [23]). The start and stop columns reflect the beginning and end of the open-reading frame, while the minutes column lists the location of the gene on the circular chromosome (in minutes and seconds).*

Enzyme	Putative gene	B. cereus 14579			B. subtilis 168		
		Start	Stop	Minutes	Start	Stop	Minutes
methionine adenosyltransferase	metK	4695519	4694323	52.03	3126877	3128076	44.31
S-adenosylmethionine decarboxylase	speH	4527578	4527189	50.11	2965456	296839	42.13
spermidine synthase	speE	5289145	5288321	58.38	3847812	3848639	54.47
methylthioadenosine nucleosidase	mtnA	4309131	4308439	47.46	2786360	2787052	39.39
methylthioribose kinase	ykrT	4007752	4006574	44.25	1422552	1423748	20.15
methylthioribose-phosphate isomerase	ykrY	4012243	4012878	44.28	1428248	1428874	20.19
methylthioribulose-phosphate dehydratase	ykrW	4010346	4011587	44.27	1426342	1427583	20.18
enolase-phosphatase	ykrX	4011587	4012243	44.28	1427583	1428287	20.19
dioxygenase	ykrZ	4012859	4013368	44.28	1428892	1429425	20.19
aminotransferase	ilvE	1358466	1359359	15.03	259004	260071	3.41

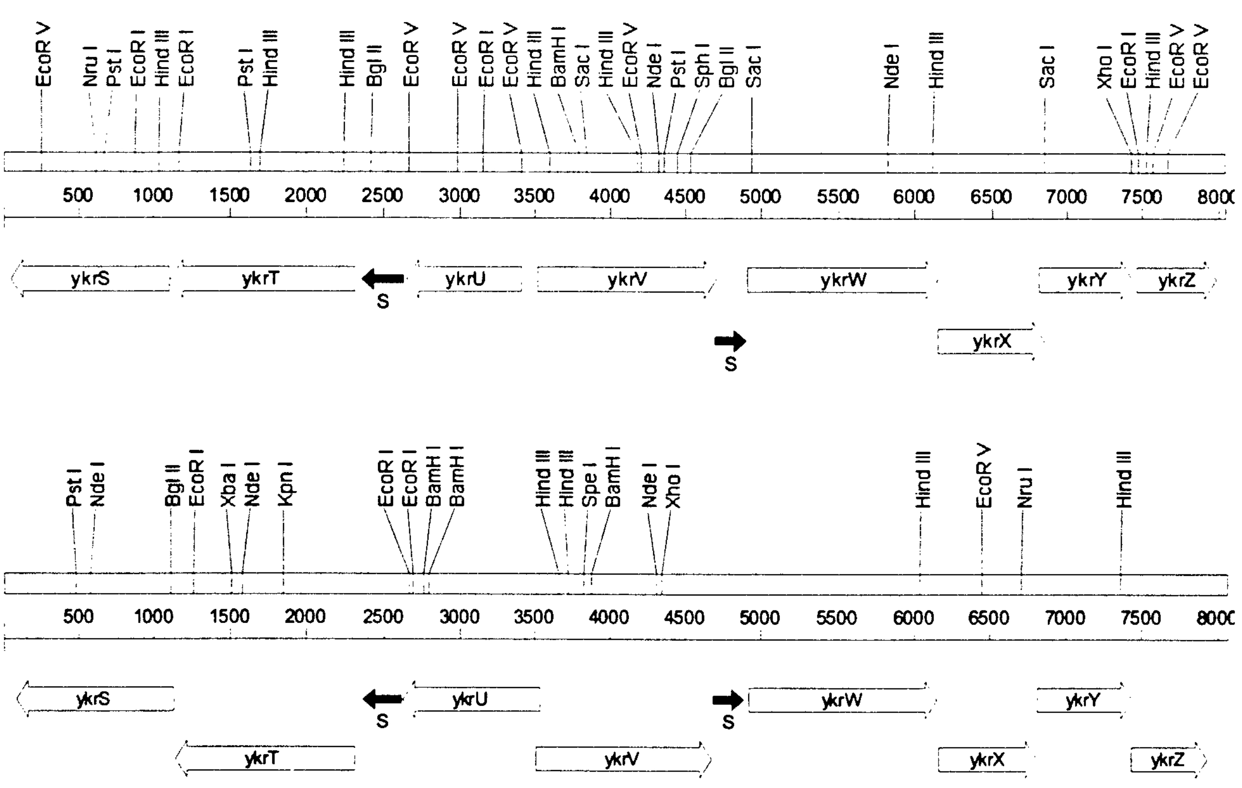

***Figure 8**. The organisation of the ykr locus involved in methionine recycling. An 8000 bp region containing the ykr locus from B. subtilis 168 (top) and B. cereus 14579 (bottom) is shown, along with restriction endonuclease sites in each sequence. The protein encoding genes are shown with the white arrows, while the S-box transcriptional control sequences [27] are shown with black arrows. Arrows are shifted to new lines where DNA sequence overlaps.*

Metabolic Pathways in *B. cereus*

The annotation contained in Table 3 was used in conjunction with the KEGG metabolic database (www.genome.ad.jp/kegg) in order to reconstruct the metabolic pathways present in *B. cereus* 14579. Figures 9-68 show KEGG metabolic pathways which have been edited to reflect only those enzymes detectable in Table 3 above. As would be expected for a versatile facultative pathogen, *B. cereus* contains a broad range of pathways for both independent, synthetic and for parasitic, acquisative lifestyles. The organism has a complete glycolytic pathway, tricarboxylic acid cycle, and oxidative phosphorylation system (Figures 9, 10, and 25). Interestingly, unlike *B. subtilis* 168, *B. cereus* appears unable to degrade a wide variety of carbohydrate polymers to simple carbohydrates and appears dependent on glycogen, starch, and chitin catabolism or on direct import of simple carbohydrates (Figures 9, 64, 65). Similarly, the range of conversion pathways between various simple carbohydrates is reduced when compared to *B. subtilis* 168 (Figures 12-15, 64, 65). Given the large number of amino acid transporters and proteases/peptidases found in the *B. cereus* genome (Table 3), it would appear that *B. cereus* is more reliant on metabolism of exogenous proteins than on complex carbohydrates as an energy source. This conclusion is supported by the insect/mammalian niche exploited by the *B. cereus* complex as opposed to the soil niche inhabited by *B. subtilis.*

B. cereus 14579 has an almost complete pentose-phosphate pathway but, like *B. subtilis* 168, lacks 6-phosphogluconolactonase (Figure 11). This gap would suggest that the pathways, as seen in Figure 11, primarily function in order to synthesize pentoses rather than to reduce $NADP^+$. *B. cereus* also has a complete glyoxylate cycle (Figure 17), facilitating energy production from exogenous acetate (Figure 16) or acetylCoA from fatty acid metabolism (Figure 23).

The organism has the ability to synthesize both purines and pyrimidines and can interconvert and salvage most nucleosides (Figures 29 and 30). As with simple sugar metabolism, *B. cereus* has a rather limited capability for nucleosugar interconversion and had enzymes for forming UDP-glucose, UDP-galactose, UDP-glucuronate, TDP-galactose, TDP-glucose, TDP-rhamnose, and GDP-rhamnose (Figure 31).

B. cereus has a complete urea cycle and the enzymes necessary for energy production from proline (Figures 32 and 42). For polyamine biosynthesis, *B. cereus* was found to contain arginine decarboxylase and agmatinase (Figure 42) rather than ornithine decarboxylase. Despite the fact that *B. cereus* is generally grown in minimal medium with supplementation of threonine, serine, leucine, valine, and alanine [28], the organism has the theoretical metabolic capability of synthesizing all amino acids (Figures 33-37, 39, 40, 42, 43, 47). While Figure 34 shows the absence of a specific alanine aminotransferase for synthesizing alanine from pyruvate, other aminotransferases should be able to catalyse the reaction. Not all amino acids appear to be possible energy sources (Figures 33-37, 38, 41, 44-46), with only glutamate, glutamine, aspartate, asparagine, serine, glycine, threonine, isoleucine, arginine, proline, and histidine having unambiguous routes to energy producing intermediates. D-alanine is also synthesized and useable as an energy source (Figure 54). Interestingly, *B. cereus* 14579 lacks the enzymes for glutathione biosynthesis and also lacks glutathione reductase (Figure 55).

However, enzymes do exist for degrading glutathione, perhaps as available exogenously. Given the large number of thioredoxins encoded in the *B. cereus* 14579 genome (Table 3) and the presence of thioredoxin reductase and thiorerdoxin peroxidase, it would appear that B. cereus uses thioredoxin as the central redox balancing and detoxification system.

B. cereus 14579 was found to contain the biosynthetic pathways for all the major vitamins and cofactors, including thiamine (Figure 56), riboflavin and FAD (Figure 57), NADH and NADPH (Figure 58), pantothenate and coenzyme A (Figure 59), biotin (Figure 60), folic acid (Figure 62), and heme (Figure 63).

Figures 9 – 68 *(next 59 pages). Metabolic pathways of B. cereus 14579. The putative proteome of B. cereus (Table 1) was searched for the presence of each enzyme contained in the KEGG metabolism database (www.genome.ac.jp/kegg). The pathway graphics from KEGG were then edited accordingly to remove non-existant or ambigous enzymes. The graphics on the following pages show the substrates, products, and EC (Enzyme Commission) numbers for enzymes present in B. cereus. White-space within each frame is due to the removal of enzymes not found in B. cereus. The graphics can be used with Appendix 1 to determine the identity of a particular enzyme. Alternatively, hyperlinked source graphics can be found at the KEGG site which wile allow access to identification and additional information on each enzyme. The source graphics at KEGG also show all the pathways which were removed in these figures.*

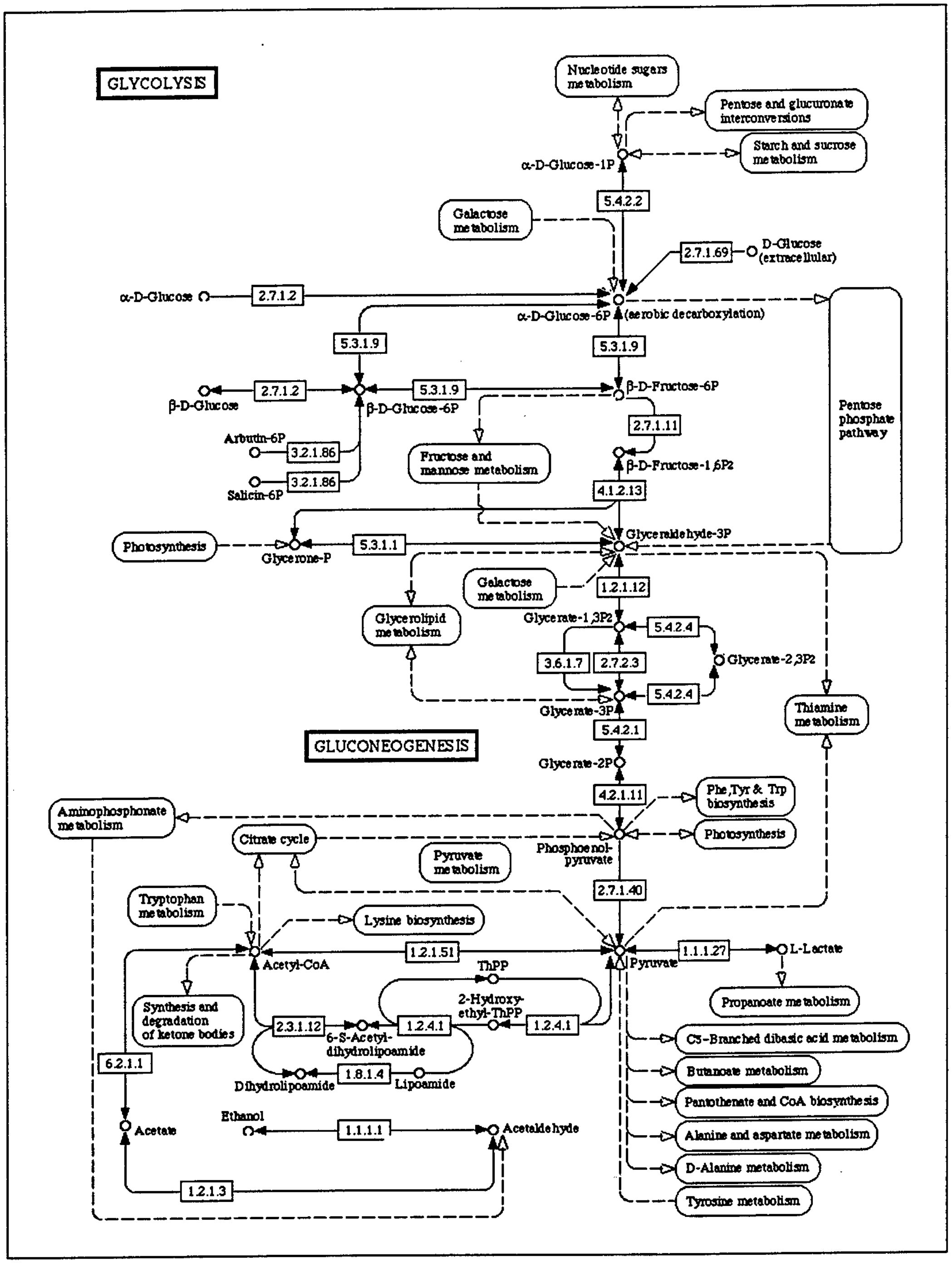

Figure 9. *Metabolic pathways of B. cereus 14579: glycolysis and gluconeogenesis.*

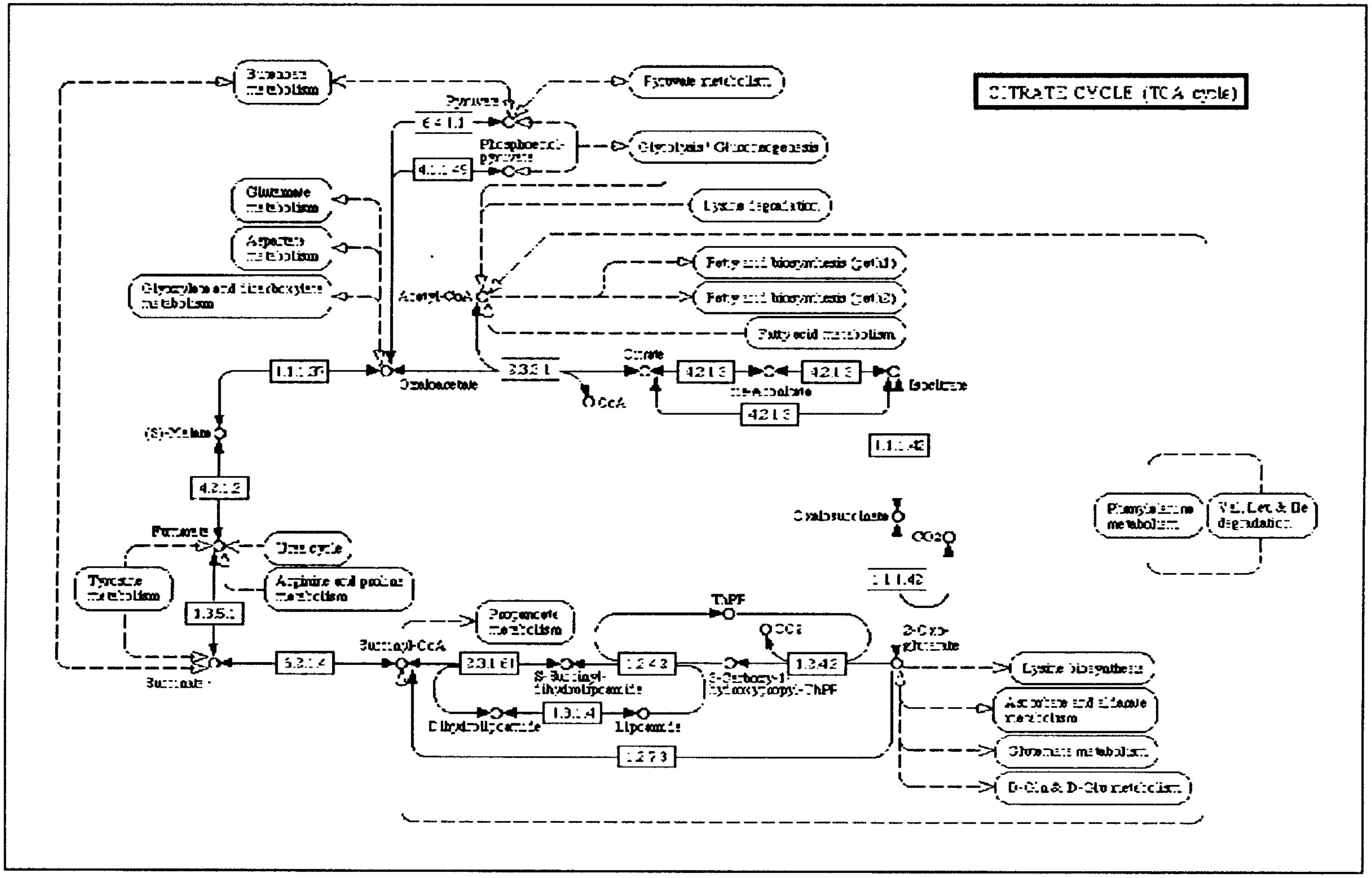

Figure 10. Metabolic pathways of B. cereus 14579: the citrate (TCA) cycle.

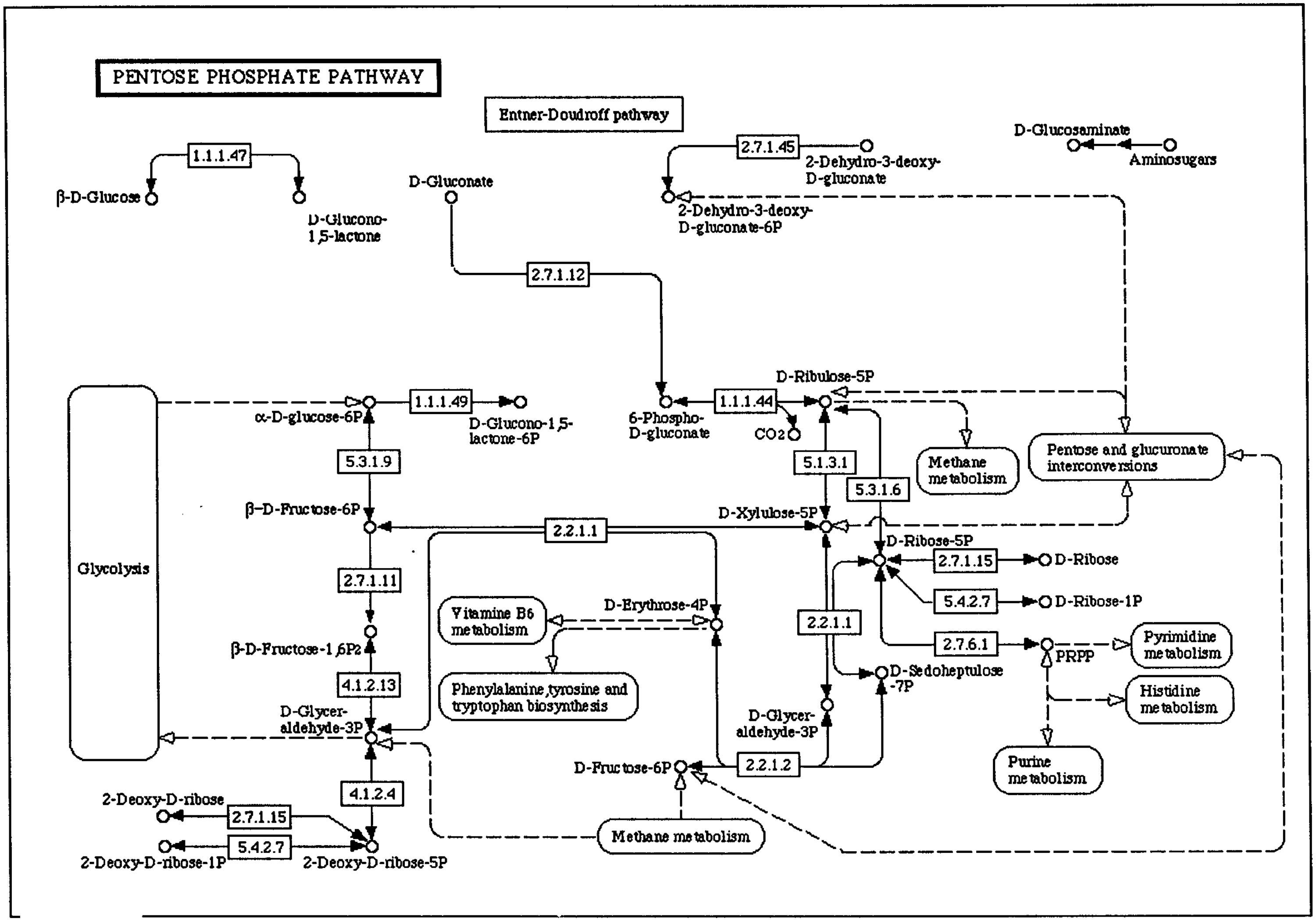

Figure 11. Metabolic pathways of B. cereus 14579: the pentose-phosphate pathway.

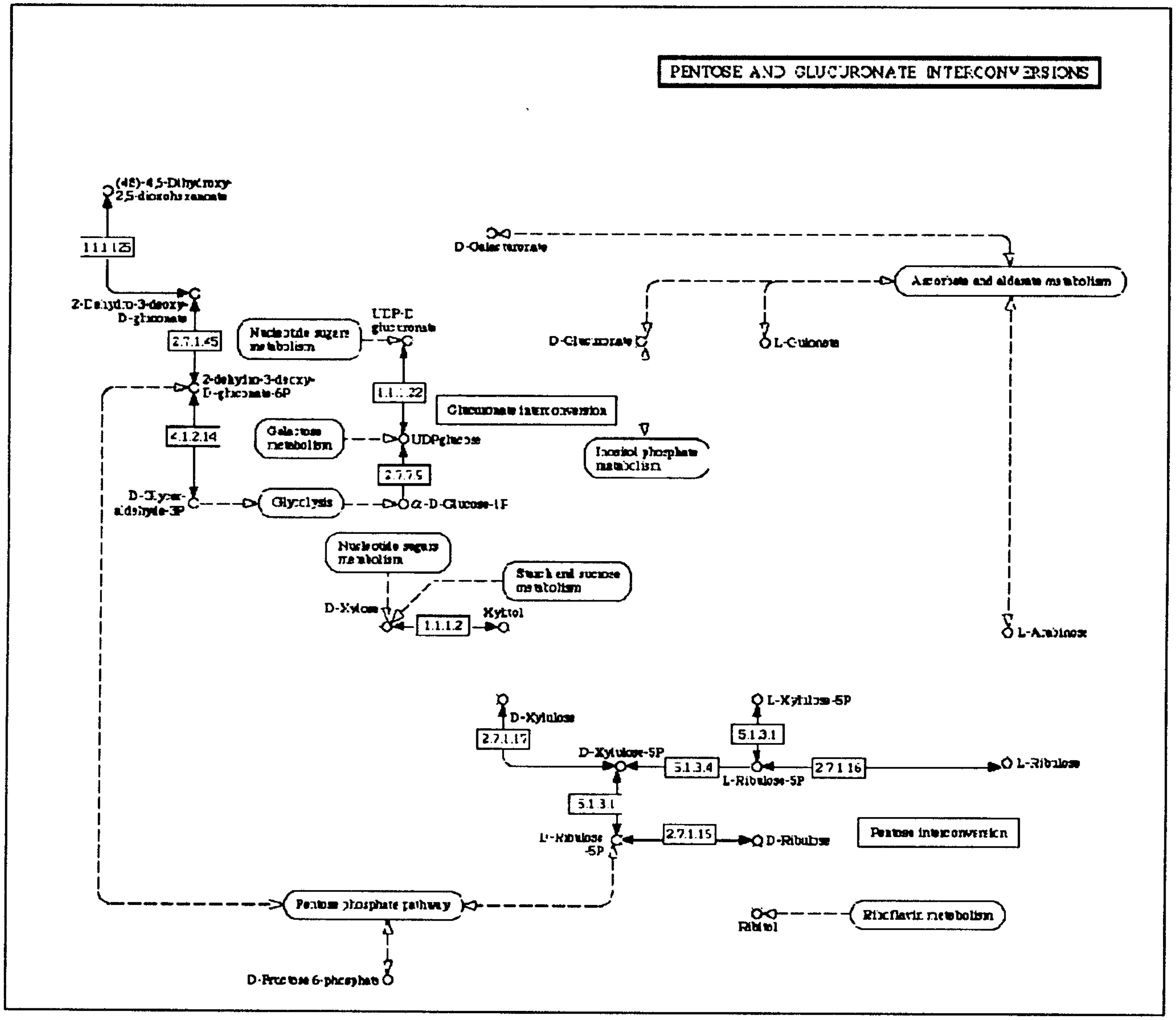

Figure 12. Metabolic pathways of B. cereus 14579: pentose and glucuronate interconversions.

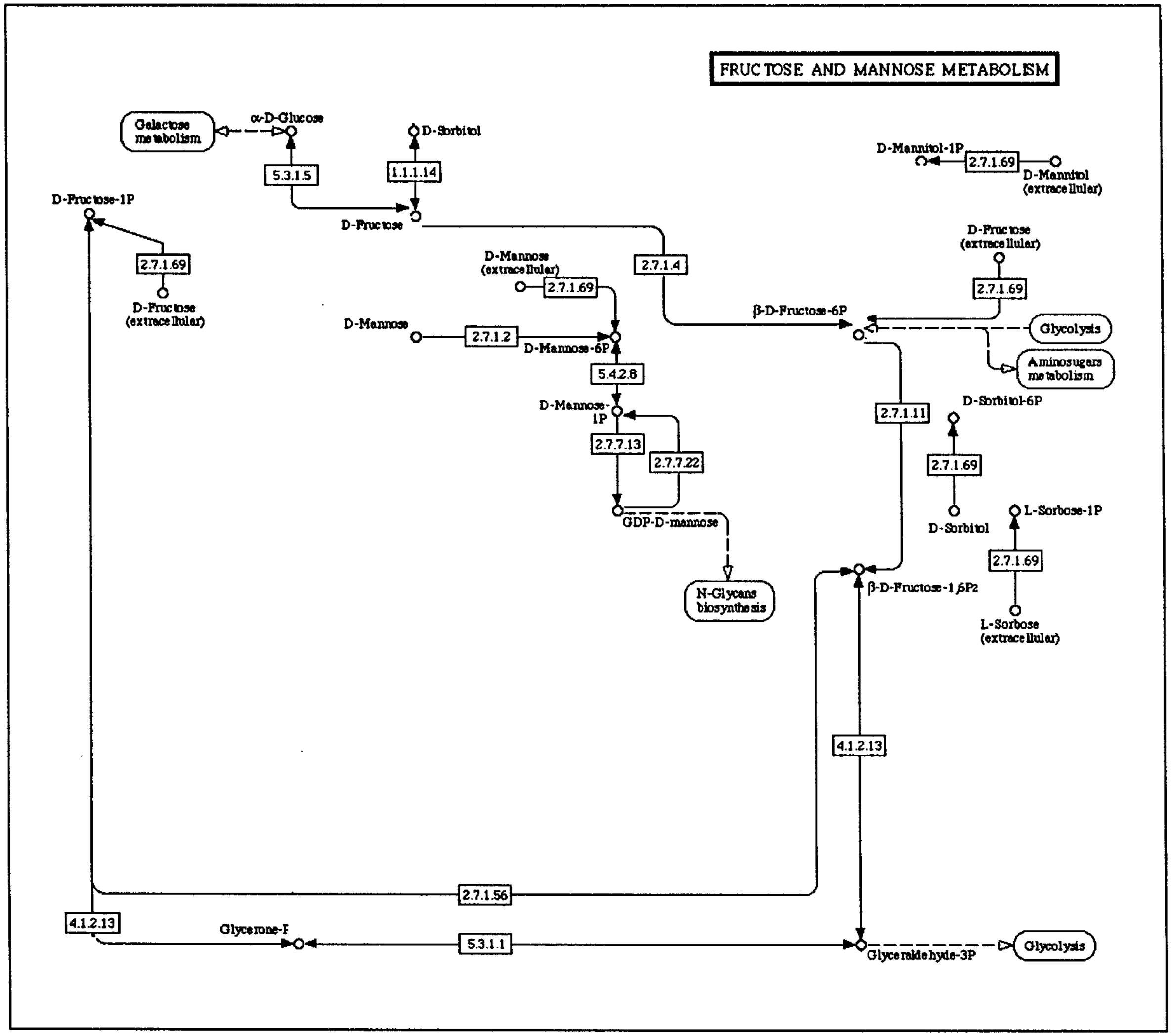

Figure 13. Metabolic pathways of B. cereus 14579: fructose and mannose metabolism

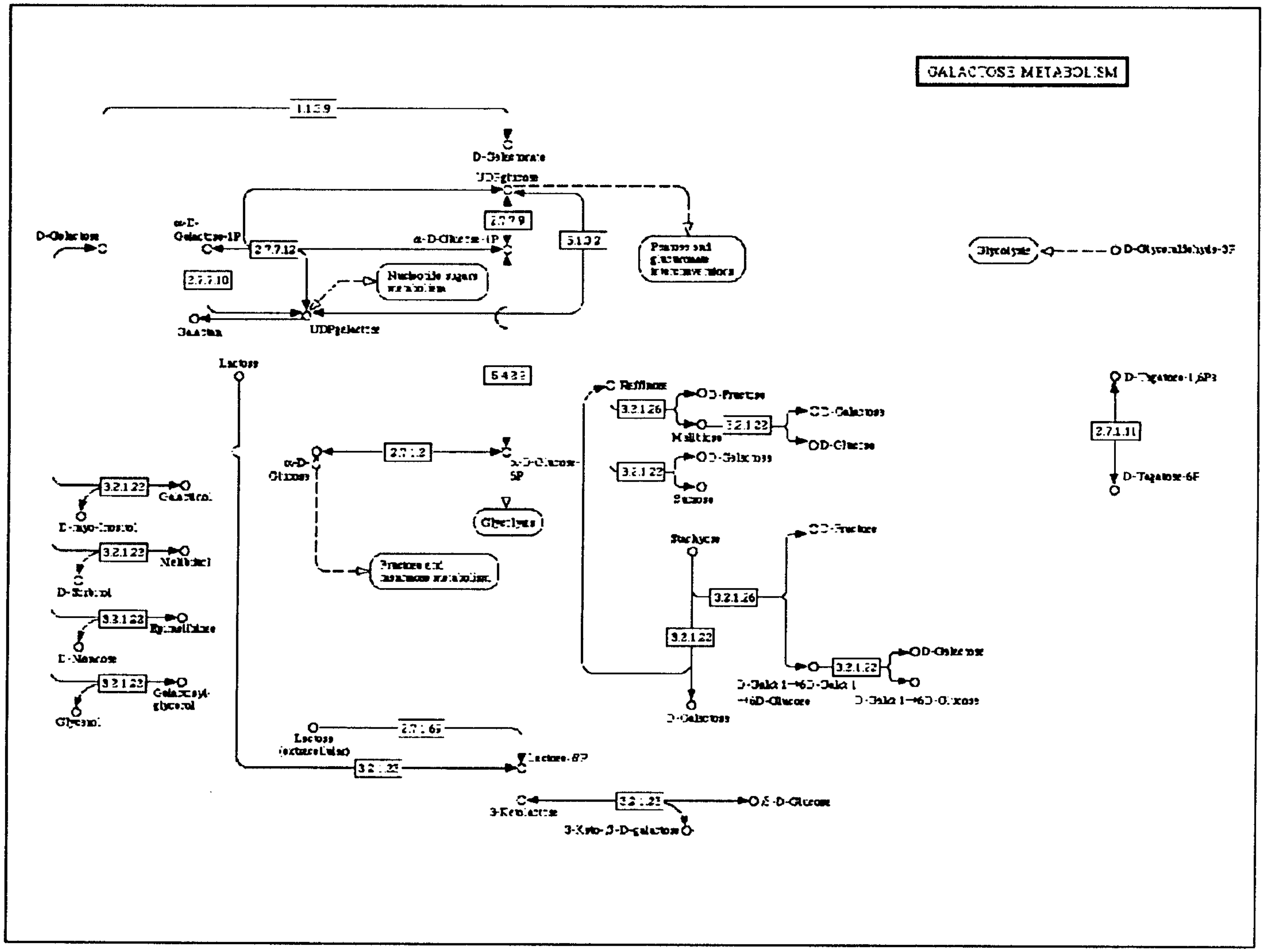

Figure 14. Metabolic pathways of B. cereus 14579: galactose metabolism

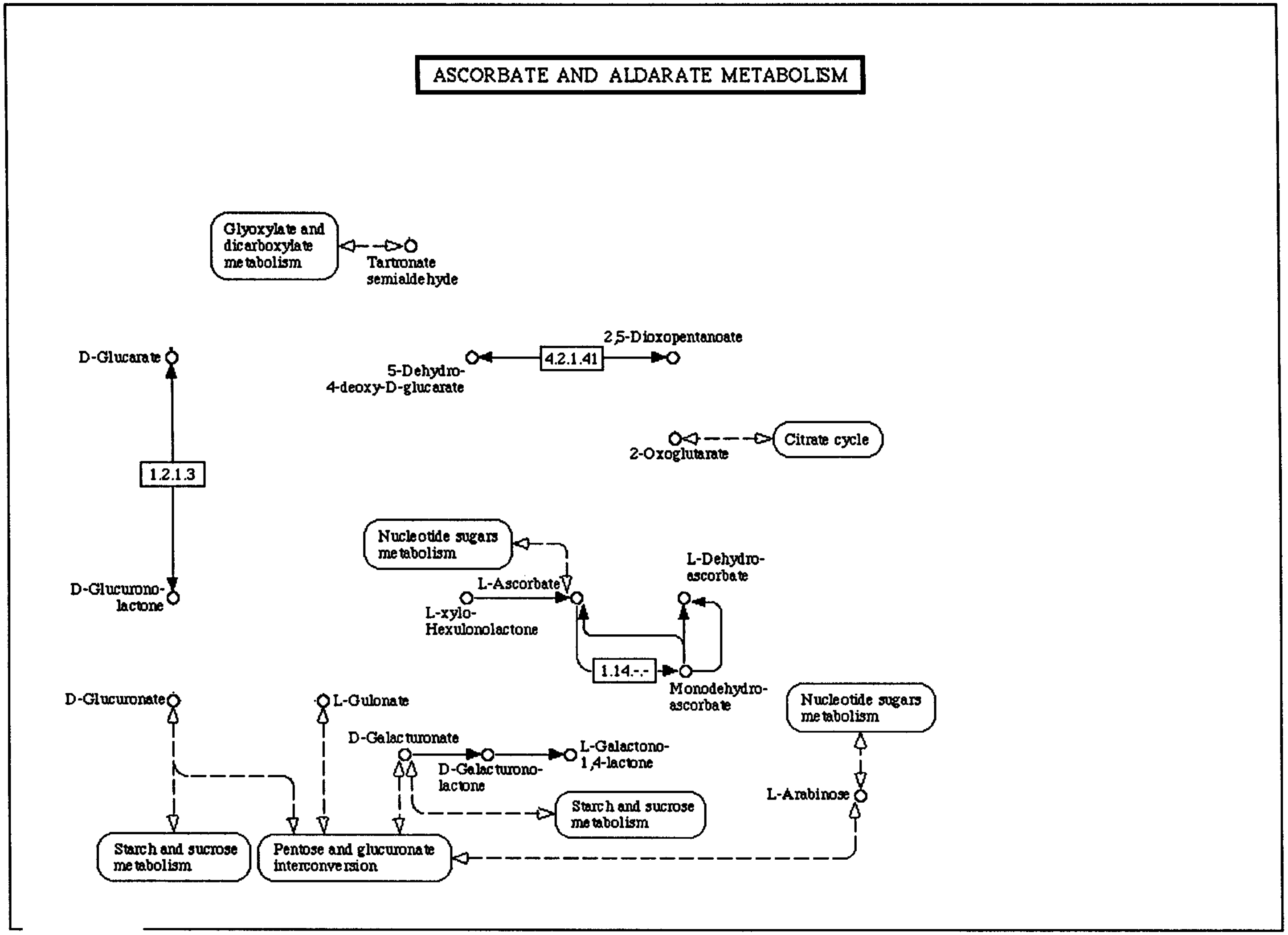

Figure 15. Metabolic pathways of B. cereus 14579: ascorbate and aldarate metabolism

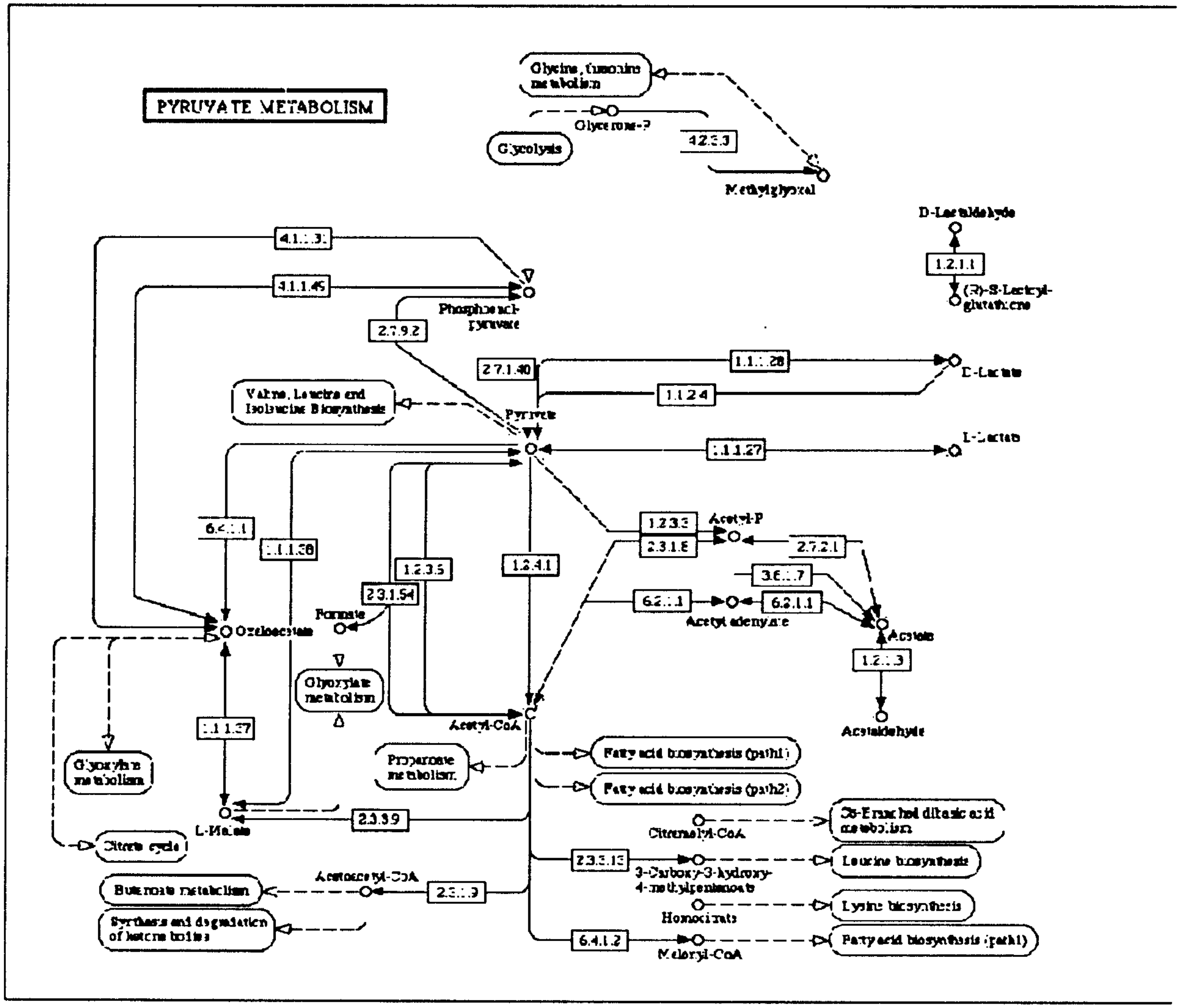

Figure 16. Metabolic pathways of B. cereus 14579: pyruvate metabolism.

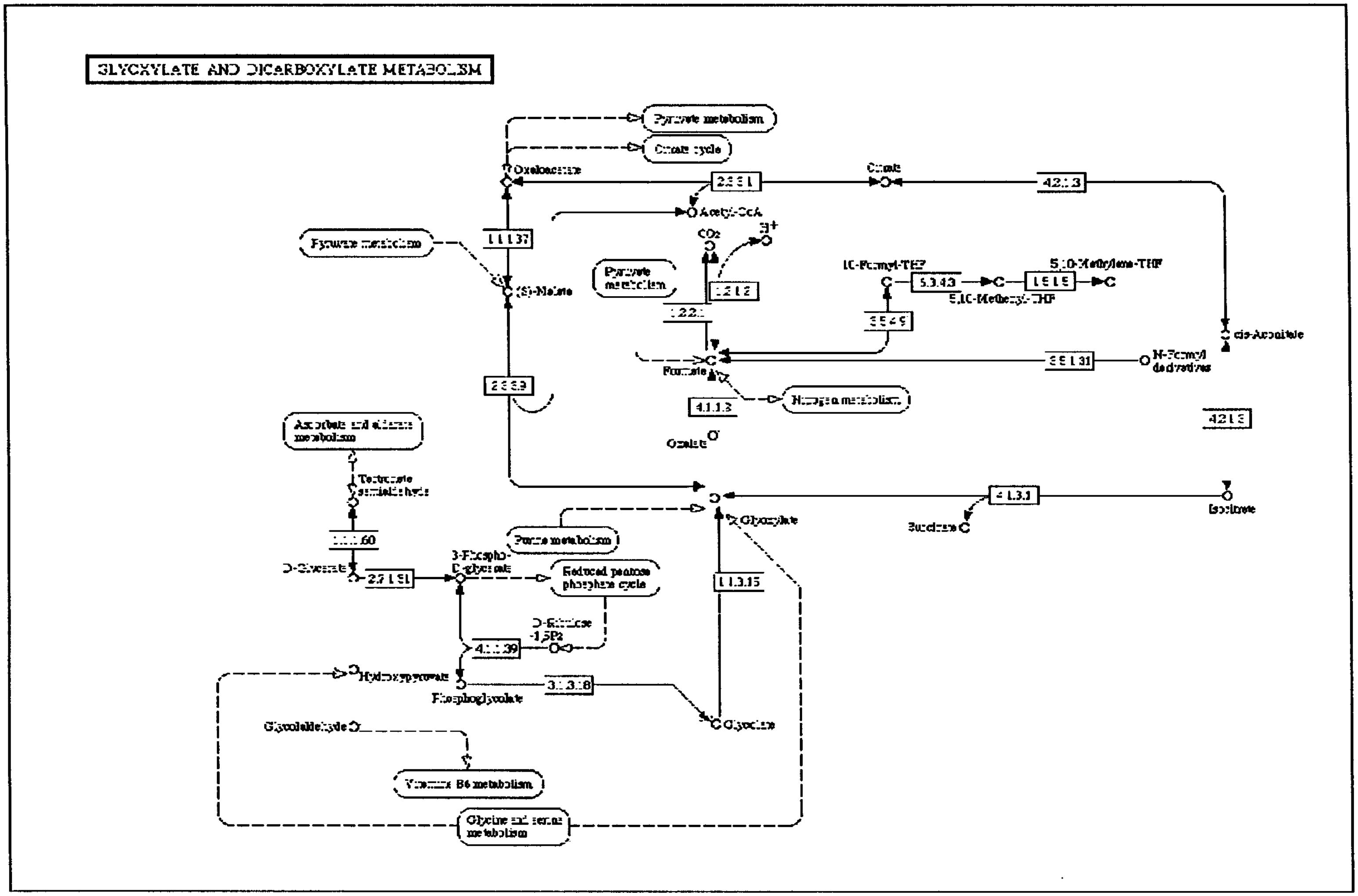

Figure 17. Metabolic pathways of B. cereus 14579: glyoxylate and dicarboxylate metabolism.

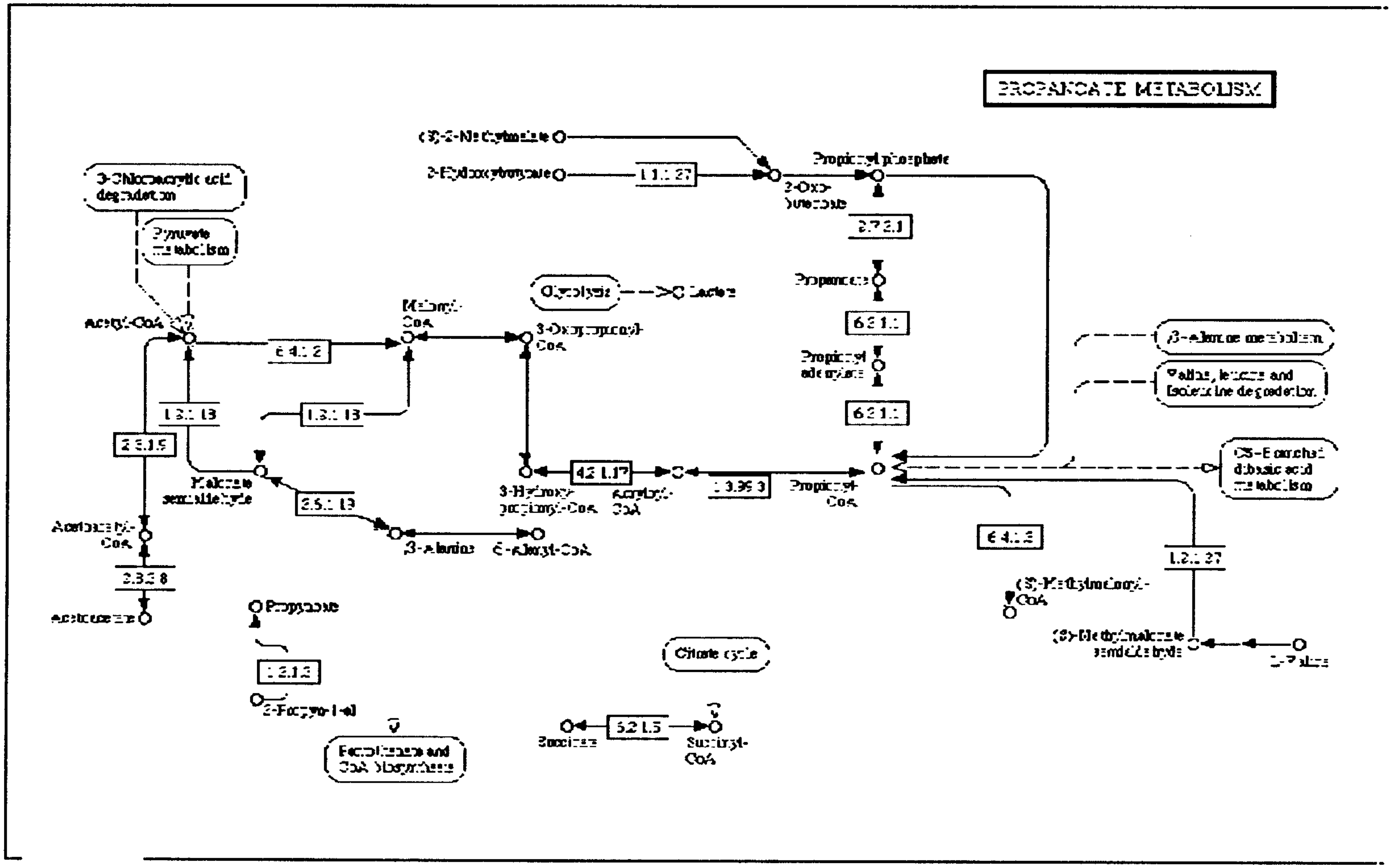

Figure 18. Metabolic pathways of B. cereus 14579: propanoate metabolism.

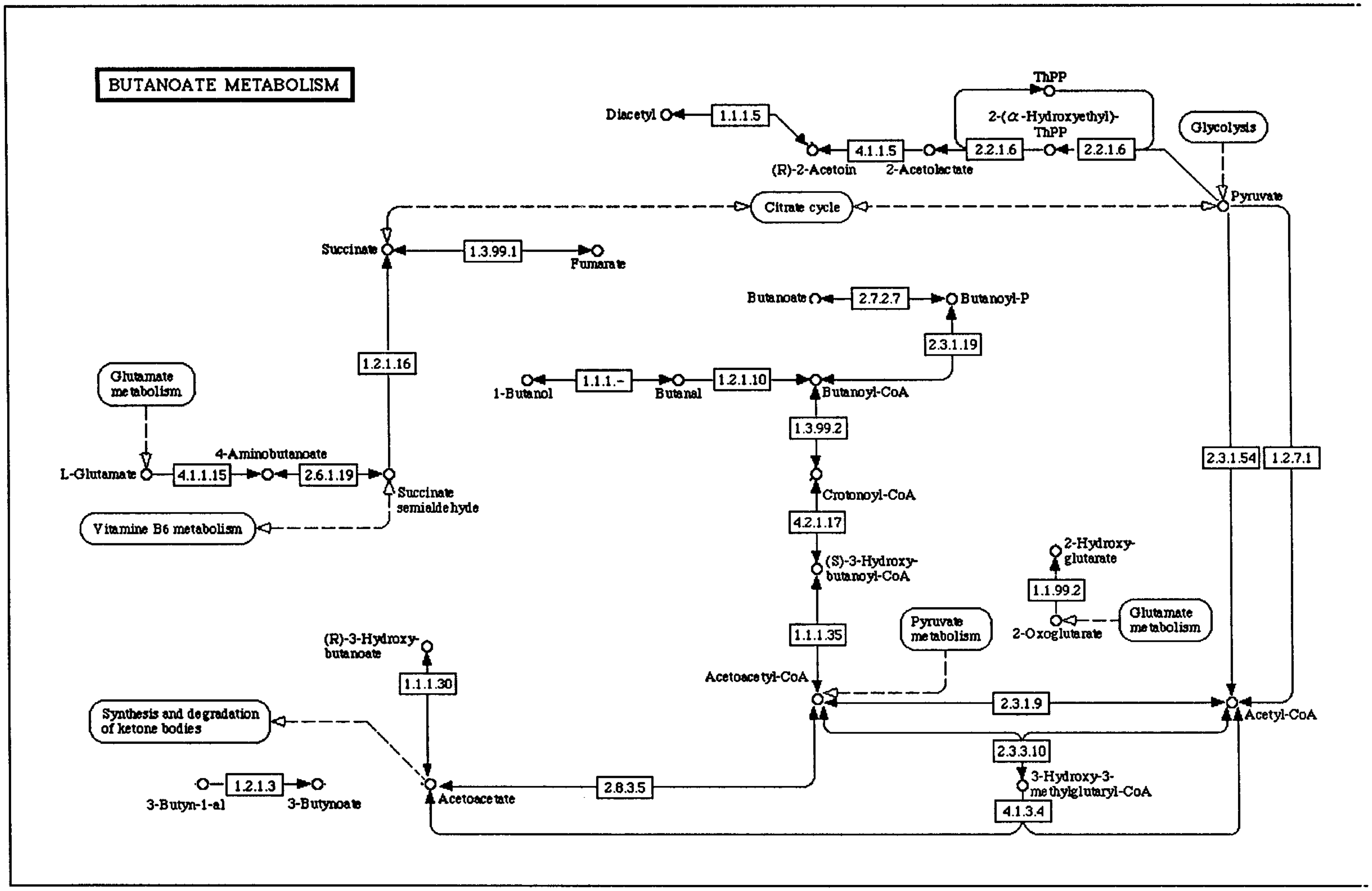

Figure 19. Metabolic pathways of B. cereus 14579: butanoate metabolism

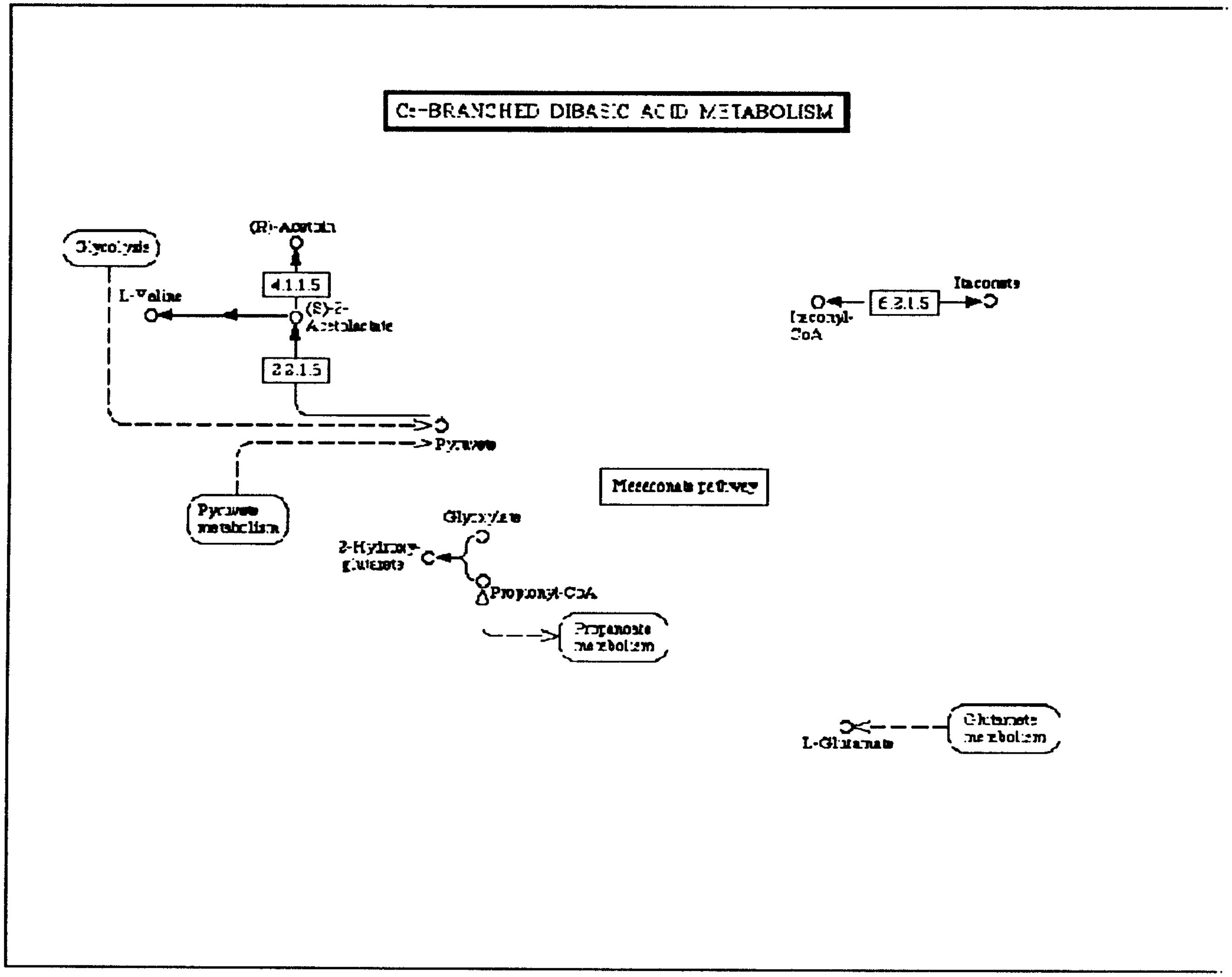

Figure 20. Metabolic pathways of B. cereus 14579: C5-branched dibasic acid metabolism.

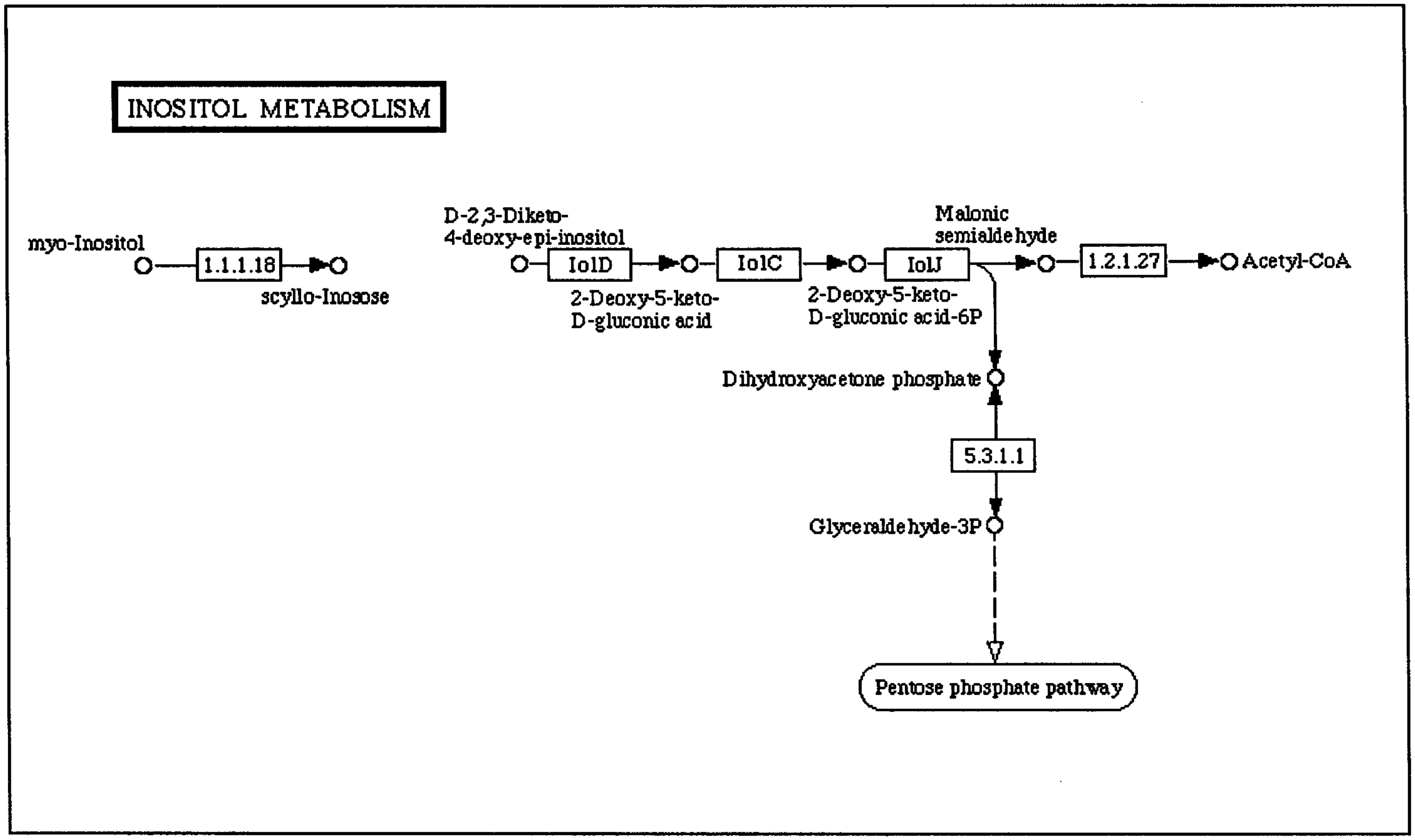

Figure 21. Metabolic pathways of B. cereus 14579: inositol metabolism

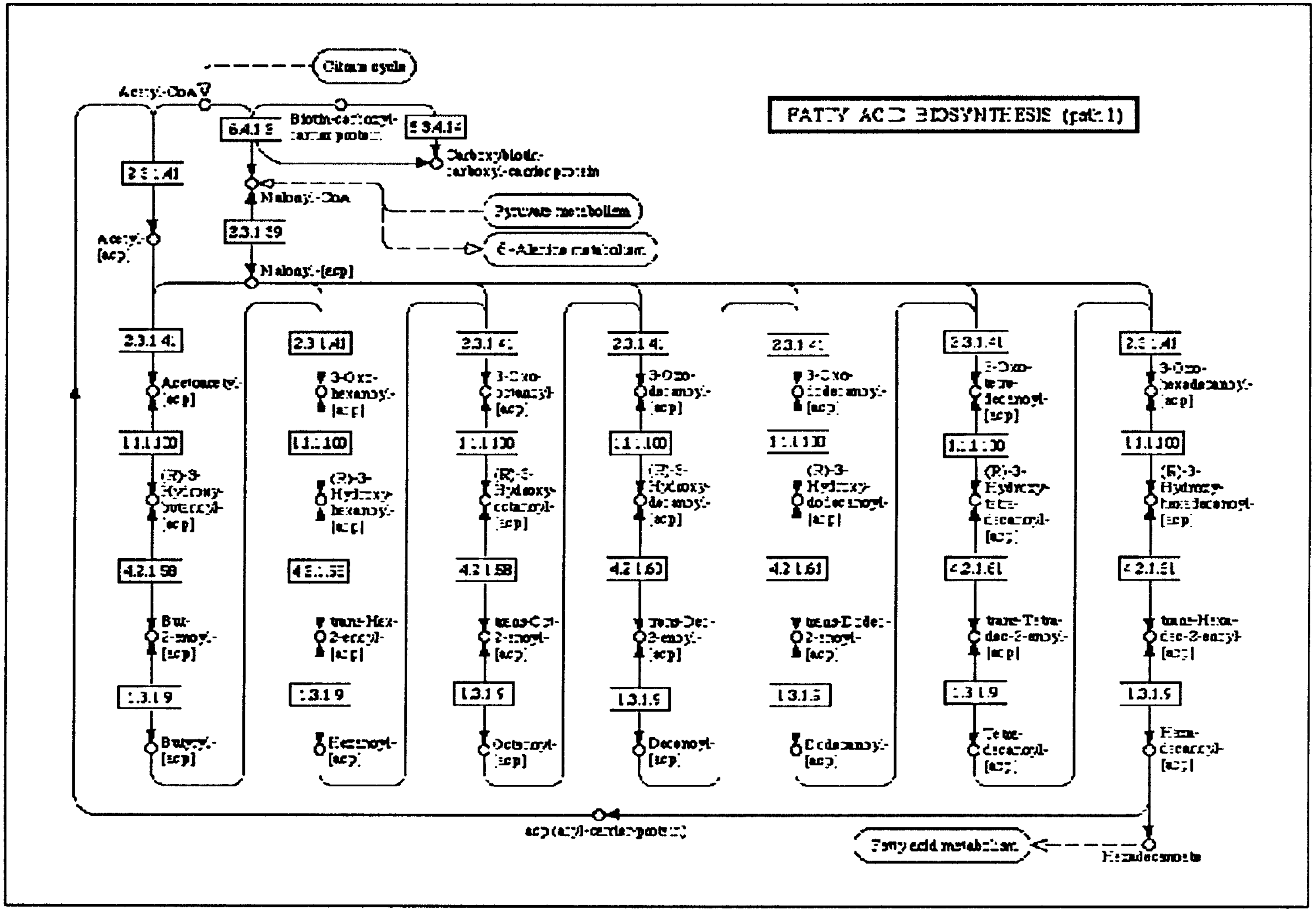

Figure 22. Metabolic pathways of B. cereus 14579: fatty acid synthesis.

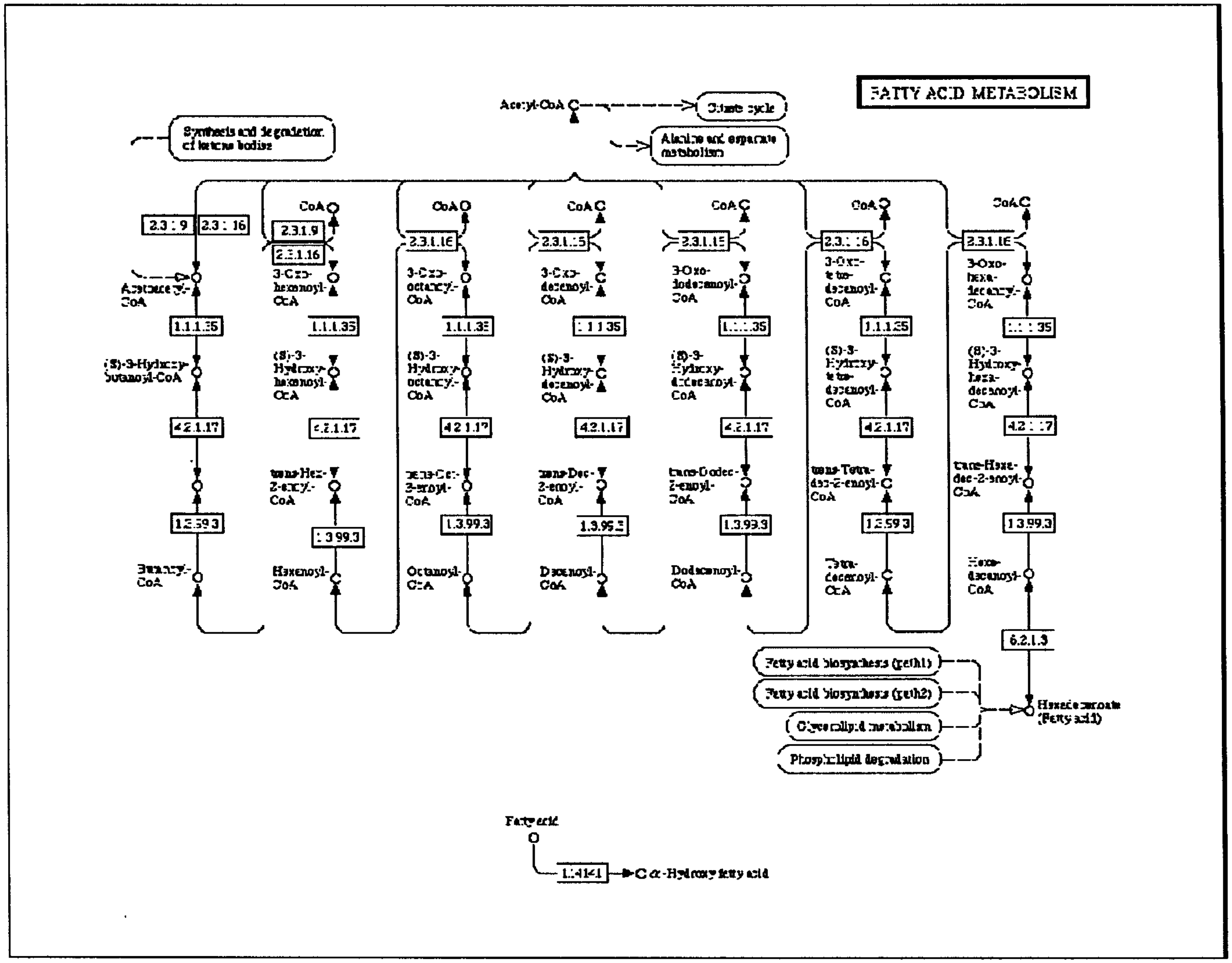

Figure 23. Metabolic pathways of B. cereus 14579: fatty acid metabolism.

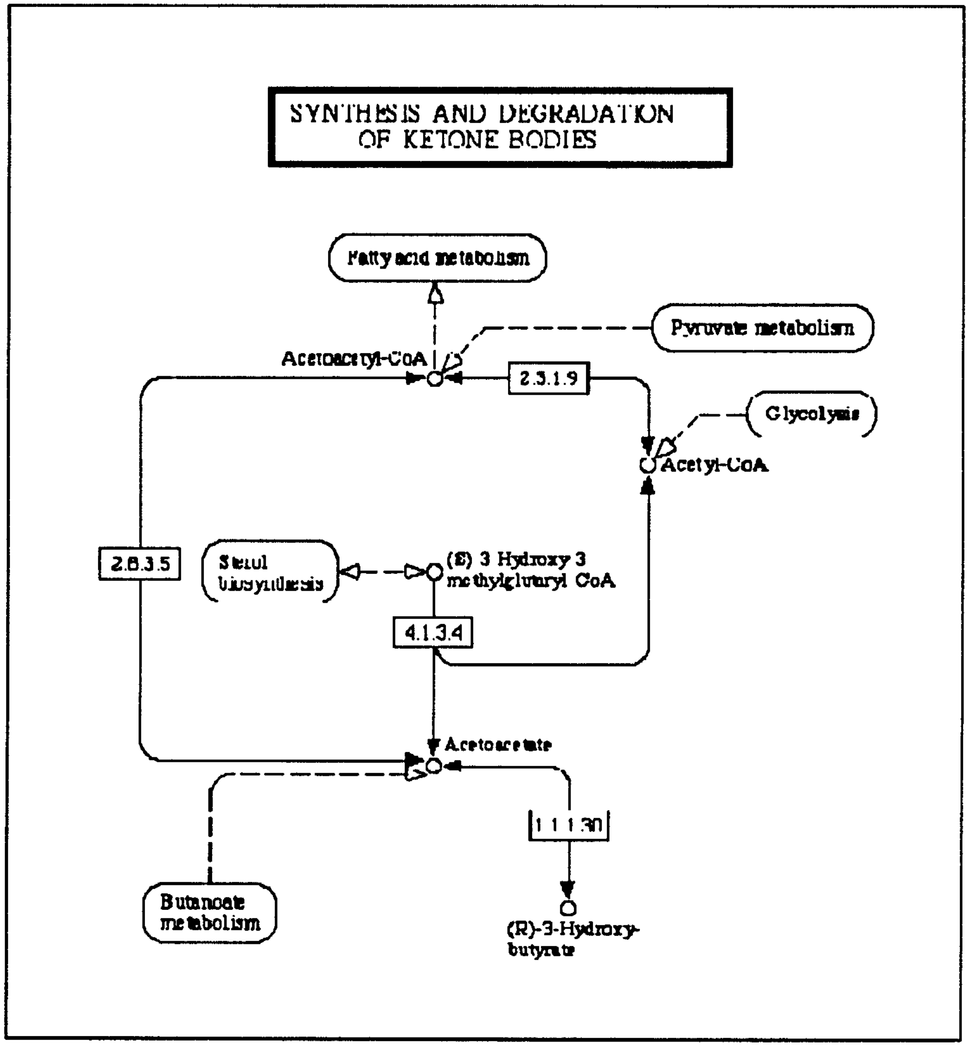

Figure 24. Metabolic pathways of B. cereus 14579: synthesis and degradation of ketone bodies.

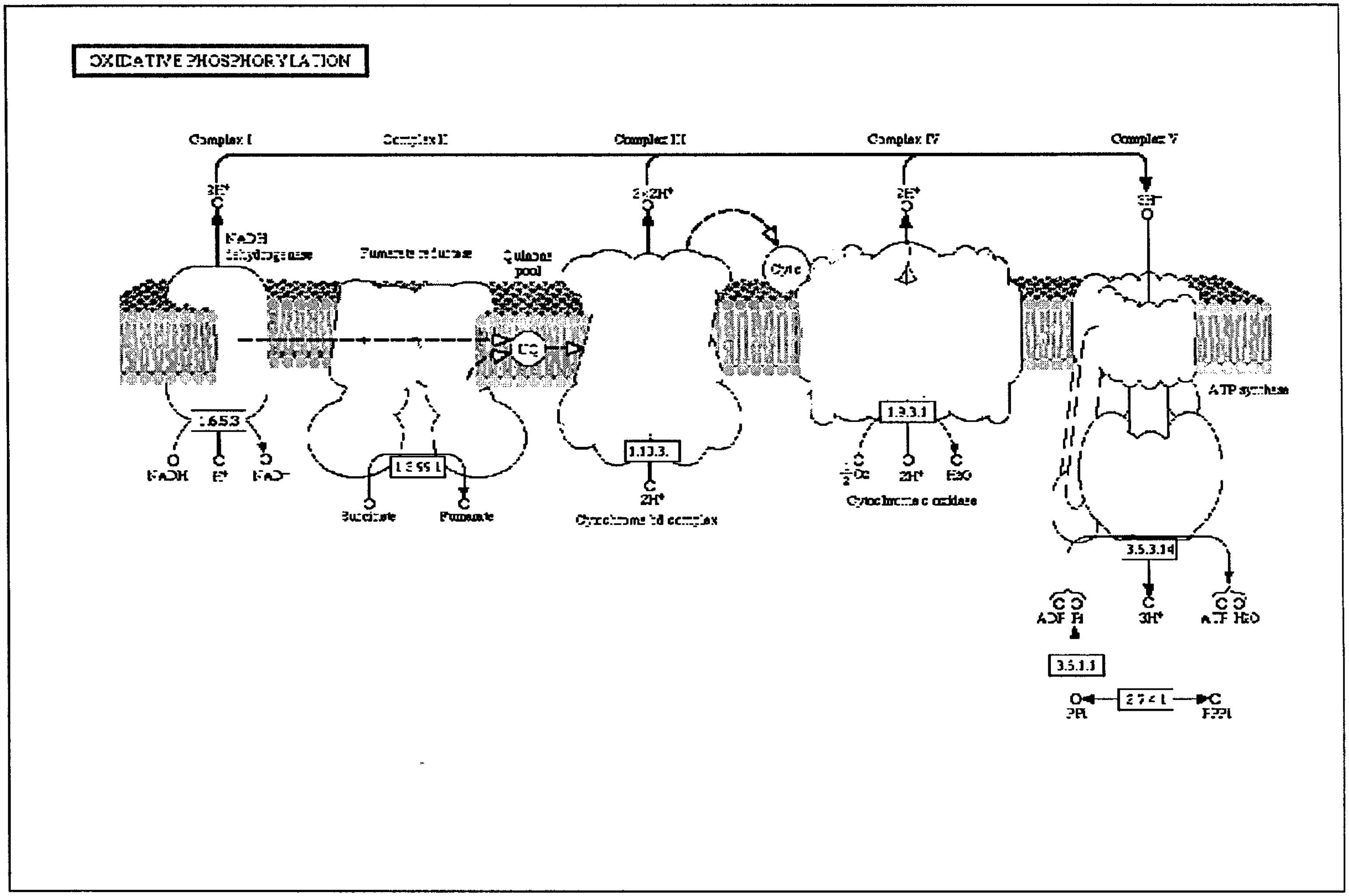

Figure 25. Metabolic pathways of B. cereus 14579: oxidative phosphorylation.

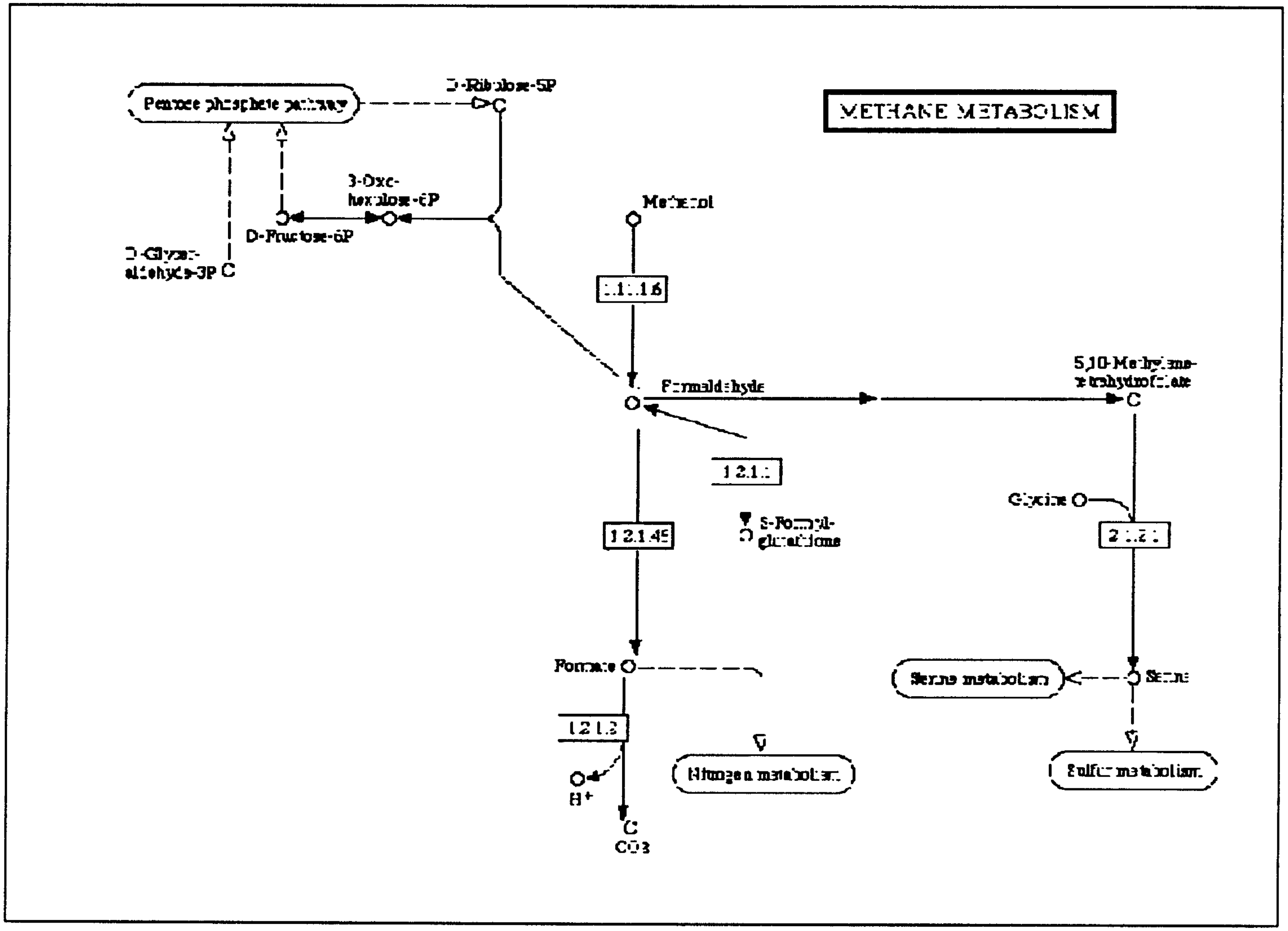

Figure 26. Metabolic pathways of B. cereus 14579: methane metabolism.

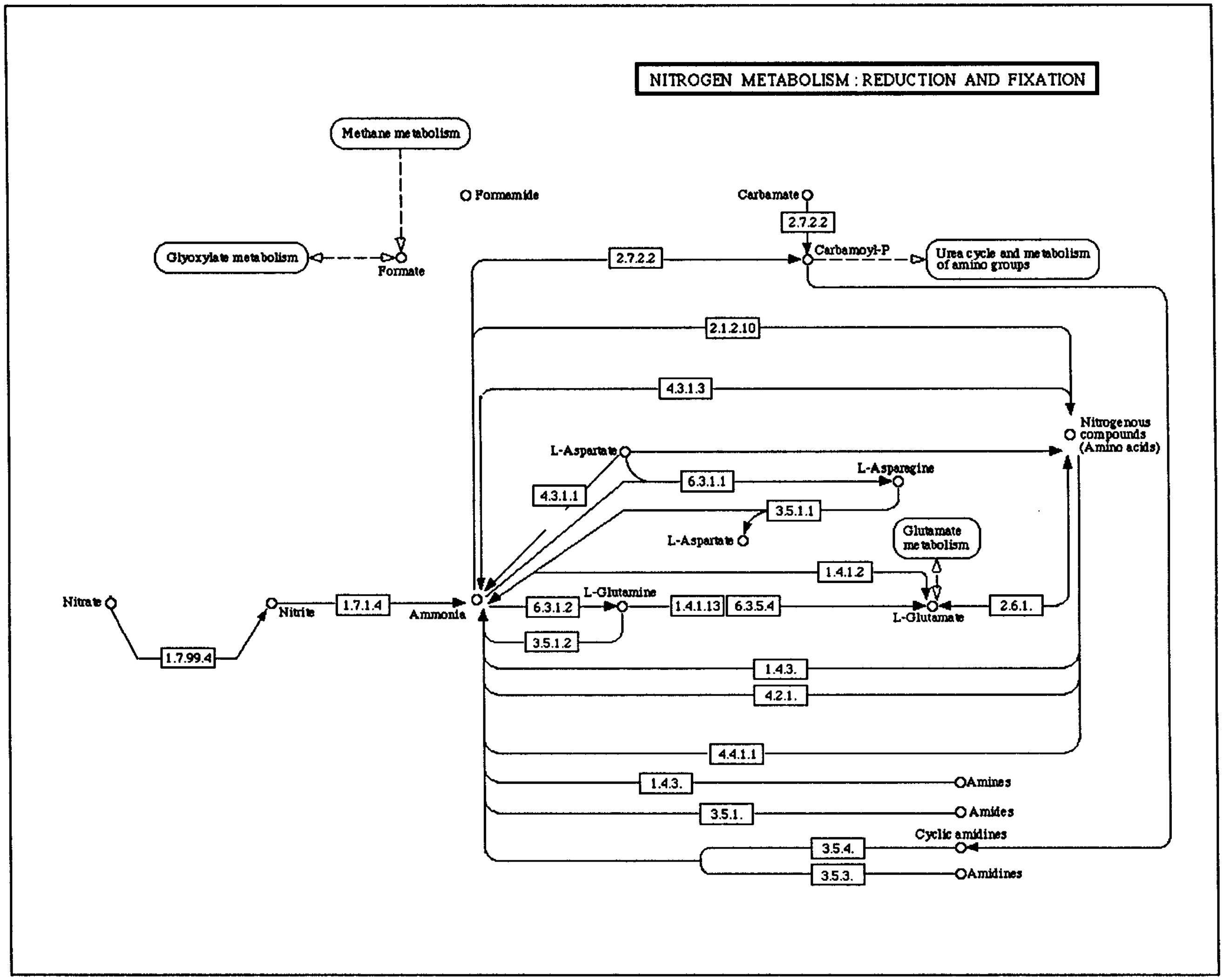

Figure 27. Metabolic pathways of B. cereus 14579: nitrogen metabolism.

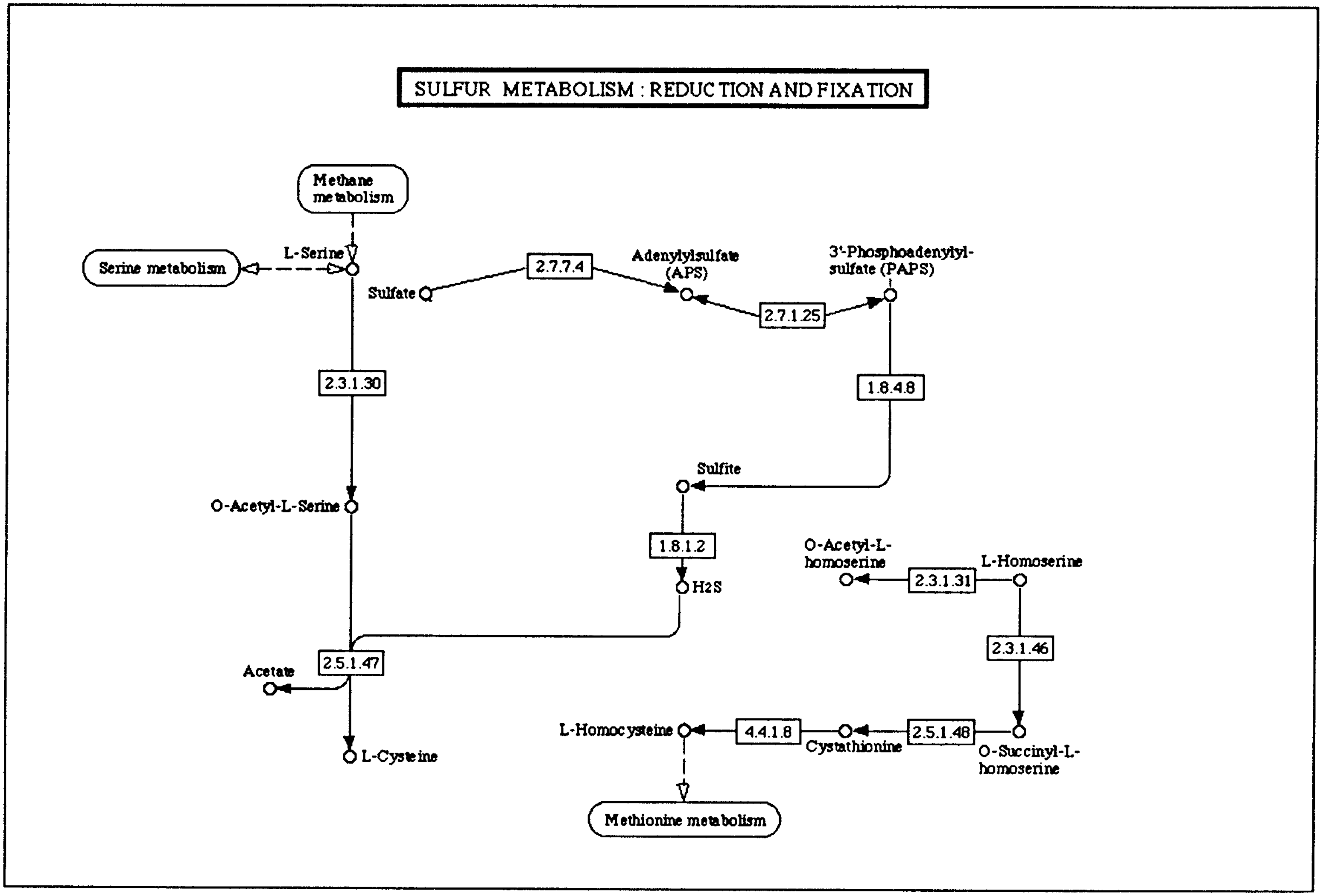

Figure 28. Metabolic pathways of B. cereus 14579: sulfur metabolism.

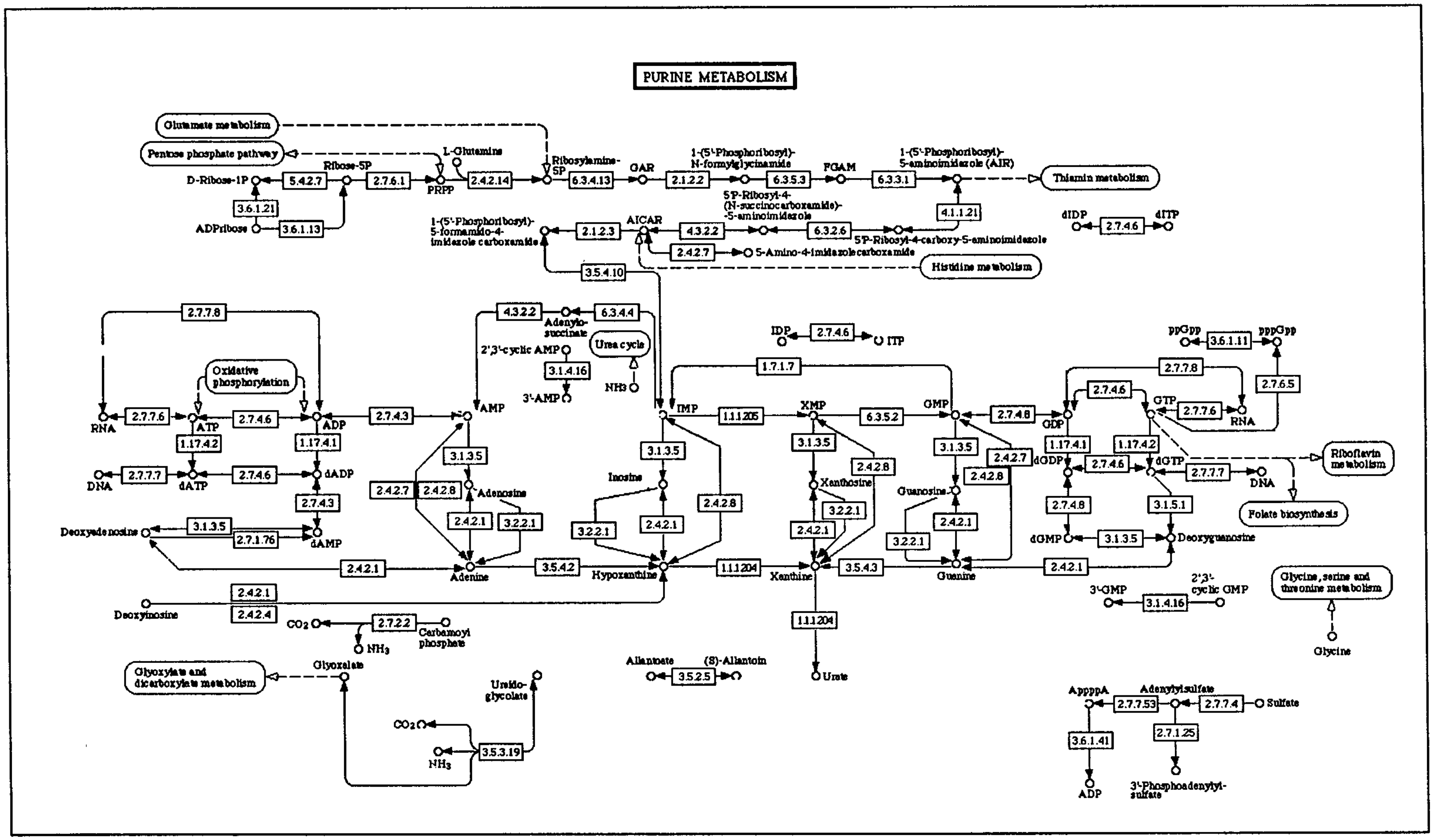

Figure 29. Metabolic pathways of B. cereus 14579: purine metabolism.

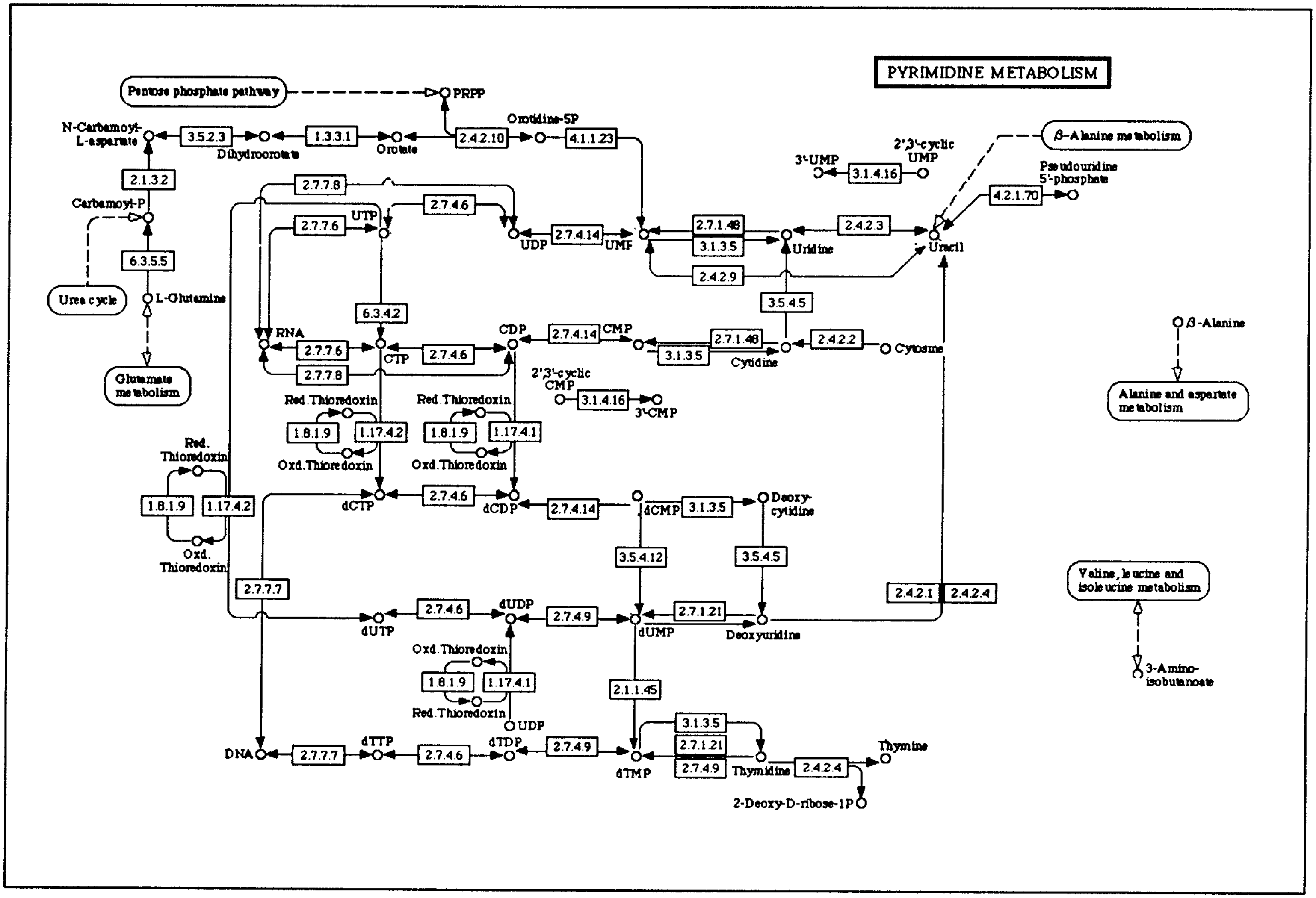

Figure 30. Metabolic pathways of B. cereus 14579: pyrimidine metabolism.

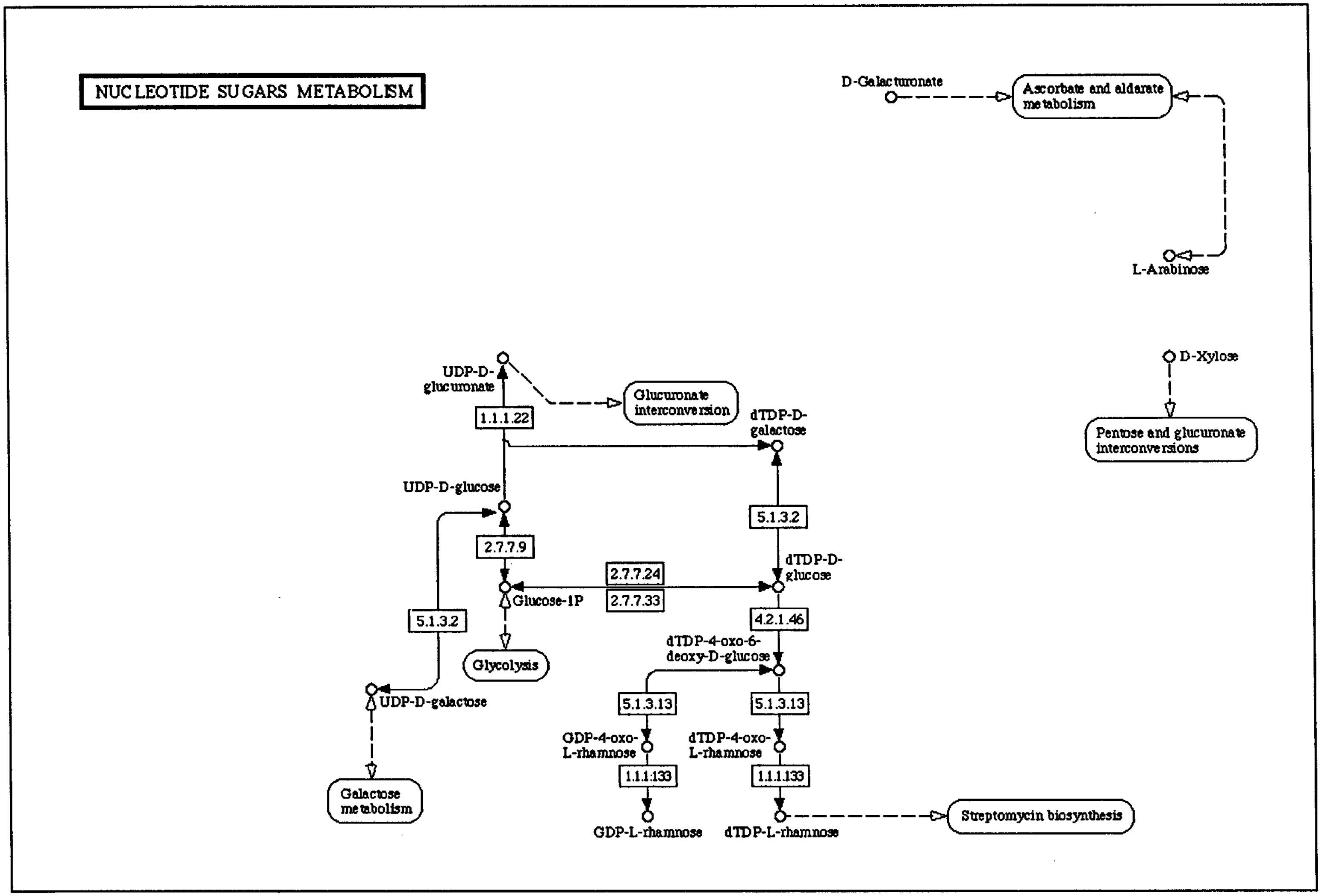

Figure 31. Metabolic pathways of B. cereus 14579: nucleotide sugar metabolism

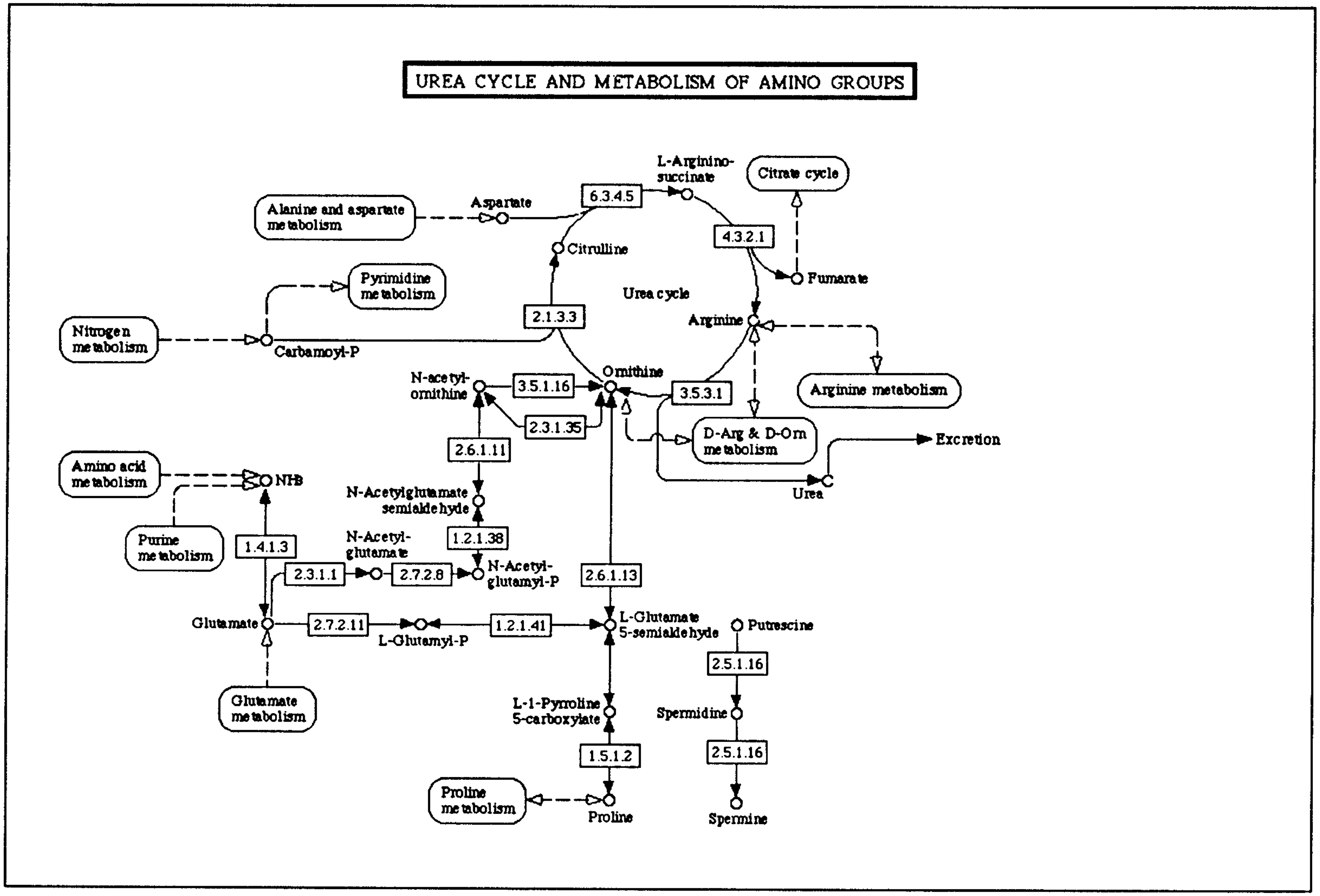

Figure 32. Metabolic pathways of B. cereus 14579: urea cycle and amino group metabolism.

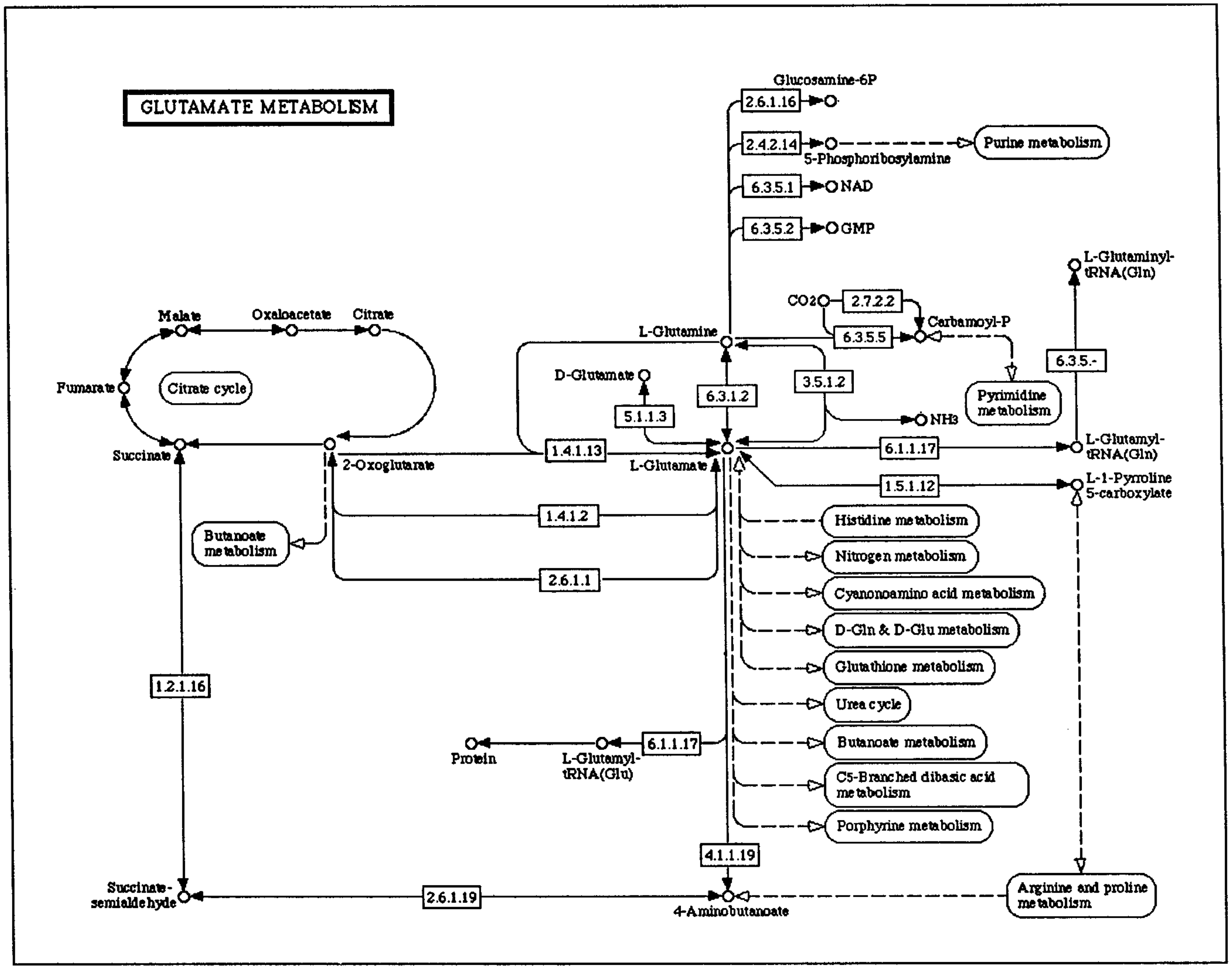

Figure 33. Metabolic pathways of B. cereus 14579: glutamate metabolism.

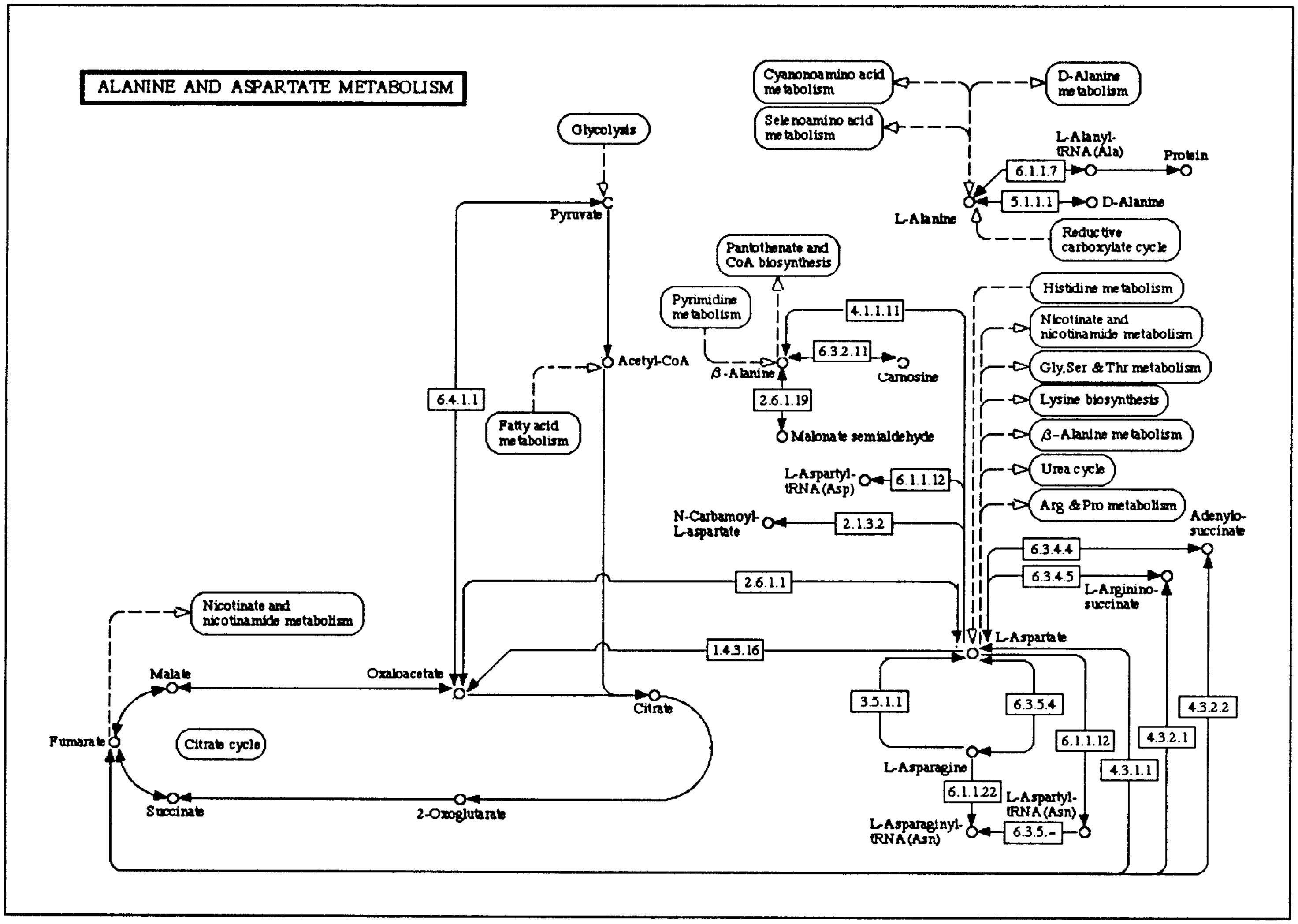

Figure 34. Metabolic pathways of B. cereus 14579: alanine and aspartate metabolism.

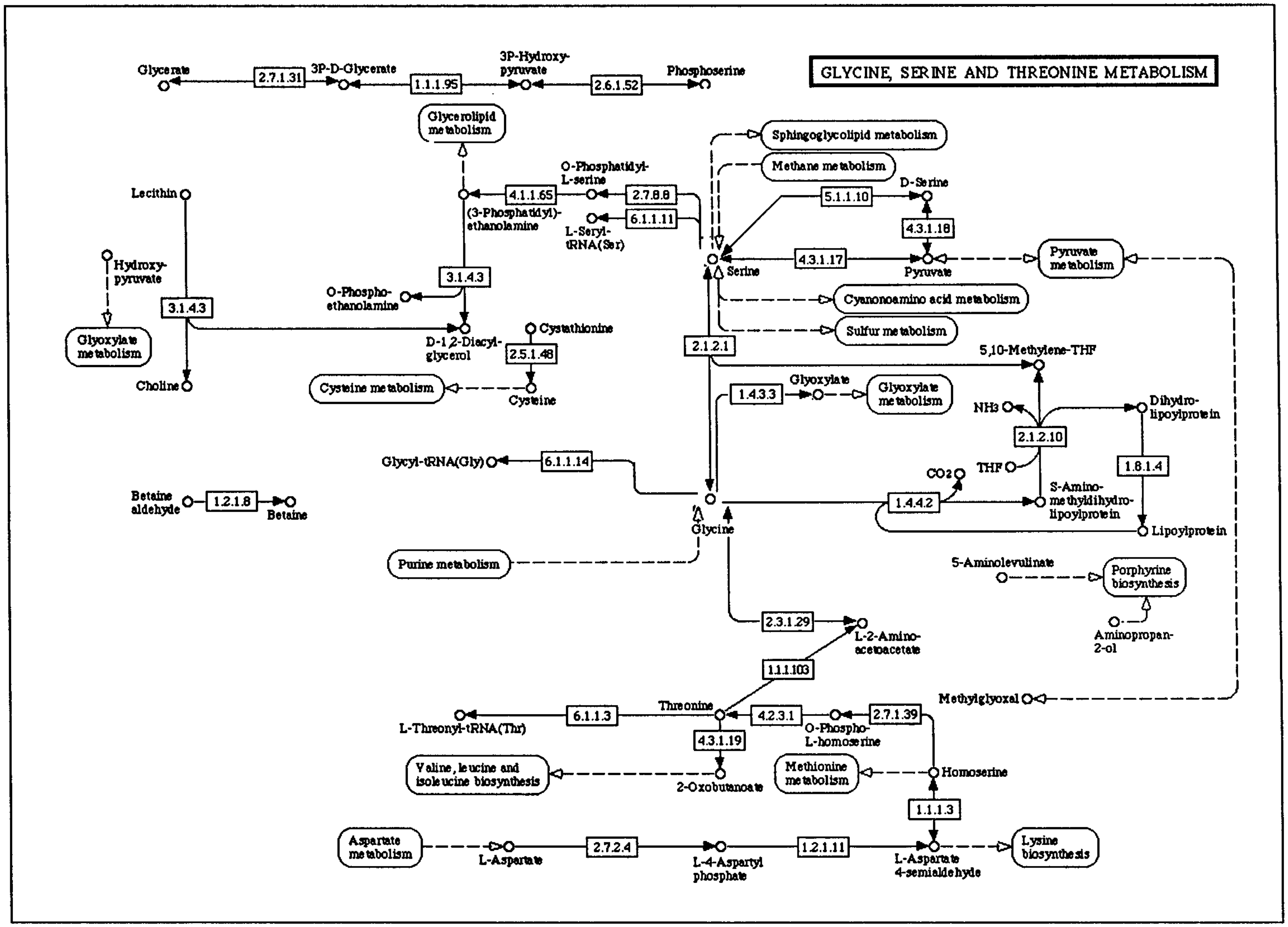

Figure 35. Metabolic pathways of B. cereus 14579: glycine, serine, and threonine metabolism.

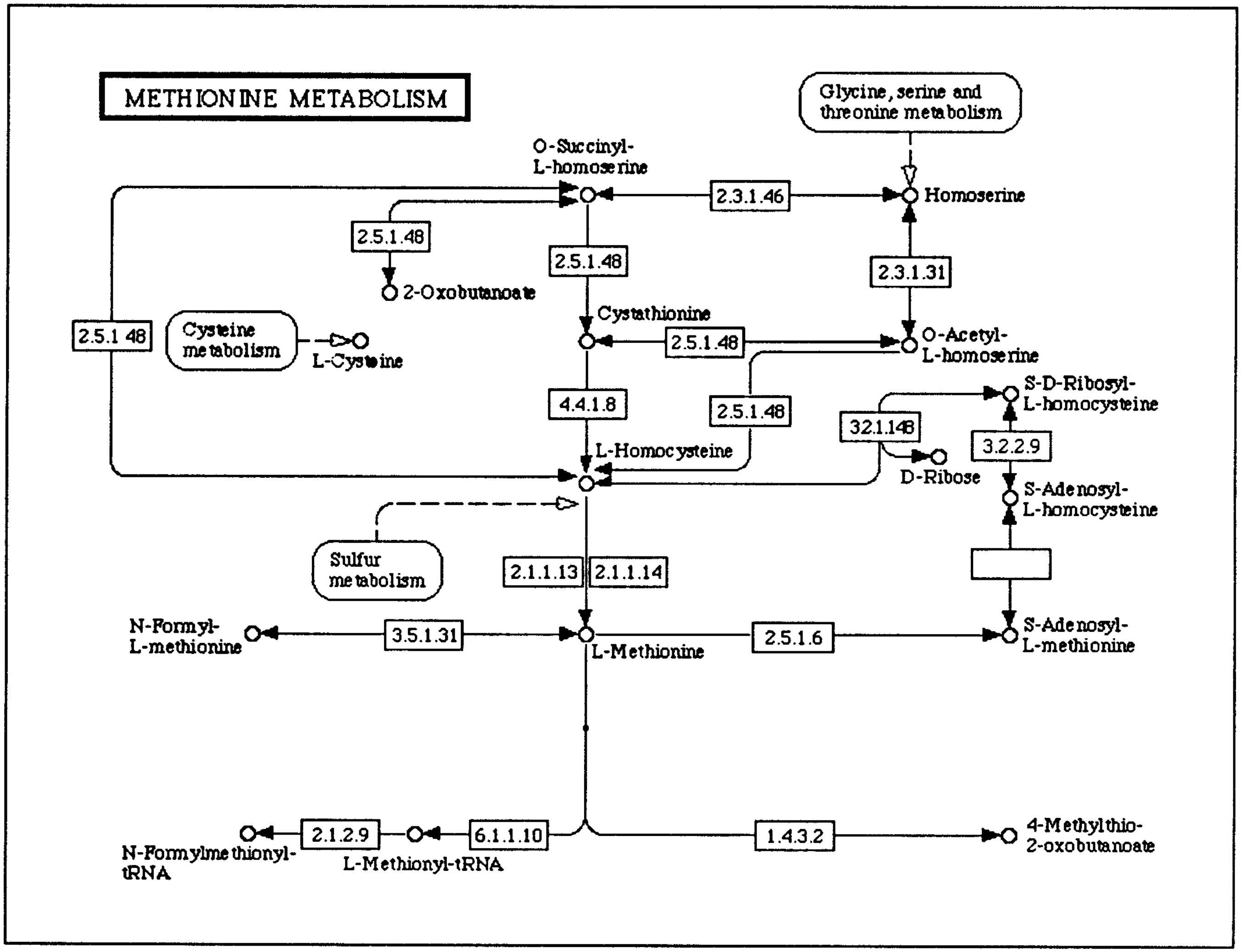

Figure 36. Metabolic pathways of B. cereus 14579: methionine metabolism.

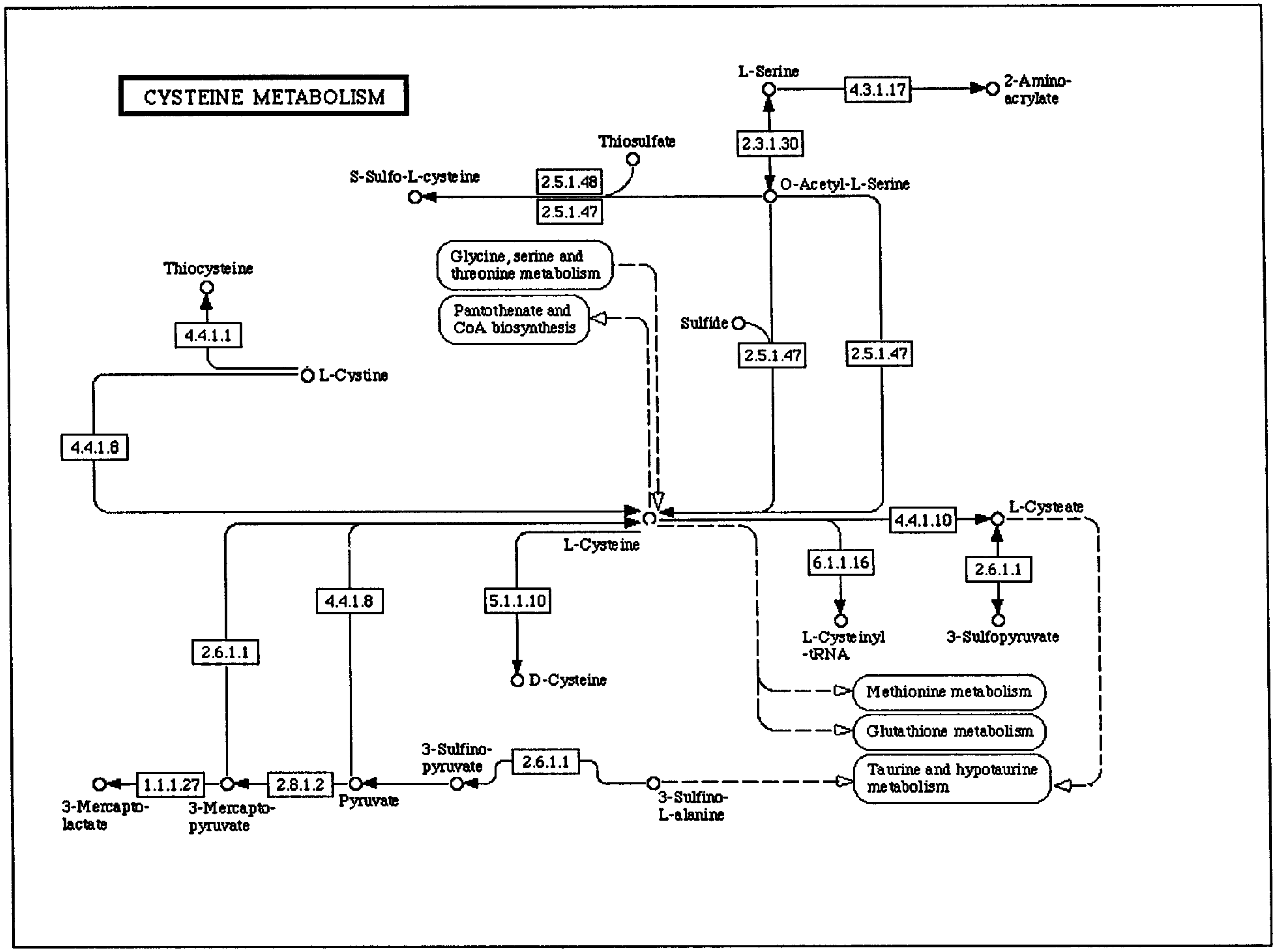

Figure 37. Metabolic pathways of B. cereus 14579: cysteine metabolism.

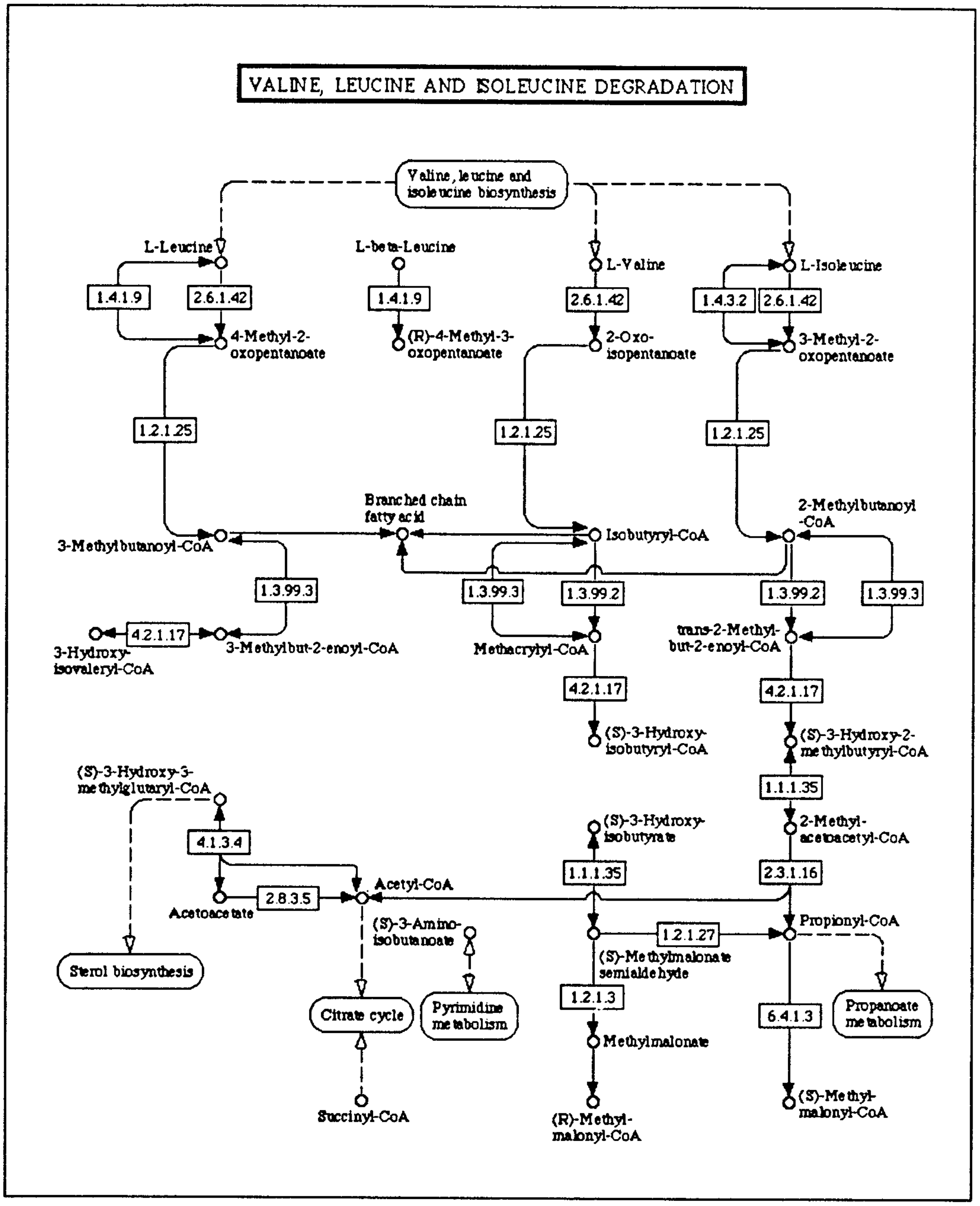

Figure 38. Metabolic pathways of B. cereus 14579: valine, leucine, and isoleucine degradation.

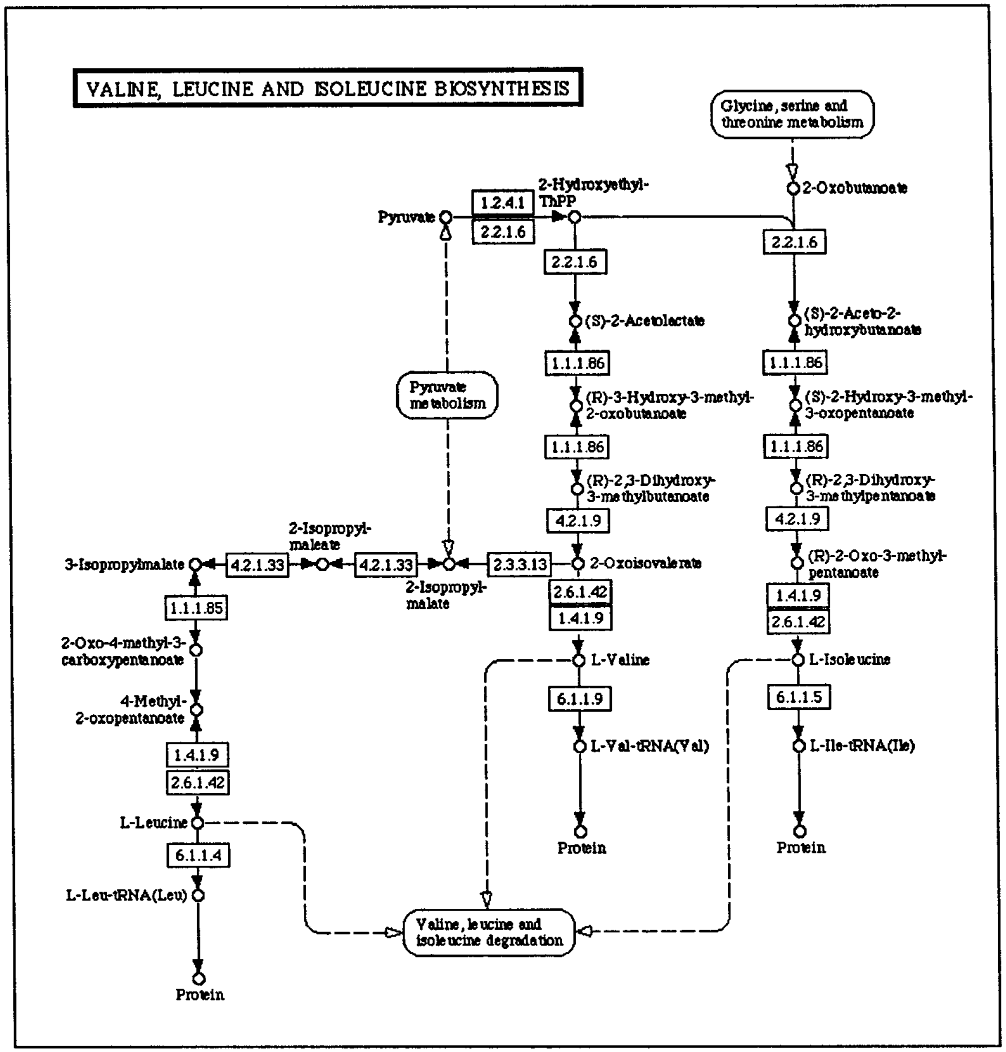

Figure 39. Metabolic pathways of B. cereus 14579: valine, leucine, isoleucine synthesis.

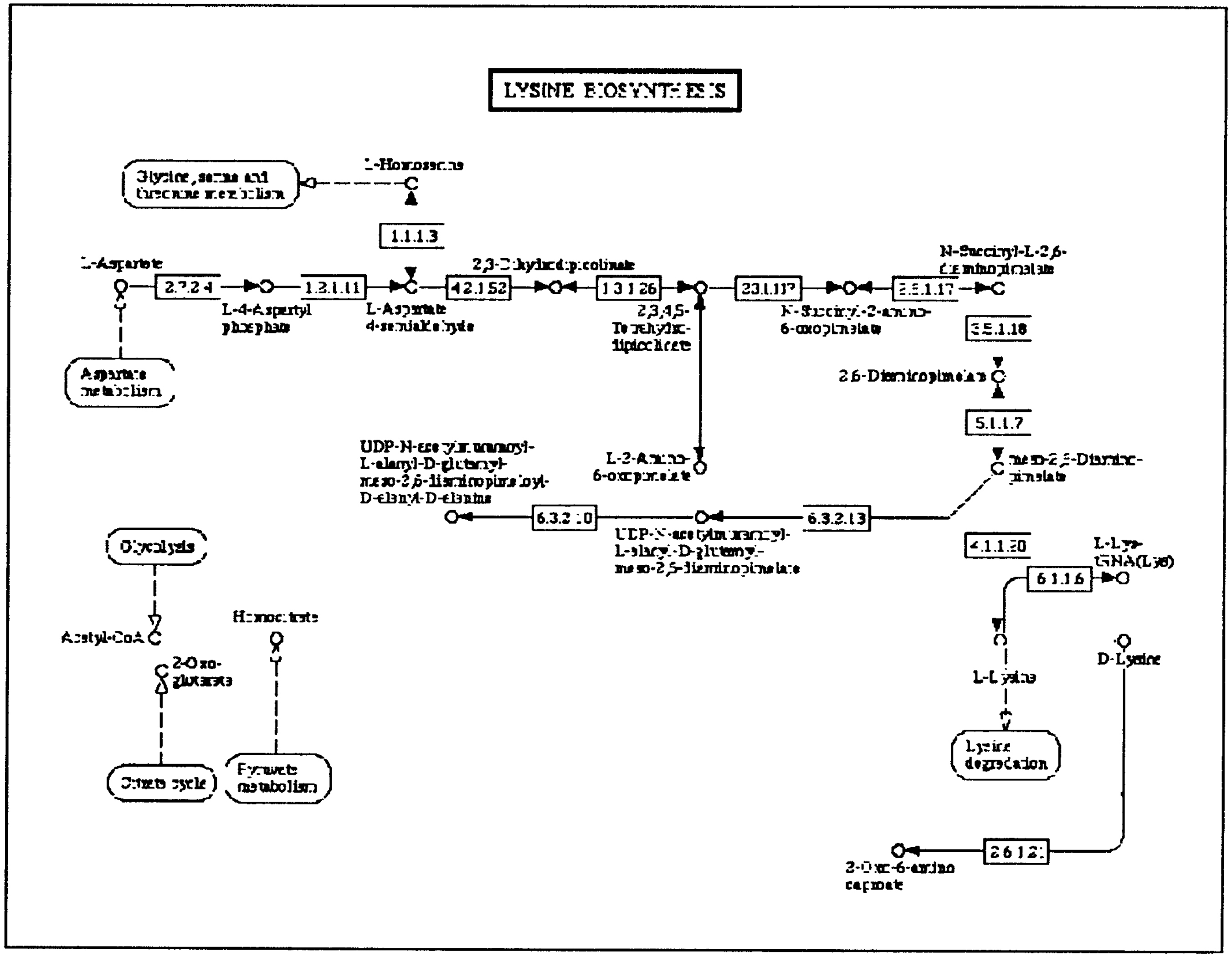

Figure 40. Metabolic pathways of B. cereus 14579: lysine synthesis.

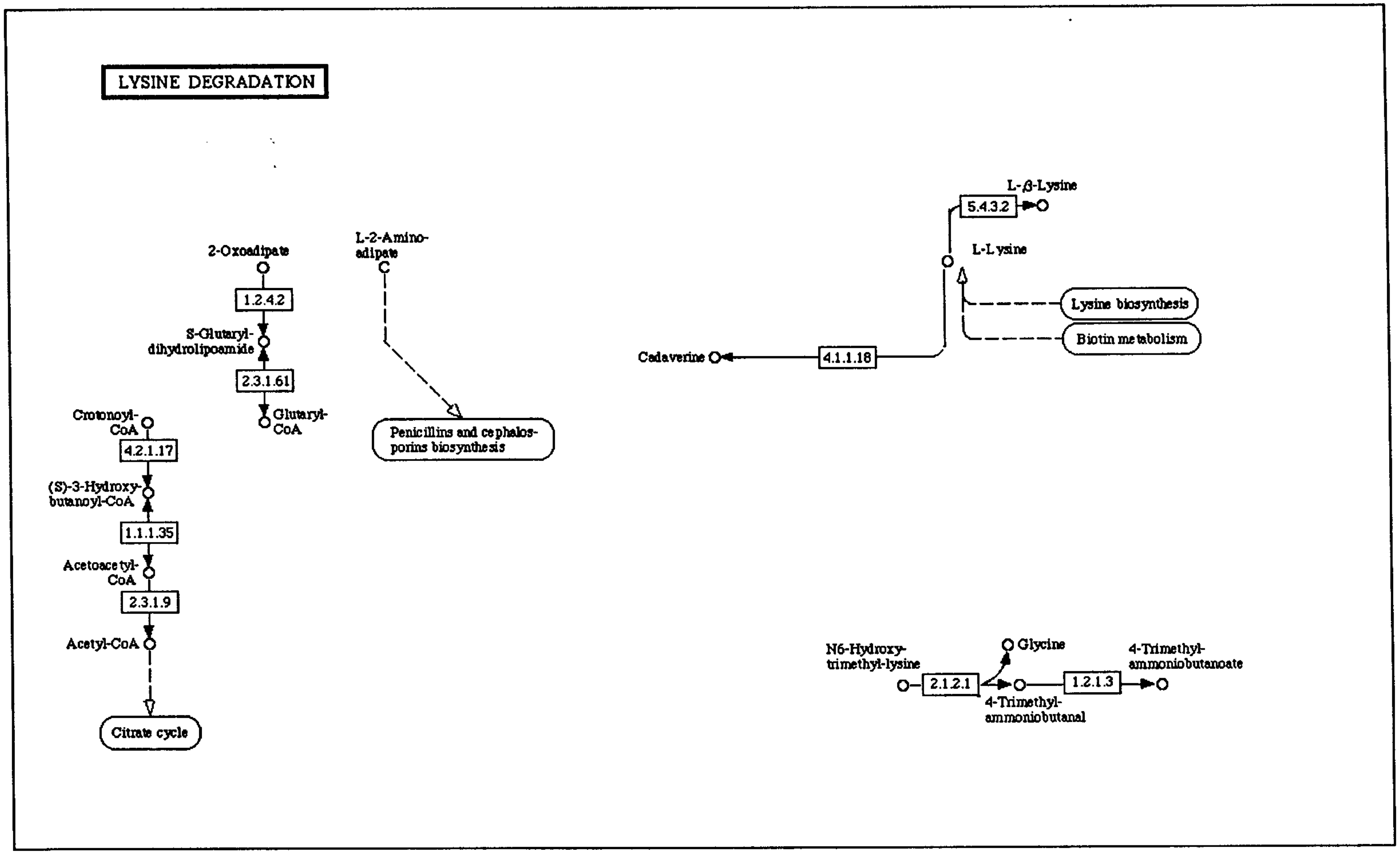

Figure 41. Metabolic pathways of B. cereus 14579: lysine degradation.

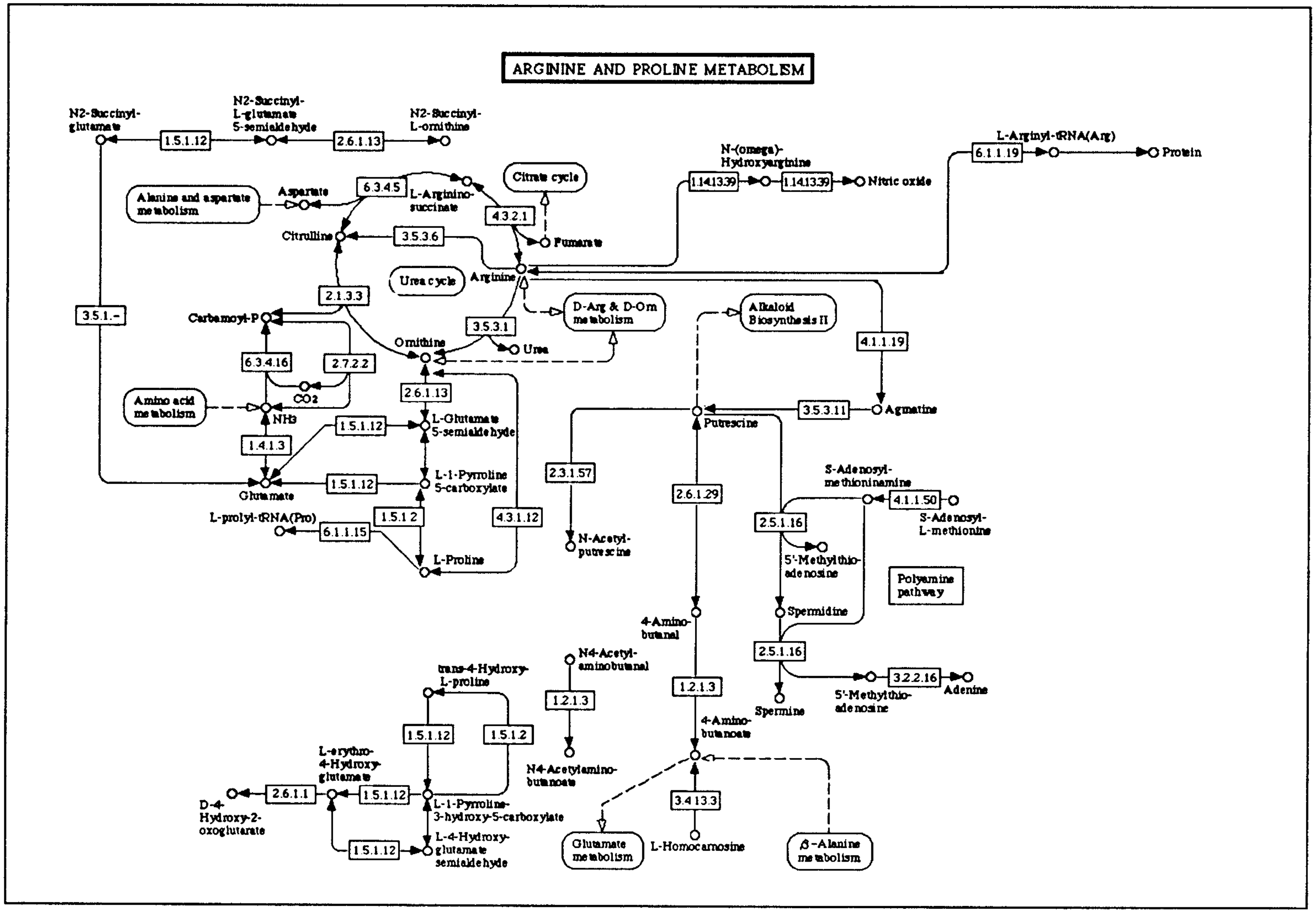

Figure 42. Metabolic pathways of B. cereus 14579: arginine and proline metabolism.

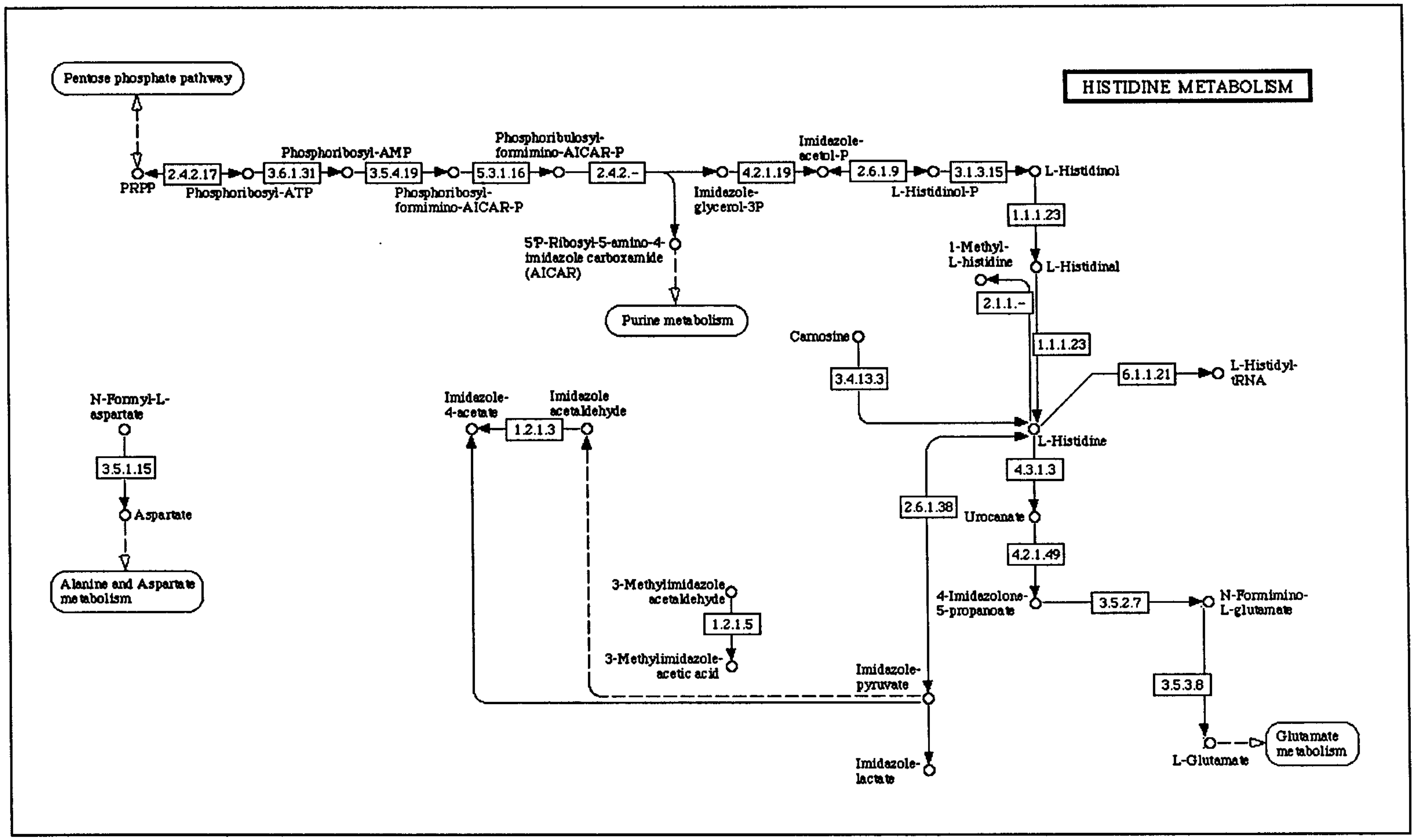

Figure 43. Metabolic pathways of B. cereus 14579: histidine metabolism.

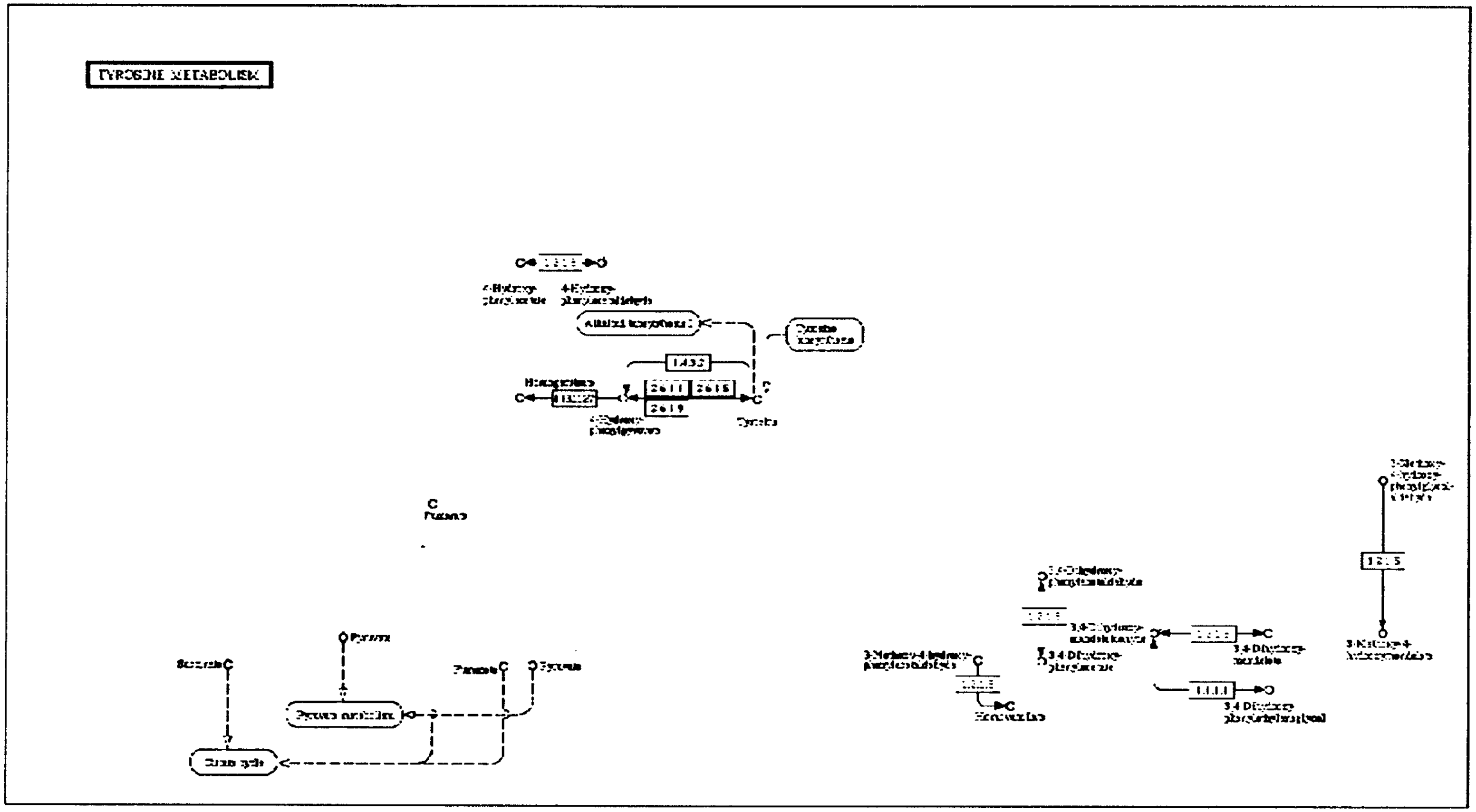

Figure 44. Metabolic pathways of B. cereus 14579: tyrosine metabolism.

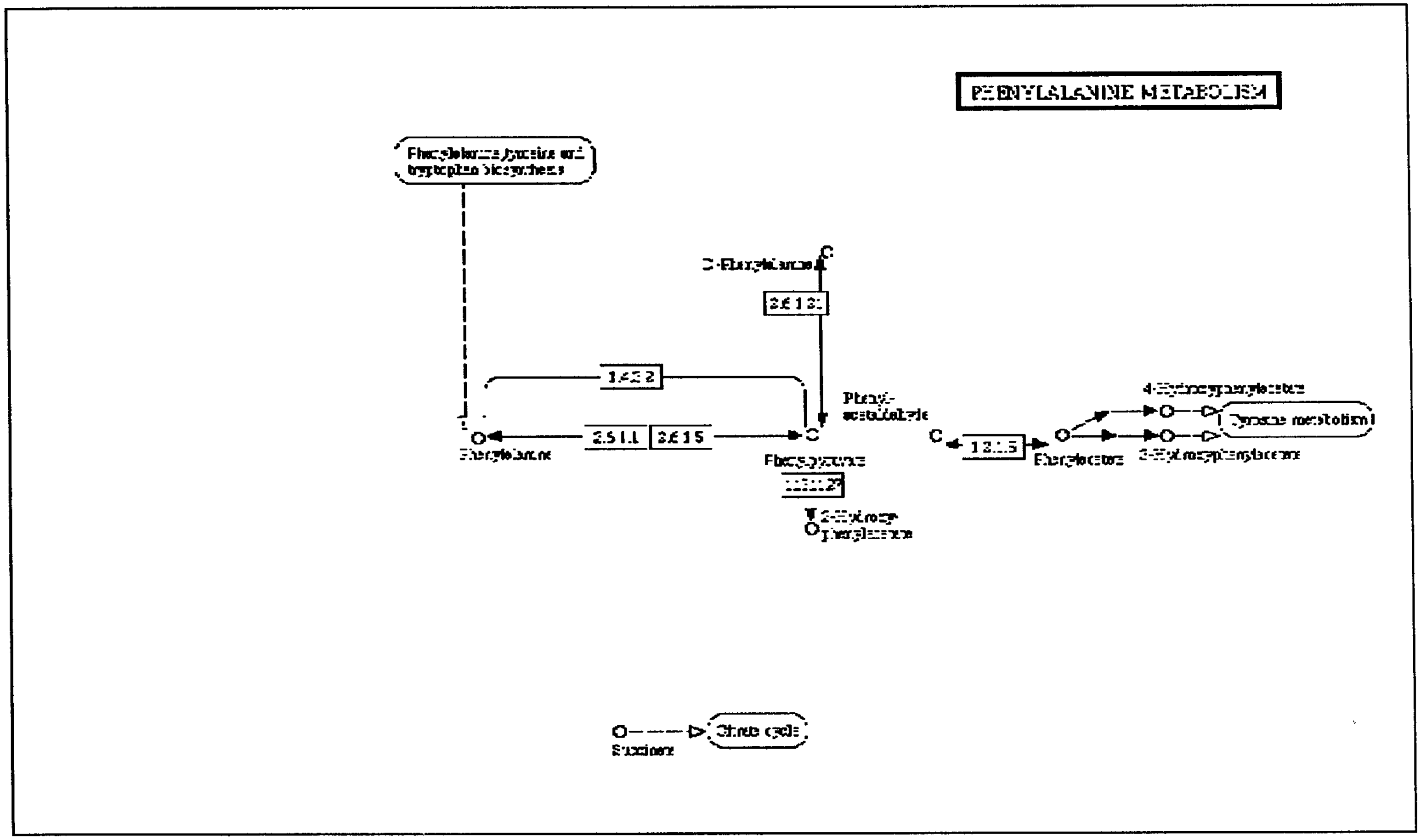

Figure 45. Metabolic pathways of B. cereus 14579: phenylalanine metabolism.

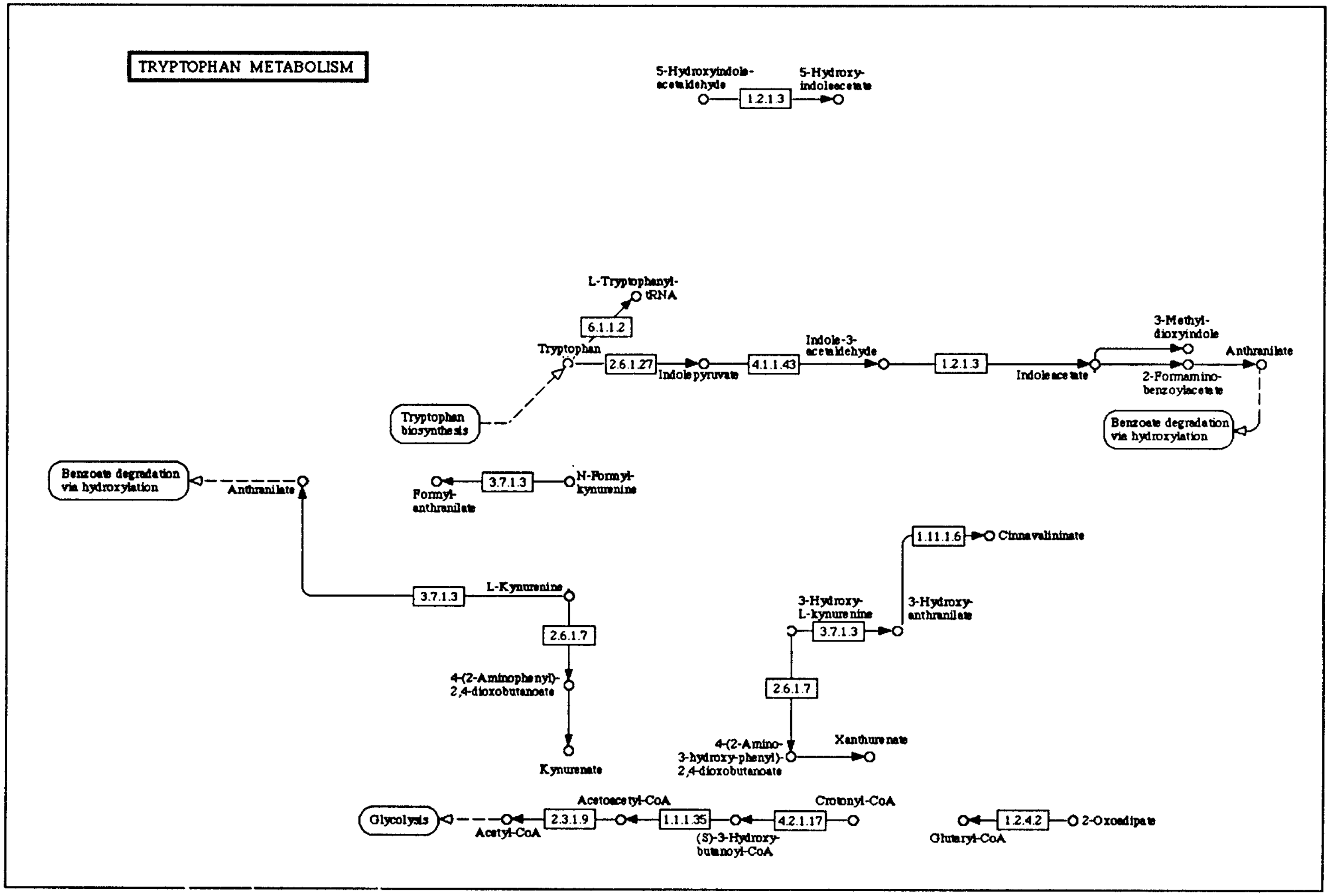

Figure 46. Metabolic pathways of B. cereus 14579: tryptophan metabolism.

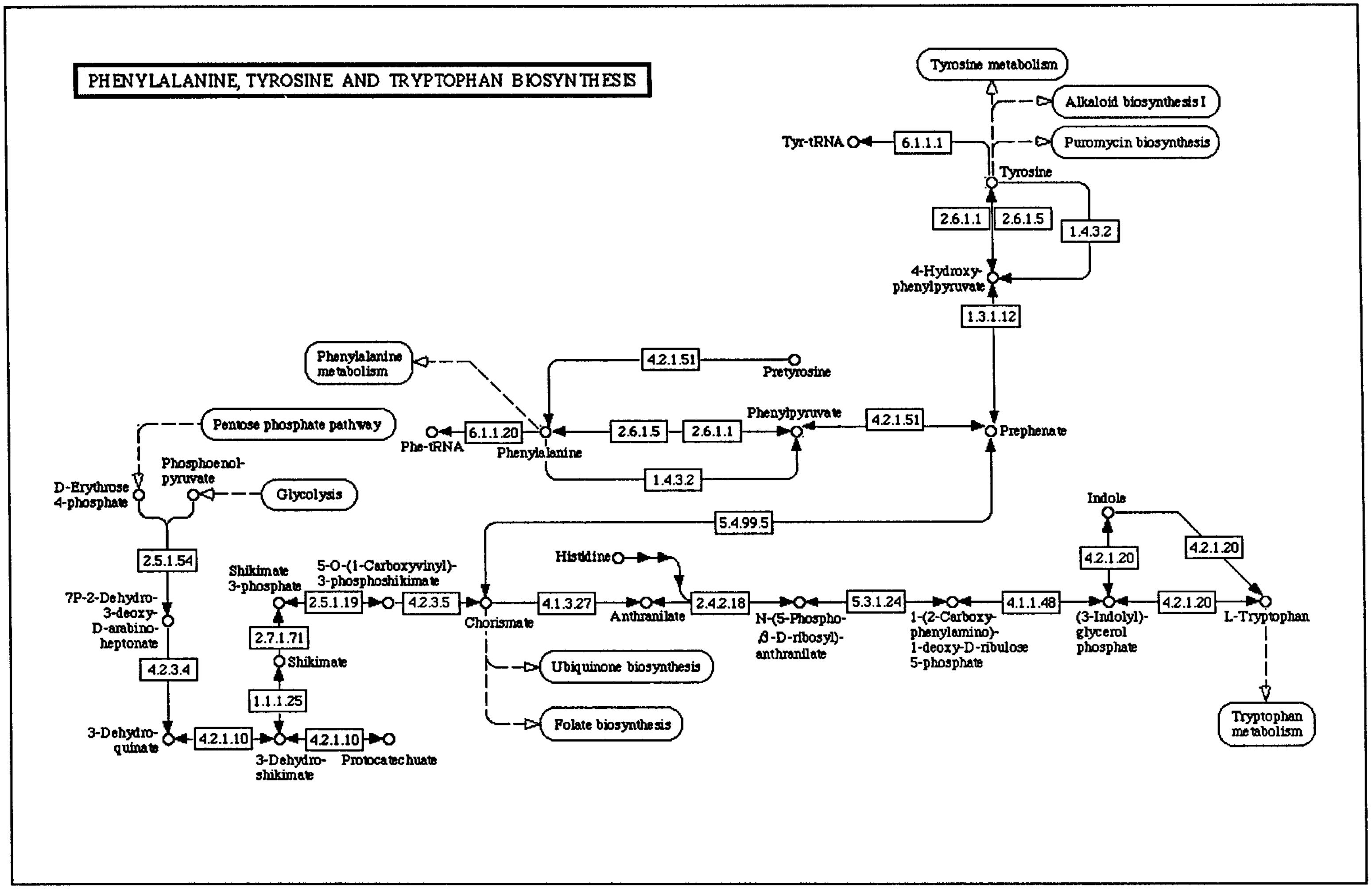

Figure 47. Metabolic pathways of B. cereus 14579: phenylalanine, tyrosine, and tryptophan metabolism.

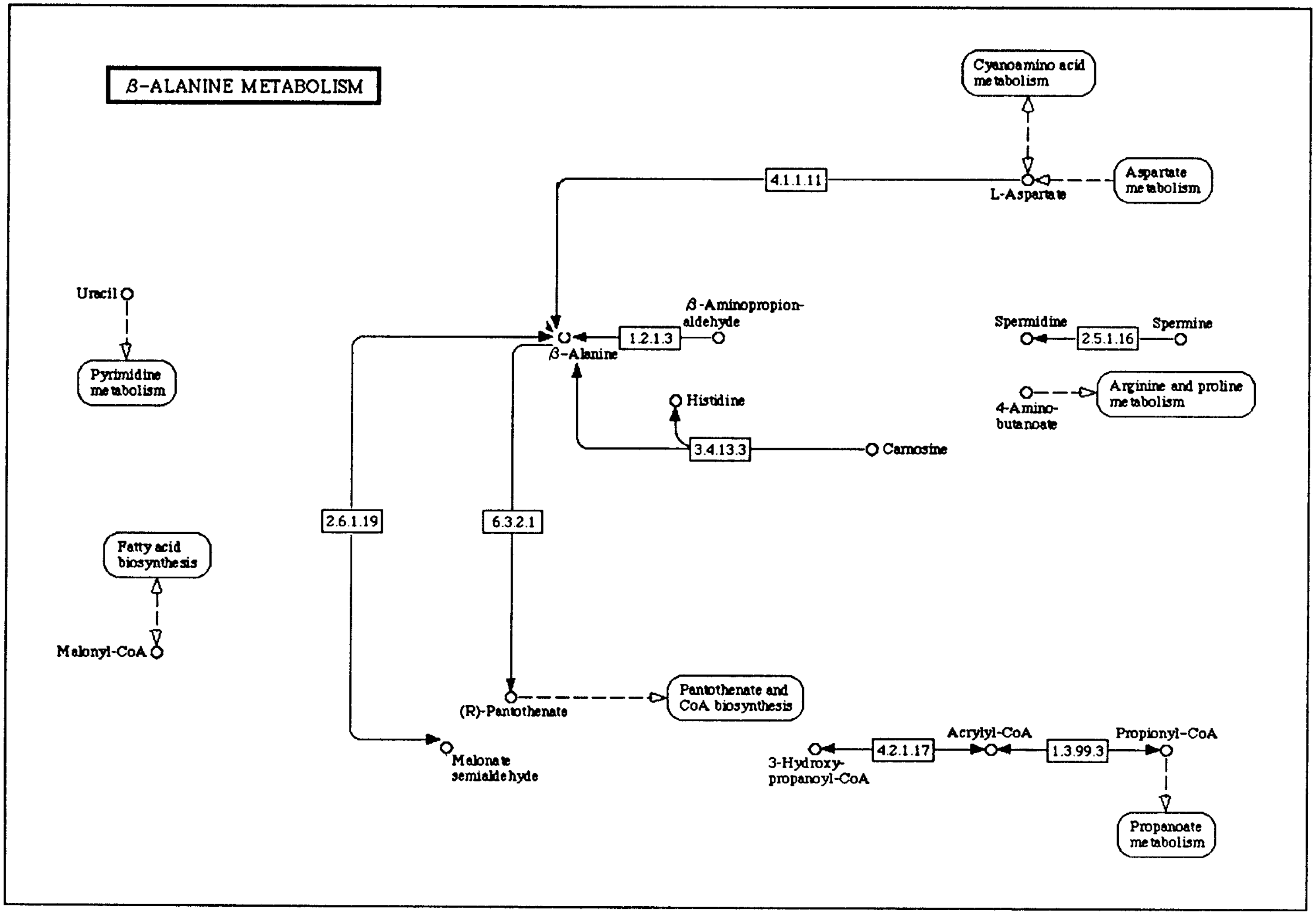

Figure 48. Metabolic pathways of B. cereus 14579: β-alanine metabolism.

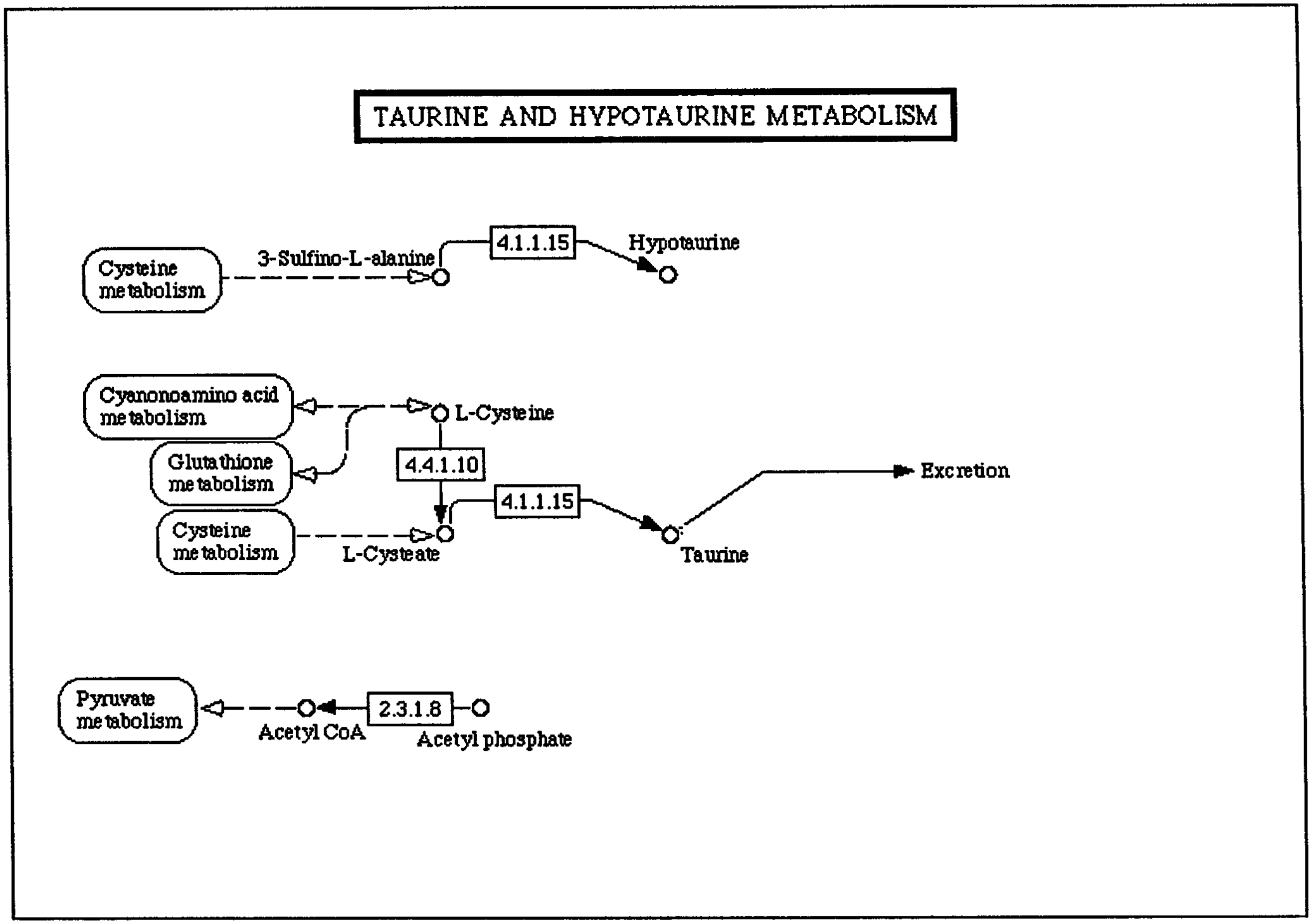

Figure 49. Metabolic pathways of B. cereus 14579: taurine and hypotaurine metabolism.

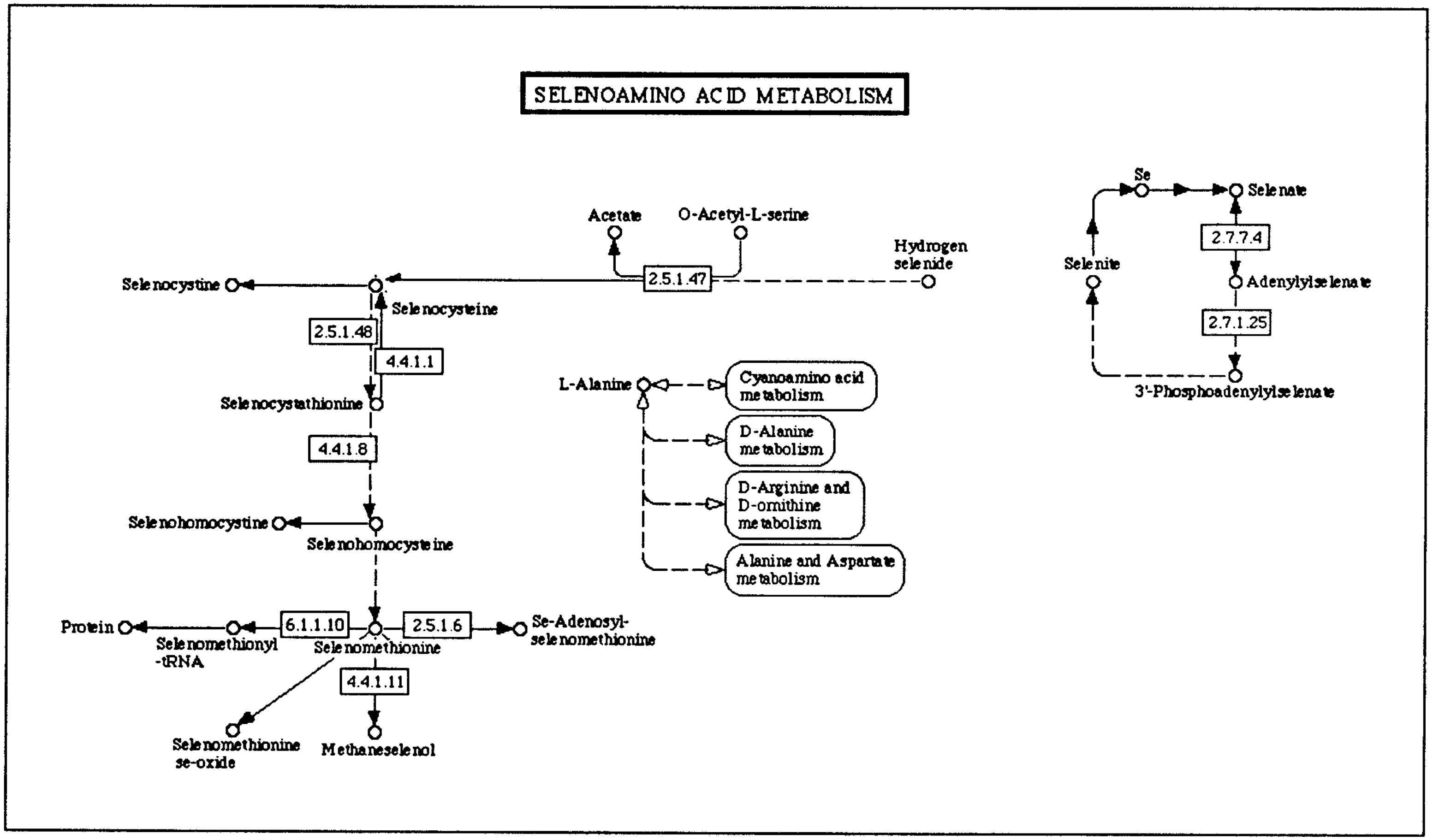

Figure 50. Metabolic pathways of B. cereus 14579: selenoamino acid metabolism.

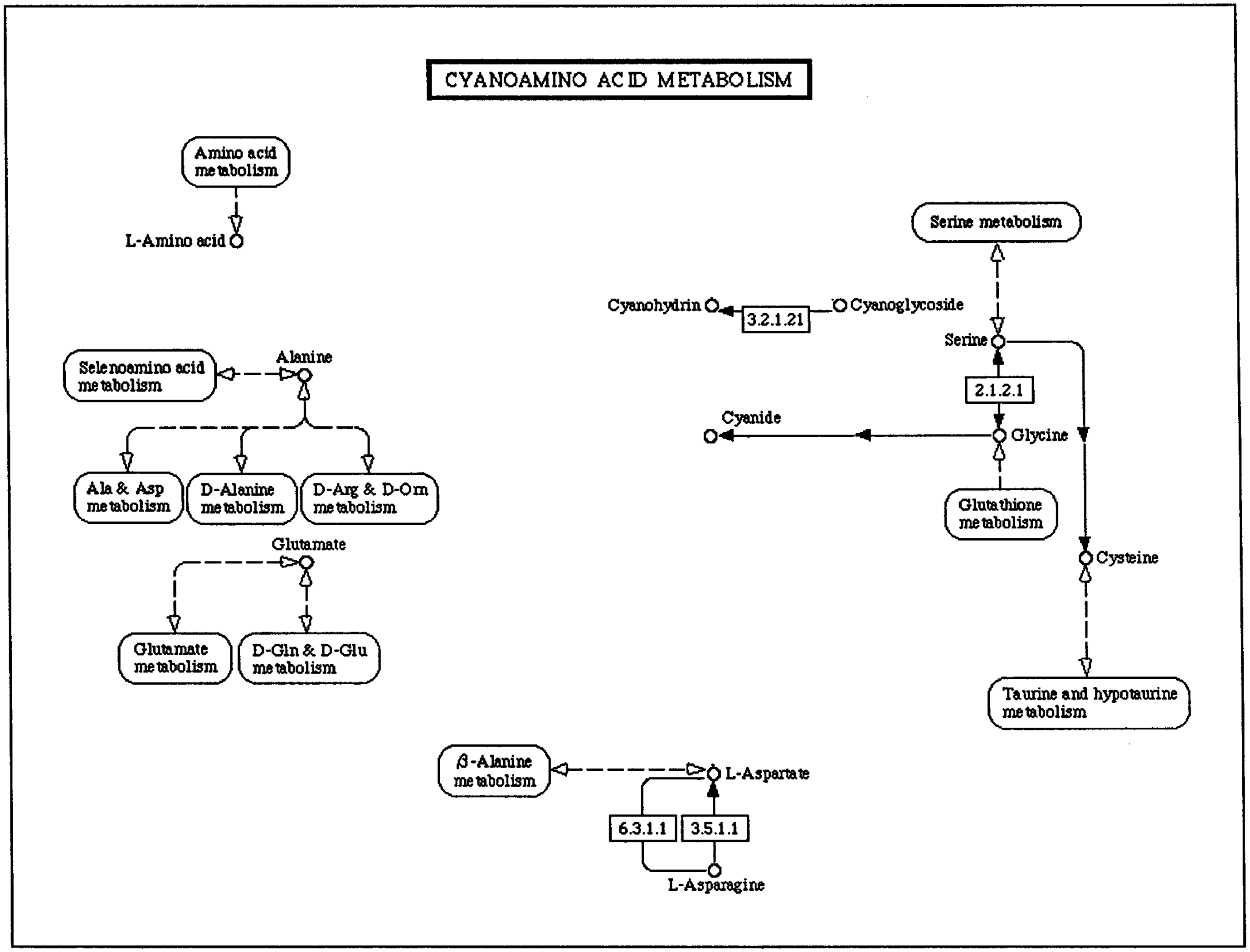

Figure 51. Metabolic pathways of B. cereus 14579: cyanoamino acid metabolism.

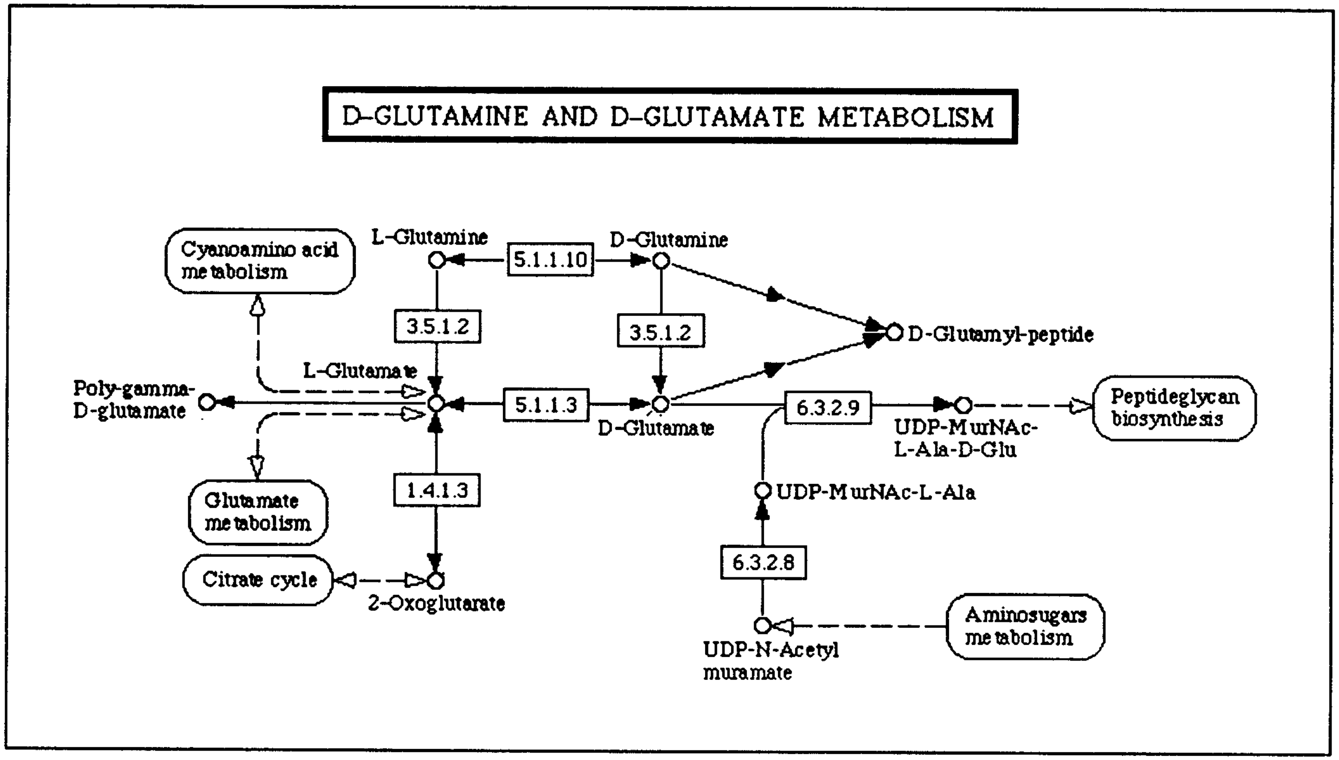

Figure 52. Metabolic pathways of B. cereus 14579: D-glutamine and D-glutamate metabolism.

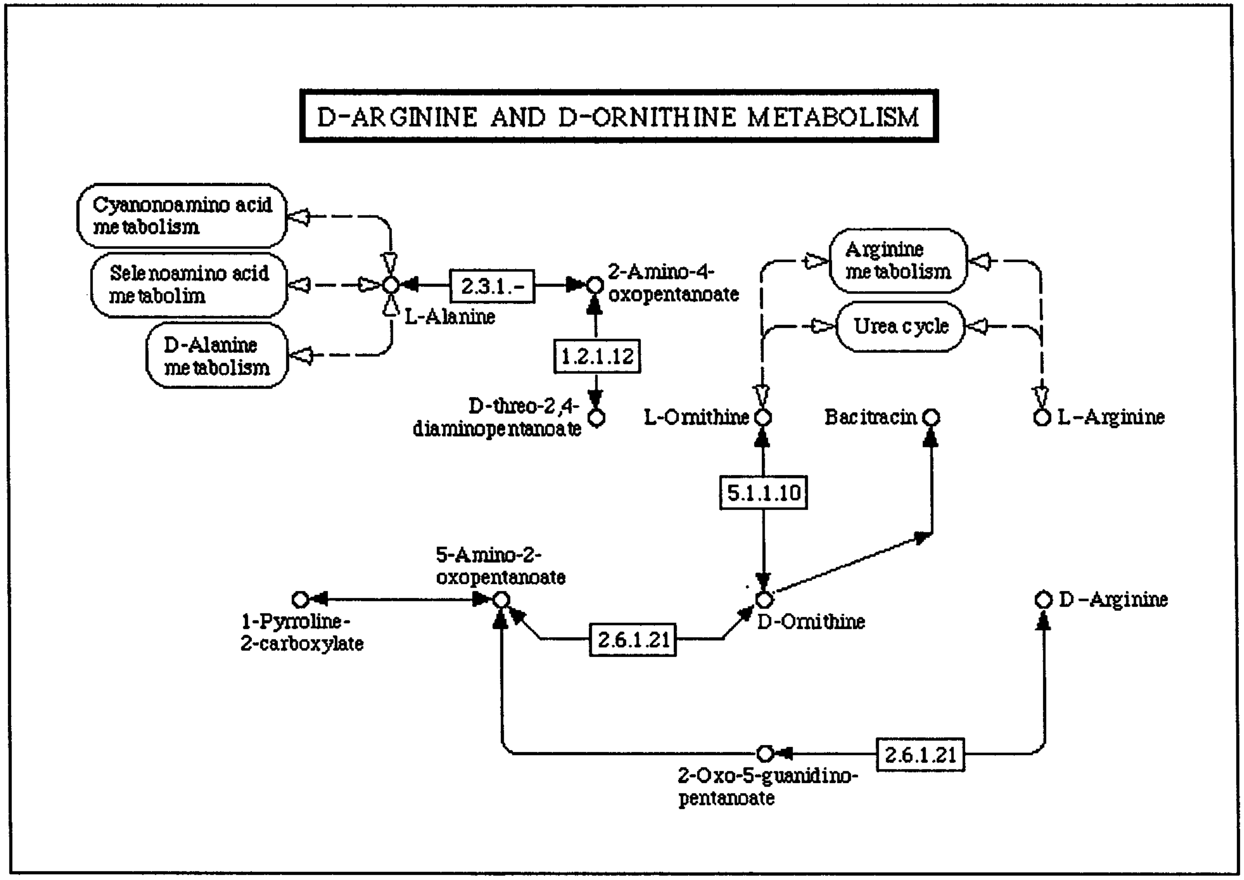

Figure 53. Metabolic pathways of B. cereus 14579: D-arginine and D-ornithine metabolism.

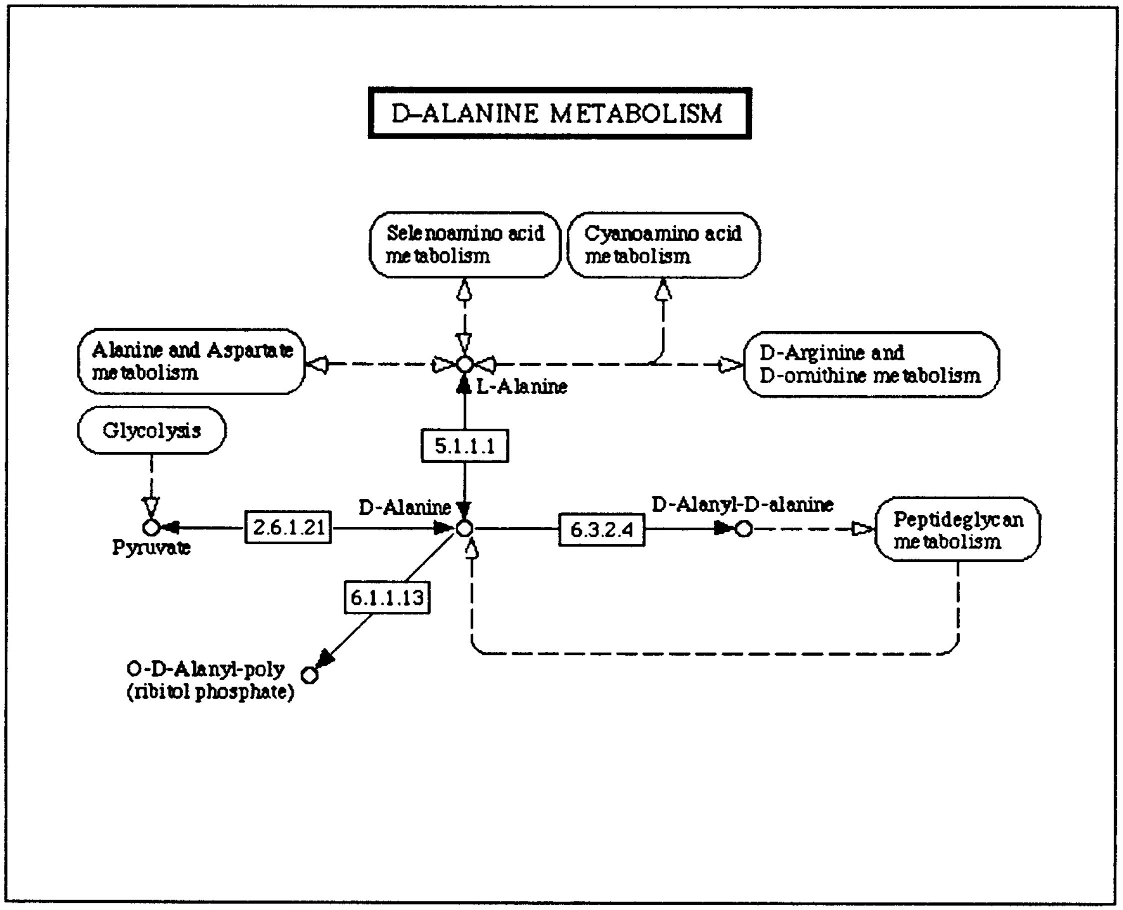

Figure 54. Metabolic pathways of B. cereus 14579: D-alanine metabolism.

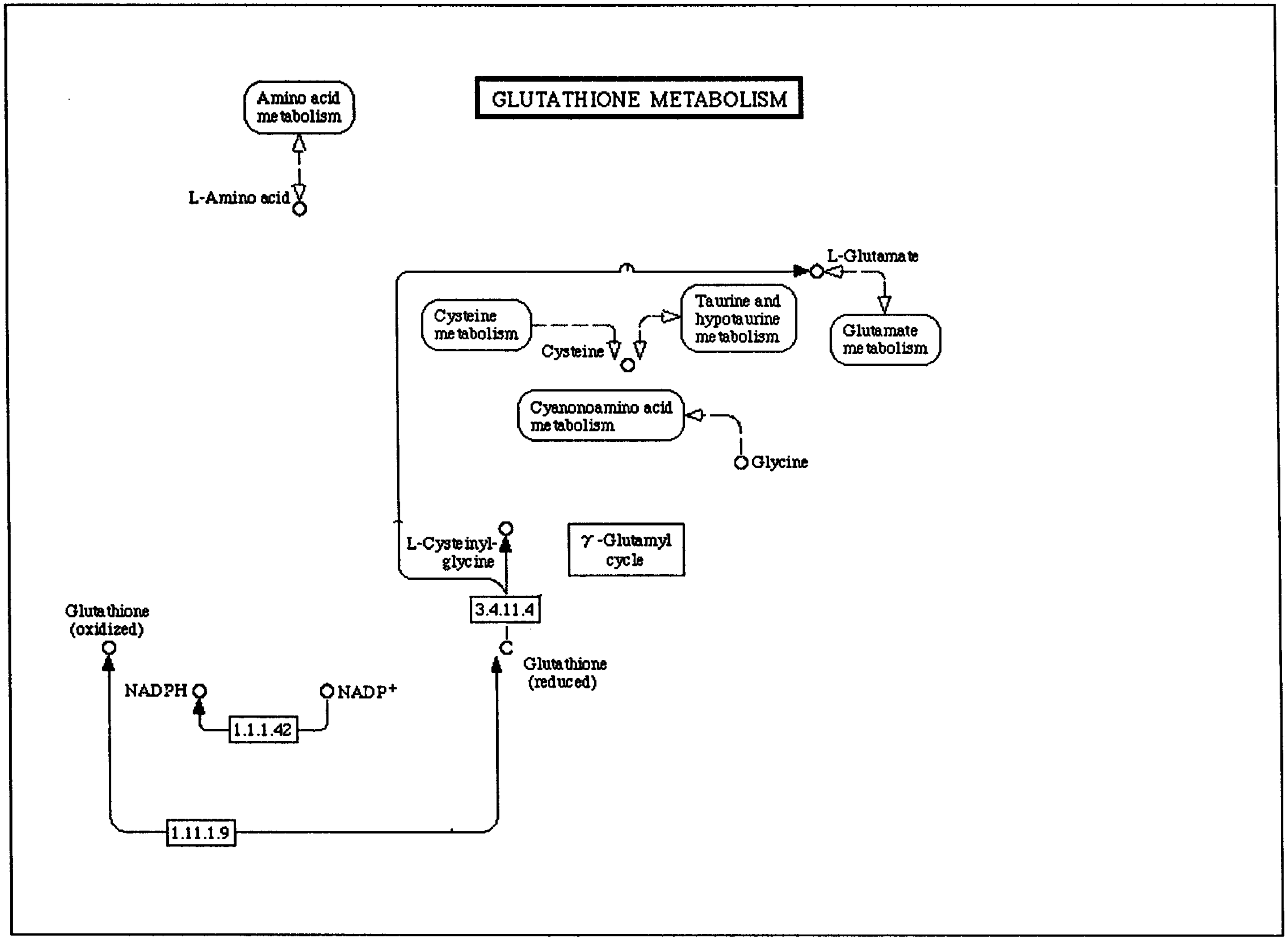

Figure 55. *Metabolic pathways of B. cereus 14579: glutathione metabolism.*

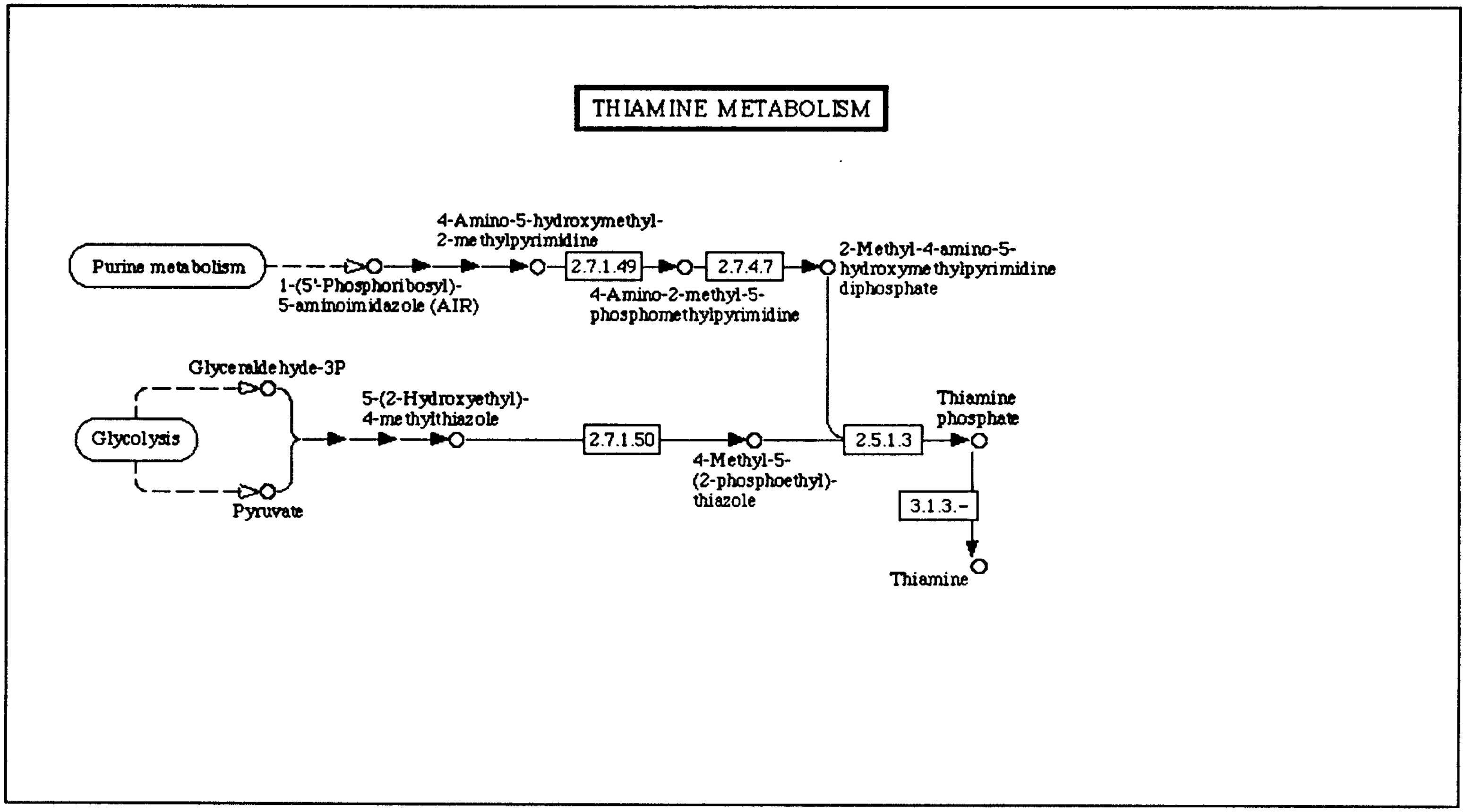

Figure 56. Metabolic pathways of B. cereus 14579: thiamine metabolism

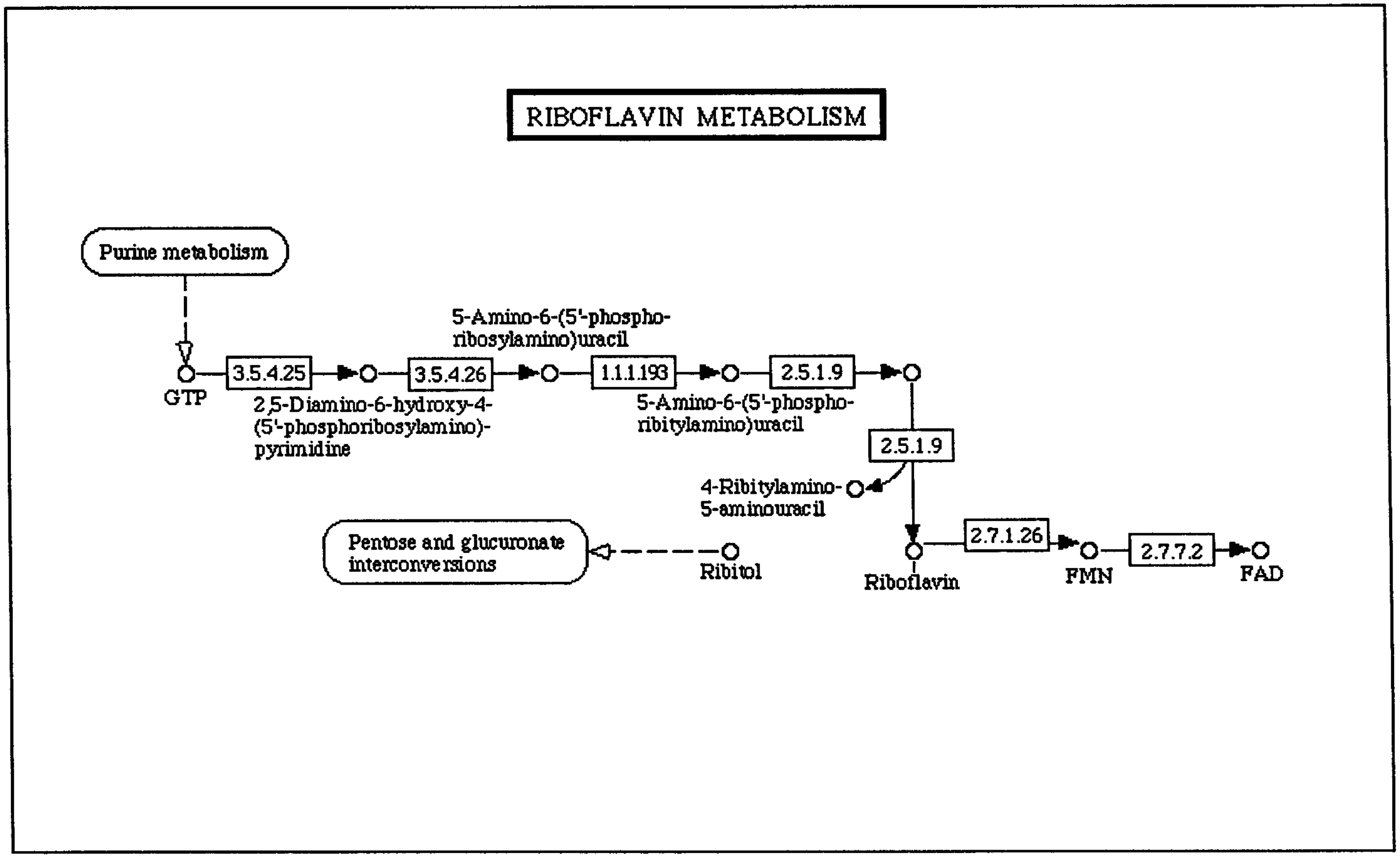

Figure 57. Metabolic pathways of B. cereus 14579: riboflavin metabolism.

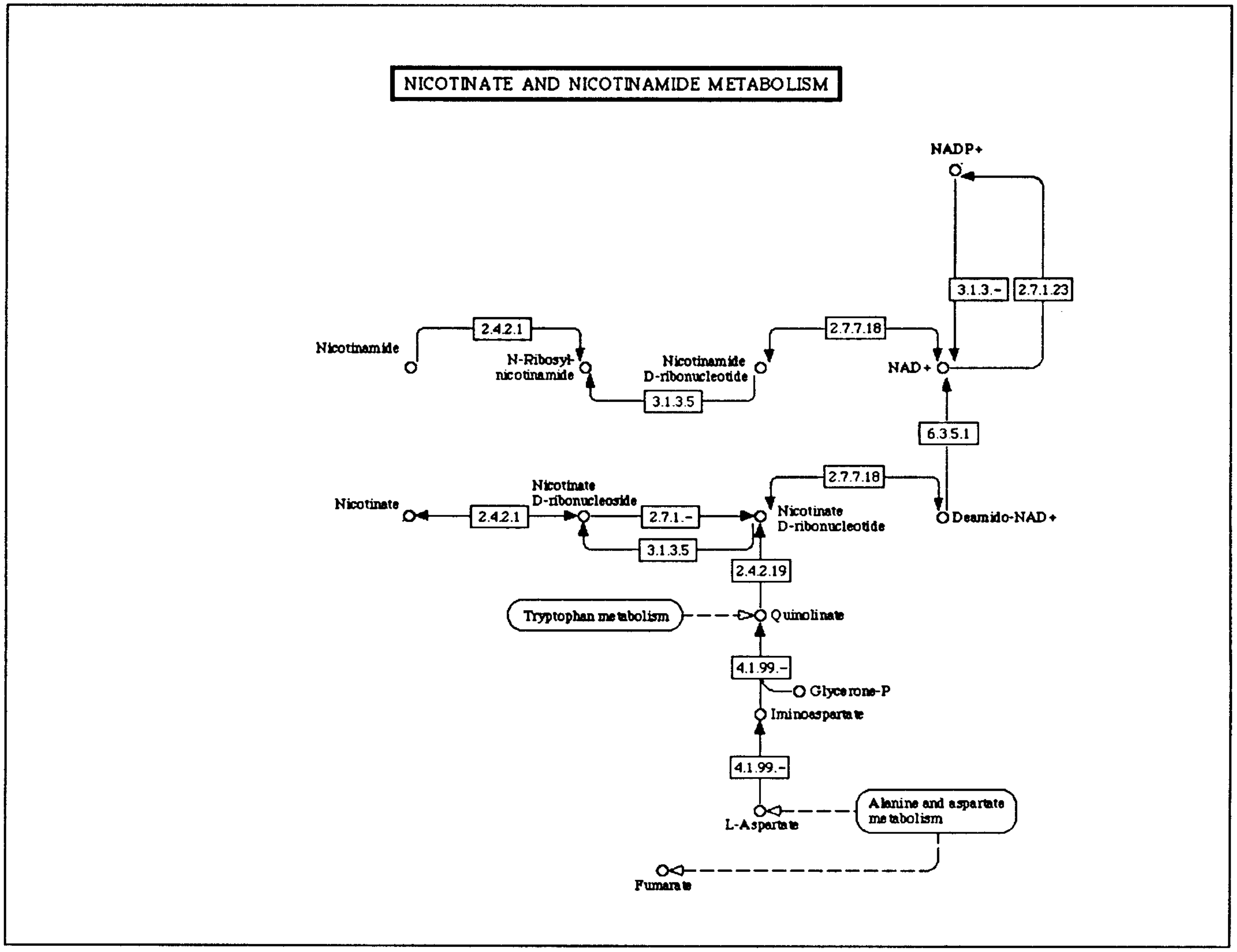

Figure 58. Metabolic pathways of B. cereus 14579: nicotinate and nicotinamide metabolism.

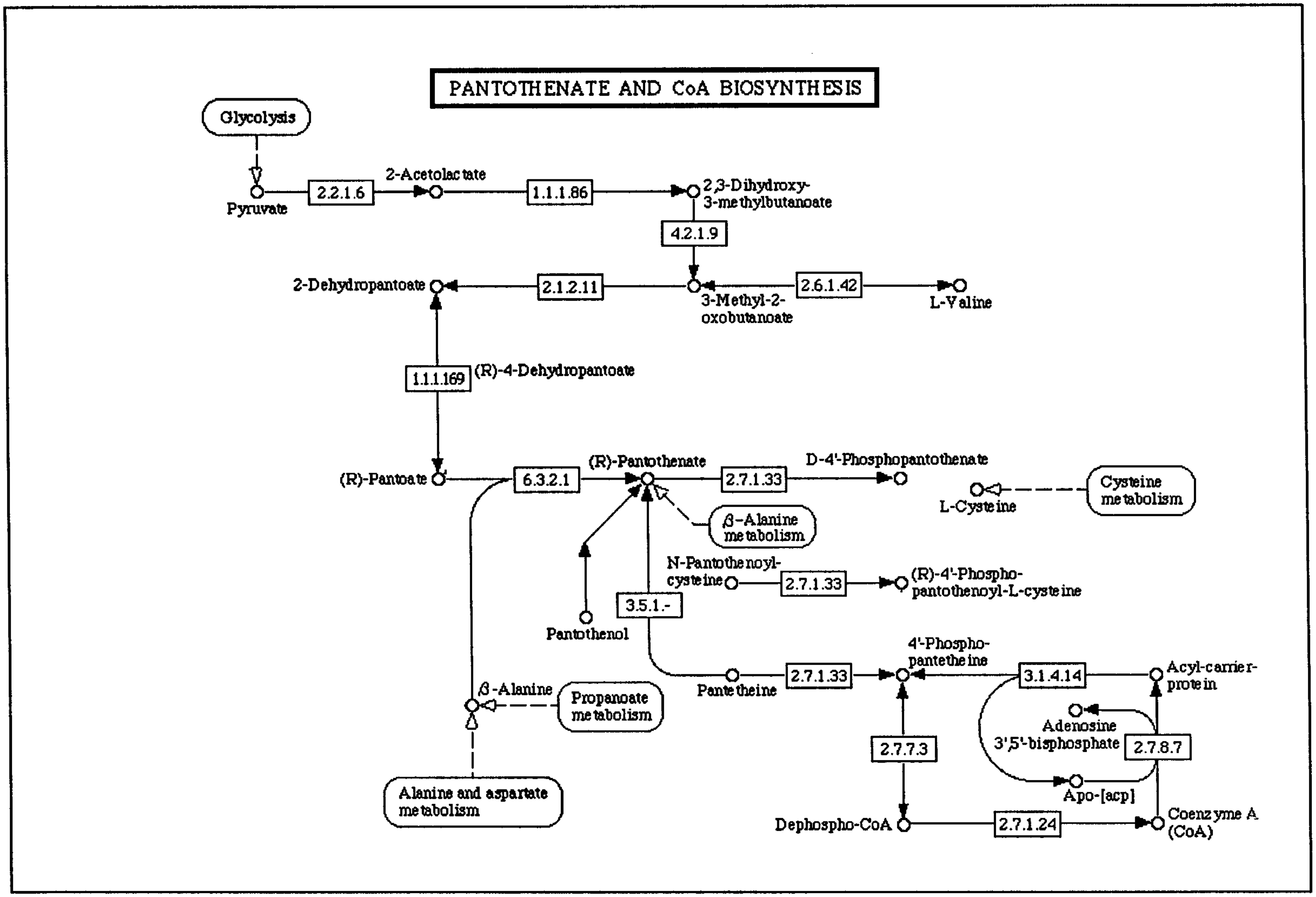

Figure 59. Metabolic pathways of B. cereus 14579: pantothenate and coenzyme A metabolism.

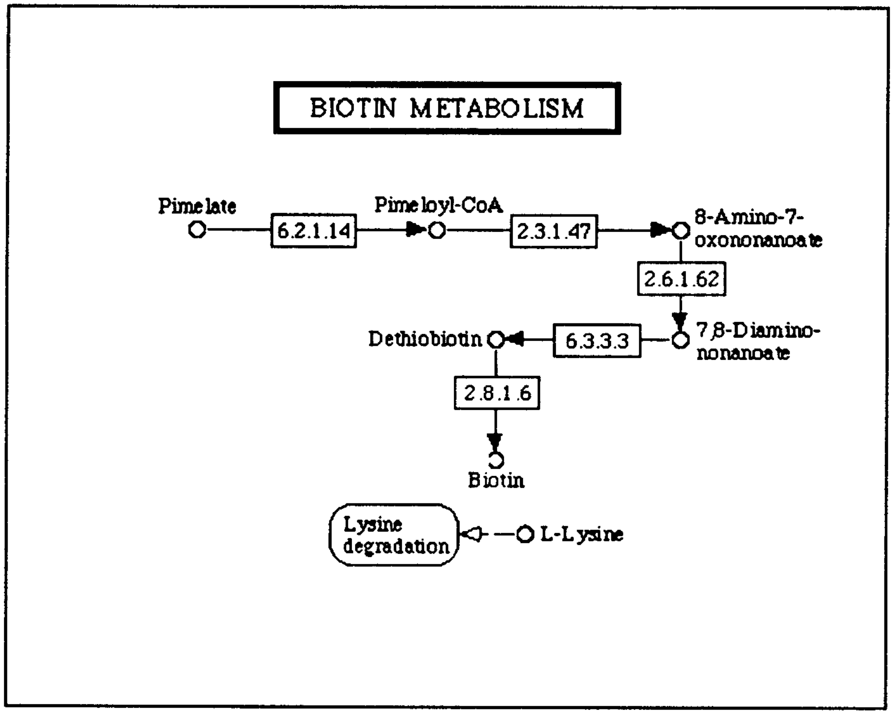

Figure 60. Metabolic pathways of B. cereus 14579: biotin metabolism.

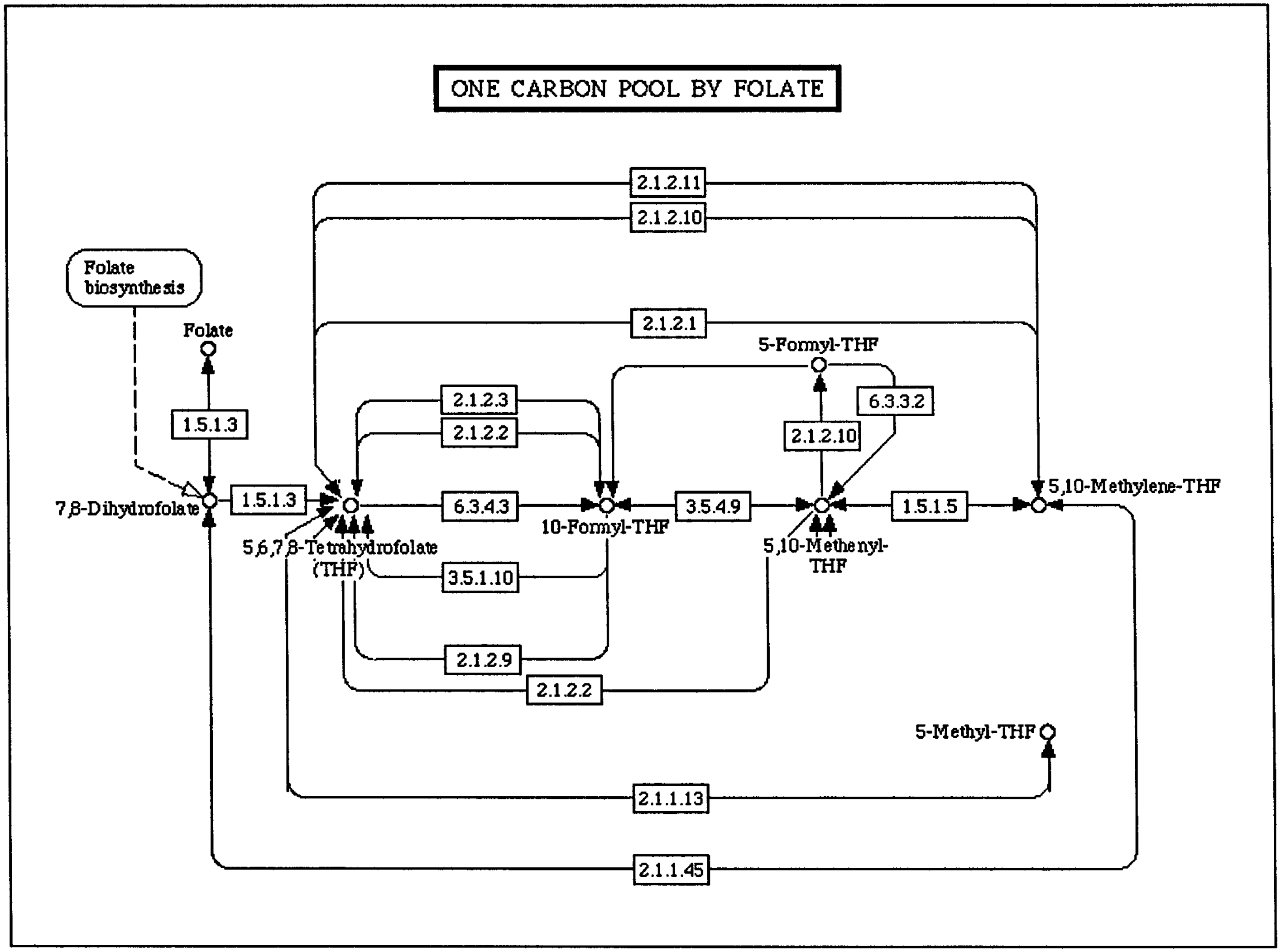

Figure 61. Metabolic pathways of B. cereus 14579: the folate one-carbon pool.

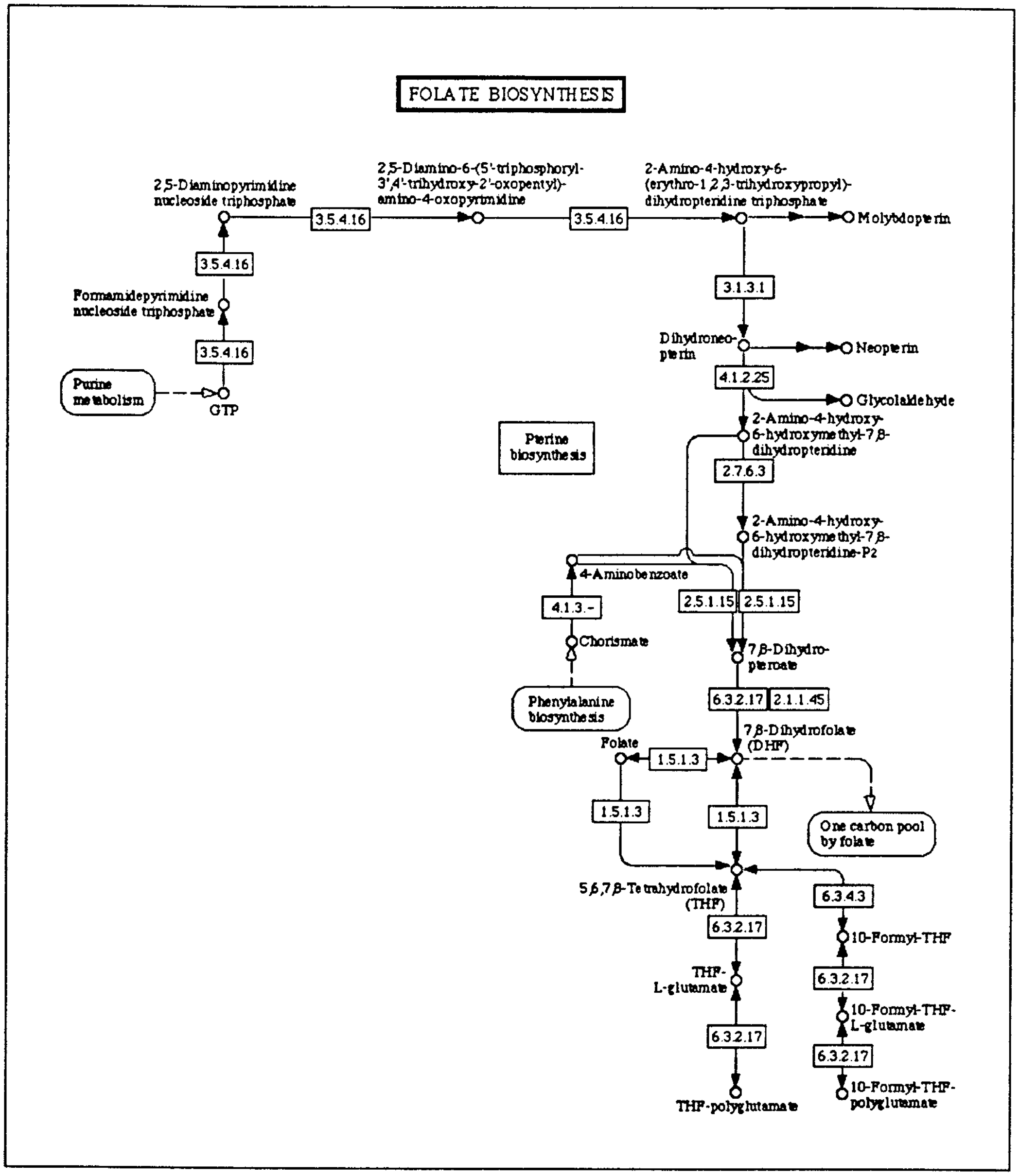

Figure 62. Metabolic pathways of B. cereus 14579: folate biosynthesis.

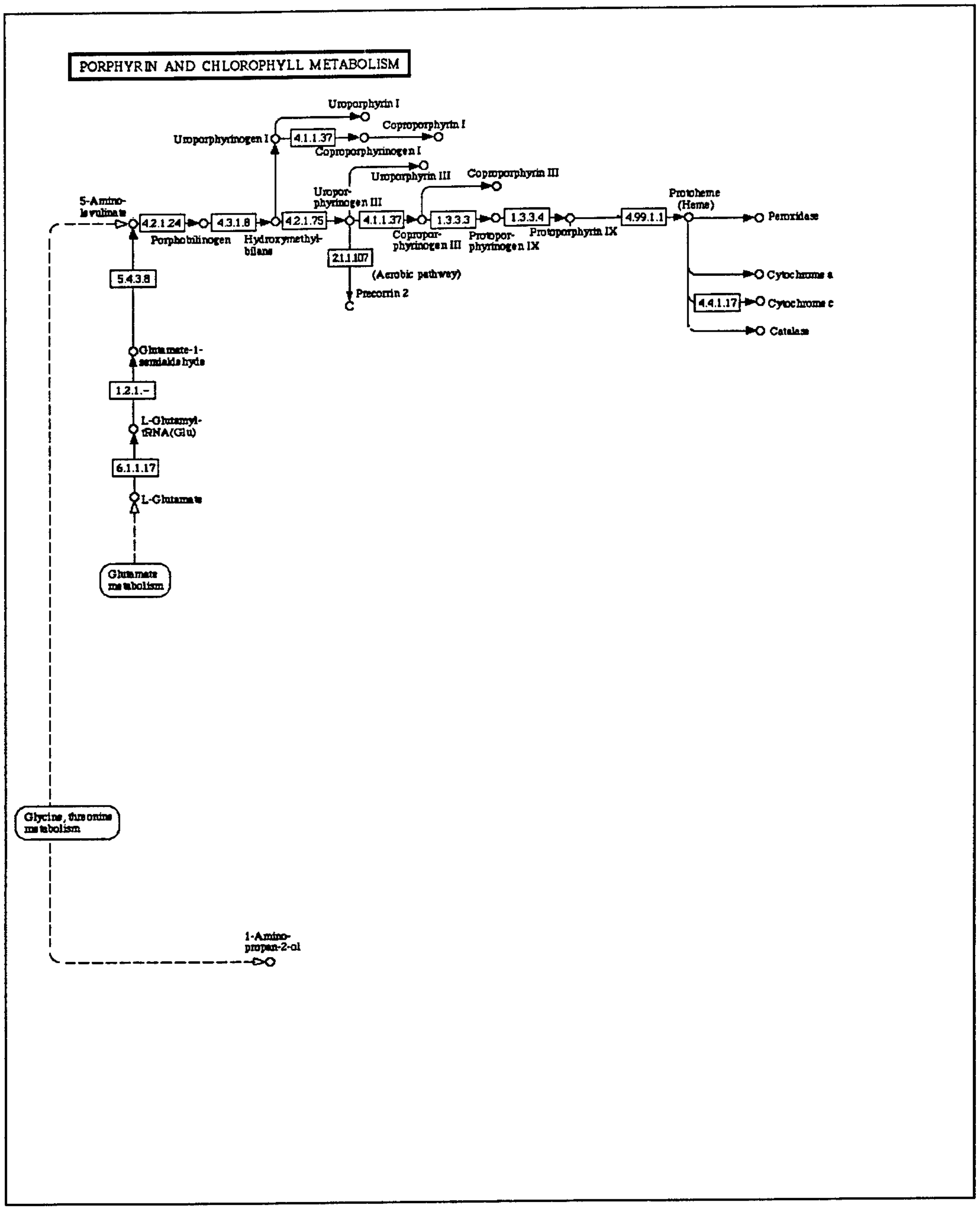

Figure 63. Metabolic pathways of B. cereus 14579: porphyrin metabolism.

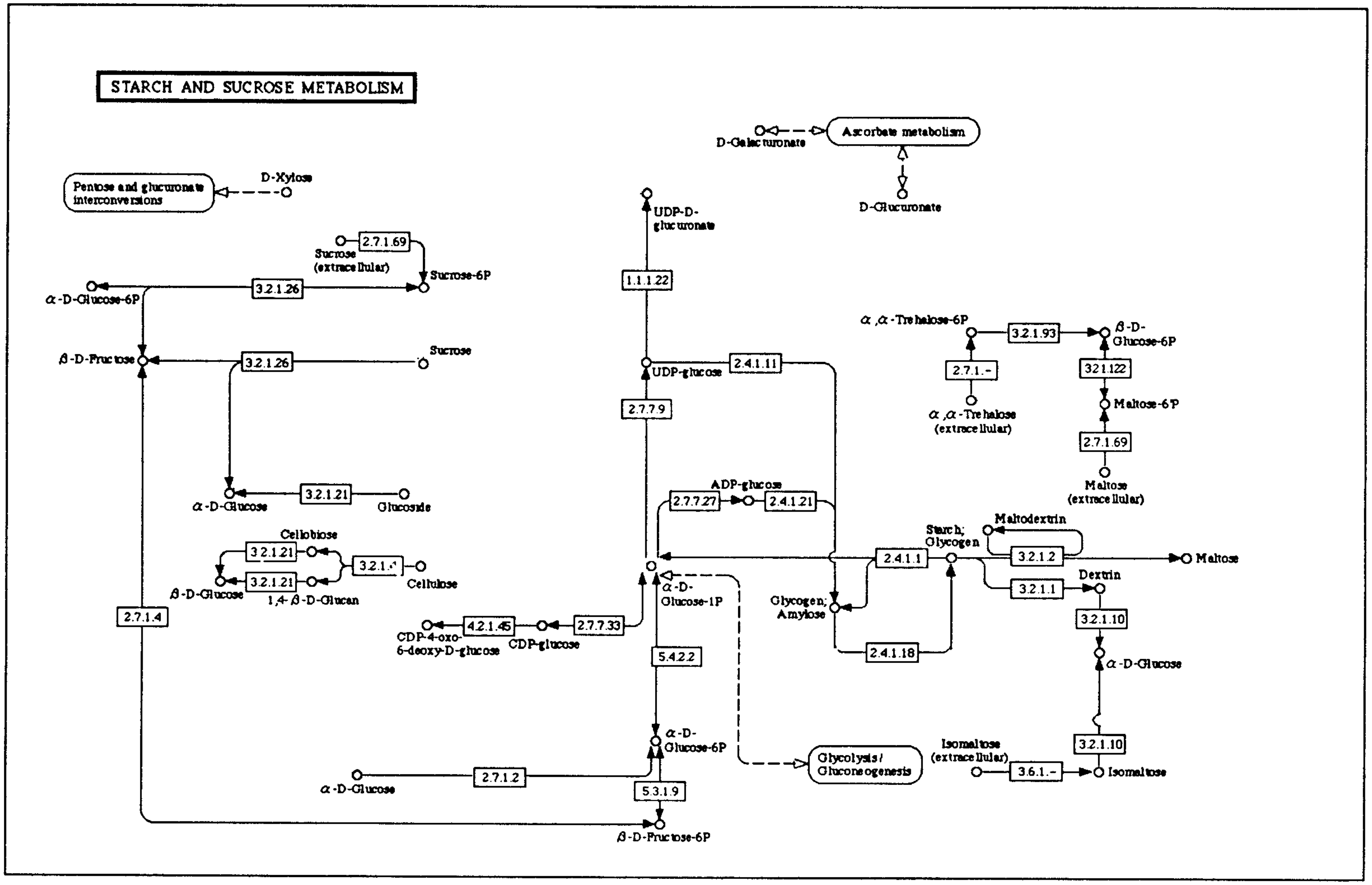

Figure 64. Metabolic pathways of B. cereus 14579: starch and sucrose metabolism.

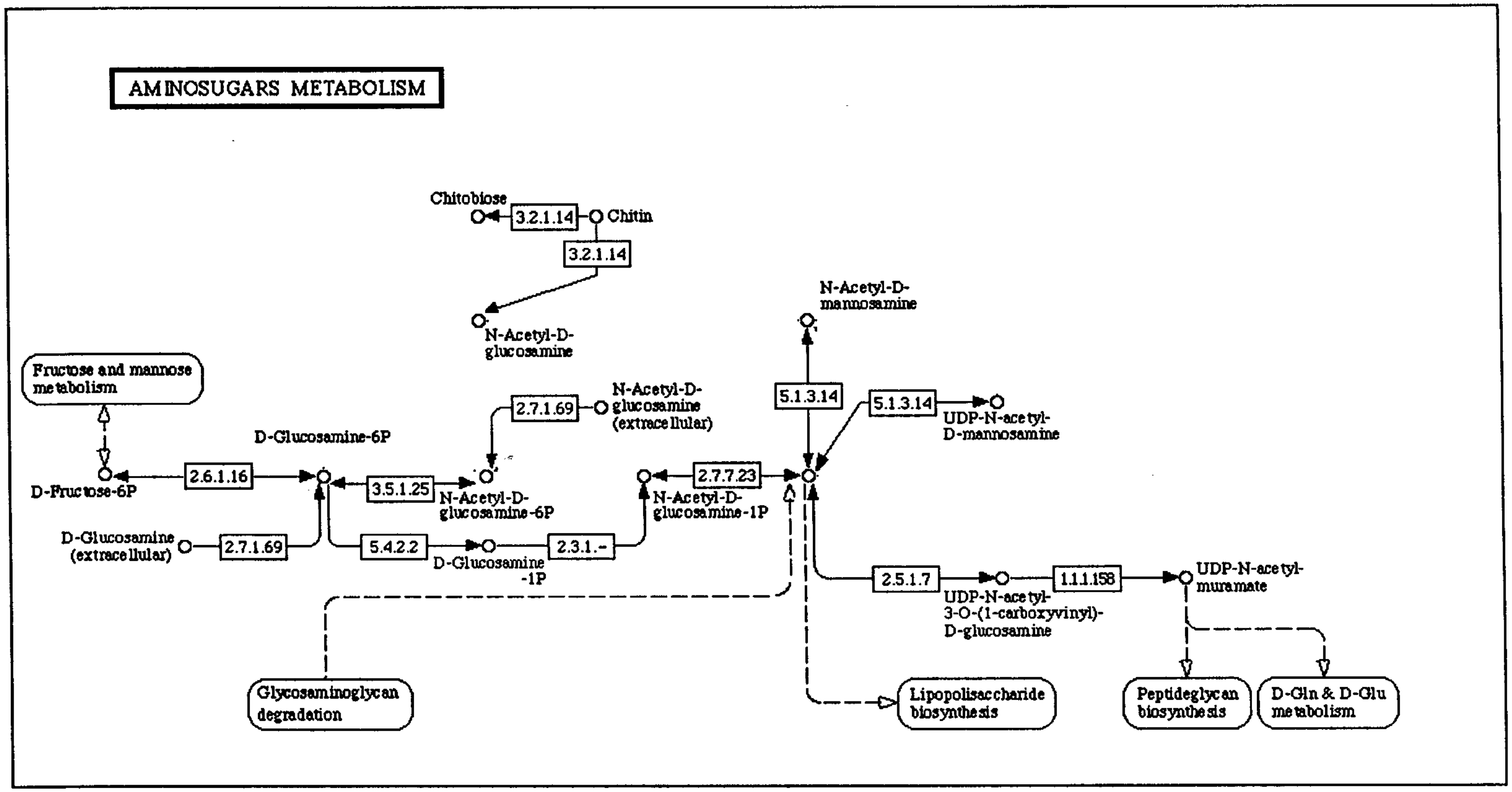

Figure 65. Metabolic pathways of B. cereus 14579: aminosugars metabolism.

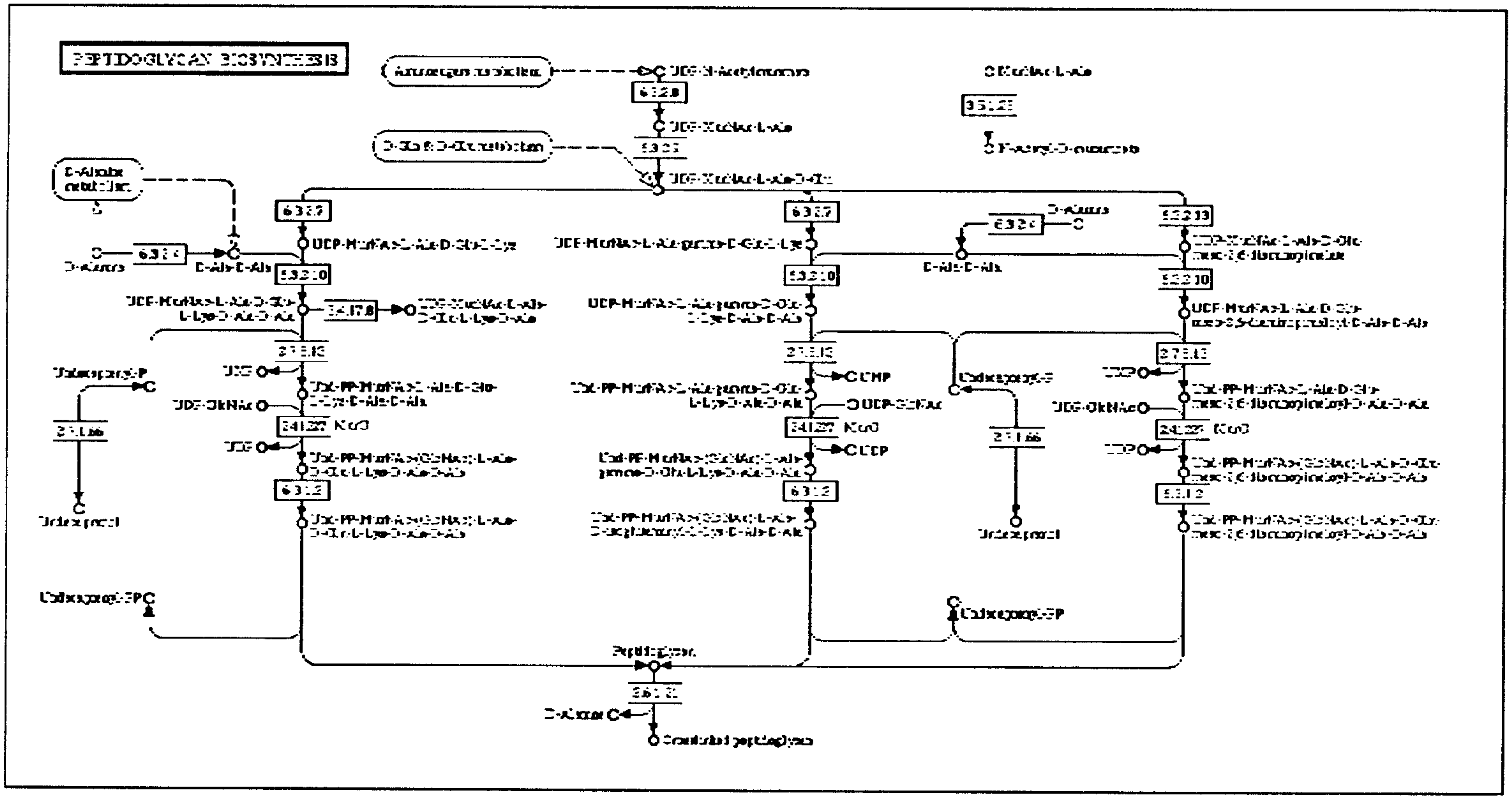

Figure 66. Metabolic pathways of B. cereus 14579: peptidoglycan metabolism.

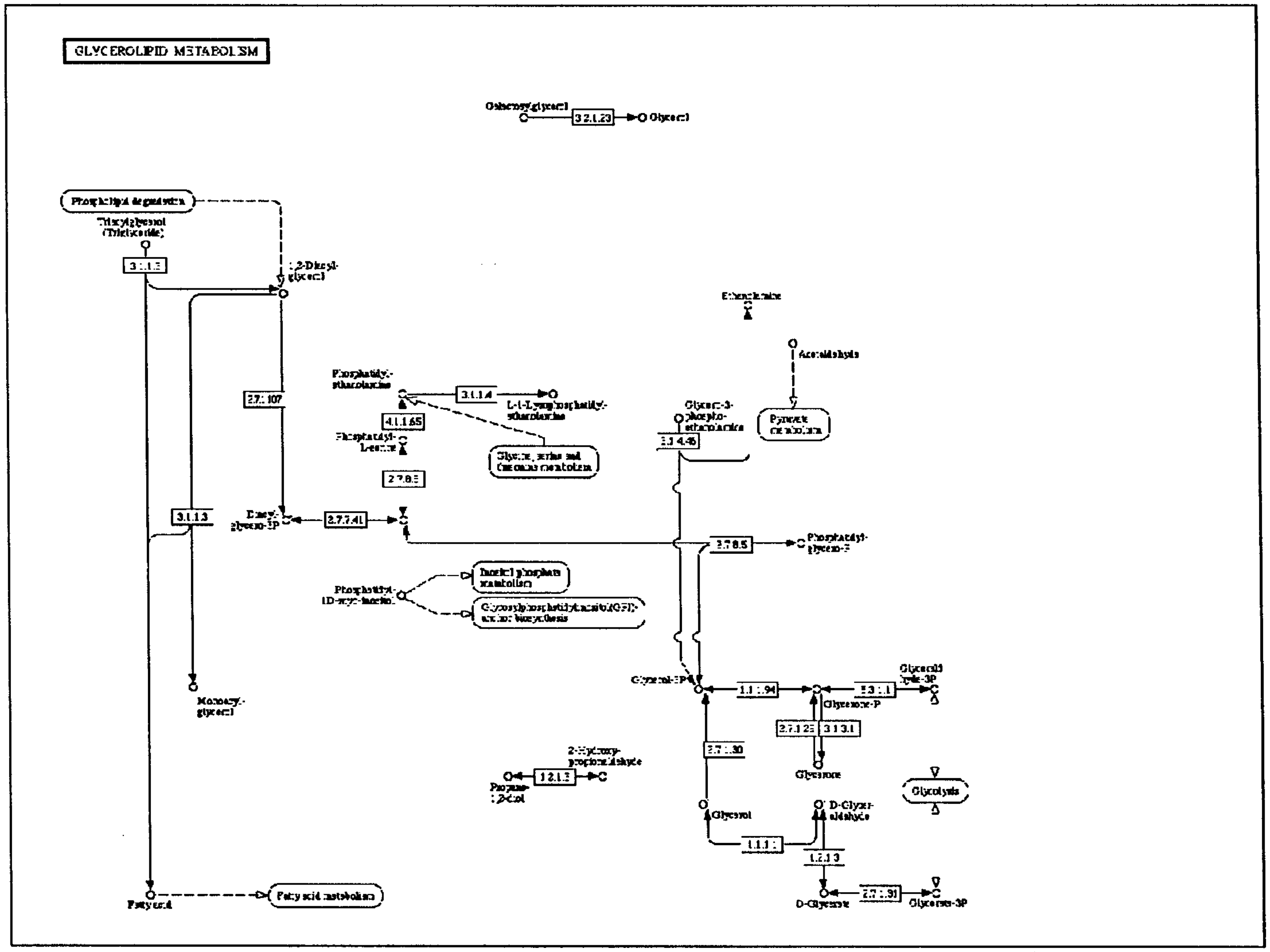

Figure 67. Metabolic pathways of B. cereus 14579: glycerolipid metabolism.

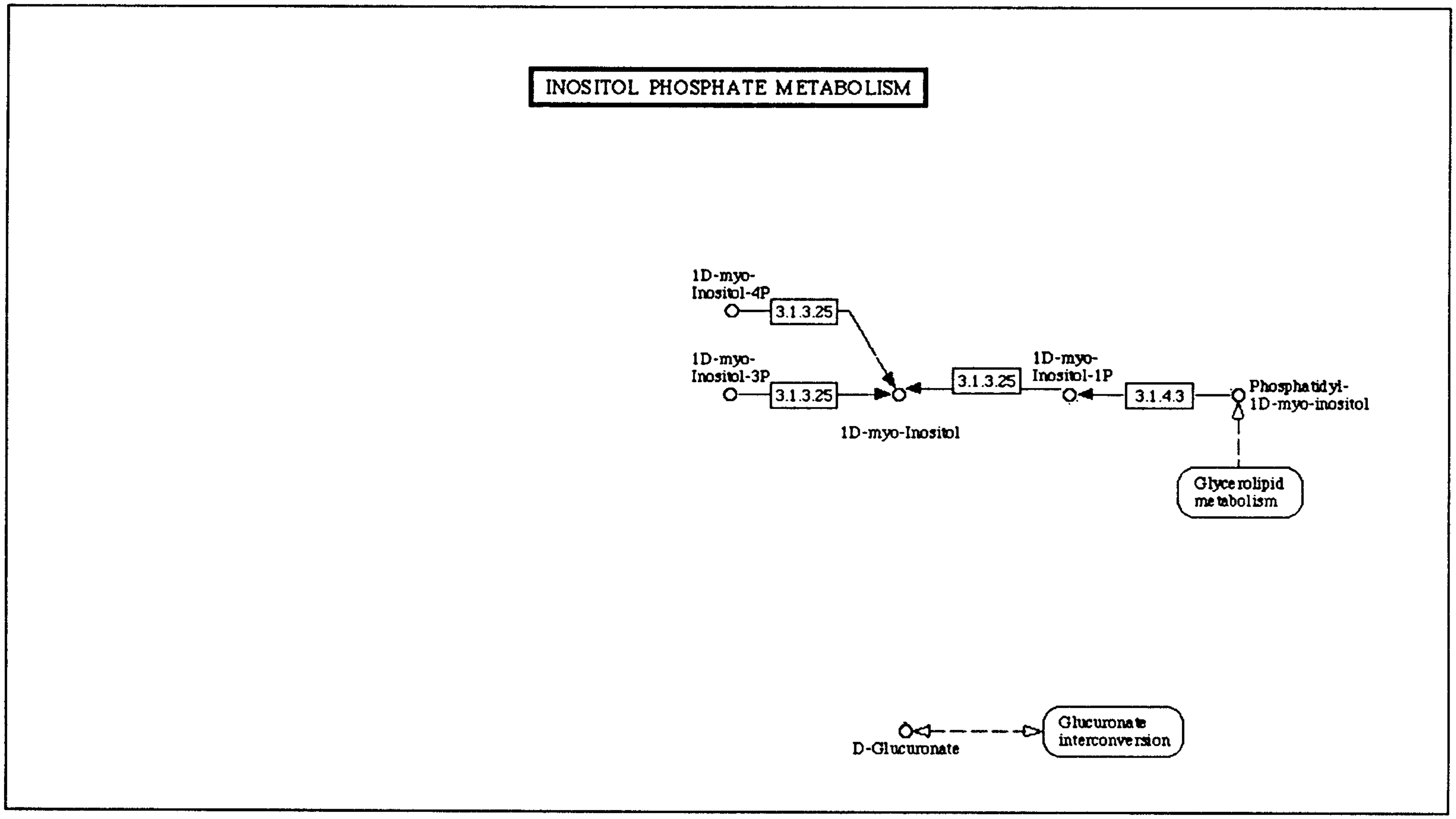

Figure 68. Metabolic pathways of B. cereus 14579: inositol phosphate metabolism.

Recent Developments

After the analyses in the preceding sections were completed, the fully annotated genomes for *B. cereus* 14579 and for *B. anthracis* Ames were published [15,16]. Those published annotations have since been integrated into the KEGG metabolic database. Close examination of these genome papers determined no serious differences with the conclusions obtained in the present document. The key difference relates to the number of putative open-reading frames discovered in the genome, with the published *B. cereus* 14579 finding 5366 genes [15], as compared with the 4885 genes annotated here. This difference can be solely related to the confidence level used as the cut-off threshold for acceptance of a particular open-reading frame as an actual protein coding sequence. The present use of $E>1^{-10}$ as a cut-off is significantly more conservative than is normally used ($E>1^{-5}$) and eliminates genes that appear marginal. It should be pointed out that any gene in *B. cereus* 14579 which has an E value of less than 1^{-10} against *B. anthracis* A2012, *B. subtilis* 168, and *B. halodurans* C-250 is either a totally new gene unique only to *B. cereus* or is a spurious identification. It is highly unlikely that the data in Table 3 is missing 481 unique *B. cereus* sequences, particularly given the completeness of the major metabolic pathways extrapolated from the Table 3 data.

While the timing of the recent genome papers is unfortunate given the effort invested in the current analyses, the open publication of the *B. cereus* 14579 genome actually does not obviate the value of the present work. As genome publications have become more routine, they have also been given less page space in journals such as Science and Nature. Thus, the *B. cereus* 14579 paper summarizes the entire genome and its contents in 5 pages (including figures and tables), while the *B. anthracis* Ames genome is covered in 6 pages (including figures and tables). Anyone desiring the complete annotation is therefore forced to reference supplementary online figures and tables, or online genome repositories (such as NCBI). In addition, there is value in having multiple, independent analysis of the genome content, particularly by people who plan on working further with the organism. Organisms such as *B. subtilis* 168, *Mycobacterium tuberculosis* H37Rv, and *Plasmodium falciparum* 3D7 have had an entire community analysing, reanalysing, and updating the genome data and its annotation based on more recent findings. The *B. anthracis* and *B. cereus* data appears much more likely to suffer the more common genome fate where the sequencing organisation has little interest in the organisms themselves and has moved on to the next challenge. At the very least, the present document will form the bench manual for the continued use of *B. cereus* 14579 at DRDC Suffield as a biochemical model system for enzyme studies in *B. anthracis*.

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Appendix

Appendix 1. Enzyme Commission (EC) numbers for enzymes.

- **EC 1 Oxidoreductases**
  - EC 1.1 Acting on the CH-OH group of donors
    - EC 1.1.1 With NAD or NADP as acceptor
      - EC 1.1.1.1 alcohol dehydrogenase
      - EC 1.1.1.2 alcohol dehydrogenase (NADP)
      - EC 1.1.1.3 homoserine dehydrogenase
      - EC 1.1.1.4 (R,R)-butanediol dehydrogenase
      - EC 1.1.1.5 acetoin dehydrogenase
      - EC 1.1.1.6 glycerol dehydrogenase
      - EC 1.1.1.7 propanediol-phosphate dehydrogenase
      - EC 1.1.1.8 glycerol-3-phosphate dehydrogenase (NAD)
      - EC 1.1.1.9 D-xylulose reductase
      - EC 1.1.1.10 L-xylulose reductase
      - EC 1.1.1.11 D-arabinitol 4-dehydrogenase
      - EC 1.1.1.12 L-arabinitol 4-dehydrogenase
      - EC 1.1.1.13 L-arabinitol 2-dehydrogenase
      - EC 1.1.1.14 L-iditol 2-dehydrogenase
      - EC 1.1.1.15 D-iditol 2-dehydrogenase
      - EC 1.1.1.16 galactitol 2-dehydrogenase
      - EC 1.1.1.17 mannitol-1-phosphate 5-dehydrogenase
      - EC 1.1.1.18 inositol 2-dehydrogenase
      - EC 1.1.1.19 L-glucuronate reductase
      - EC 1.1.1.20 glucuronolactone reductase
      - EC 1.1.1.21 aldehyde reductase
      - EC 1.1.1.22 UDP-glucose 6-dehydrogenase
      - EC 1.1.1.23 histidinol dehydrogenase
      - EC 1.1.1.24 quinate 5-dehydrogenase
      - EC 1.1.1.25 shikimate 5-dehydrogenase
      - EC 1.1.1.26 glyoxylate reductase
      - EC 1.1.1.27 L-lactate dehydrogenase
      - EC 1.1.1.28 D-lactate dehydrogenase
      - EC 1.1.1.29 glycerate dehydrogenase
      - EC 1.1.1.30 3-hydroxybutyrate dehydrogenase
      - EC 1.1.1.31 3-hydroxyisobutyrate dehydrogenase
      - EC 1.1.1.32 mevaldate reductase
      - EC 1.1.1.33 mevaldate reductase (NADPH2)
      - EC 1.1.1.34 hydroxymethylglutaryl-CoA reductase (NADPH2)
      - EC 1.1.1.35 3-hydroxyacyl-CoA dehydrogenase
      - EC 1.1.1.36 acetoacetyl-CoA reductase
      - EC 1.1.1.37 malate dehydrogenase
      - EC 1.1.1.38 malate dehydrogenase (oxaloacetate-decarboxylating)
      - EC 1.1.1.39 malate dehydrogenase (decarboxylating)
      - EC 1.1.1.40 malate dehydrogenase (oxaloacetate-decarboxylating) (NADP)
      - EC 1.1.1.41 isocitrate dehydrogenase (NAD)
      - EC 1.1.1.42 isocitrate dehydrogenase (NADP)
      - EC 1.1.1.43 phosphogluconate 2-dehydrogenase
      - EC 1.1.1.44 phosphogluconate dehydrogenase (decarboxylating)
      - EC 1.1.1.45 L-gulonate 3-dehydrogenase
      - EC 1.1.1.46 L-arabinose 1-dehydrogenase
      - EC 1.1.1.47 glucose 1-dehydrogenase
      - EC 1.1.1.48 galactose 1-dehydrogenase
      - EC 1.1.1.49 glucose-6-phosphate 1-dehydrogenase
      - EC 1.1.1.50 3a-hydroxysteroid dehydrogenase (B-specific)
      - EC 1.1.1.51 3(or 17)b-hydroxysteroid dehydrogenase
      - EC 1.1.1.52 3a-hydroxycholanate dehydrogenase
      - EC 1.1.1.53 3a(or 20b)-hydroxysteroid dehydrogenase
      - EC 1.1.1.54 allyl-alcohol dehydrogenase
      - EC 1.1.1.55 lactaldehyde reductase (NADPH2)
      - EC 1.1.1.56 ribitol 2-dehydrogenase
      - EC 1.1.1.57 fructuronate reductase
      - EC 1.1.1.58 tagaturonate reductase
      - EC 1.1.1.59 3-hydroxypropionate dehydrogenase
      - EC 1.1.1.60 2-hydroxy-3-oxopropionate reductase
      - EC 1.1.1.61 4-hydroxybutyrate dehydrogenase
      - EC 1.1.1.62 estradiol 17b-dehydrogenase
      - EC 1.1.1.63 testosterone 17b-dehydrogenase
      - EC 1.1.1.64 testosterone 17b-dehydrogenase (NADP)
      - EC 1.1.1.65 pyridoxine 4-dehydrogenase
      - EC 1.1.1.66 w-hydroxydecanoate dehydrogenase
      - EC 1.1.1.67 mannitol 2-dehydrogenase
      - EC 1.1.1.68 now EC 1.7.99.5
      - EC 1.1.1.69 gluconate 5-dehydrogenase
      - EC 1.1.1.70 deleted, included in EC 1.2.1.3
      - EC 1.1.1.71 alcohol dehydrogenase [NAD(P)]
      - EC 1.1.1.72 glycerol dehydrogenase (NADP)
      - EC 1.1.1.73 octanol dehydrogenase
      - EC 1.1.1.74 deleted
      - EC 1.1.1.75 (R)-aminopropanal dehydrogenase
      - EC 1.1.1.76 (S,S)-butanediol dehydrogenase
      - EC 1.1.1.77 lactaldehyde reductase
      - EC 1.1.1.78 D-lactaldehyde dehydrogenase
      - EC 1.1.1.79 glyoxylate reductase (NADP)
      - EC 1.1.1.80 isopropanol dehydrogenase (NADP)
      - EC 1.1.1.81 hydroxypyruvate reductase
      - EC 1.1.1.82 malate dehydrogenase (NADP)
      - EC 1.1.1.83 D-malate dehydrogenase (decarboxylating)
      - EC 1.1.1.84 dimethylmalate dehydrogenase
      - EC 1.1.1.85 3-isopropylmalate dehydrogenase
      - EC 1.1.1.86 ketol-acid reductoisomerase
      - EC 1.1.1.87 3-carboxy-2-hydroxyadipate dehydrogenase
      - EC 1.1.1.88 hydroxymethylglutaryl-CoA reductase
      - EC 1.1.1.89 deleted, included in EC 1.1.1.86
      - EC 1.1.1.90 aryl-alcohol dehydrogenase
      - EC 1.1.1.91 aryl-alcohol dehydrogenase (NADP)
      - EC 1.1.1.92 oxaloglycolate reductase (decarboxylating)
      - EC 1.1.1.93 tartrate dehydrogenase
      - EC 1.1.1.94 glycerol-3-phosphate dehydrogenase [NAD(P)]
      - EC 1.1.1.95 phosphoglycerate dehydrogenase
      - EC 1.1.1.96 diiodophenylpyruvate reductase
      - EC 1.1.1.97 3-hydroxybenzyl-alcohol dehydrogenase
      - EC 1.1.1.98 (R)-2-hydroxy-fatty-acid dehydrogenase
      - EC 1.1.1.99 (S)-2-hydroxy-fatty-acid dehydrogenase
      - EC 1.1.1.100 3-oxoacyl-[acyl-carrier-protein] reductase
      - EC 1.1.1.101 acylglycerone-phosphate reductase
      - EC 1.1.1.102 3-dehydrosphinganine reductase
      - EC 1.1.1.103 L-threonine 3-dehydrogenase
      - EC 1.1.1.104 4-oxoproline reductase
      - EC 1.1.1.105 retinol dehydrogenase
      - EC 1.1.1.106 pantoate 4-dehydrogenase
      - EC 1.1.1.107 pyridoxal 4-dehydrogenase
      - EC 1.1.1.108 carnitine 3-dehydrogenase
      - EC 1.1.1.109 now EC 1.3.1.28
      - EC 1.1.1.110 indolelactate dehydrogenase
      - EC 1.1.1.111 3-(imidazol-5-yl)lactate dehydrogenase
      - EC 1.1.1.112 indanol dehydrogenase
      - EC 1.1.1.113 L-xylose 1-dehydrogenase
      - EC 1.1.1.114 apiose 1-reductase
      - EC 1.1.1.115 ribose 1-dehydrogenase (NADP)
      - EC 1.1.1.116 D-arabinose 1-dehydrogenase
      - EC 1.1.1.117 D-arabinose 1-dehydrogenase [NAD(P)]
      - EC 1.1.1.118 glucose 1-dehydrogenase (NAD)
      - EC 1.1.1.119 glucose 1-dehydrogenase (NADP)
      - EC 1.1.1.120 galactose 1-dehydrogenase (NADP)
      - EC 1.1.1.121 aldose 1-dehydrogenase
      - EC 1.1.1.122 D-threo-aldose 1-dehydrogenase
      - EC 1.1.1.123 sorbose 5-dehydrogenase (NADP)
      - EC 1.1.1.124 fructose 5-dehydrogenase (NADP)
      - EC 1.1.1.125 2-deoxy-D-gluconate 3-dehydrogenase

EC 1.1.1.126 2-dehydro-3-deoxy-D-gluconate 6-dehydrogenase
EC 1.1.1.127 2-dehydro-3-deoxy-D-gluconate 5-dehydrogenase
EC 1.1.1.128 L-idonate 2-dehydrogenase
EC 1.1.1.129 L-threonate 3-dehydrogenase
EC 1.1.1.130 3-dehydro-L-gulonate 2-dehydrogenase
EC 1.1.1.131 mannuronate reductase
EC 1.1.1.132 GDP-mannose 6-dehydrogenase
EC 1.1.1.133 dTDP-4-dehydrorhamnose reductase
EC 1.1.1.134 dTDP-6-deoxy-L-talose 4-dehydrogenase
EC 1.1.1.135 GDP-6-deoxy-D-talose 4-dehydrogenase
EC 1.1.1.136 UDP-N-acetylglucosamine 6-dehydrogenase
EC 1.1.1.137 ribitol-5-phosphate 2-dehydrogenase
EC 1.1.1.138 mannitol 2-dehydrogenase (NADP)
EC 1.1.1.139 deleted, included in EC 1.1.1.21
EC 1.1.1.140 sorbitol-6-phosphate 2-dehydrogenase
EC 1.1.1.141 15-hydroxyprostaglandin dehydrogenase (NAD)
EC 1.1.1.142 D-pinitol dehydrogenase
EC 1.1.1.143 sequoyitol dehydrogenase
EC 1.1.1.144 perillyl-alcohol dehydrogenase
EC 1.1.1.145 3b-hydroxy-D5-steroid dehydrogenase
EC 1.1.1.146 11b-hydroxysteroid dehydrogenase
EC 1.1.1.147 16a-hydroxysteroid dehydrogenase
EC 1.1.1.148 estradiol 17a-dehydrogenase
EC 1.1.1.149 20a-hydroxysteroid dehydrogenase
EC 1.1.1.150 21-hydroxysteroid dehydrogenase (NAD)
EC 1.1.1.151 21-hydroxysteroid dehydrogenase (NADP)
EC 1.1.1.152 3a-hydroxy-5b-androstane-17-one 3a-dehydrogenase
EC 1.1.1.153 sepiapterin reductase
EC 1.1.1.154 ureidoglycolate dehydrogenase
EC 1.1.1.155 homoisocitrate dehydrogenase
EC 1.1.1.156 glycerol 2-dehydrogenase (NADP)
EC 1.1.1.157 3-hydroxybutyryl-CoA dehydrogenase
EC 1.1.1.158 UDP-N-acetylmuramate dehydrogenase
EC 1.1.1.159 7a-hydroxysteroid dehydrogenase
EC 1.1.1.160 dihydrobunolol dehydrogenase
EC 1.1.1.161 cholestanetetraol 26-dehydrogenase
EC 1.1.1.162 erythrulose reductase
EC 1.1.1.163 cyclopentanol dehydrogenase
EC 1.1.1.164 hexadecanol dehydrogenase
EC 1.1.1.165 2-alkyn-1-ol dehydrogenase
EC 1.1.1.166 hydroxycyclohexanecarboxylate dehydrogenase
EC 1.1.1.167 hydroxymalonate dehydrogenase
EC 1.1.1.168 2-dehydropantolactone reductase (A-specific)
EC 1.1.1.169 2-dehydropantoate 2-reductase
EC 1.1.1.170 3b-hydroxy-4a-methylcholestenecarboxylate 3-dehydrogenase (decarboxylating)
EC 1.1.1.171 now EC 1.5.1.20
EC 1.1.1.172 2-oxoadipate reductase
EC 1.1.1.173 L-rhamnose 1-dehydrogenase
EC 1.1.1.174 cyclohexane-1,2-diol dehydrogenase
EC 1.1.1.175 D-xylose 1-dehydrogenase
EC 1.1.1.176 12a-hydroxysteroid dehydrogenase
EC 1.1.1.177 glycerol-3-phosphate 1-dehydrogenase (NADP)
EC 1.1.1.178 3-hydroxy-2-methylbutyryl-CoA dehydrogenase
EC 1.1.1.179 D-xylose 1-dehydrogenase (NADP)
EC 1.1.1.180 deleted, included in EC 1.1.1.131
EC 1.1.1.181 cholest-5-ene-3b,7a-diol 3b-dehydrogenase
EC 1.1.1.182 deleted, included in EC 1.1.1.198, EC 1.1.1.227 and EC 1.1.1.228
EC 1.1.1.183 geraniol dehydrogenase
EC 1.1.1.184 carbonyl reductase (NADPH2)
EC 1.1.1.185 L-glycol dehydrogenase
EC 1.1.1.186 dTDP-galactose 6-dehydrogenase
EC 1.1.1.187 GDP-4-dehydro-D-rhamnose reductase
EC 1.1.1.188 prostaglandin-F synthase
EC 1.1.1.189 prostaglandin-E2 9-reductase
EC 1.1.1.190 indole-3-acetaldehyde reductase (NADH2)
EC 1.1.1.191 indole-3-acetaldehyde reductase (NADPH2)
EC 1.1.1.192 long-chain-alcohol dehydrogenase
EC 1.1.1.193 5-amino-6-(5-phosphoribosylamino)uracil reductase
EC 1.1.1.194 coniferyl-alcohol dehydrogenase
EC 1.1.1.195 cinnamyl-alcohol dehydrogenase
EC 1.1.1.196 15-hydroxyprostaglandin-D dehydrogenase (NADP)
EC 1.1.1.197 15-hydroxyprostaglandin dehydrogenase (NADP)
EC 1.1.1.198 (+)-borneol dehydrogenase
EC 1.1.1.199 (S)-usnate reductase
EC 1.1.1.200 aldose-6-phosphate reductase (NADPH2)
EC 1.1.1.201 7b-hydroxysteroid dehydrogenase (NADP)
EC 1.1.1.202 1,3-propanediol dehydrogenase
EC 1.1.1.203 uronate dehydrogenase
EC 1.1.1.204 xanthine dehydrogenase
EC 1.1.1.205 IMP dehydrogenase
EC 1.1.1.206 tropine dehydrogenase
EC 1.1.1.207 (-)-menthol dehydrogenase
EC 1.1.1.208 (+)-neomenthol dehydrogenase
EC 1.1.1.209 3(or 17)a-hydroxysteroid dehydrogenase
EC 1.1.1.210 3b(or 20a)-hydroxysteroid dehydrogenase
EC 1.1.1.211 long-chain-3-hydroxyacyl-CoA dehydrogenase
EC 1.1.1.212 3-oxoacyl-[acyl-carrier-protein] reductase (NADH2)
EC 1.1.1.213 3a-hydroxysteroid dehydrogenase (A-specific)
EC 1.1.1.214 2-dehydropantolactone reductase (B-specific)
EC 1.1.1.215 gluconate 2-dehydrogenase
EC 1.1.1.216 farnesol dehydrogenase
EC 1.1.1.217 benzyl-2-methyl-hydroxybutyrate dehydrogenase
EC 1.1.1.218 morphine 6-dehydrogenase
EC 1.1.1.219 dihydrokaempferol 4-reductase
EC 1.1.1.220 6-pyruvoyltetrahydropterin 2'-reductase
EC 1.1.1.221 vomifoliol 4'-dehydrogenase
EC 1.1.1.222 (R)-4-hydroxyphenyllactate dehydrogenase
EC 1.1.1.223 isopiperitenol dehydrogenase
EC 1.1.1.224 mannose-6-phosphate 6-reductase
EC 1.1.1.225 chlordecone reductase
EC 1.1.1.226 4-hydroxycyclohexanecarboxylate dehydrogenase
EC 1.1.1.227 (-)-borneol dehydrogenase
EC 1.1.1.228 (+)-sabinol dehydrogenase
EC 1.1.1.229 diethyl 2-methyl-3-oxosuccinate reductase
EC 1.1.1.230 3a-hydroxyglycyrrhetinate dehydrogenase
EC 1.1.1.231 15-hydroxyprostaglandin-I dehydrogenase (NADP)
EC 1.1.1.232 15-hydroxyicosatetraenoate dehydrogenase
EC 1.1.1.233 N-acylmannosamine 1-dehydrogenase
EC 1.1.1.234 flavanone 4-reductase
EC 1.1.1.235 8-oxocoformycin reductase
EC 1.1.1.236 tropinone reductase
EC 1.1.1.237 hydroxyphenylpyruvate reductase
EC 1.1.1.238 12b-hydroxysteroid dehydrogenase
EC 1.1.1.239 3a(17b)-hydroxysteroid dehydrogenase (NAD)
EC 1.1.1.240 N-acetylhexosamine 1-dehydrogenase
EC 1.1.1.241 6-endo-hydroxycineole dehydrogenase
EC 1.1.1.242 zeatin reductase now EC 1.3.1.69
EC 1.1.1.243 carveol dehydrogenase
EC 1.1.1.244 methanol dehydrogenase
EC 1.1.1.245 cyclohexanol dehydrogenase
EC 1.1.1.246 pterocarpin synthase
EC 1.1.1.247 codeinone reductase (NADPH)
EC 1.1.1.248 salutaridine reductase (NADPH)

  - EC 1.1.1.249 reinstated as EC 2.5.1.46
  - EC 1.1.1.250 D-arabinitol 2-dehydrogenase
  - EC 1.1.1.251 galactitol-1-phosphate 5-dehydrogenase
  - EC 1.1.1.252 tetrahydroxynaphthalene reductase
  - EC 1.1.1.253 pteridine reductase
  - EC 1.1.1.254 (S)-carnitine 3-dehydrogenase
  - EC 1.1.1.255 mannitol dehydrogenase
  - EC 1.1.1.256 fluoren-9-ol dehydrogenase
  - EC 1.1.1.257 4-(hydroxymethyl)benzenesulfonate dehydrogenase
  - EC 1.1.1.258 6-hydroxyhexanoate dehydrogenase
  - EC 1.1.1.259 3-hydroxypimeloyl-CoA dehydrogenase
  - EC 1.1.1.260 sulcatone reductase
  - EC 1.1.1.261 glycerol-1-phosphate dehydrogenase [NAD(P)]
  - EC 1.1.1.262 4-hydroxythreonine-4-phosphate dehydrogenase
  - EC 1.1.1.263 1,5-anhydro-D-fructose reductase
  - EC 1.1.1.264 L-idonate 5-dehydrogenase
  - EC 1.1.1.265 3-methylbutanal reductase
  - EC 1.1.1.266 dTDP-4-dehydro-6-deoxyglucose reductase
  - EC 1.1.1.267 1-deoxy-D-xylulose-5-phosphate reductoisomerase
  - EC 1.1.1.268 2-(R)-hydroxypropyl-CoM dehydrogenase
  - EC 1.1.1.269 2-(S)-hydroxypropyl-CoM dehydrogenase
  - EC 1.1.1.270 3-keto-steroid reductase
  - EC 1.1.1.271 GDP-L-fucose synthase
  - EC 1.1.1.272 (R)-2-hydroxyacid dehydrogenase
  - EC 1.1.1.273 vellosimine dehydrogenase
  - EC 1.1.1.274 2,5-didehydrogluconate reductase
- EC 1.1.2 With a cytochrome as acceptor
  - EC 1.1.2.1 now EC 1.1.99.5
  - EC 1.1.2.2 mannitol dehydrogenase (cytochrome)
  - EC 1.1.2.3 L-lactate dehydrogenase (cytochrome)
  - EC 1.1.2.4 D-lactate dehydrogenase (cytochrome)
  - EC 1.1.2.5 D-lactate dehydrogenase (cytochrome c-553)
- EC 1.1.3 With oxygen as acceptor
  - EC 1.1.3.1 deleted, included in EC 1.1.3.15
  - EC 1.1.3.2 now EC 1.13.12.4
  - EC 1.1.3.3 malate oxidase
  - EC 1.1.3.4 glucose oxidase
  - EC 1.1.3.5 hexose oxidase
  - EC 1.1.3.6 cholesterol oxidase
  - EC 1.1.3.7 aryl-alcohol oxidase
  - EC 1.1.3.8 L-gulonolactone oxidase
  - EC 1.1.3.9 galactose oxidase
  - EC 1.1.3.10 pyranose oxidase
  - EC 1.1.3.11 L-sorbose oxidase
  - EC 1.1.3.12 pyridoxine 4-oxidase
  - EC 1.1.3.13 alcohol oxidase
  - EC 1.1.3.14 catechol oxidase (dimerizing)
  - EC 1.1.3.15 (S)-2-hydroxy-acid oxidase
  - EC 1.1.3.16 ecdysone oxidase
  - EC 1.1.3.17 choline oxidase
  - EC 1.1.3.18 secondary-alcohol oxidase
  - EC 1.1.3.19 4-hydroxymandelate oxidase
  - EC 1.1.3.20 long-chain-alcohol oxidase
  - EC 1.1.3.21 glycerol-3-phosphate oxidase
  - EC 1.1.3.22 xanthine oxidase
  - EC 1.1.3.23 thiamin oxidase
  - EC 1.1.3.24 L-galactonolactone oxidase
  - EC 1.1.3.25 cellobiose oxidase
  - EC 1.1.3.26 now EC 1.21.3.2
  - EC 1.1.3.27 hydroxyphytanate oxidase
  - EC 1.1.3.28 nucleoside oxidase
  - EC 1.1.3.29 N-acylhexosamine oxidase
  - EC 1.1.3.30 polyvinyl-alcohol oxidase
  - EC 1.1.3.31 methanol oxidase
  - EC 1.1.3.32 now EC 1.14.21.1
  - EC 1.1.3.33 now EC 1.14.21.2
  - EC 1.1.3.34 now EC 1.14.21.3
  - EC 1.1.3.35 now EC 1.14.21.4
  - EC 1.1.3.36 now EC 1.14.21.5
  - EC 1.1.3.37 D-arabinono-1,4-lactone oxidase
  - EC 1.1.3.38 vanillyl-alcohol oxidase
  - EC 1.1.3.39 nucleoside oxidase (H2O2-forming)
  - EC 1.1.3.40 D-mannitol oxidase
  - EC 1.1.3.41 xylitol oxidase
- EC 1.1.4 With a disulfide as acceptor
  - EC 1.1.4.1 vitamin-K-epoxide reductase (warfarin-sensitive)
  - EC 1.1.4.2 vitamin-K-epoxide reductase (warfarin-insensitive)
- EC 1.1.5 With a quinone or similar compound as acceptor
  - EC 1.1.5.1 Deleted, see EC 1.1.99.18 cellobiose dehydrogenase (acceptor)
- EC 1.1.99 With other acceptors
  - EC 1.1.99.1 choline dehydrogenase
  - EC 1.1.99.2 2-hydroxyglutarate dehydrogenase
  - EC 1.1.99.3 gluconate 2-dehydrogenase (acceptor)
  - EC 1.1.99.4 dehydrogluconate dehydrogenase
  - EC 1.1.99.5 glycerol-3-phosphate dehydrogenase
  - EC 1.1.99.6 D-2-hydroxy-acid dehydrogenase
  - EC 1.1.99.7 lactate—malate transhydrogenase
  - EC 1.1.99.8 alcohol dehydrogenase (acceptor)
  - EC 1.1.99.9 pyridoxine 5-dehydrogenase
  - EC 1.1.99.10 glucose dehydrogenase (acceptor)
  - EC 1.1.99.11 fructose 5-dehydrogenase
  - EC 1.1.99.12 sorbose dehydrogenase
  - EC 1.1.99.13 glucoside 3-dehydrogenase
  - EC 1.1.99.14 glycolate dehydrogenase
  - EC 1.1.99.15 now EC 1.7.99.5
  - EC 1.1.99.16 malate dehydrogenase (acceptor)
  - EC 1.1.99.17 glucose dehydrogenase (pyrroloquinoline-quinone)
  - EC 1.1.99.18 cellobiose dehydrogenase (acceptor)
  - EC 1.1.99.19 uracil dehydrogenase
  - EC 1.1.99.20 alkan-1-ol dehydrogenase (acceptor)
  - EC 1.1.99.21 D-sorbitol dehydrogenase (acceptor)
  - EC 1.1.99.22 glycerol dehydrogenase (acceptor)
  - EC 1.1.99.23 polyvinyl-alcohol dehydrogenase (acceptor)
  - EC 1.1.99.24 hydroxyacid-oxoacid transhydrogenase
  - EC 1.1.99.25 quinate dehydrogenase (pyrroloquinoline-quinone)
  - EC 1.1.99.26 3-hydroxycyclohexanone dehydrogenase
  - EC 1.1.99.27 (R)-pantolactone dehydrogenase (flavin)
  - EC 1.1.99.28 glucose-fructose oxidoreductase

- EC 1.2 Acting on the aldehyde or oxo group of donors
  - EC 1.2.1 With NAD or NADP as acceptor
    - EC 1.2.1.1 formaldehyde dehydrogenase (glutathione)
    - EC 1.2.1.2 formate dehydrogenase
    - EC 1.2.1.3 aldehyde dehydrogenase (NAD)
    - EC 1.2.1.4 aldehyde dehydrogenase (NADP)
    - EC 1.2.1.5 aldehyde dehydrogenase [NAD(P)]
    - EC 1.2.1.6 deleted
    - EC 1.2.1.7 benzaldehyde dehydrogenase (NADP)
    - EC 1.2.1.8 betaine-aldehyde dehydrogenase
    - EC 1.2.1.9 glyceraldehyde-3-phosphate dehydrogenase (NADP)
    - EC 1.2.1.10 acetaldehyde dehydrogenase (acetylating)
    - EC 1.2.1.11 aspartate-semialdehyde dehydrogenase
    - EC 1.2.1.12 glyceraldehyde-3-phosphate dehydrogenase (phosphorylating)
    - EC 1.2.1.13 glyceraldehyde-3-phosphate dehydrogenase (NADP) (phosphorylating)
    - EC 1.2.1.14 now EC 1.1.1.205
    - EC 1.2.1.15 malonate-semialdehyde dehydrogenase
    - EC 1.2.1.16 succinate-semialdehyde dehydrogenase [NAD(P)]
    - EC 1.2.1.17 glyoxylate dehydrogenase (acylating)
    - EC 1.2.1.18 malonate-semialdehyde dehydrogenase (acetylating)
    - EC 1.2.1.19 aminobutyraldehyde dehydrogenase
    - EC 1.2.1.20 glutarate-semialdehyde dehydrogenase
    - EC 1.2.1.21 glycolaldehyde dehydrogenase
    - EC 1.2.1.22 lactaldehyde dehydrogenase
    - EC 1.2.1.23 2-oxoaldehyde dehydrogenase (NAD)
    - EC 1.2.1.24 succinate-semialdehyde dehydrogenase
    - EC 1.2.1.25 2-oxoisovalerate dehydrogenase (acylating)
    - EC 1.2.1.26 2,5-dioxovalerate dehydrogenase

        - EC 1.2.1.27 methylmalonate-semialdehyde dehydrogenase (acylating)
        - EC 1.2.1.28 benzaldehyde dehydrogenase (NAD)
        - EC 1.2.1.29 aryl-aldehyde dehydrogenase
        - EC 1.2.1.30 aryl-aldehyde dehydrogenase (NADP)
        - EC 1.2.1.31 L-aminoadipate-semialdehyde dehydrogenase
        - EC 1.2.1.32 aminomuconate-semialdehyde dehydrogenase
        - EC 1.2.1.33 (R)-dehydropantoate dehydrogenase
        - EC 1.2.1.34 deleted, included in EC 1.1.1.131
        - EC 1.2.1.35 now EC 1.1.1.203
        - EC 1.2.1.36 retinal dehydrogenase
        - EC 1.2.1.37 now EC 1.1.1.204
        - EC 1.2.1.38 N-acetyl-g-glutamyl-phosphate reductase
        - EC 1.2.1.39 phenylacetaldehyde dehydrogenase
        - EC 1.2.1.40 3a,7a,12a-trihydroxycholestan-26-al 26-oxidoreductase
        - EC 1.2.1.41 glutamate-5-semialdehyde dehydrogenase
        - EC 1.2.1.42 hexadecanal dehydrogenase (acylating)
        - EC 1.2.1.43 formate dehydrogenase (NADP)
        - EC 1.2.1.44 cinnamoyl-CoA reductase
        - EC 1.2.1.45 4-carboxy-2-hydroxymuconate-6-semialdehyde dehydrogenase
        - EC 1.2.1.46 formaldehyde dehydrogenase
        - EC 1.2.1.47 4-trimethylammoniobutyraldehyde dehydrogenase
        - EC 1.2.1.48 long-chain-aldehyde dehydrogenase
        - EC 1.2.1.49 2-oxoaldehyde dehydrogenase (NADP)
        - EC 1.2.1.50 long-chain-fatty-acyl-CoA reductase
        - EC 1.2.1.51 pyruvate dehydrogenase (NADP)
        - EC 1.2.1.52 oxoglutarate dehydrogenase (NADP)
        - EC 1.2.1.53 4-hydroxyphenylacetaldehyde dehydrogenase
        - EC 1.2.1.54 g-guanidinobutyraldehyde dehydrogenase
        - EC 1.2.1.55 (R)-3-hydroxyacid ester dehydrogenase
        - EC 1.2.1.56 (S)-3-hydroxyacid ester dehydrogenase
        - EC 1.2.1.57 butanal dehydrogenase
        - EC 1.2.1.58 phenylglyoxylate dehydrogenase (acylating)
        - EC 1.2.1.59 glyceraldehyde-3-phosphate dehydrogenase (NAD(P)) (phosphorylating)
        - EC 1.2.1.60 5-carboxymethyl-2-hydroxymuconic-semialdehyde dehydrogenase
        - EC 1.2.1.61 4-hydroxymuconic semialdehyde dehydrogenase
        - EC 1.2.1.62 4-formylbenzenesulfonate dehydrogenase
        - EC 1.2.1.63 6-oxohexanoate dehydrogenase
        - EC 1.2.1.64 4-hydroxybenzaldehyde dehydrogenase
        - EC 1.2.1.65 salicylaldehyde dehydrogenase
        - EC 1.2.1.66 mycothiol-dependent formaldehyde dehydrogenase
        - EC 1.2.1.67 vanillin dehydrogenase
        - EC 1.2.1.68 coniferyl-aldehyde dehydrogenase
    - EC 1.2.2 With a cytochrome as acceptor
        - EC 1.2.2.1 formate dehydrogenase (cytochrome)
        - EC 1.2.2.2 pyruvate dehydrogenase (cytochrome)
        - EC 1.2.2.3 formate dehydrogenase (cytochrome-c-553)
        - EC 1.2.2.4 carbon-monoxide oxygenase (cytochrome b-561)
    - EC 1.2.3 With oxygen as acceptor
        - EC 1.2.3.1 aldehyde oxidase
        - EC 1.2.3.2 now EC 1.1.3.22
        - EC 1.2.3.3 pyruvate oxidase
        - EC 1.2.3.4 oxalate oxidase
        - EC 1.2.3.5 glyoxylate oxidase
        - EC 1.2.3.6 pyruvate oxidase (CoA-acetylating)
        - EC 1.2.3.7 indole-3-acetaldehyde oxidase
        - EC 1.2.3.8 pyridoxal oxidase
        - EC 1.2.3.9 aryl-aldehyde oxidase
        - EC 1.2.3.10 carbon-monoxide oxidase
        - EC 1.2.3.11 retinal oxidase
        - EC 1.2.3.12 vanillate demethylase
        - EC 1.2.3.13 4-hydroxyphenylpyruvate oxidase
    - EC 1.2.4 With a disulfide as acceptor
        - EC 1.2.4.1 pyruvate dehydrogenase (lipoamide)
        - EC 1.2.4.2 oxoglutarate dehydrogenase (lipoamide)
        - EC 1.2.4.3 deleted, included in EC 1.2.4.4
        - EC 1.2.4.4 3-methyl-2-oxobutanoate dehydrogenase (lipoamide)
    - EC 1.2.7 With an iron-sulfur protein as acceptor
        - EC 1.2.7.1 pyruvate synthase
        - EC 1.2.7.2 2-oxobutyrate synthase
        - EC 1.2.7.3 2-oxoglutarate synthase
    - EC 1.2.99 With other acceptors
        - EC 1.2.99.1 now EC 1.1.99.19
        - EC 1.2.99.2 carbon-monoxide dehydrogenase
        - EC 1.2.99.3 aldehyde dehydrogenase (pyrroloquinoline-quinone)
        - EC 1.2.99.4 formaldehyde dismutase
        - EC 1.2.99.5 formylmethanofuran dehydrogenase
        - EC 1.2.99.6 carboxylate reductase
- EC 1.3 Acting on the CH-CH group of donors
    - EC 1.3.1 With NAD or NADP as acceptor
        - EC 1.3.1.1 dihydrouracil dehydrogenase (NAD)
        - EC 1.3.1.2 dihydropyrimidine dehydrogenase (NADP)
        - EC 1.3.1.3 cortisone b-reductase
        - EC 1.3.1.4 cortisone a-reductase
        - EC 1.3.1.5 cucurbitacin D23-reductase
        - EC 1.3.1.6 fumarate reductase (NADH2)
        - EC 1.3.1.7 meso-tartrate dehydrogenase
        - EC 1.3.1.8 acyl-CoA dehydrogenase (NADP)
        - EC 1.3.1.9 enoyl-[acyl-carrier-protein] reductase (NADH2)
        - EC 1.3.1.10 enoyl-[acyl-carrier-protein] reductase (NADPH2, B-specific)
        - EC 1.3.1.11 2-coumarate reductase
        - EC 1.3.1.12 prephenate dehydrogenase
        - EC 1.3.1.13 prephenate dehydrogenase (NADP)
        - EC 1.3.1.14 orotate reductase (NADH2)
        - EC 1.3.1.15 orotate reductase (NADPH2)
        - EC 1.3.1.16 b-nitroacrylate reductase
        - EC 1.3.1.17 3-methyleneoxindole reductase
        - EC 1.3.1.18 kynurenate-7,8-dihydrodiol dehydrogenase
        - EC 1.3.1.19 cis-1,2-dihydrobenzene-1,2-diol dehydrogenase
        - EC 1.3.1.20 trans-1,2-dihydrobenzene-1,2-diol dehydrogenase
        - EC 1.3.1.21 7-dehydrocholesterol reductase
        - EC 1.3.1.22 cholestenone 5a-reductase
        - EC 1.3.1.23 cholestenone 5b-reductase
        - EC 1.3.1.24 biliverdin reductase
        - EC 1.3.1.25 1,6-dihydroxycyclohexa-2,4-diene-1-carboxylate dehydrogenase
        - EC 1.3.1.26 dihydrodipicolinate reductase
        - EC 1.3.1.27 2-hexadecenal reductase
        - EC 1.3.1.28 2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase
        - EC 1.3.1.29 cis-1,2-dihydro-1,2-dihydroxynaphthalene dehydrogenase
        - EC 1.3.1.30 progesterone 5a-reductase
        - EC 1.3.1.31 2-enoate reductase
        - EC 1.3.1.32 maleylacetate reductase
        - EC 1.3.1.33 protochlorophyllide reductase
        - EC 1.3.1.34 2,4-dienoyl-CoA reductase (NADPH2)
        - EC 1.3.1.35 phosphatidylcholine desaturase
        - EC 1.3.1.36 geissoschizine dehydrogenase
        - EC 1.3.1.37 cis-2-enoyl-CoA reductase (NADPH2)
        - EC 1.3.1.38 trans-2-enoyl-CoA reductase (NADPH2)
        - EC 1.3.1.39 enoyl-[acyl-carrier-protein] reductase (NADPH2, A-specific)
        - EC 1.3.1.40 2-hydroxy-6-oxo-6-phenylhexa-2,4-dienoate reductase
        - EC 1.3.1.41 xanthommatin reductase
        - EC 1.3.1.42 12-oxophytodienoate reductase
        - EC 1.3.1.43 cyclohexadienyl dehydrogenase
        - EC 1.3.1.44 trans-2-enoyl-CoA reductase (NAD)
        - EC 1.3.1.45 2'-hydroxyisoflavone reductase
        - EC 1.3.1.46 biochanin-A reductase
        - EC 1.3.1.47 a-santonin 1,2-reductase
        - EC 1.3.1.48 15-oxoprostaglandin 13-oxidase
        - EC 1.3.1.49 cis-3,4-dihydrophenanthrene-3,4-diol dehydrogenase
        - EC 1.3.1.50 now EC 1.1.1.252
        - EC 1.3.1.51 2'-hydroxydaidzein reductase
        - EC 1.3.1.52 2-methyl-branched-chain-enoyl-CoA reductase

EC 1.3.1.53 (3S,4R)-3,4-dihydroxycyclohexa-1,5-diene-1,4-dicarboxylate dehydrogenase
EC 1.3.1.54 precorrin-6X reductase
EC 1.3.1.55 cis-1,2-dihydroxycyclohexa-3,5-diene-1-carboxylate dehydrogenase
EC 1.3.1.56 cis-2,3-dihydrobiphenyl-2,3-diol dehydrogenase
EC 1.3.1.57 phloroglucinol reductase
EC 1.3.1.58 2,3-dihydroxy-2,3-dihydro-p-cumate dehydrogenase
EC 1.3.1.59 1,6-dihydroxy-5-methylcyclohexa-2,4-dienecarboxylate dehydrogenase
EC 1.3.1.60 dibenzothiophene dihydrodiol dehydrogenase
EC 1.3.1.61 terephthalate 1,2-cis-dihydrodiol dehydrogenase
EC 1.3.1.62 pimeloyl-CoA dehydrogenase
EC 1.3.1.63 2,4-dichlorobenzoyl-CoA reductase
EC 1.3.1.64 phthalate 4,5-cis-dihydrodiol dehydrogenase
EC 1.3.1.65 5,6-dihydroxy-3-methyl-2-oxo-1,2,5,6-tetrahydroquinoline dehydrogenase
EC 1.3.1.66 cis-dihydroethylcatechol dehydrogenase
EC 1.3.1.67 cis-1,2-dihydroxy-4-methylcyclohexa-3,5-diene-1-carboxylate dehydrogenase
EC 1.3.1.68 1,2-dihydroxy-6-methylcyclohexa-3,5-dienecarboxylate dehydrogenase
EC 1.3.1.69 zeatin reductase
EC 1.3.1.70 D14-sterol reductase
EC 1.3.1.71 D24(241)-sterol reductase
EC 1.3.1.72 D24-sterol reductase
EC 1.3.1.73 1,2-dihydrovomilenine reductase
EC 1.3.2 With a cytochrome as acceptor
EC 1.3.2.1 now EC 1.3.99.2
EC 1.3.2.2 now EC 1.3.99.3
EC 1.3.2.3 galactonolactone dehydrogenase
EC 1.3.3 With oxygen as acceptor
EC 1.3.3.1 dihydroorotate oxidase
EC 1.3.3.2 lathosterol oxidase
EC 1.3.3.3 coproporphyrinogen oxidase
EC 1.3.3.4 protoporphyrinogen oxidase
EC 1.3.3.5 bilirubin oxidase
EC 1.3.3.6 acyl-CoA oxidase
EC 1.3.3.7 dihydrouracil oxidase
EC 1.3.3.8 tetrahydroberberine oxidase
EC 1.3.3.9 secologanin synthase
EC 1.3.5 With a quinone or related compound as acceptor
EC 1.3.5.1 succinate dehydrogenase (ubiquinone)
EC 1.3.7 With an iron-sulfur protein as acceptor
EC 1.3.7.1 6-hydroxynicotinate reductase
EC 1.3.7.2 15,16-dihydrobiliverdin:ferredoxin oxidoreductase
EC 1.3.7.3 phycoerythrobilin:ferredoxin oxidoreductase
EC 1.3.7.4 phytochromobilin:ferredoxin oxidoreductase
EC 1.3.7.5 phycocyanobilin:ferredoxin oxidoreductase
EC 1.3.99 With other acceptors
EC 1.3.99.1 succinate dehydrogenase
EC 1.3.99.2 butyryl-CoA dehydrogenase
EC 1.3.99.3 acyl-CoA dehydrogenase
EC 1.3.99.4 3-oxosteroid 1-dehydrogenase
EC 1.3.99.5 3-oxo-5a-steroid 4-dehydrogenase
EC 1.3.99.6 3-oxo-5b-steroid 4-dehydrogenase
EC 1.3.99.7 glutaryl-CoA dehydrogenase
EC 1.3.99.8 2-furoyl-CoA dehydrogenase
EC 1.3.99.9 now EC 1.21.99.1
EC 1.3.99.10 isovaleryl-CoA dehydrogenase
EC 1.3.99.11 dihydroorotate dehydrogenase
EC 1.3.99.12 2-methylacyl-CoA dehydrogenase
EC 1.3.99.13 long-chain-acyl-CoA dehydrogenase
EC 1.3.99.14 cyclohexanone dehydrogenase
EC 1.3.99.15 benzoyl-CoA reductase
EC 1.3.99.16 isoquinoline 1-oxidoreductase
EC 1.3.99.17 quinoline 2-oxidoreductase
EC 1.3.99.18 quinaldate 4-oxidoreductase
EC 1.3.99.19 quinoline-4-carboxylate 2-oxidoreductase
EC 1.3.99.20 4-hydroxybenzoyl-CoA reductase
EC 1.4 Acting on the CH-NH2 group of donors
EC 1.4.1 With NAD or NADP as acceptor
EC 1.4.1.1 alanine dehydrogenase
EC 1.4.1.2 glutamate dehydrogenase
EC 1.4.1.3 glutamate dehydrogenase [NAD(P)]
EC 1.4.1.4 glutamate dehydrogenase (NADP)
EC 1.4.1.5 L-amino-acid dehydrogenase
EC 1.4.1.6 deleted, included in EC 1.4.4.1
EC 1.4.1.7 serine dehydrogenase
EC 1.4.1.8 valine dehydrogenase (NADP)
EC 1.4.1.9 leucine dehydrogenase
EC 1.4.1.10 glycine dehydrogenase
EC 1.4.1.11 L-erythro-3,5-diaminohexanoate dehydrogenase
EC 1.4.1.12 2,4-diaminopentanoate dehydrogenase
EC 1.4.1.13 glutamate synthase (NADPH2)
EC 1.4.1.14 glutamate synthase (NADH2)
EC 1.4.1.15 lysine dehydrogenase
EC 1.4.1.16 diaminopimelate dehydrogenase
EC 1.4.1.17 N-methylalanine dehydrogenase
EC 1.4.1.18 lysine 6-dehydrogenase
EC 1.4.1.19 tryptophan dehydrogenase
EC 1.4.1.20 phenylalanine dehydrogenase
EC 1.4.2 With a cytochrome as acceptor
EC 1.4.2.1 glycine dehydrogenase (cytochrome)
EC 1.4.3 With oxygen as acceptor
EC 1.4.3.1 D-aspartate oxidase
EC 1.4.3.2 L-amino-acid oxidase
EC 1.4.3.3 D-amino-acid oxidase
EC 1.4.3.4 amine oxidase (flavin-containing)
EC 1.4.3.5 pyridoxamine-phosphate oxidase
EC 1.4.3.6 amine oxidase (copper-containing)
EC 1.4.3.7 D-glutamate oxidase
EC 1.4.3.8 ethanolamine oxidase
EC 1.4.3.9 deleted, included in EC 1.4.3.4
EC 1.4.3.10 putrescine oxidase
EC 1.4.3.11 L-glutamate oxidase
EC 1.4.3.12 cyclohexylamine oxidase
EC 1.4.3.13 protein-lysine 6-oxidase
EC 1.4.3.14 L-lysine oxidase
EC 1.4.3.15 D-glutamate(D-aspartate) oxidase
EC 1.4.3.16 L-aspartate oxidase
EC 1.4.3.17 tryptophan a,b-oxidase
EC 1.4.3.18 cytokinin oxidase proposed addition
EC 1.4.3.19 glycine oxidase
EC 1.4.4 With a disulfide as acceptor
EC 1.4.4.1 D-proline reductase (dithiol)
EC 1.4.4.2 glycine dehydrogenase (decarboxylating)
EC 1.4.7 With an iron-sulfur protein as acceptor
EC 1.4.7.1 glutamate synthase (ferredoxin)
EC 1.4.99 With other acceptors
EC 1.4.99.1 D-amino-acid dehydrogenase
EC 1.4.99.2 taurine dehydrogenase
EC 1.4.99.3 amine dehydrogenase
EC 1.4.99.4 aralkylamine dehydrogenase
EC 1.4.99.5 glycine dehydrogenase (cyanide-forming)
EC 1.5 Acting on the CH-NH group of donors
EC 1.5.1 With NAD or NADP as acceptor
EC 1.5.1.1 pyrroline-2-carboxylate reductase
EC 1.5.1.2 pyrroline-5-carboxylate reductase
EC 1.5.1.3 dihydrofolate reductase
EC 1.5.1.4 deleted, included in EC 1.5.1.3
EC 1.5.1.5 methylenetetrahydrofolate dehydrogenase (NADP)
EC 1.5.1.6 formyltetrahydrofolate dehydrogenase
EC 1.5.1.7 saccharopine dehydrogenase (NAD, L-lysine-forming)
EC 1.5.1.8 saccharopine dehydrogenase (NADP, L-lysine-forming)
EC 1.5.1.9 saccharopine dehydrogenase (NAD, L-glutamate-forming)
EC 1.5.1.10 saccharopine dehydrogenase (NADP, L-glutamate-forming)
EC 1.5.1.11 D-octopine dehydrogenase
EC 1.5.1.12 1-pyrroline-5-carboxylate dehydrogenase
EC 1.5.1.13 nicotinate dehydrogenase
EC 1.5.1.14 deleted, included in EC 1.5.1.21
EC 1.5.1.15 methylenetetrahydrofolate dehydrogenase (NAD)
EC 1.5.1.16 D-lysopine dehydrogenase
EC 1.5.1.17 alanopine dehydrogenase
EC 1.5.1.18 ephedrine dehydrogenase
EC 1.5.1.19 D-nopaline dehydrogenase
EC 1.5.1.20 methylenetetrahydrofolate reductase (NADPH2)
EC 1.5.1.21 D1-piperideine-2-carboxylate reductase
EC 1.5.1.22 strombine dehydrogenase
EC 1.5.1.23 tauropine dehydrogenase

- EC 1.5.1.24 N5-(carboxyethyl)ornithine synthase
- EC 1.5.1.25 thiomorpholine-carboxylate dehydrogenase
- EC 1.5.1.26 b-alanopine dehydrogenase
- EC 1.5.1.27 1,2-dehydroreticulinium reductase (NADPH2)
- EC 1.5.1.28 opine dehydrogenase
- EC 1.5.1.29 FMN reductase
- EC 1.5.1.30 flavin reductase
- EC 1.5.1.31 berberine reductase
- EC 1.5.1.32 vomilenine reductase
- EC 1.5.3 With oxygen as acceptor
  - EC 1.5.3.1 sarcosine oxidase
  - EC 1.5.3.2 N-methyl-L-amino-acid oxidase
  - EC 1.5.3.3 deleted
  - EC 1.5.3.4 N6-methyl-lysine oxidase
  - EC 1.5.3.5 (S)-6-hydroxynicotine oxidase
  - EC 1.5.3.6 (R)-6-hydroxynicotine oxidase
  - EC 1.5.3.7 L-pipecolate oxidase
  - EC 1.5.3.8 deleted, included in EC 1.3.3.8
  - EC 1.5.3.9 now EC 1.21.3.3
  - EC 1.5.3.10 dimethylglycine oxidase
  - EC 1.5.3.11 polyamine oxidase
  - EC 1.5.3.12 dihydrobenzophenanthridine oxidase
- EC 1.5.4 With a disulfide as acceptor
  - EC 1.5.4.1 pyrimidodiazepine synthase
- EC 1.5.5 With a quinone or similar compound as acceptor
  - EC 1.5.5.1 electron-transferring-flavoprotein dehydrogenase
- EC 1.5.8 With a flavin as acceptor
  - EC 1.5.8.1 dimethylamine dehydrogenase
  - EC 1.5.8.2 trimethylamine dehydrogenase
- EC 1.5.99 With other acceptors
  - EC 1.5.99.1 sarcosine dehydrogenase
  - EC 1.5.99.2 dimethylglycine dehydrogenase
  - EC 1.5.99.3 L-pipecolate dehydrogenase
  - EC 1.5.99.4 nicotine dehydrogenase
  - EC 1.5.99.5 methylglutamate dehydrogenase
  - EC 1.5.99.6 spermidine dehydrogenase
  - EC 1.5.99.7 now EC 1.5.8.2
  - EC 1.5.99.8 proline dehydrogenase
  - EC 1.5.99.9 methylenetetrahydromethanopterin dehydrogenase
  - EC 1.5.99.10 now EC 1.5.8.1
  - EC 1.5.99.11 coenzyme F420-dependent N5,N10-methenyltetrahydromethanopterin reductase
  - EC 1.5.99.12 cytokinin dehydrogenase
- EC 1.6 Acting on NADH or NADPH
  - EC 1.6.1 With NAD or NADP as acceptor
    - EC 1.6.1.1 NAD(P) transhydrogenase (B-specific)
    - EC 1.6.1.2 NAD(P) transhydrogenase (AB-specific)
  - EC 1.6.2 With a heme protein as acceptor
    - EC 1.6.2.1 now EC 1.6.99.3
    - EC 1.6.2.2 cytochrome-b5 reductase
    - EC 1.6.2.3 deleted
    - EC 1.6.2.4 NADPH—ferrihemoprotein reductase
    - EC 1.6.2.5 NADPH—cytochrome-c2 reductase
    - EC 1.6.2.6 leghemoglobin reductase
  - EC 1.6.4 With a disulfide as acceptor
    - EC 1.6.4.1 now EC 1.8.1.6
    - EC 1.6.4.2 now EC 1.8.1.7
    - EC 1.6.4.3 now EC 1.8.1.4
    - EC 1.6.4.4 now EC 1.8.1.8
    - EC 1.6.4.5 now EC 1.8.1.9
    - EC 1.6.4.6 now EC 1.8.1.10
    - EC 1.6.4.7 now EC 1.8.1.11
    - EC 1.6.4.8 now EC 1.8.1.12
    - EC 1.6.4.9 now EC 1.8.1.13
    - EC 1.6.4.10 now EC 1.8.1.14
  - EC 1.6.5 With a quinone or similar compound as acceptor
    - EC 1.6.5.1 deleted
    - EC 1.6.5.2 now EC 1.6.99.2
    - EC 1.6.5.3 NADH2 dehydrogenase (ubiquinone)
    - EC 1.6.5.4 monodehydroascorbate reductase (NADH2)
    - EC 1.6.5.5 NADPH:quinone reductase
    - EC 1.6.5.6 p-benzoquinone reductase (NADPH)
    - EC 1.6.5.7 2-hydroxy-1,4-benzoquinone reductase
  - EC 1.6.6 With a nitrogenous group as acceptor
    - EC 1.6.6.1 now EC 1.7.1.1
    - EC 1.6.6.2 now EC 1.7.1.2
    - EC 1.6.6.3 now EC 1.7.1.3
    - EC 1.6.6.4 now EC 1.7.1.4
    - EC 1.6.6.5 now EC 1.7.99.3
    - EC 1.6.6.6 now EC 1.7.1.5
    - EC 1.6.6.7 now EC 1.7.1.6
    - EC 1.6.6.8 now EC 1.7.1.7
    - EC 1.6.6.9 trimethylamine-N-oxide reductase
    - EC 1.6.6.10 now EC 1.7.1.9
    - EC 1.6.6.11 now EC 1.7.1.10
    - EC 1.6.6.12 now EC 1.7.1.11
    - EC 1.6.6.13 now EC 1.7.1.12
  - EC 1.6.7 With a iron-sulfur protein as acceptor
    - EC 1.6.7.1 now EC 1.18.1.2
    - EC 1.6.7.2 now EC 1.18.1.1
  - EC 1.6.8 With a flavin as acceptor
    - EC 1.6.8.1 EC 1.5.1.29
    - EC 1.6.8.2 EC 1.5.1.30
  - EC 1.6.99 With other acceptors
    - EC 1.6.99.1 NADPH2 dehydrogenase
    - EC 1.6.99.2 NAD(P)H2 dehydrogenase (quinone)
    - EC 1.6.99.3 NADH2 dehydrogenase
    - EC 1.6.99.4 now EC 1.18.1.2
    - EC 1.6.99.5 NADH2 dehydrogenase (quinone)
    - EC 1.6.99.6 NADPH2 dehydrogenase (quinone)
    - EC 1.6.99.7 dihydropteridine reductase
    - EC 1.6.99.8 now EC 1.16.1.3
    - EC 1.6.99.9 now EC 1.16.1.4
    - EC 1.6.99.10 deleted, included in EC 1.6.99.7
    - EC 1.6.99.11 now EC 1.16.1.5
    - EC 1.6.99.12 now EC 1.16.1.6
    - EC 1.6.99.13 now EC 1.16.1.7
- EC 1.7 Acting on other nitrogenous compounds as donors
  - EC 1.7.1 With NAD or NADP as acceptor
    - EC 1.7.1.1 nitrate reductase (NADH)
    - EC 1.7.1.2 nitrate reductase [NAD(P)H]
    - EC 1.7.1.3 nitrate reductase (NADPH)
    - EC 1.7.1.4 nitrite reductase [NAD(P)H]
    - EC 1.7.1.5 hyponitrite reductase
    - EC 1.7.1.6 azobenzene reductase
    - EC 1.7.1.7 GMP reductase
    - EC 1.7.1.8 deleted entry
    - EC 1.7.1.9 nitroquinoline-N-oxide reductase
    - EC 1.7.1.10 hydroxylamine reductase (NADH)
    - EC 1.7.1.11 4-(dimethylamino)phenylazoxybenzene reductase
    - EC 1.7.1.12 N-hydroxy-2-acetamidofluorene reductase
  - EC 1.7.2 With a cytochrome as acceptor
    - EC 1.7.2.1 nitrite reductase (NO-forming)
    - EC 1.7.2.2 nitrite reductase (cytochrome; ammonia-forming)
    - EC 1.7.2.3 trimethylamine-N-oxide reductase (cytochrome c)
  - EC 1.7.3 With oxygen as acceptor
    - EC 1.7.3.1 nitroethane oxidase
    - EC 1.7.3.2 acetylindoxyl oxidase
    - EC 1.7.3.3 urate oxidase
    - EC 1.7.3.4 hydroxylamine oxidase
    - EC 1.7.3.5 3-aci-nitropropanoate oxidase
  - EC 1.7.7 With an iron-sulfur protein as acceptor
    - EC 1.7.7.1 ferredoxin—nitrite reductase
    - EC 1.7.7.2 ferredoxin—nitrate reductase
  - EC 1.7.99 With other acceptors
    - EC 1.7.99.1 hydroxylamine reductase
    - EC 1.7.99.2 deleted
    - EC 1.7.99.3 included with EC 1.7.2.1
    - EC 1.7.99.4 nitrate reductase
    - EC 1.7.99.5 5,10-methylenetetrahydrofolate reductase (FADH2)
    - EC 1.7.99.6 nitrous-oxide reductase
    - EC 1.7.99.7 nitric-oxide reductase
- EC 1.8 Acting on a sulfur group of donors
  - EC 1.8.1 With NAD or NADP as acceptor
    - EC 1.8.1.1 deleted
    - EC 1.8.1.2 sulfite reductase (NADPH2)
    - EC 1.8.1.3 hypotaurine dehydrogenase
    - EC 1.8.1.4 dihydrolipoamide dehydrogenase
    - EC 1.8.1.5 2-oxopropyl-CoM reductase (carboxylating)
    - EC 1.8.1.6 cystine reductase
    - EC 1.8.1.7 glutathione-disulfide reductase
    - EC 1.8.1.8 protein-disulfide reductase
    - EC 1.8.1.9 thioredoxin-disulfide reductase
    - EC 1.8.1.10 CoA-glutathione reductase
    - EC 1.8.1.11 asparagusate reductase
    - EC 1.8.1.12 trypanothione-disulfide reductase
    - EC 1.8.1.13 bis-g-glutamylcystine reductase
    - EC 1.8.1.14 CoA-disulfide reductase
    - EC 1.8.1.15 mycothione reductase
  - EC 1.8.2 With a cytochrome as acceptor
    - EC 1.8.2.1 sulfite dehydrogenase
    - EC 1.8.2.2 thiosulfate dehydrogenase

- EC 1.8.3 With oxygen as acceptor
    - EC 1.8.3.1 sulfite oxidase
    - EC 1.8.3.2 thiol oxidase
    - EC 1.8.3.3 glutathione oxidase
    - EC 1.8.3.4 methanethiol oxidase
    - EC 1.8.3.5 prenylcysteine oxidase
- EC 1.8.4 With a disulfide as acceptor
    - EC 1.8.4.1 glutathione—homocystine transhydrogenase
    - EC 1.8.4.2 protein-disulfide reductase (glutathione)
    - EC 1.8.4.3 glutathione—CoA-glutathione transhydrogenase
    - EC 1.8.4.4 glutathione—cystine transhydrogenase
    - EC 1.8.4.5 methionine-S-oxide reductase
    - EC 1.8.4.6 protein-methionine-S-oxide reductase
    - EC 1.8.4.7 enzyme-thiol transhydrogenase (glutathione-disulfide)
    - EC 1.8.4.8 phosphoadenylyl-sulfate reductase (thioredoxin)
    - EC 1.8.4.9 adenylyl-sulfate reductase (glutathione)
- EC 1.8.5 With a quinone or similar compound as acceptor
    - EC 1.8.5.1 glutathione dehydrogenase (ascorbate)
- EC 1.8.6 With an nitrogenous group as acceptor
    - EC 1.8.6.1 deleted, included in EC 2.5.1.18
- EC 1.8.7 With an iron-sulfur protein as acceptor
    - EC 1.8.7.1 sulfite reductase (ferredoxin)
- EC 1.8.99 With other acceptors
    - EC 1.8.99.1 sulfite reductase
    - EC 1.8.99.2 adenylyl-sulfate reductase
    - EC 1.8.99.3 hydrogensulfite reductase
    - EC 1.8.99.4 now EC 1.8.4.8

EC 1.9 Acting on a heme group of donors
- EC 1.9.3 With oxygen as acceptor
    - EC 1.9.3.1 cytochrome-c oxidase
    - EC 1.9.3.2 included with EC 1.7.2.1
- EC 1.9.6 With a nitrogenous group as acceptor
    - EC 1.9.6.1 nitrate reductase (cytochrome)
- EC 1.9.99 With other acceptors
    - EC 1.9.99.1 iron—cytochrome-c reductase

EC 1.10 Acting on diphenols and related substances as donors
- EC 1.10.1 With NAD or NADP as acceptor
    - EC 1.10.1.1 trans-acenaphthene-1,2-diol dehydrogenase
- EC 1.10.2 With a cytochrome as acceptor
    - EC 1.10.2.1 L-ascorbate—cytochrome-b5 reductase
    - EC 1.10.2.2 ubiquinol—cytochrome-c reductase
- EC 1.10.3 With oxygen as acceptor
    - EC 1.10.3.1 catechol oxidase
    - EC 1.10.3.2 laccase
    - EC 1.10.3.3 L-ascorbate oxidase
    - EC 1.10.3.4 o-aminophenol oxidase
    - EC 1.10.3.5 3-hydroxyanthranilate oxidase
    - EC 1.10.3.6 rifamycin-B oxidase
    - EC 1.10.3.7 now EC 1.21.3.4
    - EC 1.10.3.8 now EC 1.21.3.5
- EC 1.10.99 With other acceptors
    - EC 1.10.99.1 plastoquinol—plastocyanin reductase

EC 1.11 Acting on a peroxide as acceptor
- EC 1.11.1 Peroxidases
    - EC 1.11.1.1 NADH2 peroxidase
    - EC 1.11.1.2 NADPH2 peroxidase
    - EC 1.11.1.3 fatty-acid peroxidase
    - EC 1.11.1.4 now EC 1.13.11.11
    - EC 1.11.1.5 cytochrome-c peroxidase
    - EC 1.11.1.6 catalase
    - EC 1.11.1.7 peroxidase
    - EC 1.11.1.8 iodide peroxidase
    - EC 1.11.1.9 glutathione peroxidase
    - EC 1.11.1.10 chloride peroxidase
    - EC 1.11.1.11 L-ascorbate peroxidase
    - EC 1.11.1.12 phospholipid-hydroperoxide glutathione peroxidase
    - EC 1.11.1.13 manganese peroxidase
    - EC 1.11.1.14 diarylpropane peroxidase

EC 1.12 Acting on hydrogen as donor
- EC 1.12.1 With NAD or NADP as acceptor
    - EC 1.12.1.1 now EC 1.18.99.1
    - EC 1.12.1.2 hydrogen dehydrogenase
    - EC 1.12.1.3 hydrogen dehydrogenase (NADP)
- EC 1.12.2 With a cytochrome as acceptor
    - EC 1.12.2.1 cytochrome-c3 hydrogenase
- EC 1.12.5 With a quinone or similar compound as acceptor
    - EC 1.12.5.1 hydrogen:quinone oxidoreductase
- EC 1.12.7 With an iron-sulfur protein as acceptor
    - EC 1.12.7.1 now EC 1.18.99.1
    - EC 1.12.7.2 ferredoxin hydrogenase
- EC 1.12.98 With other known acceptors
    - EC 1.12.98.1 coenzyme F420 hydrogenase
    - EC 1.12.98.2 N5,N10-methenyltetrahydromethanopterin hydrogenase
    - EC 1.12.98.3 Methanosarcina-phenazine hydrogenase

EC 1.12.99 With other acceptors
- EC 1.12.99.1 now EC 1.12.98.1
- EC 1.12.99.2 deleted
- EC 1.12.99.3 now EC 1.12.5.1
- EC 1.12.99.4 now EC 1.12.98.2
- EC 1.12.99.5 identical to EC 1.13.11.47
- EC 1.12.99.6 hydrogenase (acceptor)

EC 1.13 Acting on single donors with incorporation of molecular oxygen (oxygenases)
- EC 1.13.1.1 now EC 1.13.11.1
- EC 1.13.1.2 now EC 1.13.11.2
- EC 1.13.1.3 now EC 1.13.11.3
- EC 1.13.1.4 now EC 1.13.11.4
- EC 1.13.1.5 now EC 1.13.11.5
- EC 1.13.1.6 now EC 1.13.11.6
- EC 1.13.1.7 now EC 1.13.11.7
- EC 1.13.1.8 now EC 1.13.11.8
- EC 1.13.1.9 now EC 1.13.11.9
- EC 1.13.1.10 now EC 1.13.11.10
- EC 1.13.1.11 now EC 1.13.99.1
- EC 1.13.1.12 now EC 1.13.11.11
- EC 1.13.1.13 now EC 1.13.11.12
- EC 1.13.11 With incorporation of two atoms of oxygen
    - EC 1.13.11.1 catechol 1,2-dioxygenase
    - EC 1.13.11.2 catechol 2,3-dioxygenase
    - EC 1.13.11.3 protocatechuate 3,4-dioxygenase
    - EC 1.13.11.4 gentisate 1,2-dioxygenase
    - EC 1.13.11.5 homogentisate 1,2-dioxygenase
    - EC 1.13.11.6 3-hydroxyanthranilate 3,4-dioxygenase
    - EC 1.13.11.7 deleted
    - EC 1.13.11.8 protocatechuate 4,5-dioxygenase
    - EC 1.13.11.9 2,5-dihydroxypyridine 5,6-dioxygenase
    - EC 1.13.11.10 7,8-dihydroxykynurenate 8,8a-dioxygenase
    - EC 1.13.11.11 tryptophan 2,3-dioxygenase
    - EC 1.13.11.12 lipoxygenase
    - EC 1.13.11.13 ascorbate 2,3-dioxygenase
    - EC 1.13.11.14 2,3-dihydroxybenzoate 3,4-dioxygenase
    - EC 1.13.11.15 3,4-dihydroxyphenylacetate 2,3-dioxygenase
    - EC 1.13.11.16 3-carboxyethylcatechol 2,3-dioxygenase
    - EC 1.13.11.17 indole 2,3-dioxygenase
    - EC 1.13.11.18 sulfur dioxygenase
    - EC 1.13.11.19 cysteamine dioxygenase
    - EC 1.13.11.20 cysteine dioxygenase
    - EC 1.13.11.21 now EC 1.14.99.36
    - EC 1.13.11.22 caffeate 3,4-dioxygenase
    - EC 1.13.11.23 2,3-dihydroxyindole 2,3-dioxygenase
    - EC 1.13.11.24 quercetin 2,3-dioxygenase
    - EC 1.13.11.25 3,4-dihydroxy-9,10-secoandrosta-1,3,5(10)-triene-9,17-dione 4,5-dioxygenase
    - EC 1.13.11.26 peptide-tryptophan 2,3-dioxygenase
    - EC 1.13.11.27 4-hydroxyphenylpyruvate dioxygenase
    - EC 1.13.11.28 2,3-dihydroxybenzoate 2,3-dioxygenase
    - EC 1.13.11.29 stizolobate synthase
    - EC 1.13.11.30 stizolobinate synthase
    - EC 1.13.11.31 arachidonate 12-lipoxygenase
    - EC 1.13.11.32 2-nitropropane dioxygenase
    - EC 1.13.11.33 arachidonate 15-lipoxygenase
    - EC 1.13.11.34 arachidonate 5-lipoxygenase
    - EC 1.13.11.35 pyrogallol 1,2-oxygenase
    - EC 1.13.11.36 chloridazon-catechol dioxygenase
    - EC 1.13.11.37 hydroxyquinol 1,2-dioxygenase
    - EC 1.13.11.38 1-hydroxy-2-naphtboate 1,2-dioxygenase
    - EC 1.13.11.39 biphenyl-2,3-diol 1,2-dioxygenase
    - EC 1.13.11.40 arachidonate 8-lipoxygenase
    - EC 1.13.11.41 2,4'-dihydroxyacetophenone dioxygenase

EC 1.13.11.42 indoleamine-pyrrole 2,3-dioxygenase
EC 1.13.11.43 lignostilbene ab-dioxygenase
EC 1.13.11.44 linoleate diol synthase
EC 1.13.11.45 linoleate 11-lipoxygenase
EC 1.13.11.46 4-hydroxymandelate synthase
EC 1.13.11.47 3-hydroxy-4-oxoquinoline 2,4-dioxygenase
EC 1.13.11.48 3-hydroxy-2-methyl-quinolin-4-one 2,4-dioxygenase
EC 1.13.11.49 chlorite O2-lyase
EC 1.13.12 With incorporation of one atom of oxygen (internal monooxygenases or internal mixed function oxidases)
EC 1.13.12.1 arginine 2-monooxygenase
EC 1.13.12.2 lysine 2-monooxygenase
EC 1.13.12.3 tryptophan 2-monooxygenase
EC 1.13.12.4 lactate 2-monooxygenase
EC 1.13.12.5 Renilla-luciferin 2-monooxygenase
EC 1.13.12.6 Cypridina-luciferin 2-monooxygenase
EC 1.13.12.7 Photinus-luciferin 4-monooxygenase (ATP-hydrolysing)
EC 1.13.12.8 Watasenia-luciferin 2-monooxygenase
EC 1.13.12.9 phenylalanine 2-monooxygenase
EC 1.13.12.10 covered by EC 1.14.13.59
EC 1.13.12.11 methylphenyltetrahydropyridine N-monooxygenase
EC 1.13.12.12 apo-b-carotenoid-14',13'-dioxygenase
EC 1.13.99 Miscellaneous
EC 1.13.99.1 inositol oxygenase
EC 1.13.99.2 now EC 1.14.12.10
EC 1.13.99.3 tryptophan 2'-dioxygenase
EC 1.13.99.4 now EC 1.14.12.9
EC 1.13.99.5 now EC 1.13.11.47
EC 1.14 Acting on paired donors, with incorporation or reduction of molecular oxygen
EC 1.14.1.1 now EC 1.14.14.1
EC 1.14.1.2 now EC 1.14.13.9
EC 1.14.1.3 deleted, covered by EC 1.14.99.7, EC 5.4.99.7
EC 1.14.1.4 now EC 1.14.99.2
EC 1.14.1.5 now EC 1.14.13.5
EC 1.14.1.6 now EC 1.14.15.4
EC 1.14.1.7 now EC 1.14.99.9
EC 1.14.1.8 now EC 1.14.99.10
EC 1.14.1.9 deleted
EC 1.14.1.10 now EC 1.14.99.11
EC 1.14.1.11 deleted
EC 1.14.2 With ascorbate as one donor
EC 1.14.2.1 now EC 1.14.17.1
EC 1.14.2.2 now EC 1.13.11.27
EC 1.14.3 With reduced pteridine as one donor
EC 1.14.3.1 now EC 1.14.16.1
EC 1.14.11 With 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors
EC 1.14.11.1 g-butyrobetaine dioxygenase
EC 1.14.11.2 procollagen-proline dioxygenase
EC 1.14.11.3 pyrimidine-deoxynucleoside 2'-dioxygenase
EC 1.14.11.4 procollagen-lysine 5-dioxygenase
EC 1.14.11.5 deleted, included in EC 1.14.11.6
EC 1.14.11.6 thymine dioxygenase
EC 1.14.11.7 procollagen-proline 3-dioxygenase
EC 1.14.11.8 trimethyllysine dioxygenase
EC 1.14.11.9 naringenin 3-dioxygenase
EC 1.14.11.10 pyrimidine-deoxynucleoside 1'-dioxygenase
EC 1.14.11.11 hyoscyamine (6S)-dioxygenase
EC 1.14.11.12 gibberellin-44 dioxygenase
EC 1.14.11.13 gibberellin 2b-dioxygenase
EC 1.14.11.14 6b-hydroxyhyoscyamine epoxidase
EC 1.14.11.15 gibberellin 3b-dioxygenase
EC 1.14.11.16 peptide-aspartate b-dioxygenase
EC 1.14.11.17 taurine dioxygenase
EC 1.14.11.18 phytanoyl-CoA dioxygenase
EC 1.14.11.19 leucocyanidin oxygenase
EC 1.14.11.20 desacetoxyvindoline 4-hydroxylase
EC 1.14.12 With NADH2 or NADPH2 as one donor, and incorporation of two atoms of oxygen into one donor
EC 1.14.12.1 anthranilate 1,2-dioxygenase (deaminating, decarboxylating)
EC 1.14.12.2 now EC 1.14.13.35
EC 1.14.12.3 benzene 1,2-dioxygenase
EC 1.14.12.4 3-hydroxy-3-methylpyridinecarboxylate dioxygenase
EC 1.14.12.5 5-pyridoxate dioxygenase
EC 1.14.12.6 now EC 1.14.13.66
EC 1.14.12.7 phthalate 4,5-dioxygenase
EC 1.14.12.8 4-sulfobenzoate 3,4-dioxygenase
EC 1.14.12.9 4-chlorophenylacetate 3,4-dioxygenase
EC 1.14.12.10 benzoate 1,2-dioxygenase
EC 1.14.12.11 toluene dioxygenase
EC 1.14.12.12 naphthalene 1,2-dioxygenase
EC 1.14.12.13 2-chlorobenzoate 1,2-dioxygenase
EC 1.14.12.14 2-aminobenzenesulfonate 2,3-dioxygenase
EC 1.14.12.15 terephthalate 1,2-dioxygenase
EC 1.14.12.16 2-hydroxyquinoline 5,6-dioxygenase
EC 1.14.12.17 nitric oxide dioxygenase
EC 1.14.12.18 biphenyl 2,3-dioxygenase
EC 1.14.13 With NADH2 or NADPH2 as one donor, and incorporation of one atom of oxygen
EC 1.14.13.1 salicylate 1-monooxygenase
EC 1.14.13.2 4-hydroxybenzoate 3-monooxygenase
EC 1.14.13.3 4-hydroxyphenylacetate 3-monooxygenase
EC 1.14.13.4 melilotate 3-monooxygenase
EC 1.14.13.5 imidazoleacetate 4-monooxygenase
EC 1.14.13.6 orcinol 2-monooxygenase
EC 1.14.13.7 phenol 2-monooxygenase
EC 1.14.13.8 dimethylaniline monooxygenase (N-oxide-forming)
EC 1.14.13.9 kynurenine 3-monooxygenase
EC 1.14.13.10 2,6-dihydroxypyridine 3-monooxygenase
EC 1.14.13.11 trans-cinnamate 4-monooxygenase
EC 1.14.13.12 benzoate 4-monooxygenase
EC 1.14.13.13 calcidiol 1-monooxygenase
EC 1.14.13.14 trans-cinnamate 2-monooxygenase
EC 1.14.13.15 cholestanetriol 26-monooxygenase
EC 1.14.13.16 cyclopentanone monooxygenase
EC 1.14.13.17 cholesterol 7a-monooxygenase
EC 1.14.13.18 4-hydroxyphenylacetate 1-monooxygenase
EC 1.14.13.19 taxifolin 8-monooxygenase
EC 1.14.13.20 2,4-dichlorophenol 6-monooxygenase
EC 1.14.13.21 flavonoid 3'-monooxygenase
EC 1.14.13.22 cyclohexanone monooxygenase
EC 1.14.13.23 3-hydroxybenzoate 4-monooxygenase
EC 1.14.13.24 3-hydroxybenzoate 6-monooxygenase
EC 1.14.13.25 methane monooxygenase
EC 1.14.13.26 phosphatidylcholine 12-monooxygenase
EC 1.14.13.27 4-aminobenzoate 1-monooxygenase
EC 1.14.13.28 3,9-dihydroxypterocarpan 6a-monooxygenase
EC 1.14.13.29 4-nitrophenol 2-monooxygenase
EC 1.14.13.30 leukotriene-B4 20-monooxygenase
EC 1.14.13.31 2-nitrophenol 2-monooxygenase
EC 1.14.13.32 albendazole monooxygenase
EC 1.14.13.33 4-hydroxybenzoate 3-monooxygenase [NAD(P)H2]
EC 1.14.13.34 leukotriene-E4 20-monooxygenase
EC 1.14.13.35 anthranilate 3-monooxygenase (deaminating)
EC 1.14.13.36 5-O-(4-coumaroyl)-D-quinate 3'-monooxygenase
EC 1.14.13.37 methyltetrahydroprotoberberine 14-monooxygenase
EC 1.14.13.38 anhydrotetracycline monooxygenase
EC 1.14.13.39 nitric-oxide synthase
EC 1.14.13.40 anthraniloyl-CoA monooxygenase
EC 1.14.13.41 tyrosine N-monooxygenase
EC 1.14.13.42 hydroxyphenylacetonitrile 2-monooxygenase
EC 1.14.13.43 questin monooxygenase

    - EC 1.14.13.44 2-hydroxybiphenyl 3-monooxygenase
    - EC 1.14.13.45 CMP-N-acetylneuraminate monooxygenase
    - EC 1.14.13.46 (-)-menthol monooxygenase
    - EC 1.14.13.47 (-)-limonene 3-monooxygenase
    - EC 1.14.13.48 (-)-limonene 6-monooxygenase
    - EC 1.14.13.49 (-)-limonene 7-monooxygenase
    - EC 1.14.13.50 pentachlorophenol monooxygenase
    - EC 1.14.13.51 6-oxocineole dehydrogenase
    - EC 1.14.13.52 isoflavone 3'-hydroxylase
    - EC 1.14.13.53 isoflavone 2'-hydroxylase
    - EC 1.14.13.54 ketosteroid monooxygenase
    - EC 1.14.13.55 protopine 6-monooxygenase
    - EC 1.14.13.56 dihydrosanguinarine 10-monooxygenase
    - EC 1.14.13.57 dihydrochelirubine 12-monooxygenase
    - EC 1.14.13.58 benzoyl-CoA 3-monooxygenase
    - EC 1.14.13.59 L-lysine 6-monooxygenase (NADPH2)
    - EC 1.14.13.60 27-hydroxycholesterol 7a-monooxygenase
    - EC 1.14.13.61 2-hydroxyquinoline 8-monooxygenase
    - EC 1.14.13.62 4-hydroxyquinoline 3-monooxygenase
    - EC 1.14.13.63 3-hydroxyphenylacetate 6-hydroxylase
    - EC 1.14.13.64 4-hydroxybenzoate 1-hydroxylase
    - EC 1.14.13.65 2-hydroxyquinoline 8-monooxygenase
    - EC 1.14.13.66 2-hydroxycyclohexanone 2-monooxygenase
    - EC 1.14.13.67 quinine 3-monooxygenase
    - EC 1.14.13.68 4-hydroxyphenylacetaldehyde oxime monooxygenase
    - EC 1.14.13.69 alkene monooxygenase
    - EC 1.14.13.70 sterol 14-demethylase
    - EC 1.14.13.71 N-methylcoclaurine 3'-monooxygenase
    - EC 1.14.13.72 methylsterol monooxygenase
    - EC 1.14.13.73 tabersonine 16-hydroxylase
    - EC 1.14.13.74 7-deoxyloganin 7-hydroxylase
    - EC 1.14.13.75 vinorine hydroxylase
    - EC 1.14.13.76 taxane 10b-hydroxylase
    - EC 1.14.13.77 taxane 13a-hydroxylase
    - EC 1.14.13.78 ent-kaurene oxidase
    - EC 1.14.13.79 ent-kaurenoic acid oxidase
  - EC 1.14.14 With reduced flavin or flavoprotein as one donor, and incorporation of one atom of oxygen
    - EC 1.14.14.1 unspecific monooxygenase
    - EC 1.14.14.2 deleted, included in EC 1.14.14.1
    - EC 1.14.14.3 alkanal monooxygenase (FMN-linked)
    - EC 1.14.14.4 deleted, identical to EC 1.14.15.7
    - EC 1.14.14.5 alkanesulfonate monooxygenase
  - EC 1.14.15 With reduced iron-sulfur protein as one donor, and incorporation of one atom of oxygen
    - EC 1.14.15.1 camphor 5-monooxygenase
    - EC 1.14.15.2 camphor 1,2-monooxygenase
    - EC 1.14.15.3 alkane 1-monooxygenase
    - EC 1.14.15.4 steroid 11b-monooxygenase
    - EC 1.14.15.5 corticosterone 18-monooxygenase
    - EC 1.14.15.6 cholesterol monooxygenase (side-chain-cleaving)
    - EC 1.14.15.7 choline monooxygenase
  - EC 1.14.16 With reduced pteridine as one donor, and incorporation of one atom of oxygen
    - EC 1.14.16.1 phenylalanine 4-monooxygenase
    - EC 1.14.16.2 tyrosine 3-monooxygenase
    - EC 1.14.16.3 anthranilate 3-monooxygenase
    - EC 1.14.16.4 tryptophan 5-monooxygenase
    - EC 1.14.16.5 glyceryl-ether monooxygenase
    - EC 1.14.16.6 mandelate 4-monooxygenase
  - EC 1.14.17 With reduced ascorbate as one donor, and incorporation of one atom of oxygen
    - EC 1.14.17.1 dopamine b-monooxygenase
    - EC 1.14.17.2 deleted, included in EC 1.14.18.1
    - EC 1.14.17.3 peptidylglycine monooxygenase
  - EC 1.14.18 With another compound as one donor, and incorporation of one atom of oxygen
    - EC 1.14.18.1 monophenol monooxygenase
  - EC 1.14.19 With oxidation of a pair of donors resulting in the reduction of molecular oxygen to two molecules of water
    - EC 1.14.19.1 stearoyl-CoA 9-desaturase
    - EC 1.14.19.2 acyl-[acyl-carrier-protein] desaturase
    - EC 1.14.19.3 linoleoyl-CoA desaturase
  - EC 1.14.20 With 2-oxoglutarate as one donor, and the other dehydrogenated
    - EC 1.14.20.1 deacetoxycephalosporin-C synthase
  - EC 1.14.21 With NADH or NADPH as one donor, and the other dehydrogenated
    - EC 1.14.21.1 (S)-stylopine synthase
    - EC 1.14.21.2 (S)-cheilanthifoline synthase
    - EC 1.14.21.3 berbamunine synthase
    - EC 1.14.21.4 salutaridine synthase
    - EC 1.14.21.5 (S)-canadine synthase
  - EC 1.14.99 Miscellaneous
    - EC 1.14.99.1 prostaglandin-endoperoxide synthase
    - EC 1.14.99.2 kynurenine 7,8-hydroxylase
    - EC 1.14.99.3 heme oxygenase (decyclizing)
    - EC 1.14.99.4 progesterone monooxygenase
    - EC 1.14.99.5 now EC 1.14.19.1
    - EC 1.14.99.6 now EC 1.14.19.2
    - EC 1.14.99.7 squalene monooxygenase
    - EC 1.14.99.8 deleted, included in EC 1.14.14.1
    - EC 1.14.99.9 steroid 17a-monooxygenase
    - EC 1.14.99.10 steroid 21-monooxygenase
    - EC 1.14.99.11 estradiol 6b-monooxygenase
    - EC 1.14.99.12 4-androstene-3,17-dione monooxygenase
    - EC 1.14.99.13 now EC 1.14.13.23
    - EC 1.14.99.14 progesterone 11a-monooxygenase
    - EC 1.14.99.15 4-methoxybenzoate monooxygenase (O-demethylating)
    - EC 1.14.99.16 now EC 1.14.13.72
    - EC 1.14.99.17 now EC 1.14.16.5
    - EC 1.14.99.18 N-acetylneuraminate monooxygenase
    - EC 1.14.99.19 plasmanylethanolamine desaturase
    - EC 1.14.99.20 phylloquinone monooxygenase (2,3-epoxidizing)
    - EC 1.14.99.21 Latia-luciferin monooxygenase (demethylating)
    - EC 1.14.99.22 ecdysone 20-monooxygenase
    - EC 1.14.99.23 3-hydroxybenzoate 2-monooxygenase
    - EC 1.14.99.24 steroid 9a-monooxygenase
    - EC 1.14.99.25 now EC 1.14.19.3
    - EC 1.14.99.26 2-hydroxypyridine 5-monooxygenase
    - EC 1.14.99.27 juglone 3-monooxygenase
    - EC 1.14.99.28 linalool 8-monooxygenase
    - EC 1.14.99.29 deoxyhypusine monooxygenase
    - EC 1.14.99.30 carotene 7,8-desaturase
    - EC 1.14.99.31 myristoyl-CoA 11-(E) desaturase
    - EC 1.14.99.32 myristoyl-CoA 11-(Z) desaturase
    - EC 1.14.99.33 D12-fatty acid dehydrogenase
    - EC 1.14.99.34 monoprenyl isoflavone epoxidase
    - EC 1.14.99.35 thiophene-2-carbonyl-CoA monooxygenase
    - EC 1.14.99.36 b-carotene 15,15'-monooxygenase
    - EC 1.14.99.37 taxadiene 5a-hydroxylase
- EC 1.15 Acting on superoxide as acceptor
    - EC 1.15.1.1 superoxide dismutase
    - EC 1.15.1.2 superoxide reductase
- EC 1.16 Oxidising metal ions
  - EC 1.16.1 With NAD or NADP as acceptor
    - EC 1.16.1.1 mercury(II) reductase
    - EC 1.16.1.2 diferric-transferrin reductase
    - EC 1.16.1.3 aquacobalamin reductase
    - EC 1.16.1.4 cob(II)alamin reductase
    - EC 1.16.1.5 aquacobalamin reductase (NADPH)
    - EC 1.16.1.6 cyanocobalamin reductase (cyanide-eliminating)
    - EC 1.16.1.7 ferric-chelate reductase
  - EC 1.16.3 With oxygen as acceptor
    - EC 1.16.3.1 ferroxidase
- EC 1.17 Acting on CH2 groups
  - EC 1.17.1 With NAD or NADP as acceptor
    - EC 1.17.1.1 CDP-4-dehydro-6-deoxyglucose reductase
  - EC 1.17.3 With oxygen as acceptor
    - EC 1.17.3.1 pteridine oxidase
  - EC 1.17.4 With a disulfide as acceptor
    - EC 1.17.4.1 ribonucleoside-diphosphate reductase

        - EC 1.17.4.2 ribonucleoside-triphosphate reductase
    - EC 1.17.99 With other acceptors
        - EC 1.17.99.1 4-cresol dehydrogenase (hydroxylating)
        - EC 1.17.99.2 ethylbenzene hydroxylase
- EC 1.18 Acting on iron-sulfur proteins as donors
    - EC 1.18.1 With NAD or NADP as acceptor
        - EC 1.18.1.1 rubredoxin—NAD+ reductase
        - EC 1.18.1.2 ferredoxin—NADP reductase
        - EC 1.18.1.3 ferredoxin—NAD reductase
        - EC 1.18.1.4 rubredoxin—NAD(P)+ reductase
    - EC 1.18.2 With dinitrogen as acceptor (now EC 1.18.6)
        - EC 1.18.2.1 now EC 1.18.6.1
    - EC 1.18.3 With H+ as acceptor
        - EC 1.18.3.1 now EC 1.18.99.1
    - EC 1.18.6 With dinitrogen as acceptor
        - EC 1.18.6.1 nitrogenase
    - EC 1.18.96 With other, known, acceptors
        - EC 1.18.96.1 now EC 1.15.1.2
    - EC 1.18.99 With H+ as acceptors
        - EC 1.18.99.1 now EC 1.12.7.2
- EC 1.19 Acting on reduced flavodoxin as donor
    - EC 1.19.6 With dinitrogen as acceptor
        - EC 1.19.6.1 nitrogenase (flavodoxin)
- EC 1.20 Acting on phosphorus or arsenic in donors
    - EC 1.20.1 Acting on phosphorus or arsenic in donors, with NAD(P)+ as acceptor
        - EC 1.20.1.1 phosphonate dehydrogenase
    - EC 1.20.4 Acting on phosphorus or arsenic in donors, with disulfide as acceptor
        - EC 1.20.4.1 arsenate reductase (glutaredoxin)
        - EC 1.20.4.2 methylarsonate reductase
    - EC 1.20.98 Acting on phosphorus or arsenic in donors, with other, known acceptors
        - EC 1.20.98.1 arsenate reductase (azurin)
    - EC 1.20.99 Acting on phosphorus or arsenic in donors, with other acceptors
        - EC 1.20.99.1 arsenate reductase (donor)
- EC 1.21 Acting on X-H and Y-H to form an X-Y bond
    - EC 1.21.3 With oxygen as acceptor
        - EC 1.21.3.1 isopenicillin-N synthase
        - EC 1.21.3.2 columbamine oxidase
        - EC 1.21.3.3 reticuline oxidase
        - EC 1.21.3.4 sulochrin oxidase [(+)-bisdechlorogeodin-forming]
        - EC 1.21.3.5 sulochrin oxidase [(-)-bisdechlorogeodin-forming]
    - EC 1.21.99 With other acceptors
        - EC 1.21.99.1 b-cyclopiazonate dehydrogenase
- EC 1.97 Other oxidoreductases
        - EC 1.97.1.1 chlorate reductase
        - EC 1.97.1.2 pyrogallol hydroxyltransferase
        - EC 1.97.1.3 sulfur reductase
        - EC 1.97.1.4 formate acetyltransferase activating enzyme
        - EC 1.97.1.5 now EC 1.20.4.1
        - EC 1.97.1.6 now EC 1.20.99.1
        - EC 1.97.1.7 now EC 1.20.4.2
        - EC 1.97.1.8 tetrachloroethene reductive dehalogenase
- EC 1.98 Enzymes using H2 as reductant
        - EC 1.98.1.1 now EC 1.18.99.1
- EC 1.99 Other enzymes using O2 as oxidant
    - EC 1.99.1 Hydroxylases (now EC 1.14)
        - EC 1.99.1.1 deleted, now EC 1.14.14.1
        - EC 1.99.1.2 deleted, now EC 1.14.16.1
        - EC 1.99.1.3 deleted
        - EC 1.99.1.4 deleted
        - EC 1.99.1.5 deleted, now EC 1.14.13.9
        - EC 1.99.1.6 deleted
        - EC 1.99.1.7 deleted, now EC 1.14.15.4
        - EC 1.99.1.8 deleted
        - EC 1.99.1.9 deleted, now EC 1.14.99.9
        - EC 1.99.1.10 deleted
        - EC 1.99.1.11 deleted, now EC 1.14.99.10
        - EC 1.99.1.12 deleted
        - EC 1.99.1.13 deleted, covered by EC 1.14.99.7 and EC 5.4.99.7
        - EC 1.99.1.14 deleted, now EC 1.13.11.27
    - EC 1.99.2 Oxygenases (now EC 1.13)
        - EC 1.99.2.1 deleted, now EC 1.13.11.12
        - EC 1.99.2.2 deleted, now EC 1.13.11.1
        - EC 1.99.2.3 deleted, now EC 1.13.11.3
        - EC 1.99.2.4 deleted, now EC 1.13.11.4
        - EC 1.99.2.5 deleted, now EC 1.13.11.5
        - EC 1.99.2.6 deleted, now EC 1.13.99.1

EC 2 Transferases

- EC 2.1 Transferring One-Carbon Groups
    - EC 2.1.1 Methyltransferases
        - EC 2.1.1.1 nicotinamide N-methyltransferase
        - EC 2.1.1.2 guanidinoacetate N-methyltransferase
        - EC 2.1.1.3 thetin—homocysteine S-methyltransferase
        - EC 2.1.1.4 acetylserotonin O-methyltransferase
        - EC 2.1.1.5 betaine—homocysteine S-methyltransferase
        - EC 2.1.1.6 catechol O-methyltransferase
        - EC 2.1.1.7 nicotinate N-methyltransferase
        - EC 2.1.1.8 histamine N-methyltransferase
        - EC 2.1.1.9 thiol S-methyltransferase
        - EC 2.1.1.10 homocysteine S-methyltransferase
        - EC 2.1.1.11 magnesium-protoporphyrin O-methyltransferase
        - EC 2.1.1.12 methionine S-methyltransferase
        - EC 2.1.1.13 5-methyltetrahydrofolate—homocysteine S-methyltransferase
        - EC 2.1.1.14 5-methyltetrahydropteroyltriglutamate—homocysteine S-methyltransferase
        - EC 2.1.1.15 fatty-acid O-methyltransferase
        - EC 2.1.1.16 methylene-fatty-acyl-phospholipid synthase
        - EC 2.1.1.17 phosphatidylethanolamine N-methyltransferase
        - EC 2.1.1.18 polysaccharide O-methyltransferase
        - EC 2.1.1.19 trimethylsulfonium—tetrahydrofolate N-methyltransferase
        - EC 2.1.1.20 glycine N-methyltransferase
        - EC 2.1.1.21 methylamine—glutamate N-methyltransferase
        - EC 2.1.1.22 carnosine N-methyltransferase
        - EC 2.1.1.23 now covered by EC 2.1.1.124, EC 2.1.1.125 and EC 2.1.1.126
        - EC 2.1.1.24 now covered by EC 2.1.1.77, EC 2.1.1.80 and EC 2.1.1.100
        - EC 2.1.1.25 phenol O-methyltransferase
        - EC 2.1.1.26 iodophenol O-methyltransferase
        - EC 2.1.1.27 tyramine N-methyltransferase
        - EC 2.1.1.28 phenylethanolamine N-methyltransferase
        - EC 2.1.1.29 tRNA (cytosine-5-)-methyltransferase
        - EC 2.1.1.30 deleted
        - EC 2.1.1.31 tRNA (guanine-N1-)-methyltransferase
        - EC 2.1.1.32 tRNA (guanine-N2-)-methyltransferase
        - EC 2.1.1.33 tRNA (guanine-N7-)-methyltransferase
        - EC 2.1.1.34 tRNA (guanosine-2'-O-)-methyltransferase
        - EC 2.1.1.35 tRNA (uracil-5-)-methyltransferase
        - EC 2.1.1.36 tRNA (adenine-N1-)-methyltransferase
        - EC 2.1.1.37 DNA (cytosine-5-)-methyltransferase
        - EC 2.1.1.38 O-demethylpuromycin O-methyltransferase
        - EC 2.1.1.39 inositol 3-methyltransferase
        - EC 2.1.1.40 inositol 1-methyltransferase
        - EC 2.1.1.41 sterol 24-C-methyltransferase
        - EC 2.1.1.42 luteolin O-methyltransferase
        - EC 2.1.1.43 histone-lysine N-methyltransferase
        - EC 2.1.1.44 dimethylhistidine N-methyltransferase
        - EC 2.1.1.45 thymidylate synthase
        - EC 2.1.1.46 isoflavone 4'-O-methyltransferase
        - EC 2.1.1.47 indolepyruvate C-methyltransferase
        - EC 2.1.1.48 rRNA (adenine-N6-)-methyltransferase
        - EC 2.1.1.49 amine N-methyltransferase
        - EC 2.1.1.50 loganate O-methyltransferase
        - EC 2.1.1.51 rRNA (guanine-N1-)-methyltransferase
        - EC 2.1.1.52 rRNA (guanine-N2-)-methyltransferase
        - EC 2.1.1.53 putrescine N-methyltransferase
        - EC 2.1.1.54 deoxycytidylate C-methyltransferase
        - EC 2.1.1.55 tRNA (adenine-N6-)-methyltransferase
        - EC 2.1.1.56 mRNA (guanine-N7-)-methyltransferase
        - EC 2.1.1.57 mRNA (nucleoside-2'-O-)-methyltransferase
        - EC 2.1.1.58 deleted, included in EC 2.1.1.57

  - EC 2.1.1.59 [cytochrome c]-lysine N-methyltransferase
  - EC 2.1.1.60 calmodulin-lysine N-methyltransferase
  - EC 2.1.1.61 tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase
  - EC 2.1.1.62 mRNA (2'-O-methyladenosine-N6-)-methyltransferase
  - EC 2.1.1.63 methylated-DNA—[protein]-cysteine S-methyltransferase
  - EC 2.1.1.64 3-demethylubiquinone-9 3-O-methyltransferase
  - EC 2.1.1.65 licodione 2'-O-methyltransferase
  - EC 2.1.1.66 rRNA (adenosine-2'-O-)-methyltransferase
  - EC 2.1.1.67 thiopurine S-methyltransferase
  - EC 2.1.1.68 caffeate O-methyltransferase
  - EC 2.1.1.69 5-hydroxyfuranocoumarin 5-O-methyltransferase
  - EC 2.1.1.70 8-hydroxyfuranocoumarin 8-O-methyltransferase
  - EC 2.1.1.71 phosphatidyl-N-methylethanolamine N-methyltransferase
  - EC 2.1.1.72 site-specific DNA-methyltransferase (adenine-specific)
  - EC 2.1.1.73 site-specific DNA-methyltransferase (cytosine-specific)
  - EC 2.1.1.74 methylenetetrahydrofolate—tRNA-(uracil-5-)-methyltransferase (FADH2-oxidizing)
  - EC 2.1.1.75 apigenin 4'-O-methyltransferase
  - EC 2.1.1.76 quercetin 3-O-methyltransferase
  - EC 2.1.1.77 protein-L-isoaspartate(D-aspartate) O-methyltransferase
  - EC 2.1.1.78 isoorientin 3'-O-methyltransferase
  - EC 2.1.1.79 cyclopropane-fatty-acyl-phospholipid synthase
  - EC 2.1.1.80 protein-glutamate O-methyltransferase
  - EC 2.1.1.81 deleted, included in EC 2.1.1.49
  - EC 2.1.1.82 3-methylquercitin 7-O-methyltransferase
  - EC 2.1.1.83 3,7-dimethylquercitin 4'-O-methyltransferase
  - EC 2.1.1.84 methylquercetagetin 6-O-methyltransferase
  - EC 2.1.1.85 protein-histidine N-methyltransferase
  - EC 2.1.1.86 tetrahydromethanopterin S-methyltransferase
  - EC 2.1.1.87 pyridine N-methyltransferase
  - EC 2.1.1.88 8-hydroxyquercitin 8-O-methyltransferase
  - EC 2.1.1.89 tetrahydrocolumbamine 2-O-methyltransferase
  - EC 2.1.1.90 methanol—5-hydroxybenzimidazolylcobamide Co-methyltransferase
  - EC 2.1.1.91 isobutyraldoxime O-methyltransferase
  - EC 2.1.1.92 bergaptol O-methyltransferase
  - EC 2.1.1.93 xanthotoxol O-methyltransferase
  - EC 2.1.1.94 11-O-demethyl-17-O-deacetylvindoline O-methyltransferase
  - EC 2.1.1.95 tocopherol O-methyltransferase
  - EC 2.1.1.96 thioether S-methyltransferase
  - EC 2.1.1.97 3-hydroxyanthranilate 4-C-methyltransferase
  - EC 2.1.1.98 diphthine synthase
  - EC 2.1.1.99 16-methoxy-2,3-dihydro-3-hydroxytabersonine N-methyltransferase
  - EC 2.1.1.100 protein-S-isoprenylcysteine O-methyltransferase
  - EC 2.1.1.101 macrocin O-methyltransferase
  - EC 2.1.1.102 demethylmacrocin O-methyltransferase
  - EC 2.1.1.103 phosphoethanolamine N-methyltransferase
  - EC 2.1.1.104 caffeoyl-CoA O-methyltransferase
  - EC 2.1.1.105 N-benzoyl-4-hydroxyanthranilate 4-O-methyltransferase
  - EC 2.1.1.106 tryptophan 2-C-methyltransferase
  - EC 2.1.1.107 uroporphyrin-III C-methyltransferase
  - EC 2.1.1.108 6-hydroxymellein O-methyltransferase
  - EC 2.1.1.109 demethylsterigmatocystin 6-O-methyltransferase
  - EC 2.1.1.110 sterigmatocystin 7-O-methyltransferase
  - EC 2.1.1.111 anthranilate N-methyltransferase
  - EC 2.1.1.112 glucuronoxylan 4-O-methyltransferase
  - EC 2.1.1.113 site-specific DNA-methyltransferase (cytosine-N4-specific)
  - EC 2.1.1.114 hexaprenyldihydroxybenzoate methyltransferase
  - EC 2.1.1.115 (RS)-1-benzyl-1,2,3,4-tetrahydroisoquinoline N-methyltransferase
  - EC 2.1.1.116 3'-hydroxy-N-methyl-(S)-coclaurine 4'-O-methyltransferase
  - EC 2.1.1.117 (S)-scoulerine 9-O-methyltransferase
  - EC 2.1.1.118 columbamine O-methyltransferase
  - EC 2.1.1.119 10-hydroxydihydrosanguinarine 10-O-methyltransferase
  - EC 2.1.1.120 12-hydroxydihydrochelirubine 12-O-methyltransferase
  - EC 2.1.1.121 6-O-methylnorlaudanosoline 5'-O-methyltransferase
  - EC 2.1.1.122 (S)-tetrahydroprotoberberine N-methyltransferase
  - EC 2.1.1.123 [cytochrome c]-methionine S-methyltransferase
  - EC 2.1.1.124 [cytochrome c]-arginine N-methyltransferase
  - EC 2.1.1.125 histone-arginine N-methyltransferase
  - EC 2.1.1.126 [myelin basic protein]-arginine N-methyltransferase
  - EC 2.1.1.127 [ribulose-bisphosphate carboxylase]-lysine N-methyltransferase
  - EC 2.1.1.128 (RS)-norcoclaurine 6-O-methyltransferase
  - EC 2.1.1.129 inositol 4-methyltransferase
  - EC 2.1.1.130 precorrin-2 C20-methyltransferase
  - EC 2.1.1.131 precorrin-3B C17-methyltransferase
  - EC 2.1.1.132 precorrin-6Y C5,15-methyltransferase (decarboxylating)
  - EC 2.1.1.133 precorrin-4 C11-methyltransferase
  - EC 2.1.1.134 now with EC 2.1.1.129
  - EC 2.1.1.135 [methionine synthase]-cobalamin methyltransferase (cob(II)alamin reducing)
  - EC 2.1.1.136 chlorophenol O-methyltransferase
  - EC 2.1.1.137 arsenite methyltransferase
  - EC 2.1.1.138 methylarsonite methyltransferase
  - EC 2.1.1.139 3'-demethylstaurosporine O-methyltransferase
  - EC 2.1.1.140 (S)-coclaurine-N-methyltransferase
  - EC 2.1.1.141 jasmonate O-methyltransferase
  - EC 2.1.1.142 cycloartenol 24-C-methyltransferase
  - EC 2.1.1.143 24-methylenesterol C-methyltransferase
  - EC 2.1.1.144 trans-aconitate 2-methyltransferase
  - EC 2.1.1.145 trans-aconitate 3-methyltransferase
  - EC 2.1.1.146 (iso)eugenol O-methyltransferase
  - EC 2.1.1.147 corydaline synthase
- EC 2.1.2 Hydroxymethyl-, Formyl- and Related Transferases
  - EC 2.1.2.1 glycine hydroxymethyltransferase
  - EC 2.1.2.2 phosphoribosylglycinamide formyltransferase
  - EC 2.1.2.3 phosphoribosylaminoimidazolecarboxamide formyltransferase
  - EC 2.1.2.4 glycine formiminotransferase
  - EC 2.1.2.5 glutamate formiminotransferase
  - EC 2.1.2.6 deleted, included in EC 2.1.2.5
  - EC 2.1.2.7 D-alanine 2-hydroxymethyltransferase
  - EC 2.1.2.8 deoxycytidylate 5-hydroxymethyltransferase
  - EC 2.1.2.9 methionyl-tRNA formyltransferase
  - EC 2.1.2.10 aminomethyltransferase
  - EC 2.1.2.11 3-methyl-2-oxobutanoate hydroxymethyltransferase
  - EC 2.1.2.12 now EC 2.1.1.74
- EC 2.1.3 Carboxyl- and Carbamoyltransferases
  - EC 2.1.3.1 methylmalonyl-CoA carboxyltransferase
  - EC 2.1.3.2 aspartate carbamoyltransferase
  - EC 2.1.3.3 ornithine carbamoyltransferase
  - EC 2.1.3.4 deleted
  - EC 2.1.3.5 oxamate carbamoyltransferase
  - EC 2.1.3.6 putrescine carbamoyltransferase
  - EC 2.1.3.7 3-hydroxymethylcephem carbamoyltransferase
  - EC 2.1.3.8 lysine carbamoyltransferase
- EC 2.1.4 Amidinotransferases

        - EC 2.1.4.1 glycine amidinotransferase
        - EC 2.1.4.2 inosamine-phosphate amidinotransferase
- EC 2.2 Transferring Aldehyde or Ketone Residues
    - EC 2.2.1 Transketolases and Transaldolases
        - EC 2.2.1.1 transketolase
        - EC 2.2.1.2 transaldolase
        - EC 2.2.1.3 formaldehyde transketolase
        - EC 2.2.1.4 acetoin—ribose-5-phosphate transaldolase
        - EC 2.2.1.5 2-hydroxy-3-oxoadipate synthase
        - EC 2.2.1.6 acetolactate synthase
        - EC 2.2.1.7 1-deoxy-D-xylulose-5-phosphate synthase
- EC 2.3 Acyltransferases
    - EC 2.3.1 Transferring groups other than amino-acyl groups
        - EC 2.3.1.1 amino-acid N-acetyltransferase
        - EC 2.3.1.2 imidazole N-acetyltransferase
        - EC 2.3.1.3 glucosamine N-acetyltransferase
        - EC 2.3.1.4 glucosamine 6-phosphate N-acetyltransferase
        - EC 2.3.1.5 arylamine N-acetyltransferase
        - EC 2.3.1.6 choline O-acetyltransferase
        - EC 2.3.1.7 carnitine O-acetyltransferase
        - EC 2.3.1.8 phosphate acetyltransferase
        - EC 2.3.1.9 acetyl-CoA C-acetyltransferase
        - EC 2.3.1.10 hydrogen-sulfide S-acetyltransferase
        - EC 2.3.1.11 thioethanolamine S-acetyltransferase
        - EC 2.3.1.12 dihydrolipoamide S-acetyltransferase
        - EC 2.3.1.13 glycine N-acyltransferase
        - EC 2.3.1.14 glutamine N-phenylacetyltransferase
        - EC 2.3.1.15 glycerol-3-phosphate O-acyltransferase
        - EC 2.3.1.16 acetyl-CoA C-acyltransferase
        - EC 2.3.1.17 aspartate N-acetyltransferase
        - EC 2.3.1.18 galactoside O-acetyltransferase
        - EC 2.3.1.19 phosphate butyryltransferase
        - EC 2.3.1.20 diacylglycerol O-acyltransferase
        - EC 2.3.1.21 carnitine O-palmitoyltransferase
        - EC 2.3.1.22 2-acylglycerol O-acyltransferase
        - EC 2.3.1.23 1-acylglycerophosphocholine O-acyltransferase
        - EC 2.3.1.24 sphingosine N-acyltransferase
        - EC 2.3.1.25 plasmalogen synthase
        - EC 2.3.1.26 sterol O-acyltransferase
        - EC 2.3.1.27 cortisol O-acetyltransferase
        - EC 2.3.1.28 chloramphenicol O-acetyltransferase
        - EC 2.3.1.29 glycine C-acetyltransferase
        - EC 2.3.1.30 serine O-acetyltransferase
        - EC 2.3.1.31 homoserine O-acetyltransferase
        - EC 2.3.1.32 lysine N-acetyltransferase
        - EC 2.3.1.33 histidine N-acetyltransferase
        - EC 2.3.1.34 D-tryptophan N-acetyltransferase
        - EC 2.3.1.35 glutamate N-acetyltransferase
        - EC 2.3.1.36 D-amino-acid N-acetyltransferase
        - EC 2.3.1.37 5-aminolevulinate synthase
        - EC 2.3.1.38 [acyl-carrier-protein] S-acetyltransferase
        - EC 2.3.1.39 [acyl-carrier-protein] S-malonyltransferase
        - EC 2.3.1.40 acyl-[acyl-carrier-protein]—phospholipid O-acyltransferase
        - EC 2.3.1.41 3-oxoacyl-[acyl-carrier-protein] synthase
        - EC 2.3.1.42 glycerone-phosphate O-acyltransferase
        - EC 2.3.1.43 phosphatidylcholine—sterol O-acyltransferase
        - EC 2.3.1.44 N-acetylneuraminate 4-O-acetyltransferase
        - EC 2.3.1.45 N-acetylneuraminate 7-O(or 9-O)-acetyltransferase
        - EC 2.3.1.46 homoserine O-succinyltransferase
        - EC 2.3.1.47 8-amino-7-oxononanoate synthase
        - EC 2.3.1.48 histone acetyltransferase
        - EC 2.3.1.49 deacetyl-[citrate-(pro-3S)-lyase] S-acetyltransferase
        - EC 2.3.1.50 serine C-palmitoyltransferase
        - EC 2.3.1.51 1-acylglycerol-3-phosphate O-acyltransferase
        - EC 2.3.1.52 2-acylglycerol-3-phosphate O-acyltransferase
        - EC 2.3.1.53 phenylalanine N-acetyltransferase
        - EC 2.3.1.54 formate C-acetyltransferase
        - EC 2.3.1.55 now EC 2.3.1.82
        - EC 2.3.1.56 aromatic-hydroxylamine O-acetyltransferase
        - EC 2.3.1.57 diamine N-acetyltransferase
        - EC 2.3.1.58 2,3-diaminopropionate N-oxalyltransferase
        - EC 2.3.1.59 gentamycin 2'-N-acetyltransferase
        - EC 2.3.1.60 gentamycin 3'-N-acetyltransferase
        - EC 2.3.1.61 dihydrolipoamide S-succinyltransferase
        - EC 2.3.1.62 2-acylglycerophosphocholine O-acyltransferase
        - EC 2.3.1.63 1-alkylglycerophosphocholine O-acyltransferase
        - EC 2.3.1.64 agmatine N4-coumaroyltransferase
        - EC 2.3.1.65 glycine N-choloyltransferase
        - EC 2.3.1.66 leucine N-acetyltransferase
        - EC 2.3.1.67 1-alkylglycerophosphocholine O-acetyltransferase
        - EC 2.3.1.68 glutamine N-acyltransferase
        - EC 2.3.1.69 monoterpenol O-acetyltransferase
        - EC 2.3.1.70 CDP-acylglycerol O-arachidonyltransferase
        - EC 2.3.1.71 glycine N-benzoyltransferase
        - EC 2.3.1.72 indoleacetylglucose—inositol O-acyltransferase
        - EC 2.3.1.73 diacylglycerol—sterol O-acyltransferase
        - EC 2.3.1.74 naringenin-chalcone synthase
        - EC 2.3.1.75 long-chain-alcohol O-fatty-acyltransferase
        - EC 2.3.1.76 retinol O-fatty-acyltransferase
        - EC 2.3.1.77 triacylglycerol—sterol O-acyltransferase
        - EC 2.3.1.78 heparan-a-glucosaminide N-acetyltransferase
        - EC 2.3.1.79 maltose O-acetyltransferase
        - EC 2.3.1.80 cysteine-S-conjugate N-acetyltransferase
        - EC 2.3.1.81 aminoglycoside N3'-acetyltransferase
        - EC 2.3.1.82 aminoglycoside N6'-acetyltransferase
        - EC 2.3.1.83 phosphatidylcholine—dolichol O-acyltransferase
        - EC 2.3.1.84 alcohol O-acetyltransferase
        - EC 2.3.1.85fatty-acid synthase
        - EC 2.3.1.86 fatty-acyl-CoA synthase
        - EC 2.3.1.87 aralkylamine N-acetyltransferase
        - EC 2.3.1.88 peptide a-N-acetyltransferase
        - EC 2.3.1.89 tetrahydrodipicolinate N-acetyltransferase
        - EC 2.3.1.90 b-glucogallin O-galloyltransferase
        - EC 2.3.1.91 sinapoylglucose—choline O-sinapoyltransferase
        - EC 2.3.1.92 sinapoylglucose—malate O-sinapoyltransferase
        - EC 2.3.1.93 13-hydroxylupinine O-tigloyltransferase
        - EC 2.3.1.94 erythronolide synthase
        - EC 2.3.1.95 trihydroxystilbene synthase
        - EC 2.3.1.96 glycoprotein N-palmitoyltransferase
        - EC 2.3.1.97 glycylpeptide N-tetradecanoyltransferase
        - EC 2.3.1.98 chlorogenate—glucarate O-hydroxycinnamoyltransferase
        - EC 2.3.1.99 quinate O-hydroxycinnamoyltransferase
        - EC 2.3.1.100 myelin-proteolipid O-palmitoyltransferase
        - EC 2.3.1.101 formylmethanofuran—tetrahydromethanopterin N-formyltransferase
        - EC 2.3.1.102 N6-hydroxylysine O-acetyltransferase
        - EC 2.3.1.103 sinapoylglucose—sinapoylglucose O-sinapoyltransferase
        - EC 2.3.1.104 1-alkenylglycerophosphocholine O-acyltransferase
        - EC 2.3.1.105 alkylglycerophosphate 2-O-acetyltransferase
        - EC 2.3.1.106 tartronate O-hydroxycinnamoyltransferase
        - EC 2.3.1.107 17-O-deacetylvindoline O-acetyltransferase
        - EC 2.3.1.108 tubulin N-acetyltransferase
        - EC 2.3.1.109 arginine N-succinyltransferase
        - EC 2.3.1.110 tyramine N-feruloyltransferase
        - EC 2.3.1.111 mycocerosate synthase
        - EC 2.3.1.112 D-tryptophan N-malonyltransferase
        - EC 2.3.1.113 anthranilate N-malonyltransferase
        - EC 2.3.1.114 3,4-dichloroaniline N-malonyltransferase

- EC 2.3.1.115 isoflavone-7-O-b-glucoside 6"-O-malonyltransferase
- EC 2.3.1.116 flavonol-3-O-b-glucoside O-malonyltransferase
- EC 2.3.1.117 2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-succinyltransferase
- EC 2.3.1.118 N-hydroxyarylamine O-acetyltransferase
- EC 2.3.1.119 icosanoyl-CoA synthase
- EC 2.3.1.120 deleted
- EC 2.3.1.121 1-alkenylglycerophosphoethanolamine O-acyltransferase
- EC 2.3.1.122 trehalose O-mycolyltransferase
- EC 2.3.1.123 dolichol O-acyltransferase
- EC 2.3.1.124 deleted
- EC 2.3.1.125 1-alkyl-2-acetylglycerol O-acyltransferase
- EC 2.3.1.126 isocitrate O-dihydroxycinnamoyltransferase
- EC 2.3.1.127 ornithine N-benzoyltransferase
- EC 2.3.1.128 ribosomal-protein-alanine N-acetyltransferase
- EC 2.3.1.129 acyl-[acyl-carrier-protein]—UDP-N-acetylglucosamine O-acyltransferase
- EC 2.3.1.130 galactarate O-hydroxycinnamoyltransferase
- EC 2.3.1.131 glucarate O-hydroxycinnamoyltransferase
- EC 2.3.1.132 glucarolactone O-hydroxycinnamoyltransferase
- EC 2.3.1.133 shikimate O-hydroxycinnamoyltransferase
- EC 2.3.1.134 galactolipid O-acyltransferase
- EC 2.3.1.135 phosphatidylcholine—retinol O-acyltransferase
- EC 2.3.1.136 polysialic-acid O-acetyltransferase
- EC 2.3.1.137 carnitine O-octanoyltransferase
- EC 2.3.1.138 putrescine N-hydroxycinnamoyltransferase
- EC 2.3.1.139 ecdysone O-acyltransferase
- EC 2.3.1.140 rosmarinate synthase
- EC 2.3.1.141 galactosylacylglycerol O-acyltransferase
- EC 2.3.1.142 glycoprotein O-fatty-acyltransferase
- EC 2.3.1.143 b-glucogallin—tetrakisgalloylglucose O-galloyltransferase
- EC 2.3.1.144 anthranilate N-benzoyltransferase
- EC 2.3.1.145 piperidine N-piperoyltransferase
- EC 2.3.1.146 pinosylvin synthase
- EC 2.3.1.147 glycerophospholipid arachidonoyl-transferase (CoA-independent)
- EC 2.3.1.148 glycerophospholipid acyltransferase (CoA-dependent)
- EC 2.3.1.149 platelet-activating factor acetyltransferase
- EC 2.3.1.150 salutaridinol 7-O-acetyltransferase
- EC 2.3.1.151 benzophenone synthase
- EC 2.3.1.152 alcohol O-cinnamoyltransferase
- EC 2.3.1.153 anthocyanin 5-aromatic acyltransferase
- EC 2.3.1.154 propionyl-CoA C2-trimethyltridecanoyltransferase
- EC 2.3.1.155 acetyl-CoA C-myristoyltransferase
- EC 2.3.1.156 phloroisovalerophenone synthase
- EC 2.3.1.157 glucosamine-1-phosphate N-acetyltransferase
- EC 2.3.1.158 phospholipid:diacylglycerol acyltransferase
- EC 2.3.1.159 acridone synthase
- EC 2.3.1.160 vinorine synthase
- EC 2.3.1.161 lovastatin nonaketide synthase
- EC 2.3.1.162 taxadien-5a-ol O-acetyltransferase
- EC 2.3.1.163 10-hydroxytaxane O-acetyltransferase
- EC 2.3.1.164 isopenicillin-N N-acyltransferase
- EC 2.3.1.165 6-methylsalicylic acid synthase
- EC 2.3.1.166 2a-hydroxytaxane 2-O-benzoyltransferase
- EC 2.3.1.167 10-deacetylbaccatin III 10-O-acetyltransferase

- EC 2.3.2 Aminoacyltransferases
  - EC 2.3.2.1 D-glutamyltransferase
  - EC 2.3.2.2 g-glutamyltransferase
  - EC 2.3.2.3 lysyltransferase
  - EC 2.3.2.4 g-glutamylcyclotransferase
  - EC 2.3.2.5 glutaminyl-peptide cyclotransferase
  - EC 2.3.2.6 leucyltransferase
  - EC 2.3.2.7 aspartyltransferase
  - EC 2.3.2.8 arginyltransferase
  - EC 2.3.2.9 agantine g-glutamyltransferase
  - EC 2.3.2.10 UDP-N-acetylmuramoylpentapeptide-lysine N6-alanyltransferase
  - EC 2.3.2.11 alanylphosphatidylglycerol synthase
  - EC 2.3.2.12 peptidyltransferase
  - EC 2.3.2.13 protein-glutamine g-glutamyltransferase
  - EC 2.3.2.14 D-alanine g-glutamyltransferase
  - EC 2.3.2.15 glutathione g-glutamylcysteinyltransferase
- EC 2.3.3 Acyl groups converted into alkyl on transfer
  - EC 2.3.3.1 citrate (Si)-synthase
  - EC 2.3.3.2 decylcitrate synthase
  - EC 2.3.3.3 citrate (Re)-synthase
  - EC 2.3.3.4 decylhomocitrate synthase
  - EC 2.3.3.5 2-methylcitrate synthase
  - EC 2.3.3.6 2-ethylmalate synthase
  - EC 2.3.3.7 3-ethylmalate synthase
  - EC 2.3.3.8 ATP citrate synthase
  - EC 2.3.3.9 malate synthase
  - EC 2.3.3.10 hydroxymethylglutaryl-CoA synthase
  - EC 2.3.3.11 2-hydroxyglutarate synthase
  - EC 2.3.3.12 3-propylmalate synthase
  - EC 2.3.3.13 2-isopropylmalate synthase
  - EC 2.3.3.14 homocitrate synthase

- EC 2.4 Glycosyltransferases
  - EC 2.4.1 Hexosyltransferases
    - EC 2.4.1.1 phosphorylase
    - EC 2.4.1.2 dextrin dextranase
    - EC 2.4.1.3 deleted, included in EC 2.4.1.25
    - EC 2.4.1.4 amylosucrase
    - EC 2.4.1.5 dextransucrase
    - EC 2.4.1.6 deleted
    - EC 2.4.1.7 sucrose phosphorylase
    - EC 2.4.1.8 maltose phosphorylase
    - EC 2.4.1.9 inulosucrase
    - EC 2.4.1.10 levansucrase
    - EC 2.4.1.11 glycogen(starch) synthase
    - EC 2.4.1.12 cellulose synthase (UDP-forming)
    - EC 2.4.1.13 sucrose synthase
    - EC 2.4.1.14 sucrose-phosphate synthase
    - EC 2.4.1.15 a,a-trehalose-phosphate synthase (UDP-forming)
    - EC 2.4.1.16 chitin synthase
    - EC 2.4.1.17 glucuronosyltransferase
    - EC 2.4.1.18 1,4-a-glucan branching enzyme
    - EC 2.4.1.19 cyclomaltodextrin glucanotransferase
    - EC 2.4.1.20 cellobiose phosphorylase
    - EC 2.4.1.21 starch synthase
    - EC 2.4.1.22 lactose synthase
    - EC 2.4.1.23 sphingosine b-galactosyltransferase
    - EC 2.4.1.24 1,4-a-glucan 6-a-glucosyltransferase
    - EC 2.4.1.25 4-a-glucanotransferase
    - EC 2.4.1.26 DNA a-glucosyltransferase
    - EC 2.4.1.27 DNA b-glucosyltransferase
    - EC 2.4.1.28 glucosyl-DNA b-glucosyltransferase
    - EC 2.4.1.29 cellulose synthase (GDP-forming)
    - EC 2.4.1.30 1,3-b-oligoglucan phosphorylase
    - EC 2.4.1.31 laminaribiose phosphorylase
    - EC 2.4.1 32 glucomannan 4-b-mannosyltransferase
    - EC 2.4.1.33 alginate synthase
    - EC 2.4.1.34 1,3-b-glucan synthase
    - EC 2.4.1.35 phenol b-glucosyltransferase
    - EC 2.4.1.36 a,a-trehalose-phosphate synthase (GDP-forming)
    - EC 2.4.1.37 fucosylgalactoside 3-a-galactosyltransferase
    - EC 2.4.1.38 b-N-acetylglucosaminylglycopeptide b-1,4-galactosyltransferase
    - EC 2.4.1.39 steroid N-acetylglucosaminyltransferase
    - EC 2.4.1.40 glycoprotein-fucosylgalactoside a-N-acetylgalactosaminyltransferase
    - EC 2.4.1.41 polypeptide N-acetylgalactosaminyltransferase
    - EC 2.4.1.42 deleted, included in EC 2.4.1.17
    - EC 2.4.1.43 polygalacturonate 4-a-galacturonosyltransferase
    - EC 2.4.1.44 lipopolysaccharide 3-a-galactosyltransferase
    - EC 2.4.1.45 2-hydroxyacylsphingosine 1-b-galactosyltransferase
    - EC 2.4.1.46 1,2-diacylglycerol 3-b-galactosyltransferase

EC 2.4.1.47 N-acylsphingosine galactosyltransferase
EC 2.4.1.48 heteroglycan a-mannosyltransferase
EC 2.4.1.49 cellodextrin phosphorylase
EC 2.4.1.50 procollagen galactosyltransferase
EC 2.4.1.51 now covered by EC 2.4.1.101, EC 2.4.1.143, EC 2.4.1.144 and EC 2.4.1.145
EC 2.4.1.52 poly(glycerol-phosphate) a-glucosyltransferase
EC 2.4.1.53 poly(ribitol-phosphate) b-glucosyltransferase
EC 2.4.1.54 undecaprenyl-phosphate mannosyltransferase
EC 2.4.1.55 now EC 2.7.8.14
EC 2.4.1.56 lipopolysaccharide N-acetylglucosaminyltransferase
EC 2.4.1.57 phosphatidyl-myo-inositol a-mannosyltransferase
EC 2.4.1.58 lipopolysaccharide glucosyltransferase I
EC 2.4.1.59 deleted, included in EC 2.4.1.17
EC 2.4.1.60 abequosyltransferase
EC 2.4.1.61 deleted, included in EC 2.4.1.17
EC 2.4.1.62 ganglioside galactosyltransferase
EC 2.4.1.63 linamarin synthase
EC 2.4.1.64 a,a-trehalose phosphorylase
EC 2.4.1.65 3-galactosyl-N-acetylglucosaminide 4-a-L-fucosyltransferase
EC 2.4.1.66 procollagen glucosyltransferase
EC 2.4.1.67 galactinol—raffinose galactosyltransferase
EC 2.4.1.68 glycoprotein 6-a-L-fucosyltransferase
EC 2.4.1.69 galactoside 2-a-L-fucosyltransferase
EC 2.4.1.70 poly(ribitol-phosphate) N-acetylglucosaminyl-transferase
EC 2.4.1.71 arylamine glucosyltransferase
EC 2.4.1.72 now EC 2.4.2.24
EC 2.4.1.73 lipopolysaccharide glucosyltransferase II
EC 2.4.1.74 glycosaminoglycan galactosyltransferase
EC 2.4.1.75 UDP-galacturonosyltransferase
EC 2.4.1.76 deleted, included in EC 2.4.1.17
EC 2.4.1.77 deleted, included in EC 2.4.1.17
EC 2.4.1.78 phosphopolyprenol glucosyltransferase
EC 2.4.1.79 galactosylgalactosylglucosylceramide b-D-acetylgalactosaminyltransferase
EC 2.4.1.80 ceramide glucosyltransferase
EC 2.4.1.81 flavone 7-O-b-glucosyltransferase
EC 2.4.1.82 galactinol—sucrose galactosyltransferase
EC 2.4.1.83 dolichyl-phosphate b-D-mannosyltransferase
EC 2.4.1.84 deleted, included in EC 2.4.1.17
EC 2.4.1.85 cyanohydrin b-glucosyltransferase
EC 2.4.1.86 glucosaminylgalactosylglucosylceramide b-galactosyltransferase
EC 2.4.1.87 N-acetyllactosaminide 3-a-galactosyltransferase
EC 2.4.1.88 globoside a-N-acetylgalactosaminyltransferase
EC 2.4.1.89 deleted, included in EC 2.4.1.69
EC 2.4.1.90 N-acetyllactosamine synthase
EC 2.4.1.91 flavonol 3-O-glucosyltransferase
EC 2.4.1.92 (N-acetylneuraminyl)-galactosylglucosylceramide N-acetylgalactosaminyltransferase
EC 2.4.1.93 inulin fructotransferase (depolymerizing, difructofuranose-1,2':2,3'-dianhydride-forming)
EC 2.4.1.94 protein N-acetylglucosaminyltransferase
EC 2.4.1.95 bilirubin-glucuronoside glucuronosyltransferase
EC 2.4.1.96 sn-glycerol-3-phosphate 1-galactosyltransferase
EC 2.4.1.97 1,3-b-D-glucan phosphorylase
EC 2.4.1.98 deleted, included in EC 2.4.1.90
EC 2.4.1.99 sucrose 1F-fructosyltransferase
EC 2.4.1.100 1,2-b-fructan 1F-fructosyltransferase
EC 2.4.1.101 a-1,3-mannosyl-glycoprotein 2-b-N-acetylglucosaminyltransferase
EC 2.4.1.102 b-1,3-galactosyl-O-glycosyl-glycoprotein b-1,6-N-acetylglucosaminyltransferase
EC 2.4.1.103 alizarin 2-b-glucosyltransferase
EC 2.4.1.104 o-dihydroxycoumarin 7-O-glucosyltransferase
EC 2.4.1.105 vitexin b-glucosyltransferase
EC 2.4.1.106 isovitexin b-glucosyltransferase
EC 2.4.1.107 deleted, included in EC 2.4.1.17
EC 2.4.1.108 deleted, included in EC 2.4.1.17
EC 2.4.1.109 dolichyl-phosphate-mannose-protein mannosyltransferase
EC 2.4.1.110 tRNA-queuosine b-mannosyltransferase
EC 2.4.1.111 coniferyl-alcohol glucosyltransferase
EC 2.4.1.112 a-1,4-glucan-protein synthase (UDP-forming)
EC 2.4.1.113 a-1,4-glucan-protein synthase (ADP-forming)
EC 2.4.1.114 2-coumarate O-b-glucosyltransferase
EC 2.4.1.115 anthocyanidin 3-O-glucosyltransferase
EC 2.4.1.116 cyanidin-3-rhamnosylglucoside 5-O-glucosyltransferase
EC 2.4.1.117 dolichyl-phosphate b-glucosyltransferase
EC 2.4.1.118 cytokinin 7-b-glucosyltransferase
EC 2.4.1.119 dolichyl-diphosphooligosaccharide—protein glycotransferase
EC 2.4.1.120 sinapate 1-glucosyltransferase
EC 2.4.1.121 indole-3-acetate b-glucosyltransferase
EC 2.4.1.122 glycoprotein-N-acetylgalactosamine 3-b-galactosyltransferase
EC 2.4.1.123 inositol 1-a-galactosyltransferase
EC 2.4.1.124 now included with EC 2.4.1.87
EC 2.4.1.125 sucrose—1,6-a-glucan 3(6)-a-glucosyltransferase
EC 2.4.1.126 hydroxycinnamate 4-b-glucosyltransferase
EC 2.4.1.127 monoterpenol b-glucosyltransferase
EC 2.4.1.128 scopoletin glucosyltransferase
EC 2.4.1.129 peptidoglycan glycosyltransferase
EC 2.4.1.130 dolichyl-phosphate-mannose—glycolipid a-mannosyltransferase
EC 2.4.1.131 glycolipid 2-a-mannosyltransferase
EC 2.4.1.132 glycolipid 3-a-mannosyltransferase
EC 2.4.1.133 xylosylprotein 4-b-galactosyltransferase
EC 2.4.1.134 galactosylxylosylprotein 3-b-galactosyltransferase
EC 2.4.1.135 galactosylgalactosylxylosylprotein 3-b-glucuronosyltransferase
EC 2.4.1.136 gallate 1-b-glucosyltransferase
EC 2.4.1.137 sn-glycerol-3-phosphate 2-a-galactosyltransferase
EC 2.4.1.138 mannotetraose 2-a-N-acetylglucosaminyltransferase
EC 2.4.1.139 maltose synthase
EC 2.4.1.140 alternansucrase
EC 2.4.1.141 N-acetylglucosaminyldiphosphodolichol N-acetylglucosaminyltransferase
EC 2.4.1.142 chitobiosyldiphosphodolichol b-mannosyltransferase
EC 2.4.1.143 a-1,6-mannosyl-glycoprotein 2-b-N-acetylglucosaminyltransferase
EC 2.4.1.144 b-1,4-mannosyl-glycoprotein 4-b-N-acetylglucosaminyltransferase
EC 2.4.1.145 a-1,3-mannosyl-glycoprotein 4-b-N-acetylglucosaminyltransferase
EC 2.4.1.146 b-1,3-galactosyl-O-glycosyl-glycoprotein b-1,3-N-acetylglucosaminyltransferase
EC 2.4.1.147 acetylgalactosaminyl-O-glycosyl-glycoprotein b-1,3-N-acetylglucosaminyltransferase
EC 2.4.1.148 acetylgalactosaminyl-O-glycosyl-glycoprotein b-1,6-N-acetylglucosaminyltransferase
EC 2.4.1.149 N-acetyllactosaminide b-1,3-N-acetylglucosaminyltransferase
EC 2.4.1.150 N-acetyllactosaminide b-1,6-N-acetylglucosaminyl-transferase
EC 2.4.1.151 included with EC 2.4.1.87

  - EC 2.4.1.152 galactoside 3-fucosyltransferase
  - EC 2.4.1.153 dolichyl-phosphate a-N-acetylglucosaminyltransferase
  - EC 2.4.1.154 globotriosylceramide b-1,6-N-acetylgalactosaminyl-transferase
  - EC 2.4.1.155 a-1,6-mannosyl-glycoprotein 6-b-N-acetylglucosaminyltransferase
  - EC 2.4.1.156 indolylacetyl-myo-inositol galactosyltransferase
  - EC 2.4.1.157 1,2-diacylglycerol 3-glucosyltransferase
  - EC 2.4.1.158 13-hydroxydocosanoate 13-b-glucosyltransferase
  - EC 2.4.1.159 flavonol-3-O-glucoside L-rhamnosyltransferase
  - EC 2.4.1.160 pyridoxine 5'-O-b-D-glucosyltransferase
  - EC 2.4.1.161 oligosaccharide 4-a-D-glucosyltransferase
  - EC 2.4.1.162 aldose b-D-fructosyltransferase
  - EC 2.4.1.163 b-galactosyl-N-acetylglucosaminylgalactosylglucosyl-ceramide b-1,3-acetylglucosaminyltransferase
  - EC 2.4.1.164 galactosyl-N-acetylglucosaminylgalactosylglucosyl-ceramide b-1,6-N-acetylglucosaminyltransferase
  - EC 2.4.1.165 N-acetylneuraminylgalactosylglucosylceramide b-1,4-N-acetylgalactosaminyltransferase
  - EC 2.4.1.166 raffinose—raffinose a-galactotransferase
  - EC 2.4.1.167 sucrose 6F-a-galactotransferase
  - EC 2.4.1.168 xyloglucan 4-glucosyltransferase
  - EC 2.4.1.169 xyloglucan 6-xylosyltransferase
  - EC 2.4.1.170 isoflavone 7-O-glucosyltransferase
  - EC 2.4.1.171 methyl-ONN-azoxymethanol b-D-glucosyltransferase
  - EC 2.4.1.172 salicyl-alcohol b-D-glucosyltransferase
  - EC 2.4.1.173 sterol 3b-glucosyltransferase
  - EC 2.4.1.174 glucuronylgalactosylproteoglycan 4-b-N-acetylgalactosaminyltransferase
  - EC 2.4.1.175 glucuronosyl-N-acetylgalactosaminyl-proteoglycan 4-b-N-acetylgalactosaminyltransferase
  - EC 2.4.1.176 gibberellin b-D-glucosyltransferase
  - EC 2.4.1.177 cinnamate b-D-glucosyltransferase
  - EC 2.4.1.178 hydroxymandelonitrile glucosyltransferase
  - EC 2.4.1.179 lactosylceramide b-1,3-galactosyltransferase
  - EC 2.4.1.180 lipopolysaccharide N-acetylmannosaminouronosyltransferase
  - EC 2.4.1.181 hydroxyanthraquinone glucosyltransferase
  - EC 2.4.1.182 lipid-A-disaccharide synthase
  - EC 2.4.1.183 a-1,3-glucan synthase
  - EC 2.4.1.184 galactolipid galactosyltransferase
  - EC 2.4.1.185 flavanone 7-O-b-glucosyltransferase
  - EC 2.4.1.186 glycogenin glucosyltransferase
  - EC 2.4.1.187 N-acetylglucosaminyldiphosphoundecaprenol N-acetyl-b-D-mannosaminyltransferase
  - EC 2.4.1.188 N-acetylglucosaminyldiphosphoundecaprenol glucosyltransferase
  - EC 2.4.1.189 luteolin 7-O-glucuronosyltransferase
  - EC 2.4.1.190 luteolin-7-O-glucuronide 7-O-glucuronosyltransferase
  - EC 2.4.1.191 luteolin-7-O-diglucuronide 4'-O-glucuronosyltransferase
  - EC 2.4.1.192 nuatigenin 3b-glucosyltransferase
  - EC 2.4.1.193 sarsapogenin 3b-glucosyltransferase
  - EC 2.4.1.194 4-hydroxybenzoate 4-O-b-D-glucosyltransferase
  - EC 2.4.1.195 thiohydroximate b-D-glucosyltransferase
  - EC 2.4.1.196 nicotinate glucosyltransferase
  - EC 2.4.1.197 high-mannose-oligosaccharide b-1,4-N-acetylglucosaminyltransferase
  - EC 2.4.1.198 phosphatidylinositol N-acetylglucosaminyltransferase
  - EC 2.4.1.199 b-mannosylphosphodecaprenol—mannooligosaccharide 6-mannosyltransferase
  - EC 2.4.1.200 inulin fructotransferase (depolymerizing, difructofuranose-1,2':2',1-dianhydride-forming)
  - EC 2.4.1.201 a-1,6-mannosyl-glycoprotein 4-b-N-acetylglucosaminyltransferase
  - EC 2.4.1.202 2,4-dihydroxy-7-methoxy-2H-1,4-benzoxazin-3(4H)-one 2 -D-glucosyltransferase
  - EC 2.4.1.203 trans-zeatin O-b-D-glucosyltransferase
  - EC 2.4.1.204 zeatin O-b-D-xylosyltransferase
  - EC 2.4.1.205 galactogen 6b-galactosyltransferase
  - EC 2.4.1.206 lactosylceramide 1,3-N-acetyl-b-D-glucosaminyltransferase
  - EC 2.4.1.207 xyloglucan:xyloglucosyl transferase
  - EC 2.4.1.208 diglucosyl diacylglycerol synthase
  - EC 2.4.1.209 cis-p-coumarate glucosyltransferase
  - EC 2.4.1.210 limonoid glucosyltransferase
  - EC 2.4.1.211 1,3-b-galactosyl-N-acetylhexosamine phosphorylase
  - EC 2.4.1.212 hyaluronan synthase
  - EC 2.4.1.213 glucosylglycerol-phosphate synthase
  - EC 2.4.1.214 glycoprotein 3-a-L-fucosyltransferase
  - EC 2.4.1.215 cis-zeatin O-b-D-glucosyltransferase
  - EC 2.4.1.216 trehalose 6-phosphate phosphorylase
  - EC 2.4.1.217 mannosyl-3-phosphoglycerate synthase
  - EC 2.4.1.218 hydroquinone glucosyltransferase
  - EC 2.4.1.219 vomilenine glucosyltransferase
  - EC 2.4.1.220 indoxyl-UDPG glucosyltransferase
  - EC 2.4.1.221 peptide-O-fucosyltransferase
  - EC 2.4.1.222 O-fucosylpeptide 3-b-N-acetylglucosaminyltransferase
  - EC 2.4.1.223 glucuronyl-galactosyl-proteoglycan 4-a-N-acetylglucosaminyltransferase
  - EC 2.4.1.224 glucuronosyl-N-acetylglucosaminyl-proteoglycan 4-a-N-acetylglucosaminyltransferase
  - EC 2.4.1.225 N-acetylglucosaminyl-proteoglycan 4-b-glucuronosyltransferase
  - EC 2.4.1.226 N-acetylgalactosaminyl-proteoglycan 3-b-glucuronosyltransferase
  - EC 2.4.1.227 undecaprenyldiphospho-muramoylpentapeptide b-N-acetylglucosaminyltransferase
  - EC 2.4.1.228 lactosylceramide 4-a-galactosyltransferase
- EC 2.4.2 Pentosyltransferases
  - EC 2.4.2.1 purine-nucleoside phosphorylase
  - EC 2.4.2.2 pyrimidine-nucleoside phosphorylase
  - EC 2.4.2.3 uridine phosphorylase
  - EC 2.4.2.4 thymidine phosphorylase
  - EC 2.4.2.5 nucleoside ribosyltransferase
  - EC 2.4.2.6 nucleoside deoxyribosyltransferase
  - EC 2.4.2.7 adenine phosphoribosyltransferase
  - EC 2.4.2.8 hypoxanthine phosphoribosyltransferase
  - EC 2.4.2.9 uracil phosphoribosyltransferase
  - EC 2.4.2.10 orotate phosphoribosyltransferase
  - EC 2.4.2.11 nicotinate phosphoribosyltransferase
  - EC 2.4.2.12 nicotinamide phosphoribosyltransferase
  - EC 2.4.2.13 now EC 2.5.1.6
  - EC 2.4.2.14 amidophosphoribosyltransferase
  - EC 2.4.2.15 guanosine phosphorylase
  - EC 2.4.2.16 urate-ribonucleotide phosphorylase
  - EC 2.4.2.17 ATP phosphoribosyltransferase
  - EC 2.4.2.18 anthranilate phosphoribosyltransferase
  - EC 2.4.2.19 nicotinate-nucleotide diphosphorylase (carboxylating)
  - EC 2.4.2.20 dioxotetrahydropyrimidine phosphoribosyltransferase
  - EC 2.4.2.21 nicotinate-nucleotide—dimethylbenzimidazole phosphoribosyltransferase
  - EC 2.4.2.22 xanthine phosphoribosyltransferase
  - EC 2.4.2.23 deoxyuridine phosphorylase
  - EC 2.4.2.24 1,4-b-D-xylan synthase
  - EC 2.4.2.25 flavone apiosyltransferase
  - EC 2.4.2.26 protein xylosyltransferase
  - EC 2.4.2.27 dTDP-dihydrostreptose—streptidine-6-phosphate dihydrostreptosyltransferase

- EC 2.4.2.28 5'-methylthioadenosine phosphorylase
- EC 2.4.2.29 queuine tRNA-ribosyltransferase
- EC 2.4.2.30 NAD ADP-ribosyltransferase
- EC 2.4.2.31 NAD(P)—arginine ADP-ribosyltransferase
- EC 2.4.2.32 dolichyl-phosphate D-xylosyltransferase
- EC 2.4.2.33 dolichyl-xylosyl-phosphate—protein xylosyltransferase
- EC 2.4.2.34 indolylacetylinositol arabinosyltransferase
- EC 2.4.2.35 flavonol-3-O-glycoside xylosyltransferase
- EC 2.4.2.36 NAD—diphthamide ADP-ribosyltransferase
- EC 2.4.2.37 NAD—dinitrogen-reductase ADP-D-ribosyltransferase
- EC 2.4.2.38 glycoprotein 2-b-D-xylosyltransferase
- EC 2.4.99 Transferring Other Glycosyl Groups
  - EC 2.4.99.1 b-galactoside a-2,6-sialyltransferase
  - EC 2.4.99.2 monosialoganglioside sialyltransferase
  - EC 2.4.99.3 a-N-acetylgalactosaminide a-2,6-sialyltransferase
  - EC 2.4.99.4 b-galactoside a-2,3-sialyltransferase
  - EC 2.4.99.5 galactosyldiacylglycerol a-2,3-sialyltransferase
  - EC 2.4.99.6 N-acetyllactosaminide a-2,3-sialyltransferase
  - EC 2.4.99.7 (a-N-acetylneuraminyl-2,3-a-galactosyl-1,3)-N-acetyl-galactosaminide a-2,6-sialyltransferase
  - EC 2.4.99.8 a-N-acetylneuraminate a-2,8-sialyltransferase
  - EC 2.4.99.9 lactosylceramide a-2,3-sialyltransferase
  - EC 2.4.99.10 neolactotetraosylceramide a-2,3-sialyltransferase
  - EC 2.4.99.11 lactosylceramide a-2,6-N-sialyltransferase
- EC 2.5 Transferring Alkyl or Aryl Groups, Other than Methyl Groups
  - EC 2.5.1.1 dimethylallyltranstransferase
  - EC 2.5.1.2 thiamine pyridinylase
  - EC 2.5.1.3 thiamine-phosphate diphosphorylase
  - EC 2.5.1.4 adenosylmethionine cyclotransferase
  - EC 2.5.1.5 galactose-6-sulfurylase
  - EC 2.5.1.6 methionine adenosyltransferase
  - EC 2.5.1.7 UDP-N-acetylglucosamine 1-carboxyvinyltransferase
  - EC 2.5.1.8 tRNA isopentenyltransferase
  - EC 2.5.1.9 riboflavin synthase
  - EC 2.5.1.10 geranyltranstransferase
  - EC 2.5.1.11 trans-octaprenyltranstransferase
  - EC 2.5.1.12 deleted, included in EC 2.5.1.18
  - EC 2.5.1.13 deleted, included in EC 2.5.1.18
  - EC 2.5.1.14 deleted, included in EC 2.5.1.18
  - EC 2.5.1.15 dihydropteroate synthase
  - EC 2.5.1.16 spermidine synthase
  - EC 2.5.1.17 cob(I)alamin adenosyltransferase
  - EC 2.5.1.18 glutathione transferase
  - EC 2.5.1.19 3-phosphoshikimate 1-carboxyvinyltransferase
  - EC 2.5.1.20 rubber cis-polyprenylcistransferase
  - EC 2.5.1.21 farnesyl-diphosphate farnesyltransferase
  - EC 2.5.1.22 spermine synthase
  - EC 2.5.1.23 sym-norspermidine synthase
  - EC 2.5.1.24 discadenine synthase
  - EC 2.5.1.25 tRNA-uridine aminocarboxypropyltransferase
  - EC 2.5.1.26 alkylglycerone-phosphate synthase
  - EC 2.5.1.27 adenylate dimethylallyltransferase
  - EC 2.5.1.28 dimethylallylcistransferase
  - EC 2.5.1.29 farnesyltranstransferase
  - EC 2.5.1.30 trans-hexaprenyltranstransferase
  - EC 2.5.1.31 di-trans,poly-cis-decaprenylcistransferase
  - EC 2.5.1.32 geranylgeranyl-diphosphate geranylgeranyltransferase
  - EC 2.5.1.33 trans-pentaprenyltranstransferase
  - EC 2.5.1.34 tryptophan dimethylallyltransferase
  - EC 2.5.1.35 aspulvinone dimethylallyltransferase
  - EC 2.5.1.36 trihydroxypterocarpan dimethylallyltransferase
  - EC 2.5.1.37 leukotriene-C4 synthase
  - EC 2.5.1.38 isonocardicin synthase
  - EC 2.5.1.39 4-hydroxybenzoate nonaprenyltransferase
  - EC 2.5.1.40 now EC 4.2.3.9
  - EC 2.5.1.41 phosphoglycerol geranylgeranyltransferase
  - EC 2.5.1.42 geranylgeranylglycerol-phosphate geranylgeranyltransferase
  - EC 2.5.1.43 nicotianamine synthase
  - EC 2.5.1.44 homospermidine synthase
  - EC 2.5.1.45 homospermidine synthase (spermidine-specific)
  - EC 2.5.1.46 deoxyhypusine synthase
  - EC 2.5.1.47 cysteine synthase
  - EC 2.5.1.48 cystathionine g-synthase
  - EC 2.5.1.49 O-acetylhomoserine aminocarboxypropyltransferase
  - EC 2.5.1.50 zeatin 9-aminocarboxyethyltransferase
  - EC 2.5.1.51 b-pyrazolylalanine synthase
  - EC 2.5.1.52 L-mimosine synthase
  - EC 2.5.1.53 uracilylalanine synthase
  - EC 2.5.1.54 3-deoxy-7-phosphoheptulonate synthase
  - EC 2.5.1.55 3-deoxy-8-phosphooctulonate synthase
  - EC 2.5.1.56 N-acetylneuraminate synthase
  - EC 2.5.1.57 N-acylneuraminate-9-phosphate synthase
- EC 2.6 Transferring Nitrogenous Groups
  - EC 2.6.1 Transaminases
    - EC 2.6.1.1 aspartate transaminase
    - EC 2.6.1.2 alanine transaminase
    - EC 2.6.1.3 cysteine transaminase
    - EC 2.6.1.4 glycine transaminase
    - EC 2.6.1.5 tyrosine transaminase
    - EC 2.6.1.6 leucine transaminase
    - EC 2.6.1.7 kynurenine—oxoglutarate transaminase
    - EC 2.6.1.8 2,5-diaminovalerate transaminase
    - EC 2.6.1.9 histidinol-phosphate transaminase
    - EC 2.6.1.10 deleted, included in EC 2.6.1.21
    - EC 2.6.1.11 acetylornithine transaminase
    - EC 2.6.1.12 alanine—oxo-acid transaminase
    - EC 2.6.1.13 ornithine—oxo-acid transaminase
    - EC 2.6.1.14 asparagine—oxo-acid transaminase
    - EC 2.6.1.15 glutamine—pyruvate transaminase
    - EC 2.6.1.16 glutamine—fructose-6-phosphate transaminase (isomerizing)
    - EC 2.6.1.17 succinyldiaminopimelate transaminase
    - EC 2.6.1.18 b-alanine—pyruvate transaminase
    - EC 2.6.1.19 4-aminobutyrate transaminase
    - EC 2.6.1.20 deleted
    - EC 2.6.1.21 D-alanine transaminase
    - EC 2.6.1.22 (S)-3-amino-2-methylpropionate transaminase
    - EC 2.6.1.23 4-hydroxyglutamate transaminase
    - EC 2.6.1.24 diiodotyrosine transaminase
    - EC 2.6.1.25 deleted, included in EC 2.6.1.24
    - EC 2.6.1.26 thyroid-hormone transaminase
    - EC 2.6.1.27 tryptophan transaminase
    - EC 2.6.1.28 tryptophan—phenylpyruvate transaminase
    - EC 2.6.1.29 diamine transaminase
    - EC 2.6.1.30 pyridoxamine—pyruvate transaminase
    - EC 2.6.1.31 pyridoxamine—oxaloacetate transaminase
    - EC 2.6.1.32 valine—3-methyl-2-oxovalerate transaminase
    - EC 2.6.1.33 dTDP-4-amino-4,6-dideoxy-D-glucose transaminase
    - EC 2.6.1.34 UDP-2-acetamido-4-amino-2,4,6-trideoxyglucose transaminase
    - EC 2.6.1.35 glycine—oxaloacetate transaminase
    - EC 2.6.1.36 L-lysine 6-transaminase
    - EC 2.6.1.37 (2-aminoethyl)phosphonate—pyruvate transaminase
    - EC 2.6.1.38 histidine transaminase
    - EC 2.6.1.39 2-aminoadipate transaminase
    - EC 2.6.1.40 (R)-3-amino-2-methylpropionate—pyruvate transaminase
    - EC 2.6.1.41 D-methionine—pyruvate transaminase
    - EC 2.6.1.42 branched-chain-amino-acid transaminase
    - EC 2.6.1.43 aminolevulinate transaminase
    - EC 2.6.1.44 alanine—glyoxylate transaminase

- EC 2.6.1.45 serine—glyoxylate transaminase
- EC 2.6.1.46 diaminobutyrate—pyruvate transaminase
- EC 2.6.1.47 alanine—oxomalonate transaminase
- EC 2.6.1.48 5-aminovalerate transaminase
- EC 2.6.1.49 dihydroxyphenylalanine transaminase
- EC 2.6.1.50 glutamine—scyllo-inositol transaminase
- EC 2.6.1.51 serine—pyruvate transaminase
- EC 2.6.1.52 phosphoserine transaminase
- EC 2.6.1.53 now EC 1.4.1.13
- EC 2.6.1.54 pyridoxamine-phosphate transaminase
- EC 2.6.1.55 taurine transaminase
- EC 2.6.1.56 1D-1-guanidino-3-amino-1,3-dideoxy-scyllo-inositol transaminase
- EC 2.6.1.57 aromatic-amino-acid transaminase
- EC 2.6.1.58 phenylalanine(histidine) transaminase
- EC 2.6.1.59 dTDP-4-amino-4,6-dideoxygalactose transaminase
- EC 2.6.1.60 aromatic-amino-acid—glyoxylate transaminase
- EC 2.6.1.61 (R)-3-amino-2-methylpropionate transaminase
- EC 2.6.1.62 adenosylmethionine—8-amino-7-oxononanoate transaminase
- EC 2.6.1.63 kynurenine—glyoxylate transaminase
- EC 2.6.1.64 glutamine—phenylpyruvate transaminase
- EC 2.6.1.65 N6-acetyl-b-lysine transaminase
- EC 2.6.1.66 valine—pyruvate transaminase
- EC 2.6.1.67 2-aminohexanoate transaminase
- EC 2.6.1.68 ornithine(lysine) transaminase
- EC 2.6.1.69 N2-acetylornithine 5-transaminase
- EC 2.6.1.70 aspartate—phenylpyruvate transaminase
- EC 2.6.1.71 lysine—pyruvate 6-transaminase
- EC 2.6.1.72 D-4-hydroxyphenylglycine transaminase
- EC 2.6.1.73 methionine—glyoxylate transaminase
- EC 2.6.1.74 cephalosporin-C transaminase
- EC 2.6.1.75 cysteine-conjugate transaminase
- EC 2.6.1.76 diaminobutyrate—2-oxoglutarate transaminase
- EC 2.6.2 Amidinotransferases
  - EC 2.6.2.1 now EC 2.1.4.1
- EC 2.6.3 Oximinotransferases
  - EC 2.6.3.1 oximinotransferase
- 2.6.99 Transferring Other Nitrogenous Groups
  - EC 2.6.99.1 dATP(dGTP)—DNA purinetransferase

EC 2.7 Transferring Phosphorus-Containing Groups

- EC 2.7.1 Phosphotransferases with an Alcohol Group as Acceptor
  - EC 2.7.1.1 hexokinase
  - EC 2.7.1.2 glucokinase
  - EC 2.7.1.3 ketohexokinase
  - EC 2.7.1.4 fructokinase
  - EC 2.7.1.5 rhamnulokinase
  - EC 2.7.1.6 galactokinase
  - EC 2.7.1.7 mannokinase
  - EC 2.7.1.8 glucosamine kinase
  - EC 2.7.1.9 deleted
  - EC 2.7.1.10 phosphoglucokinase
  - EC 2.7.1.11 6-phosphofructokinase
  - EC 2.7.1.12 gluconokinase
  - EC 2.7.1.13 dehydrogluconokinase
  - EC 2.7.1.14 sedoheptulokinase
  - EC 2.7.1.15 ribokinase
  - EC 2.7.1.16 ribulokinase
  - EC 2.7.1.17 xylulokinase
  - EC 2.7.1.18 phosphoribokinase
  - EC 2.7.1.19 phosphoribulokinase
  - EC 2.7.1.20 adenosine kinase
  - EC 2.7.1.21 thymidine kinase
  - EC 2.7.1.22 ribosylnicotinamide kinase
  - EC 2.7.1.23 NAD kinase
  - EC 2.7.1.24 dephospho-CoA kinase
  - EC 2.7.1.25 adenylyl-sulfate kinase
  - EC 2.7.1.26 riboflavin kinase
  - EC 2.7.1.27 erythritol kinase
  - EC 2.7.1.28 triokinase
  - EC 2.7.1.29 glycerone kinase
  - EC 2.7.1.30 glycerol kinase
  - EC 2.7.1.31 glycerate kinase
  - EC 2.7.1.32 choline kinase
  - EC 2.7.1.33 pantothenate kinase
  - EC 2.7.1.34 pantetheine kinase
  - EC 2.7.1.35 pyridoxal kinase
  - EC 2.7.1.36 mevalonate kinase
  - EC 2.7.1.37 protein kinase
  - EC 2.7.1.38 phosphorylase kinase
  - EC 2.7.1.39 homoserine kinase
  - EC 2.7.1.40 pyruvate kinase
  - EC 2.7.1.41 glucose-1-phosphate phosphodismutase
  - EC 2.7.1.42 riboflavin phosphotransferase
  - EC 2.7.1.43 glucuronokinase
  - EC 2.7.1.44 galacturonokinase
  - EC 2.7.1.45 2-dehydro-3-deoxygluconokinase
  - EC 2.7.1.46 L-arabinokinase
  - EC 2.7.1.47 D-ribulokinase
  - EC 2.7.1.48 uridine kinase
  - EC 2.7.1.49 hydroxymethylpyrimidine kinase
  - EC 2.7.1.50 hydroxyethylthiazole kinase
  - EC 2.7.1.51 L-fuculokinase
  - EC 2.7.1.52 fucokinase
  - EC 2.7.1.53 L-xylulokinase
  - EC 2.7.1.54 D-arabinokinase
  - EC 2.7.1.55 allose kinase
  - EC 2.7.1.56 1-phosphofructokinase
  - EC 2.7.1.57 deleted
  - EC 2.7.1.58 2-dehydro-3-deoxygalactonokinase
  - EC 2.7.1.59 N-acetylglucosamine kinase
  - EC 2.7.1.60 N-acylmannosamine kinase
  - EC 2.7.1.61 acyl-phosphate—hexose phosphotransferase
  - EC 2.7.1.62 phosphoramidate—hexose phosphotransferase
  - EC 2.7.1.63 polyphosphate—glucose phosphotransferase
  - EC 2.7.1.64 inositol 3-kinase
  - EC 2.7.1.65 scyllo-inosamine 4-kinase
  - EC 2.7.1.66 undecaprenol kinase
  - EC 2.7.1.67 1-phosphatidylinositol 4-kinase
  - EC 2.7.1.68 1-phosphatidylinositol-4-phosphate 5-kinase
  - EC 2.7.1.69 protein—Np-phosphohistidine-sugar phosphotransferase
  - EC 2.7.1.70 protamine kinase
  - EC 2.7.1.71 shikimate kinase
  - EC 2.7.1.72 streptomycin 6-kinase
  - EC 2.7.1.73 inosine kinase
  - EC 2.7.1.74 deoxycytidine kinase
  - EC 2.7.1.75 now EC 2.7.1.21
  - EC 2.7.1.76 deoxyadenosine kinase
  - EC 2.7.1.77 nucleoside phosphotransferase
  - EC 2.7.1.78 polynucleotide 5'-hydroxyl-kinase
  - EC 2.7.1.79 diphosphate—glycerol phosphotransferase
  - EC 2.7.1.80 diphosphate—serine phosphotransferase
  - EC 2.7.1.81 hydroxylysine kinase
  - EC 2.7.1.82 ethanolamine kinase
  - EC 2.7.1.83 pseudouridine kinase
  - EC 2.7.1.84 alkylglycerone kinase
  - EC 2.7.1.85 b-glucoside kinase
  - EC 2.7.1.86 NADH2 kinase
  - EC 2.7.1.87 streptomycin 3"-kinase
  - EC 2.7.1.88 dihydrostreptomycin-6-phosphate 3'a-kinase
  - EC 2.7.1.89 thiamine kinase
  - EC 2.7.1.90 diphosphate—fructose-6-phosphate 1-phosphotransferase
  - EC 2.7.1.91 sphinganine kinase
  - EC 2.7.1.92 5-dehydro-2-deoxygluconokinase
  - EC 2.7.1.93 alkylglycerol kinase
  - EC 2.7.1.94 acylglycerol kinase
  - EC 2.7.1.95 kanamycin kinase
  - EC 2.7.1.96 deleted, included in EC 2.7.1.86
  - EC 2.7.1.97 deleted, identical to EC 2.7.1.125
  - EC 2.7.1.98 deleted
  - EC 2.7.1.99 [pyruvate dehydrogenase (lipoamide)] kinase
  - EC 2.7.1.100 5-methylthioribose kinase
  - EC 2.7.1.101 tagatose kinase
  - EC 2.7.1.102 hamamelose kinase
  - EC 2.7.1.103 viomycin kinase
  - EC 2.7.1.104 diphosphate—protein phosphotransferase
  - EC 2.7.1.105 6-phosphofructo-2-kinase
  - EC 2.7.1.106 glucose-1,6-bisphosphate synthase

  - EC 2.7.1.107 diacylglycerol kinase
  - EC 2.7.1.108 dolichol kinase
  - EC 2.7.1.109 [hydroxymethylglutaryl-CoA reductase (NADPH2)] kinase
  - EC 2.7.1.110 dephospho-[reductase kinase] kinase
  - EC 2.7.1.111 now EC 2.7.1.128
  - EC 2.7.1.112 protein-tyrosine kinase
  - EC 2.7.1.113 deoxyguanosine kinase
  - EC 2.7.1.114 AMP—thymidine kinase
  - EC 2.7.1.115 [3-methyl-2-oxobutanoate dehydrogenase (lipoamide)] kinase
  - EC 2.7.1.116 [isocitrate dehydrogenase (NADP)] kinase
  - EC 2.7.1.117 myosin-light-chain kinase
  - EC 2.7.1.118 ADP—thymidine kinase
  - EC 2.7.1.119 hygromycin-B kinase
  - EC 2.7.1.120 caldesmon kinase
  - EC 2.7.1.121 phosphoenolpyruvate—glycerone phosphotransferase
  - EC 2.7.1.122 xylitol kinase
  - EC 2.7.1.123 Ca2+/calmodulin-dependent protein kinase
  - EC 2.7.1.124 [tyrosine 3-monooxygenase] kinase
  - EC 2.7.1.125 rhodopsin kinase
  - EC 2.7.1.126 b-adrenergic-receptor kinase
  - EC 2.7.1.127 inositol-trisphosphate 3-kinase
  - EC 2.7.1.128 [acetyl-CoA carboxylase] kinase
  - EC 2.7.1.129 myosin-heavy-chain kinase
  - EC 2.7.1.130 tetraacyldisaccharide 4'-kinase
  - EC 2.7.1.131 low-density-lipoprotein kinase
  - EC 2.7.1.132 tropomyosin kinase
  - EC 2.7.1.133 now with EC 2.7.1.134
  - EC 2.7.1.134 inositol-tetrakisphosphate 1-kinase
  - EC 2.7.1.135 tau-protein kinase
  - EC 2.7.1.136 macrolide 2'-kinase
  - EC 2.7.1.137 phosphatidylinositol 3-kinase
  - EC 2.7.1.138 ceramide kinase
  - EC 2.7.1.139 now with EC 2.7.1.134
  - EC 2.7.1.140 inositol-tetrakisphosphate 5-kinase
  - EC 2.7.1.141 [RNA-polymerase]-subunit kinase
  - EC 2.7.1.142 glycerol—3-phosphate-glucose phosphotransferase
  - EC 2.7.1.143 diphosphate-purine nucleoside kinase
  - EC 2.7.1.144 tagatose-6-phosphate kinase
  - EC 2.7.1.145 deoxynucleoside kinase
  - EC 2.7.1.146 ADP-dependent phosphofructokinase
  - EC 2.7.1.147 ADP-dependent glucokinase
  - EC 2.7.1.148 4-(cytidine 5'-diphospho)-2-C-methyl-D-erythritol kinase
  - EC 2.7.1.149 1-phosphatidylinositol-5-phosphate 4-kinase
  - EC 2.7.1.150 1-phosphatidylinositol-3-phosphate 5-kinase
  - EC 2.7.1.151 inositol-polyphosphate multikinase
  - EC 2.7.1.152 inositol-hexakisphosphate kinase
  - EC 2.7.1.153 phosphatidylinositol-4,5-bisphosphate 3-kinase
  - EC 2.7.1.154 phosphatidylinositol-4-phosphate 3-kinase
- EC 2.7.2 Phosphotransferases with a carboxyl group as acceptor
  - EC 2.7.2.1 acetate kinase
  - EC 2.7.2.2 carbamate kinase
  - EC 2.7.2.3 phosphoglycerate kinase
  - EC 2.7.2.4 aspartate kinase
  - EC 2.7.2.5 now EC 6.3.4.16
  - EC 2.7.2.6 formate kinase
  - EC 2.7.2.7 butyrate kinase
  - EC 2.7.2.8 acetylglutamate kinase
  - EC 2.7.2.9 now EC 6.3.5.5
  - EC 2.7.2.10 phosphoglycerate kinase (GTP)
  - EC 2.7.2.11 glutamate 5-kinase
  - EC 2.7.2.12 acetate kinase (diphosphate)
  - EC 2.7.2.13 glutamate 1-kinase
  - EC 2.7.2.14 branched-chain-fatty-acid kinase
- EC 2.7.3 Phosphotransferases with a nitrogenous group as acceptor
  - EC 2.7.3.1 guanidinoacetate kinase
  - EC 2.7.3.2 creatine kinase
  - EC 2.7.3.3 arginine kinase
  - EC 2.7.3.4 taurocyamine kinase
  - EC 2.7.3.5 lombricine kinase
  - EC 2.7.3.6 hypotaurocyamine kinase
  - EC 2.7.3.7 opheline kinase
  - EC 2.7.3.8 ammonia kinase
  - EC 2.7.3.9 phosphoenolpyruvate—protein phosphotransferase
  - EC 2.7.3.10 agmatine kinase
  - EC 2.7.3.11 protein-histidine pros-kinase
  - EC 2.7.3.12 protein-histidine tele-kinase
- EC 2.7.4 Phosphotransferases with a phosphate group as acceptor
  - EC 2.7.4.1 polyphosphate kinase
  - EC 2.7.4.2 phosphomevalonate kinase
  - EC 2.7.4.3 adenylate kinase
  - EC 2.7.4.4 nucleoside-phosphate kinase
  - EC 2.7.4.5 deleted, included in EC 2.7.4.14
  - EC 2.7.4.6 nucleoside-diphosphate kinase
  - EC 2.7.4.7 phosphomethylpyrimidine kinase
  - EC 2.7.4.8 guanylate kinase
  - EC 2.7.4.9 dTMP kinase
  - EC 2.7.4.10 nucleoside-triphosphate—adenylate kinase
  - EC 2.7.4.11 (deoxy)adenylate kinase
  - EC 2.7.4.12 T2-induced deoxynucleotide kinase
  - EC 2.7.4.13 (deoxy)nucleoside-phosphate kinase
  - EC 2.7.4.14 cytidylate kinase
  - EC 2.7.4.15 thiamine-diphosphate kinase
  - EC 2.7.4.16 thiamine-phosphate kinase
  - EC 2.7.4.17 3-phosphoglyceroyl-phosphate—polyphosphate phosphotransferase
  - EC 2.7.4.18 farnesyl-diphosphate kinase
  - EC 2.7.4.19 5-methyldeoxycytidine-5'-phosphate kinase
  - EC 2.7.4.20 dolichyl-diphosphate—polyphosphate phosphotransferase
- EC 2.7.5 Phosphotransferases with regeneration of donors, apparently catalysing intramolecular transfers
  - EC 2.7.5.1 now EC 5.4.2.2
  - EC 2.7.5.2 now EC 5.4.2.3
  - EC 2.7.5.3 now EC 5.4.2.1
  - EC 2.7.5.4 now EC 5.4.2.4
  - EC 2.7.5.5 now EC 5.4.2.5
  - EC 2.7.5.6 now EC 5.4.2.7
  - EC 2.7.5.7 now EC 5.4.2.8
- EC 2.7.6 Diphosphotransferases
  - EC 2.7.6.1 ribose-phosphate diphosphokinase
  - EC 2.7.6.2 thiamine diphosphokinase
  - EC 2.7.6.3 2-amino-4-hydroxy-6-hydroxymethyldihydropteridine diphosphokinase
  - EC 2.7.6.4 nucleotide diphosphokinase
  - EC 2.7.6.5 GTP diphosphokinase
- EC 2.7.7 Nucleotidyltransferases
  - EC 2.7.7.1 nicotinamide-nucleotide adenylyltransferase
  - EC 2.7.7.2 FMN adenylyltransferase
  - EC 2.7.7.3 pantetheine-phosphate adenylyltransferase
  - EC 2.7.7.4 sulfate adenylyltransferase
  - EC 2.7.7.5 sulfate adenylyltransferase (ADP)
  - EC 2.7.7.6 DNA-directed RNA polymerase
  - EC 2.7.7.7 DNA-directed DNA polymerase
  - EC 2.7.7.8 polyribonucleotide nucleotidyltransferase
  - EC 2.7.7.9 UTP—glucose-1-phosphate uridylyltransferase
  - EC 2.7.7.10 UTP—hexose-1-phosphate uridylyltransferase
  - EC 2.7.7.11 UTP—xylose-1-phosphate uridylyltransferase
  - EC 2.7.7.12 UDP-glucose—hexose-1-phosphate uridylyltransferase
  - EC 2.7.7.13 mannose-1-phosphate guanylyltransferase
  - EC 2.7.7.14 ethanolamine-phosphate cytidylyltransferase
  - EC 2.7.7.15 choline-phosphate cytidylyltransferase
  - EC 2.7.7.16 now EC 3.1.27.5
  - EC 2.7.7.17 now EC 3.1.27.1
  - EC 2.7.7.18 nicotinate-nucleotide adenylyltransferase
  - EC 2.7.7.19 polynucleotide adenylyltransferase
  - EC 2.7.7.20 deleted
  - EC 2.7.7.21 tRNA cytidylyltransferase
  - EC 2.7.7.22 mannose-1-phosphate guanylyltransferase (GDP)
  - EC 2.7.7.23 UDP-N-acetylglucosamine diphosphorylase
  - EC 2.7.7.24 glucose-1-phosphate thymidylyltransferase
  - EC 2.7.7.25 tRNA adenylyltransferase
  - EC 2.7.7.26 now EC 3.1.27.3

        - EC 2.7.7.27 glucose-1-phosphate adenylyltransferase
        - EC 2.7.7.28 nucleoside-triphosphate-hexose-1-phosphate nucleotidyltransferase
        - EC 2.7.7.29 hexose-1-phosphate guanylyltransferase
        - EC 2.7.7.30 fucose-1-phosphate guanylyltransferase
        - EC 2.7.7.31 DNA nucleotidylexotransferase
        - EC 2.7.7.32 galactose-1-phosphate thymidylyltransferase
        - EC 2.7.7.33 glucose-1-phosphate cytidylyltransferase
        - EC 2.7.7.34 glucose-1-phosphate guanylyltransferase
        - EC 2.7.7.35 ribose-5-phosphate adenylyltransferase
        - EC 2.7.7.36 aldose-1-phosphate adenylyltransferase
        - EC 2.7.7.37 aldose-1-phosphate nucleotidyltransferase
        - EC 2.7.7.38 3-deoxy-manno-octulosonate cytidylyltransferase
        - EC 2.7.7.39 glycerol-3-phosphate cytidylyltransferase
        - EC 2.7.7.40 D-ribitol-5-phosphate cytidylyltransferase
        - EC 2.7.7.41 phosphatidate cytidylyltransferase
        - EC 2.7.7.42 [glutamate—ammonia-ligase] adenylyltransferase
        - EC 2.7.7.43 N-acylneuraminate cytidylyltransferase
        - EC 2.7.7.44 glucuronate-1-phosphate uridylyltransferase
        - EC 2.7.7.45 guanosine-triphosphate guanylyltransferase
        - EC 2.7.7.46 gentamycin 2"-nucleotidyltransferase
        - EC 2.7.7.47 streptomycin 3"-adenylyltransferase
        - EC 2.7.7.48 RNA-directed RNA polymerase
        - EC 2.7.7.49 RNA-directed DNA polymerase
        - EC 2.7.7.50 mRNA guanylyltransferase
        - EC 2.7.7.51 adenylylsulfate—ammonia adenylyltransferase
        - EC 2.7.7.52 RNA uridylyltransferase
        - EC 2.7.7.53 ATP adenylyltransferase
        - EC 2.7.7.54 phenylalanine adenylyltransferase
        - EC 2.7.7.55 anthranilate adenylyltransferase
        - EC 2.7.7.56 tRNA nucleotidyltransferase
        - EC 2.7.7.57 N-methylphosphoethanolamine cytidylyltransferase
        - EC 2.7.7.58 (2,3-dihydroxybenzoyl)adenylate synthase
        - EC 2.7.7.59 [protein-PII] uridylyltransferase
        - EC 2.7.7.60 2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase
        - EC 2.7.7.61 holo-ACP synthase
    - EC 2.7.8 Transferases for other substituted phosphate groups
        - EC 2.7.8.1 ethanolaminephosphotransferase
        - EC 2.7.8.2 diacylglycerol cholinephosphotransferase
        - EC 2.7.8.3 ceramide cholinephosphotransferase
        - EC 2.7.8.4 serine-phosphoethanolamine synthase
        - EC 2.7.8.5 CDP-diacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase
        - EC 2.7.8.6 undecaprenyl-phosphate galactose phosphotransferase
        - EC 2.7.8.7 holo-[acyl-carrier-protein] synthase
        - EC 2.7.8.8 CDP-diacylglycerol—serine O-phosphatidyltransferase
        - EC 2.7.8.9 phosphomannan mannosephosphotransferase
        - EC 2.7.8.10 sphingosine choline phosphotransferase
        - EC 2.7.8.11 CDP-diacylglycerol—inositol 3-phosphatidyltransferase
        - EC 2.7.8.12 CDP-glycerol glycerophosphotransferase
        - EC 2.7.8.13 phospho-N-acetylmuramoyl-pentapeptide-transferase
        - EC 2.7.8.14 CDP-ribitol ribitolphosphotransferase
        - EC 2.7.8.15 UDP-N-acetylglucosamine—dolichyl-phosphate N-acetylglucosaminephosphotransferase
        - EC 2.7.8.16 deleted, included in EC 2.7.8.2
        - EC 2.7.8.17 UDP-N-acetylglucosamine—lysosomal-enzyme N-acetylglucosaminephosphotransferase
        - EC 2.7.8.18 UDP-galactose—UDP-N-acetylglucosamine galactose phosphotransferase
        - EC 2.7.8.19 UDP-glucose—glycoprotein glucose phosphotransferase
        - EC 2.7.8.20 phosphatidylglycerol—membrane-oligosaccharide glycerophosphotransferase
        - EC 2.7.8.21 membrane-oligosaccharide glycerophosphotransferase
        - EC 2.7.8.22 1-alkenyl-2-acylglycerol choline phosphotransferase
        - EC 2.7.8.23 carboxyvinyl-carboxyphosphonate phosphorylmutase
        - EC 2.7.8.24 phosphatidylcholine synthase
        - EC 2.7.8.25 triphosphoribosyl-dephospho-CoA synthase
    - EC 2.7.9 Phosphotransferases with paired acceptors
        - EC 2.7.9.1 pyruvate, phosphate dikinase
        - EC 2.7.9.2 pyruvate, water dikinase
        - EC 2.7.9.3 selenide, water dikinase
        - EC 2.7.9.4 a-glucan, water dikinase
- EC 2.8 Transferring Sulfur-Containing Groups
    - EC 2.8.1 Sulfurtransferases
        - EC 2.8.1.1 thiosulfate sulfurtransferase
        - EC 2.8.1.2 3-mercaptopyruvate sulfurtransferase
        - EC 2.8.1.3 thiosulfate—thiol sulfurtransferase
        - EC 2.8.1.4 tRNA sulfurtransferase
        - EC 2.8.1.5 thiosulfate—dithiol sulfurtransferase
        - EC 2.8.1.6 biotin synthase
    - EC 2.8.2 Sulfotransferases
        - EC 2.8.2.1 aryl sulfotransferase
        - EC 2.8.2.2 alcohol sulfotransferase
        - EC 2.8.2.3 amine sulfotransferase
        - EC 2.8.2.4 estrone sulfotransferase
        - EC 2.8.2.5 chondroitin 4-sulfotransferase
        - EC 2.8.2.6 choline sulfotransferase
        - EC 2.8.2.7 UDP-N-acetylgalactosamine-4-sulfate sulfotransferase
        - EC 2.8.2.8 [heparan sulfate]-glucosamine N-sulfotransferase
        - EC 2.8.2.9 tyrosine-ester sulfotransferase
        - EC 2.8.2.10 Renilla-luciferin sulfotransferase
        - EC 2.8.2.11 galactosylceramide sulfotransferase
        - EC 2.8.2.12 deleted, identical to EC 2.8.2.8
        - EC 2.8.2.13 psychosine sulfotransferase
        - EC 2.8.2.14 bile-salt sulfotransferase
        - EC 2.8.2.15 steroid sulfotransferase
        - EC 2.8.2.16 thiol sulfotransferase
        - EC 2.8.2.17 chondroitin 6-sulfotransferase
        - EC 2.8.2.18 cortisol sulfotransferase
        - EC 2.8.2.19 triglucosylalkylacylglycerol sulfotransferase
        - EC 2.8.2.20 protein-tyrosine sulfotransferase
        - EC 2.8.2.21 keratan sulfotransferase
        - EC 2.8.2.22 arylsulfate sulfotransferase
        - EC 2.8.2.23 [heparan sulfate]-glucosamine 3-sulfotransferase 1
        - EC 2.8.2.24 desulfoglucosinolate sulfotransferase
        - EC 2.8.2.25 flavonol 3-sulfotransferase
        - EC 2.8.2.26 quercetin-3-sulfate 3'-sulfotransferase
        - EC 2.8.2.27 quercetin-3-sulfate 4'-sulfotransferase
        - EC 2.8.2.28 quercetin-3,3'-bissulfate 7-sulfotransferase
        - EC 2.8.2.29 [heparan sulfate]-glucosamine 3-sulfotransferase 2
        - EC 2.8.2.30 [heparan sulfate]-glucosamine 3-sulfotransferase 3
    - EC 2.8.3 CoA-transferases
        - EC 2.8.3.1 propionate CoA-transferase
        - EC 2.8.3.2 oxalate CoA-transferase
        - EC 2.8.3.3 malonate CoA-transferase
        - EC 2.8.3.4 deleted
        - EC 2.8.3.5 3-oxoacid CoA-transferase
        - EC 2.8.3.6 3-oxoadipate CoA-transferase
        - EC 2.8.3.7 succinate—citramalate CoA-transferase
        - EC 2.8.3.8 acetate CoA-transferase
        - EC 2.8.3.9 butyrate—acetoacetate CoA-transferase
        - EC 2.8.3.10 citrate CoA-transferase
        - EC 2.8.3.11 citramalate CoA-transferase
        - EC 2.8.3.12 glutaconate CoA-transferase
        - EC 2.8.3.13 succinate—hydroxymethylglutarate CoA-transferase
        - EC 2.8.3.14 5-hydroxypentanoate CoA-transferase
    - EC 2.8.4 Transferring alkylthio groups

- EC 2.8.4.1 coenzyme-B sulfoethylthiotransferase
- EC 2.9 Transferring Selenium-Containing Groups
  - EC 2.9.1 Selenotransferases
    - EC 2.9.1.1 L-seryl-tRNASec selenium transferase

- **EC 3 Hydrolases**
- EC 3.1 Acting on Ester Bonds
  - EC 3.1.1 Carboxylic Ester Hydrolases
    - EC 3.1.1.1 carboxylesterase
    - EC 3.1.1.2 arylesterase
    - EC 3.1.1.3 triacylglycerol lipase
    - EC 3.1.1.4 phospholipase A2
    - EC 3.1.1.5 lysophospholipase
    - EC 3.1.1.6 acetylesterase
    - EC 3.1.1.7 acetylcholinesterase
    - EC 3.1.1.8 cholinesterase
    - EC 3.1.1.9 deleted
    - EC 3.1.1.10 tropinesterase
    - EC 3.1.1.11 pectinesterase
    - EC 3.1.1.12 deleted
    - EC 3.1.1.13 sterol esterase
    - EC 3.1.1.14 chlorophyllase
    - EC 3.1.1.15 L-arabinonolactonase
    - EC 3.1.1.16 deleted, mixture of EC 5.3.3.4 and EC 3.1.1.24
    - EC 3.1.1.17 gluconolactonase
    - EC 3.1.1.18 deleted, included in EC 3.1.1.17
    - EC 3.1.1.19 uronolactonase
    - EC 3.1.1.20 tannase
    - EC 3.1.1.21 retinyl-palmitate esterase
    - EC 3.1.1.22 hydroxybutyrate-dimer hydrolase
    - EC 3.1.1.23 acylglycerol lipase
    - EC 3.1.1.24 3-oxoadipate enol-lactonase
    - EC 3.1.1.25 1,4-lactonase
    - EC 3.1.1.26 galactolipase
    - EC 3.1.1.27 4-pyridoxolactonase
    - EC 3.1.1.28 acylcarnitine hydrolase
    - EC 3.1.1.29 aminoacyl-tRNA hydrolase
    - EC 3.1.1.30 D-arabinonolactonase
    - EC 3.1.1.31 6-phosphogluconolactonase
    - EC 3.1.1.32 phospholipase A1
    - EC 3.1.1.33 6-acetylglucose deacetylase
    - EC 3.1.1.34 lipoprotein lipase
    - EC 3.1.1.35 dihydrocoumarin hydrolase
    - EC 3.1.1.36 limonin-D-ring-lactonase
    - EC 3.1.1.37 steroid-lactonase
    - EC 3.1.1.38 triacetate-lactonase
    - EC 3.1.1.39 actinomycin lactonase
    - EC 3.1.1.40 orsellinate-depside hydrolase
    - EC 3.1.1.41 cephalosporin-C deacetylase
    - EC 3.1.1.42 chlorogenate hydrolase
    - EC 3.1.1.43 a-amino-acid esterase
    - EC 3.1.1.44 4-methyloxaloacetate esterase
    - EC 3.1.1.45 carboxymethylenebutenolidase
    - EC 3.1.1.46 deoxylimonate A-ring-lactonase
    - EC 3.1.1.47 1-alkyl-2-acetylglycerophosphocholine esterase
    - EC 3.1.1.48 fusarinine-C ornithinesterase
    - EC 3.1.1.49 sinapine esterase
    - EC 3.1.1.50 wax-ester hydrolase
    - EC 3.1.1.51 phorbol-diester hydrolase
    - EC 3.1.1.52 phosphatidylinositol deacylase
    - EC 3.1.1.53 sialate O-acetylesterase
    - EC 3.1.1.54 acetoxybutynylbithiophene deacetylase
    - EC 3.1.1.55 acetylsalicylate deacetylase
    - EC 3.1.1.56 methylumbelliferyl-acetate deacetylase
    - EC 3.1.1.57 2-pyrone-4,6-dicarboxylate lactonase
    - EC 3.1.1.58 N-acetylgalactosaminoglycan deacetylase
    - EC 3.1.1.59 juvenile-hormone esterase
    - EC 3.1.1.60 bis(2-ethylhexyl)phthalate esterase
    - EC 3.1.1.61 protein-glutamate methylesterase
    - EC 3.1.1.62 now EC 3.5.1.47
    - EC 3.1.1.63 11-cis-retinyl-palmitate hydrolase
    - EC 3.1.1.64 all-trans-retinyl-palmitate hydrolase
    - EC 3.1.1.65 L-rhamnono-1,4-lactonase
    - EC 3.1.1.66 5-(3,4-diacetoxybut-1-ynyl)-2,2'-bithiophene deacetylase
    - EC 3.1.1.67 fatty-acyl-ethyl-ester synthase
    - EC 3.1.1.68 xylono-1,4-lactonase
    - EC 3.1.1.69 now EC 3.5.1.89
    - EC 3.1.1.70 cetraxate benzylesterase
    - EC 3.1.1.71 acetylalkylglycerol acetylhydrolase
    - EC 3.1.1.72 acetylxylan esterase
    - EC 3.1.1.73 feruloyl esterase
    - EC 3.1.1.74 cutinase
    - EC 3.1.1.75 poly(3-hydroxybutyrate) depolymerase
    - EC 3.1.1.76 poly(3-hydroxyoctanoate) depolymerase acyloxyacyl hydrolase
    - EC 3.1.1.77 acyloxyacyl hydrolase
    - EC 3.1.1.78 polyneuridine-aldehyde esterase
  - EC 3.1.2 Thiolester Hydrolases
    - EC 3.1.2.1 acetyl-CoA hydrolase
    - EC 3.1.2.2 palmitoyl-CoA hydrolase
    - EC 3.1.2.3 succinyl-CoA hydrolase
    - EC 3.1.2.4 3-hydroxyisobutyryl-CoA hydrolase
    - EC 3.1.2.5 hydroxymethylglutaryl-CoA hydrolase
    - EC 3.1.2.6 hydroxyacylglutathione hydrolase
    - EC 3.1.2.7 glutathione thiolesterase
    - EC 3.1.2.8 deleted, included in EC 3.1.2.6
    - EC 3.1.2.9 deleted
    - EC 3.1.2.10 formyl-CoA hydrolase
    - EC 3.1.2.11 acetoacetyl-CoA hydrolase
    - EC 3.1.2.12 S-formylglutathione hydrolase
    - EC 3.1.2.13 S-succinylglutathione hydrolase
    - EC 3.1.2.14 oleoyl-[acyl-carrier-protein] hydrolase
    - EC 3.1.2.15 ubiquitin thiolesterase
    - EC 3.1.2.16 [citrate-(pro-3S)-lyase] thiolesterase
    - EC 3.1.2.17 (S)-methylmalonyl-CoA hydrolase
    - EC 3.1.2.18 ADP-dependent short-chain-acyl-CoA hydrolase
    - EC 3.1.2.19 ADP-dependent medium-chain-acyl-CoA hydrolase
    - EC 3.1.2.20 acyl-CoA hydrolase
    - EC 3.1.2.21 dodecanoyl-[acyl-carrier protein] hydrolase
    - EC 3.1.2.22 palmitoyl-(protein) hydrolase
    - EC 3.1.2.23 4-hydroxybenzoyl-CoA thioesterase
    - EC 3.1.2.24 2-(2-hydroxyphenyl)benzenesulfinate hydrolase
  - EC 3.1.3 Phosphoric Monoester Hydrolases
    - EC 3.1.3.1 alkaline phosphatase
    - EC 3.1.3.2 acid phosphatase
    - EC 3.1.3.3 phosphoserine phosphatase
    - EC 3.1.3.4 phosphatidate phosphatase
    - EC 3.1.3.5 5'-nucleotidase
    - EC 3.1.3.6 3'-nucleotidase
    - EC 3.1.3.7 3'(2'),5'-bisphosphate nucleotidase
    - EC 3.1.3.8 3-phytase
    - EC 3.1.3.9 glucose-6-phosphatase
    - EC 3.1.3.10 glucose-1-phosphatase
    - EC 3.1.3.11 fructose-bisphosphatase
    - EC 3.1.3.12 trehalose-phosphatase
    - EC 3.1.3.13 bisphosphoglycerate phosphatase
    - EC 3.1.3.14 methylphosphothioglycerate phosphatase
    - EC 3.1.3.15 histidinol-phosphatase
    - EC 3.1.3.16 phosphoprotein phosphatase
    - EC 3.1.3.17 [phosphorylase] phosphatase
    - EC 3.1.3.18 phosphoglycolate phosphatase
    - EC 3.1.3.19 glycerol-2-phosphatase
    - EC 3.1.3.20 phosphoglycerate phosphatase
    - EC 3.1.3.21 glycerol-1-phosphatase
    - EC 3.1.3.22 mannitol-1-phosphatase
    - EC 3.1.3.23 sugar-phosphatase
    - EC 3.1.3.24 sucrose-phosphatase
    - EC 3.1.3.25 inositol-1(or 4)-monophosphatase
    - EC 3.1.3.26 4-phytase
    - EC 3.1.3.27 phosphatidylglycerophosphatase
    - EC 3.1.3.28 ADPphosphoglycerate phosphatase
    - EC 3.1.3.29 N-acylneuraminate-9-phosphatase
    - EC 3.1.3.30 deleted, included in EC 3.1.3.31
    - EC 3.1.3.31 nucleotidase
    - EC 3.1.3.32 polynucleotide 3'-phosphatase
    - EC 3.1.3.33 polynucleotide 5'-phosphatase
    - EC 3.1.3.34 deoxynucleotide 3'-phosphatase
    - EC 3.1.3.35 thymidylate 5'-phosphatase
    - EC 3.1.3.36 phosphoinositide 5-phosphatase
    - EC 3.1.3.37 sedoheptulose-bisphosphatase
    - EC 3.1.3.38 3-phosphoglycerate phosphatase
    - EC 3.1.3.39 streptomycin-6-phosphatase
    - EC 3.1.3.40 guanidinodeoxy-scyllo-inositol-4-phosphatase
    - EC 3.1.3.41 4-nitrophenylphosphatase
    - EC 3.1.3.42 [glycogen-synthase-D] phosphatase
    - EC 3.1.3.43 [pyruvate dehydrogenase (lipoamide)]-phosphatase
    - EC 3.1.3.44 [acetyl-CoA carboxylase]-phosphatase
    - EC 3.1.3.45 3-deoxy-manno-octulosonate-8-phosphatase
    - EC 3.1.3.46 fructose-2,6-bisphosphate 2-phosphatase

- EC 3.1.3.47 [hydroxymethylglutaryl-CoA reductase (NADPH)]-phosphatase
- EC 3.1.3.48 protein-tyrosine-phosphatase
- EC 3.1.3.49 [pyruvate kinase]-phosphatase
- EC 3.1.3.50 sorbitol-6-phosphatase
- EC 3.1.3.51 dolichyl-phosphatase
- EC 3.1.3.52 [3-methyl-2-oxobutanoate dehydrogenase (lipoamide)]-phosphatase
- EC 3.1.3.53 myosin-light-chain-phosphatase
- EC 3.1.3.54 fructose-2,6-bisphosphate 6-phosphatase
- EC 3.1.3.55 caldesmon-phosphatase
- EC 3.1.3.56 inositol-polyphosphate 5-phosphatase
- EC 3.1.3.57 inositol-1,4-bisphosphate 1-phosphatase
- EC 3.1.3.58 sugar-terminal-phosphatase
- EC 3.1.3.59 alkylacetylglycerophosphatase
- EC 3.1.3.60 phosphoenolpyruvate phosphatase
- EC 3.1.3.61 deleted
- EC 3.1.3.62 multiple inositol-polyphosphate phosphatase
- EC 3.1.3.63 2-carboxy-D-arabinitol-1-phosphatase
- EC 3.1.3.64 phosphatidylinositol-3-phosphatase
- EC 3.1.3.65 now with EC 3.1.3.64
- EC 3.1.3.66 phosphatidylinositol-3,4-bisphosphate 4-phosphatase
- EC 3.1.3.67 phosphatidylinositol-3,4,5-trisphosphate 3-phosphatase
- EC 3.1.3.68 2-deoxyglucose-6-phosphatase
- EC 3.1.3.69 glucosylglycerol 3-phosphatase
- EC 3.1.3.70 mannosyl-3-phosphoglycerate phosphatase
- EC 3.1.3.71 2-phosphosulfolactate phosphatase
- EC 3.1.3.72 5-phytase

EC 3.1.4 Phosphoric Diester Hydrolases

  - EC 3.1.4.1 phosphodiesterase I
  - EC 3.1.4.2 glycerophosphocholine phosphodiesterase
  - EC 3.1.4.3 phospholipase C
  - EC 3.1.4.4 phospholipase D
  - EC 3.1.4.5 now EC 3.1.21.1
  - EC 3.1.4.6 now EC 3.1.22.1
  - EC 3.1.4.7 now EC 3.1.31.1
  - EC 3.1.4.8 now EC 3.1.27.3
  - EC 3.1.4.9 now EC 3.1.30.2
  - EC 3.1.4.10 now EC 4.6.1.13
  - EC 3.1.4.11 phosphoinositide phospholipase C
  - EC 3.1.4.12 sphingomyelin phosphodiesterase
  - EC 3.1.4.13 serine-ethanolaminephosphate phosphodiesterase
  - EC 3.1.4.14 [acyl-carrier-protein] phosphodiesterase
  - EC 3.1.4.15 adenylyl-[glutamate—ammonia ligase] hydrolase
  - EC 3.1.4.16 2',3'-cyclic-nucleotide 2'-phosphodiesterase
  - EC 3.1.4.17 3',5'-cyclic-nucleotide phosphodiesterase
  - EC 3.1.4.18 now EC 3.1.16.1
  - EC 3.1.4.19 now EC 3.1.13.3
  - EC 3.1.4.20 now EC 3.1.13.1
  - EC 3.1.4.21 now EC 3.1.30.1
  - EC 3.1.4.22 now EC 3.1.27.5
  - EC 3.1.4.23 now EC 3.1.27.1
  - EC 3.1.4.24 deleted
  - EC 3.1.4.25 now EC 3.1.11.1
  - EC 3.1.4.26 deleted
  - EC 3.1.4.27 now EC 3.1.11.2
  - EC 3.1.4.28 now EC 3.1.11.3
  - EC 3.1.4.29 deleted
  - EC 3.1.4.30 now EC 3.1.21.2
  - EC 3.1.4.31 now EC 3.1.11.4
  - EC 3.1.4.32 deleted
  - EC 3.1.4.33 deleted
  - EC 3.1.4.34 deleted
  - EC 3.1.4.35 3',5'-cyclic-GMP phosphodiesterase
  - EC 3.1.4.36 now with EC 3.1.4.43
  - EC 3.1.4.37 2',3'-cyclic-nucleotide 3'-phosphodiesterase
  - EC 3.1.4.38 glycerophosphocholine cholinephosphodiesterase
  - EC 3.1.4.39 alkylglycerophosphoethanolamine phosphodiesterase
  - EC 3.1.4.40 CMP-N-acylneuraminate phosphodiesterase
  - EC 3.1.4.41 sphingomyelin phosphodiesterase D
  - EC 3.1.4.42 glycerol-1,2-cyclic-phosphate 2-phosphodiesterase
  - EC 3.1.4.43 glycerophosphoinositol inositolphosphodiesterase
  - EC 3.1.4.44 glycerophosphoinositol glycerophosphodiesterase
  - EC 3.1.4.45 N-acetylglucosamine-1-phosphodiester a-N-acetylglucosaminidase
  - EC 3.1.4.46 glycerophosphodiester phosphodiesterase
  - EC 3.1.4.47 now EC 4.6.1.14
  - EC 3.1.4.48 dolichylphosphate-glucose phosphodiesterase
  - EC 3.1.4.49 dolichylphosphate-mannose phosphodiesterase
  - EC 3.1.4.50 glycosylphosphatidylinositol phospholipase D
  - EC 3.1.4.51 glucose-1-phospho-D-mannosylglycoprotein phosphodiesterase

EC 3.1.5 Triphosphoric Monoester Hydrolases

  - EC 3.1.5.1 dGTPase

EC 3.1.6 Sulfuric Ester Hydrolases

  - EC 3.1.6.1 arylsulfatase
  - EC 3.1.6.2 steryl-sulfatase
  - EC 3.1.6.3 glycosulfatase
  - EC 3.1.6.4 N-acetylgalactosamine-6-sulfatase
  - EC 3.1.6.5 deleted
  - EC 3.1.6.6 choline-sulfatase
  - EC 3.1.6.7 cellulose-polysulfatase
  - EC 3.1.6.8 cerebroside-sulfatase
  - EC 3.1.6.9 chondro-4-sulfatase
  - EC 3.1.6.10 chondro-6-sulfatase
  - EC 3.1.6.11 disulfoglucosamine-6-sulfatase
  - EC 3.1.6.12 N-acetylgalactosamine-4-sulfatase
  - EC 3.1.6.13 iduronate-2-sulfatase
  - EC 3.1.6.14 N-acetylglucosamine-6-sulfatase
  - EC 3.1.6.15 N-sulfoglucosamine-3-sulfatase
  - EC 3.1.6.16 monomethyl-sulfatase
  - EC 3.1.6.17 D-lactate-2-sulfatase
  - EC 3.1.6.18 glucuronate-2-sulfatase

EC 3.1.7 Diphosphoric Monoester Hydrolases

  - EC 3.1.7.1 prenyl-diphosphatase
  - EC 3.1.7.2 guanosine-3',5'-bis(diphosphate) 3'-diphosphatase
  - EC 3.1.7.3 monoterpenyl-diphosphatase

EC 3.1.8 Phosphoric Triester Hydrolases

  - EC 3.1.8.1 aryldialkylphosphatase
  - EC 3.1.8.2 diisopropyl-fluorophosphatase

EC 3.1.11 Exodeoxyribonucleases Producing 5'-Phosphomonoesters

  - EC 3.1.11.1 exodeoxyribonuclease I
  - EC 3.1.11.2 exodeoxyribonuclease III
  - EC 3.1.11.3 exodeoxyribonuclease (lambda-induced)
  - EC 3.1.11.4 exodeoxyribonuclease (phage SP3-induced)
  - EC 3.1.11.5 exodeoxyribonuclease V
  - EC 3.1.11.6 exodeoxyribonuclease VII

EC 3.1.13 Exoribonucleases Producing 5'-Phosphomonoesters

  - EC 3.1.13.1 exoribonuclease II
  - EC 3.1.13.2 exoribonuclease H
  - EC 3.1.13.3 oligonucleotidase
  - EC 3.1.13.4 poly(A)-specific ribonuclease

EC 3.1.14 Exoribonucleases Producing 3'-Phosphomonoesters

  - EC 3.1.14.1 yeast ribonuclease

EC 3.1.15 Exonucleases Active with either Ribo- or Deoxyribonucleic Acids and Producing 5'-Phosphomonoesters

  - EC 3.1.15.1 venom exonuclease

EC 3.1.16 Exonucleases Active with either Ribo- or Deoxyribonucleic Acids and Producing 3'-Phosphomonoesters

  - EC 3.1.16.1 spleen exonuclease

EC 3.1.21 Endodeoxyribonucleases Producing 5'-Phosphomonoesters

  - EC 3.1.21.1 deoxyribonuclease I
  - EC 3.1.21.2 deoxyribonuclease IV (phage-T4-induced)
  - EC 3.1.21.3 type 1 site-specific deoxyribonuclease
  - EC 3.1.21.4 type II site-specific deoxyribonuclease
  - EC 3.1.21.5 type III site-specific deoxyribonuclease
  - EC 3.1.21.6 CC-preferring endodeoxyribonuclease
  - EC 3.1.21.7 deoxyribonuclease V

EC 3.1.22 Endodeoxyribonucleases Producing 3'-Phosphomonoesters

  - EC 3.1.22.1 deoxyribonuclease II

- EC 3.1.22.2 Aspergillus deoxyribonuclease K1
- EC 3.1.22.3 now EC 3.1.21.7
- EC 3.1.22.4 crossover junction endoribonuclease
- EC 3.1.22.5 deoxyribonuclease X
- EC 3.1.23 and EC 3.1.24 now EC 3.1.21.3, EC 3.1.21.4 and EC 3.1.21.5
- EC 3.1.25 Site-Specific Endodeoxyribonucleases Specific for Altered Bases
  - EC 3.1.25.1 deoxyribonuclease (pyrimidine dimer)
  - EC 3.1.25.2 now EC 4.2.99.18
- EC 3.1.26 Endoribonucleases Producing 5'-Phosphomonoesters
  - EC 3.1.26.1 Physarum polycephalum ribonuclease
  - EC 3.1.26.2 ribonculease alpha
  - EC 3.1.26.3 ribonuclease III
  - EC 3.1.26.4 calf thymus ribonuclease H
  - EC 3.1.26.5 ribonuclease P
  - EC 3.1.26.6 ribonuclease IV
  - EC 3.1.26.7 ribonuclease P4
  - EC 3.1.26.8 ribonuclease M5
  - EC 3.1.26.9 ribonuclease [poly-(U)-specific]
  - EC 3.1.26.10 ribonuclease IX
  - EC 3.1.26.11 RNase Z
- EC 3.1.27 Endoribonucleases Producing 3'-Phosphomonoesters
  - EC 3.1.27.1 ribonuclease T2
  - EC 3.1.27.2 Bacillus subtilis ribonuclease
  - EC 3.1.27.3 ribonuclease T1
  - EC 3.1.27.4 riblonuclease U2
  - EC 3.1.27.5 pancreatic ribonuclease
  - EC 3.1.27.6 Enterobacter ribonuclease
  - EC 3.1.27.7 ribonuclease F
  - EC 3.1.27.8 ribonuclease V
  - EC 3.1.27.9 tRNA-intron endonuclease
  - EC 3.1.27.10 rRNA endonuclease
- EC 3.1.30 Endoribonucleases Active with either Ribo- or Deoxyribonucleic Acids and Producing 5'-Phosphomonoesters
  - EC 3.1.30.1 Aspergillus nuclease S1
  - EC 3.1.30.2 Serratia marcescens nuclease
- EC 3.1.31 Endoribonucleases Active with either Ribo- or Deoxyribonucleic Acids and Producing 3'-Phosphomonoesters
  - EC 3.1.31.1 micrococcal nuclease

- EC 3.2 Glycosylases
  - EC 3.2.1 Glycosidases, i.e. enzymes hydrolysing O- and S-glycosyl compounds
    - EC 3.2.1.1 a-amylase
    - EC 3.2.1.2 b-amylase
    - EC 3.2.1.3 glucan 1,4-a-glucosidase
    - EC 3.2.1.4 cellulase
    - EC 3.2.1.5 deleted
    - EC 3.2.1.6 endo-1,3(4)-b-glucanase
    - EC 3.2.1.7 inulinase
    - EC 3.2.1.8 endo-1,4-b-xylanase
    - EC 3.2.1.9 deleted
    - EC 3.2.1.10 oligo-1,6-glucosidase
    - EC 3.2.1.11 dextranase
    - EC 3.2.1.12 deleted, included in EC 3.2.1.54
    - EC 3.2.1.13 deleted, included in EC 3.2.1.54
    - EC 3.2.1.14 chitinase
    - EC 3.2.1.15 polygalacturonase
    - EC 3.2.1.16 deleted
    - EC 3.2.1.17 lysozyme
    - EC 3.2.1.18 exo-a-sialidase
    - EC 3.2.1.19 deleted
    - EC 3.2.1.20 a-glucosidase
    - EC 3.2.1.21 b-glucosidase
    - EC 3.2.1.22 a-galactosidase
    - EC 3.2.1.23 b-galactosidase
    - EC 3.2.1.24 a-mannosidase
    - EC 3.2.1.25 b-mannosidase
    - EC 3.2.1.26 b-fructofuranosidase
    - EC 3.2.1.27 deleted
    - EC 3.2.1.28 a,a-trehalase
    - EC 3.2.1.29 deleted, included in EC 3.2.1.52
    - EC 3.2.1.30 deleted, included in EC 3.2.1.52
    - EC 3.2.1.31 b-glucuronidase
    - EC 3.2.1.32 xylan endo-1,3-b-xylosidase
    - EC 3.2.1.33 amylo-1,6-glucosidase
    - EC 3.2.1.34 deleted, included in EC 3.2.1.35
    - EC 3.2.1.35 hyaluronoglucosaminidase
    - EC 3.2.1.36 hyaluronoglucuronidase
    - EC 3.2.1.37 xylan 1,4-b-xylosidase
    - EC 3.2.1.38 b-D-fucosidase
    - EC 3.2.1.39 glucan endo-1,3-b-D-glucosidase
    - EC 3.2.1.40 a-L-rhamnosidase
    - EC 3.2.1.41 pullulanase
    - EC 3.2.1.42 GDP-glucosidase
    - EC 3.2.1.43 b-L-rhamnosidase
    - EC 3.2.1.44 fucoidanase
    - EC 3.2.1.45 glucosylceramidase
    - EC 3.2.1.46 galactosylceramidase
    - EC 3.2.1.47 galactosylgalactosylglucosylceramidase
    - EC 3.2.1.48 sucrose a-glucosidase
    - EC 3.2.1.49 a-N-acetylgalactosaminidase
    - EC 3.2.1.50 a-N-acetylglucosaminidase
    - EC 3.2.1.51 a-L-fucosidase
    - EC 3.2.1.52 b-L-N-acetylhexosaminidase
    - EC 3.2.1.53 b-N-acetylgalactosaminidase
    - EC 3.2.1.54 cyclomaltodextrinase
    - EC 3.2.1.55 a-N-arabinofuranosidase
    - EC 3.2.1.56 glucuronosyl-disulfoglucosamine glucuronidase
    - EC 3.2.1.57 isopullulanase
    - EC 3.2.1.58 glucan 1,3-b-glucosidase
    - EC 3.2.1.59 glucan endo-1,3-a-glucosidase
    - EC 3.2.1.60 glucan 1,4-a-maltotetraohydrolase
    - EC 3.2.1.61 mycodextranase
    - EC 3.2.1.62 glycosylceramidase
    - EC 3.2.1.63 1,2-a-L-fucosidase
    - EC 3.2.1.64 2,6-b-fructan 6-levanbiohydrolase
    - EC 3.2.1.65 levanase
    - EC 3.2.1.66 quercitrinase
    - EC 3.2.1.67 galacturan 1,4-a-galacturonidase
    - EC 3.2.1.68 isoamylase
    - EC 3.2.1.69 deleted, included in EC 3.2.1.41
    - EC 3.2.1.70 glucan 1,6-a-glucosidase
    - EC 3.2.1.71 glucan endo-1,2-b-glucosidase
    - EC 3.2.1.72 xylan 1,3-b-xylosidase
    - EC 3.2.1.73 licheninase
    - EC 3.2.1.74 glucan 1,4-b-glucosidase
    - EC 3.2.1.75 glucan endo-1,6-b-glucosidase
    - EC 3.2.1.76 L-iduronidase
    - EC 3.2.1.77 mannan 1,2-(1,3)-a-mannosidase
    - EC 3.2.1.78 mannan endo-1,4-b-mannosidase
    - EC 3.2.1.79 deleted, included in EC 3.2.1.55
    - EC 3.2.1.80 fructan b-fructosidase
    - EC 3.2.1.81 agarase
    - EC 3.2.1.82 exo-poly-a-galacturonosidase
    - EC 3.2.1.83 k-carrageenase
    - EC 3.2.1.84 glucan 1,3-a-glucosidase
    - EC 3.2.1.85 6-phospho-b-galactosidase
    - EC 3.2.1.86 6-phospho-b-glucosidase
    - EC 3.2.1.87 capsular-polysaccharide endo-1,3-a-galactosidase
    - EC 3.2.1.88 b-L-arabinosidase
    - EC 3.2.1.89 arabinogalactan endo-1,4-b-galactosidase
    - EC 3.2.1.90Deleted, not sufficiently characterised.
    - EC 3.2.1.91 cellulose 1,4-b-cellobiosidase
    - EC 3.2.1.92 peptidoglycan b-N-acetylmuramidase
    - EC 3.2.1.93 a,a-phosphotrehalase
    - EC 3.2.1.94 glucan 1,6-a-isomaltosidase
    - EC 3.2.1.95 dextran 1,6-a-isomaltotriosidase
    - EC 3.2.1.96 mannosyl-glycoprotein endo-b-N-acetylglucosaminidase
    - EC 3.2.1.97 glycopeptide a-N-acetylgalactosaminidase
    - EC 3.2.1.98 glucan 1,4-a-maltohexaosidase
    - EC 3.2.1.99 arabinan endo-1,5-a-L-arabinosidase
    - EC 3.2.1.100 mannan 1,4-mannobiosidase
    - EC 3.2.1.101 mannan endo-1,6-b-mannosidase
    - EC 3.2.1.102 blood-group-substance endo-1,4-b-galactosidase
    - EC 3.2.1.103 keratan-sulfate endo-1,4-b-galactosidase
    - EC 3.2.1.104 steryl-b-glucosidase
    - EC 3.2.1.105 strictosidine b-glucosidase
    - EC 3.2.1.106 mannosyl-oligosaccharide glucosidase
    - EC 3.2.1.107 protein-glucosylgalactosylhydroxylysine glucosidase
    - EC 3.2.1.108 lactase
    - EC 3.2.1.109 endogalactosaminidase
    - EC 3.2.1.110 mucinaminylserine mucinaminidase
    - EC 3.2.1.111 1,3-a-L-fucosidase
    - EC 3.2.1.112 2-deoxyglucosidase
    - EC 3.2.1.113 mannosyl-oligosaccharide 1,2-a-mannosidase
    - EC 3.2.1.114 mannosyl-oligosaccharide 1,3-1,6-a-mannosidase
    - EC 3.2.1.115 branched-dextran exo-1,2-a-glucosidase

- EC 3.2.1.116 glucan 1,4-a-maltotriohydrolase
- EC 3.2.1.117 amygdalin b-glucosidase
- EC 3.2.1.118 prunasin b-glucosidase
- EC 3.2.1.119 vicianin b-glucosidase
- EC 3.2.1.120 oligoxyloglucan b-glycosidase
- EC 3.2.1.121 polymannuronate hydrolase
- EC 3.2.1.122 maltose-6'-phosphate glucosidase
- EC 3.2.1.123 endoglycosylceramidase
- EC 3.2.1.124 3-deoxy-2-octulosonidase
- EC 3.2.1.125 raucaffricine b-glucosidase
- EC 3.2.1.126 coniferin b-glucosidase
- EC 3.2.1.127 1,6-a-L-fucosidase
- EC 3.2.1.128 glycyrrhizinate b-glucuronidase
- EC 3.2.1.129 endo-a-sialidase
- EC 3.2.1.130 glycoprotein endo-a-1,2-mannosidase
- EC 3.2.1.131 xylan a-1,2-glucuronosidase
- EC 3.2.1.132 chitosanase
- EC 3.2.1.133 glucan 1,4-a-maltohydrolase
- EC 3.2.1.134 difructose-anhydride synthase
- EC 3.2.1.135 neopullulanase
- EC 3.2.1.136 glucuronoarabinoxylan endo-1,4-b-xylanase
- EC 3.2.1.137 mannan exo-1,2-1,6-a-mannosidase
- EC 3.2.1.138 anhydrosialidase
- EC 3.2.1.139 a-glucuronidase
- EC 3.2.1.140 lacto-N-biosidase
- EC 3.2.1.141 4-a-D-{(1 4)-a-D-glucano}trehaose trehalohydrolase
- EC 3.2.1.142 limit dextrinase
- EC 3.2.1.143 poly(ADP-ribose) glycohydrolase
- EC 3.2.1.144 3-deoxyoctulosonase
- EC 3.2.1.145 galactan 1,3-b-galactosidase
- EC 3.2.1.146 b-galactofuranosidase
- EC 3.2.1.147 thioglucosidase
- EC 3.2.1.148 ribosylhomocysteinase
- EC 3.2.1.149 b-primeverosidase
- EC 3.2.2 Hydrolysing N-Glycosyl Compounds
  - EC 3.2.2.1 purine nucleosidase
  - EC 3.2.2.2 inosine nucleosidase
  - EC 3.2.2.3 uridine nucleosidase
  - EC 3.2.2.4 AMP nucleosidase
  - EC 3.2.2.5 NAD nucleosidase
  - EC 3.2.2.6 NAD(P) nucleosidase
  - EC 3.2.2.7 adenosine nucleosidase
  - EC 3.2.2.8 ribosylpyrimidine nucleosidase
  - EC 3.2.2.9 adenosylhomocysteine nucleosidase
  - EC 3.2.2.10 pyrimidine-5'-nucleotide nucleosidase
  - EC 3.2.2.11 b-aspartyl-N-acetylglucosaminidase
  - EC 3.2.2.12 inosinate nucleosidase
  - EC 3.2.2.13 1-methyladenosine nucleosidase
  - EC 3.2.2.14 NMN nucleosidase
  - EC 3.2.2.15 DNA-deoxyinosine glycosylase
  - EC 3.2.2.16 methylthioadenosine nucleosidase
  - EC 3.2.2.17 deoxyribodipyrimidine endonucleosidase
  - EC 3.2.2.18 deleted, included in EC 3.5.1.52
  - EC 3.2.2.19 ADPribosylarginine hydrolase
  - EC 3.2.2.20 DNA-3-methyladenine glycosylase I
  - EC 3.2.2.21 DNA-3-methyladenine glycosylase II
  - EC 3.2.2.22 rRNA N-glycosylase
  - EC 3.2.2.23 DNA-formamidopyrimidine glycosylase
  - EC 3.2.2.24 ADP-ribosyl-[dinitrogen reductase] hydrolase
- EC 3.2.3 Hydrolysing S-Glycosyl Compounds
  - EC 3.2.3.1 now EC 3.2.1.147
- EC 3.3 Acting on Ether Bonds
  - EC 3.3.1 Trialkylsulfonium hydrolases
    - EC 3.3.1.1 adenosylhomocysteinase
    - EC 3.3.1.2 adenosylmethionine hydrolase
    - EC 3.3.1.3 now EC 3.2.1.148
  - EC 3.3.2 Ether Hydrolases
    - EC 3.3.2.1 isochorismatase
    - EC 3.3.2.2 alkenylglycerophosphocholine hydrolase
    - EC 3.3.2.3 epoxide hydrolase
    - EC 3.3.2.4 trans-epoxysuccinate hydrolase
    - EC 3.3.2.5 alkenylglycerophosphoethanolamine hydrolase
    - EC 3.3.2.6 leukotriene-A4 hydrolase
    - EC 3.3.2.7 hepoxilin-epoxide hydrolase
    - EC 3.3.2.8 limonene-1,2-epoxide hydrolase
- EC 3.4 Acting on peptide bonds (Peptidases)
  - EC 3.4.1 a-Amino-Acyl-Peptide Hydrolases (discontinued)
    - EC 3.4.1.1 now EC 3.4.11.1
    - EC 3.4.1.2 now EC 3.4.11.2
    - EC 3.4.1.3 now EC 3.4.11.4
    - EC 3.4.1.4 now EC 3.4.11.5
  - EC 3.4.2 Peptidyl-Amino-Acid Hydrolases (discontinued)
    - EC 3.4.2.1 now EC 3.4.17.1
    - EC 3.4.2.2 now EC 3.4.17.2
    - EC 3.4.2.3 now EC 3.4.17.4
  - EC 3.4.3 Dipeptide Hydrolases (discontinued)
    - EC 3.4.3.1 now EC 3.4.13.18
    - EC 3.4.3.2 now EC 3.4.13.18
    - EC 3.4.3.3 now EC 3.4.13.3
    - EC 3.4.3.4 now EC 3.4.13.5
    - EC 3.4.3.5 now EC 3.4.13.6
    - EC 3.4.3.6 now EC 3.4.13.8
    - EC 3.4.3.7 now EC 3.4.13.9
  - EC 3.4.4 Peptidyl Peptide Hydrolases (discontinued)
    - EC 3.4.4.1 now EC 3.4.23.1
    - EC 3.4.4.2 now EC 3.4.23.2
    - EC 3.4.4.3 now EC 3.4.23.4
    - EC 3.4.4.4 now EC 3.4.21.4
    - EC 3.4.4.5 now EC 3.4.21.1
    - EC 3.4.4.6 now EC 3.4.21.1
    - EC 3.4.4.7 now covered by EC 3.4.21.36, EC 3.4.21.37
    - EC 3.4.4.8 now EC 3.4.21.9
    - EC 3.4.4.9 now EC 3.4.14.1
    - EC 3.4.4.10 now EC 3.4.22.2
    - EC 3.4.4.11 now EC 3.4.22.6
    - EC 3.4.4.12 now EC 3.4.22.3
    - EC 3.4.4.13 now EC 3.4.21.5
    - EC 3.4.4.14 now EC 3.4.21.7
    - EC 3.4.4.15 now EC 3.4.23.15
    - EC 3.4.4.16 now covered by EC 3.4.21.62 to EC 3.4.21.67
    - EC 3.4.4.17 now covered by EC 3.4.23.20 to EC 3.4.23.30
    - EC 3.4.4.18 now EC 3.4.22.10
    - EC 3.4.4.19 now EC 3.4.24.3
    - EC 3.4.4.20 now EC 3.4.22.8
    - EC 3.4.4.21 now EC 3.4.21.34
    - EC 3.4.4.22 now EC 3.4.23.3
    - EC 3.4.4.23 now EC 3.4.23.5
    - EC 3.4.4.24 now covered by EC 3.4.22.32 and EC 3.4.22.33
    - EC 3.4.4.25 deleted
  - EC 3.4.11 Aminopeptidases
    - EC 3.4.11.1 leucyl aminopeptidase
    - EC 3.4.11.2 membrane alanyl aminopeptidase
    - EC 3.4.11.3 cystinyl aminopeptidase
    - EC 3.4.11.4 tripeptide aminopeptidase
    - EC 3.4.11.5 prolyl aminopeptidase
    - EC 3.4.11.6 arginyl aminopeptidase
    - EC 3.4.11.7 glutamyl aminopeptidase
    - EC 3.4.11.8 now EC 3.4.19.3
    - EC 3.4.11.9 X-Pro aminopeptidase
    - EC 3.4.11.10 bacterial leucyl aminopeptidase
    - EC 3.4.11.11 deleted
    - EC 3.4.11.12 deleted (Supplement 4)
    - EC 3.4.11.13 clostridial aminopeptidase
    - EC 3.4.11.14 cytosol alanyl aminopeptidase
    - EC 3.4.11.15 lysyl aminopeptidase
    - EC 3.4.11.16 X-Trp aminopeptidase
    - EC 3.4.11.17 tryptophanyl aminopeptidase
    - EC 3.4.11.18 methionyl aminopeptidase
    - EC 3.4.11.19 D-stereospecific aminopeptidase
    - EC 3.4.11.20 aminopeptidase Ey
    - EC 3.4.11.21 aspartyl aminopeptidase
    - EC 3.4.11.22 aminopeptidase I
  - EC 3.4.12 Peptidylamino-Acid Hydrolases or Acylamino-Acid Hydrolases
    - EC 3.4.12.1 now EC 3.4.16.1
    - EC 3.4.12.2 now EC 3.4.17.1
    - EC 3.4.12.3 now EC 3.4.17.2
    - EC 3.4.12.4 now EC 3.4.16.2
    - EC 3.4.12.5 now EC 3.4.19.10
    - EC 3.4.12.6 now EC 3.4.17.8
    - EC 3.4.12.7 now EC 3.4.17.3
    - EC 3.4.12.8 now EC 3.4.17.4
    - EC 3.4.12.9 deleted
    - EC 3.4.12.10 now EC 3.4.19.9
    - EC 3.4.12.11 now EC 3.4.17.6
    - EC 3.4.12.12 now EC 3.4.16.1
    - EC 3.4.12.13 deleted
  - EC 3.4.13 Dipeptidases
    - EC 3.4.13.1 now EC 3.4.13.18
    - EC 3.4.13.2 now EC 3.4.13.18
    - EC 3.4.13.3 X-His dipeptidase
    - EC 3.4.13.4 X-Arg dipeptidase

  - EC 3.4.13.5 X-methyl-His dipeptidase
  - EC 3.4.13.6 now EC 3.4.11.2 (Supplement 4)
  - EC 3.4.13.7 Glu-Glu dipeptidase
  - EC 3.4.13.8 now EC 3.4.17.21 (Supplement 6)
  - EC 3.4.13.9 X-Pro dipeptidase
  - EC 3.4.13.10 now EC 3.4.19.5
  - EC 3.4.13.11 deleted, included in EC 3.4.13.18
  - EC 3.4.13.12 Met-X dipeptidase
  - EC 3.4.13.13 deleted, included in EC 3.4.13.3
  - EC 3.4.13.14 deleted
  - EC 3.4.13.15 deleted, included in EC 3.4.13.18
  - EC 3.4.13.16 deleted
  - EC 3.4.13.17 non-stereospecific dipeptidase
  - EC 3.4.13.18 cytosol nonspecific dipeptidase
  - EC 3.4.13.19 membrane dipeptidase
  - EC 3.4.13.20 b-Ala-His dipeptidase
  - EC 3.4.13.21 dipeptidase E
- EC 3.4.14 Dipeptidyl-peptidases and tripeptidyl-peptidases
  - EC 3.4.14.1 dipeptidyl-peptidase I
  - EC 3.4.14.2 dipeptidyl-peptidase II
  - EC 3.4.14.3 now EC 3.4.19.1
  - EC 3.4.14.4 dipeptidyl-peptidase III
  - EC 3.4.14.5 dipeptidyl-peptidase IV
  - EC 3.4.14.6 dipeptidyl-dipeptidase
  - EC 3.4.14.7 deleted
  - EC 3.4.14.8 now covered by EC 3.4.14.9, EC 3.4.14.10
  - EC 3.4.14.9 tripeptidyl-peptidase I
  - EC 3.4.14.10 tripeptidyl-peptidase II
  - EC 3.4.14.11 X-Pro dipeptidyl-peptidase
- EC 3.4.15 Peptidyl-dipeptidases
  - EC 3.4.15.1 peptidyl-dipeptidase A
  - EC 3.4.15.2 now EC 3.4.19.2
  - EC 3.4.15.3 deleted, included in EC 3.4.15.5 (supplement 2)
  - EC 3.4.15.4 peptidyl-dipeptidase B
  - EC 3.4.15.5 peptidyl-dipeptidase Dcp
- EC 3.4.16 Serine-type carboxypeptidases
  - EC 3.4.16.1 deleted, included in EC 3.4.16.5, EC 3.4.16.6 (supplement 1)
  - EC 3.4.16.2 lysosomal Pro-X carboxypeptidase
  - EC 3.4.16.3 deleted, included in EC 3.4.16.5 (supplement 1)
  - EC 3.4.16.4 serine-type D-Ala-D-Ala carboxypeptidase
  - EC 3.4.16.5 carboxypeptidase C
  - EC 3.4.16.6 carboxypeptidase D
- EC 3.4.17 Metallocarboxypeptidases
  - EC 3.4.17.1 carboxypeptidase A
  - EC 3.4.17.2 carboxypeptidase B
  - EC 3.4.17.3 lysine carboxypeptidase
  - EC 3.4.17.4 Gly-X carboxypeptidase
  - EC 3.4.17.5 deleted
  - EC 3.4.17.6 alanine carboxypeptidase
  - EC 3.4.17.7 now EC 3.4.19.10
  - EC 3.4.17.8 muramoylpentapeptide carboxypeptidase
  - EC 3.4.17.9 deleted, included in EC 3.4.17.4
  - EC 3.4.17.10 carboxypeptidase E
  - EC 3.4.17.11 glutamate carboxypeptidase
  - EC 3.4.17.12 carboxypeptidase M
  - EC 3.4.17.13 muramoyltetrapeptide carboxypeptidase
  - EC 3.4.17.14 zinc D-Ala-D-Ala carboxypeptidase
  - EC 3.4.17.15 carboxypeptidase A2
  - EC 3.4.17.16 membrane Pro-X carboxypeptidase
  - EC 3.4.17.17 tubulinyl-Tyr carboxypeptidase
  - EC 3.4.17.18 carboxypeptidase T
  - EC 3.4.17.19 carboxypeptidase Taq
  - EC 3.4.17.20 carboxypeptidase U
  - EC 3.4.17.21 glutamate carboxypeptidase II
  - EC 3.4.17.22 metallocarboxypeptidase D
- EC 3.4.18 Cysteine-type carboxypeptidases
  - EC 3.4.18.1 cathepsin X
- EC 3.4.19 Omega peptidases
  - EC 3.4.19.1 acylaminoacyl-peptidase
  - EC 3.4.19.2 peptidyl-glycinamidase
  - EC 3.4.19.3 pyroglutamyl-peptidase I
  - EC 3.4.19.4 deleted
  - EC 3.4.19.5 b-aspartyl-peptidase
  - EC 3.4.19.6 pyroglutamyl-peptidase II
  - EC 3.4.19.7 N-formylmethionyl-peptidase
  - EC 3.4.19.8 now EC 3.4.17.21 (Supplement 6)
  - EC 3.4.19.9 g-glutamyl hydrolase
  - EC 3.4.19.10 now EC 3.5.1.28 (Supplement 4)
  - EC 3.4.19.11 g-D-glutamyl-meso-diaminopimelate peptidase I
  - EC 3.4.19.12 ubiquitinyl hydrolase 1
- EC 3.4.21 Serine endopeptidases
  - EC 3.4.21.1 chymotrypsin
  - EC 3.4.21.2 chymotrypsin C
  - EC 3.4.21.3 metridin
  - EC 3.4.21.4 trypsin
  - EC 3.4.21.5 thrombin
  - EC 3.4.21.6 coagulation factor Xa
  - EC 3.4.21.7 plasmin
  - EC 3.4.21.8 now covered by EC 3.4.21.34 and EC 3.4.21.35
  - EC 3.4.21.9 enteropeptidase
  - EC 3.4.21.10 acrosin
  - EC 3.4.21.11 now covered by EC 3.4.21.36 and EC 3.4.21.37
  - EC 3.4.21.12 a-Lytic endopeptidase
  - EC 3.4.21.13 now EC 3.4.16.1
  - EC 3.4.21.14 now covered by EC 3.4.21.62 to EC 3.4.21.65 and EC 3.4.21.67
  - EC 3.4.21.15 now EC 3.4.21.63
  - EC 3.4.21.16 deleted
  - EC 3.4.21.17 deleted
  - EC 3.4.21.18 deleted
  - EC 3.4.21.19 glutamyl endopeptidase
  - EC 3.4.21.20 cathepsin G
  - EC 3.4.21.21 coagulation factor VIIa
  - EC 3.4.21.22 coagulation factor IXa
  - EC 3.4.21.23 deleted
  - EC 3.4.21.24 deleted
  - EC 3.4.21.25 cucumisin
  - EC 3.4.21.26 prolyl oligopeptidase
  - EC 3.4.21.27 coagulation factor XIa
  - EC 3.4.21.28 deleted, included in EC 3.4.21.74
  - EC 3.4.21.29 deleted, included in EC 3.4.21.74
  - EC 3.4.21.30 deleted, included in EC 3.4.21.74
  - EC 3.4.21.31 now covered by EC 3.4.21.68 and EC 3.4.21.73
  - EC 3.4.21.32 brachyurin
  - EC 3.4.21.33 deleted
  - EC 3.4.21.34 plasma kallikrein
  - EC 3.4.21.35 tissue kallikrein
  - EC 3.4.21.36 pancreatic elastase
  - EC 3.4.21.37 leukocyte elastase
  - EC 3.4.21.38 coagulation factor XIIa
  - EC 3.4.21.39 chymase
  - EC 3.4.21.40 deleted
  - EC 3.4.21.41 complement subcomponent C
  - EC 3.4.21.42 complement subcomponent C
  - EC 3.4.21.43 classical-complement-pathway C3/C5 convertase
  - EC 3.4.21.44 deleted, included in EC 3.4.21.43
  - EC 3.4.21.45 complement factor I
  - EC 3.4.21.46 complement factor D
  - EC 3.4.21.47 alternative-complement-pathway C3/C5 convertase
  - EC 3.4.21.48 cerevisin
  - EC 3.4.21.49 hypodermin C
  - EC 3.4.21.50 lysyl endopeptidase
  - EC 3.4.21.51 deleted
  - EC 3.4.21.52 deleted
  - EC 3.4.21.53 endopeptidase La
  - EC 3.4.21.54 g-renin
  - EC 3.4.21.55 venombin AB
  - EC 3.4.21.56 deleted
  - EC 3.4.21.57 leucyl endopeptidase
  - EC 3.4.21.58 deleted
  - EC 3.4.21.59 tryptase
  - EC 3.4.21.60 scutelarin
  - EC 3.4.21.61 kexin
  - EC 3.4.21.62 subtilisin
  - EC 3.4.21.63 oryzin
  - EC 3.4.21.64 endopeptidase K
  - EC 3.4.21.65 thermomycolin
  - EC 3.4.21.66 thermitase
  - EC 3.4.21.67 endopeptidase So
  - EC 3.4.21.68 t-plasminogen activator
  - EC 3.4.21.69 protein C (activated)
  - EC 3.4.21.70 pancreatic endopeptidase E
  - EC 3.4.21.71 pancreatic elastase II
  - EC 3.4.21.72 IgA-specific serine endopeptidase
  - EC 3.4.21.73 u-plasminogen activator
  - EC 3.4.21.74 venombin A
  - EC 3.4.21.75 furin
  - EC 3.4.21.76 myeloblastin
  - EC 3.4.21.77 semenogelase
  - EC 3.4.21.78 granzyme A
  - EC 3.4.21.79 granzyme B
  - EC 3.4.21.80 streptogrisin A
  - EC 3.4.21.81 streptogrisin B

  - EC 3.4.21.82 glutamyl endopeptidase II
  - EC 3.4.21.83 oligopeptidase B
  - EC 3.4.21.84 limulus clotting factor
  - EC 3.4.21.85 limulus clotting factor
  - EC 3.4.21.86 limulus clotting enzyme
  - EC 3.4.21.87 omptin
  - EC 3.4.21.88 repressor LexA
  - EC 3.4.21.89 signal peptidase I
  - EC 3.4.21.90 togavirin
  - EC 3.4.21.91 flavivirin
  - EC 3.4.21.92 endopeptidase Clp
  - EC 3.4.21.93 proprotein convertase 1
  - EC 3.4.21.94 proprotein convertase 2
  - EC 3.4.21.95 snake venom factor V activator
  - EC 3.4.21.96 lactocepin
  - EC 3.4.21.97 assemblin
  - EC 3.4.21.98 hepacivirin
  - EC 3.4.21.99 spermosin
  - EC 3.4.21.100 pseudomonapepsin
  - EC 3.4.21.101 xanthomonapepsin
  - EC 3.4.21.102 C-terminal processing peptidase
- EC 3.4.22 Cysteine endopeptidases
  - EC 3.4.22.1 cathepsin B
  - EC 3.4.22.2 papain
  - EC 3.4.22.3 ficain
  - EC 3.4.22.4 now covered by EC 3.4.22.32 and EC 3.4.22.33
  - EC 3.4.22.5 now EC 3.4.22.33
  - EC 3.4.22.6 chymopapain
  - EC 3.4.22.7 asclepain
  - EC 3.4.22.8 clostripain
  - EC 3.4.22.9 now EC 3.4.21.48
  - EC 3.4.22.10 streptopain
  - EC 3.4.22.11 now EC 3.4.24.56 (supplement 3)
  - EC 3.4.22.12 now EC 3.4.19.9
  - EC 3.4.22.13 deleted
  - EC 3.4.22.14 actinidain
  - EC 3.4.22.15 cathepsin L
  - EC 3.4.22.16 cathepsin H
  - EC 3.4.22.17 calpain
  - EC 3.4.22.18 deleted, included in EC 3.4.21.26
  - EC 3.4.22.19 deleted, included in EC 3.4.24.15
  - EC 3.4.22.20 deleted
  - EC 3.4.22.21 deleted, included in EC 3.4.99.46
  - EC 3.4.22.22 now EC 3.4.24.37
  - EC 3.4.22.23 deleted, included in EC 3.4.21.61
  - EC 3.4.22.24 cathepsin T
  - EC 3.4.22.25 glycyl endopeptidase
  - EC 3.4.22.26 cancer procoagulant
  - EC 3.4.22.27 cathepsin S
  - EC 3.4.22.28 picomain 3C
  - EC 3.4.22.29 picomain 2A
  - EC 3.4.22.30 caricain
  - EC 3.4.22.31 ananain
  - EC 3.4.22.32 stem bromelain
  - EC 3.4.22.33 fruit bromelain
  - EC 3.4.22.34 legumain
  - EC 3.4.22.35 histolysain
  - EC 3.4.22.36 caspase-1
  - EC 3.4.22.37 gingipain R
  - EC 3.4.22.38 cathepsin K
  - EC 3.4.22.39 adenain
  - EC 3.4.22.40 bleomycin hydrolase
  - EC 3.4.22.41 cathepsin F
  - EC 3.4.22.42 cathepsin O
  - EC 3.4.22.43 cathepsin V
  - EC 3.4.22.44 nuclear-inclusion-a endopeptidase
  - EC 3.4.22.45 helper-component proteinase
  - EC 3.4.22.46 L-peptidase
- EC 3.4.23 Aspartic endopeptidases
  - EC 3.4.23.1 pepsin A
  - EC 3.4.23.2 pepsin B
  - EC 3.4.23.3 gastricsin
  - EC 3.4.23.4 chymosin
  - EC 3.4.23.5 cathepsin D
  - EC 3.4.23.6 now covered by EC 3.4.23.18 to EC 3.4.23.28 and EC 3.4.23.30
  - EC 3.4.23.7 now EC 3.4.23.20
  - EC 3.4.23.8 now EC 3.4.23.25
  - EC 3.4.23.9 now EC 3.4.23.21
  - EC 3.4.23.10 now EC 3.4.23.22
  - EC 3.4.23.11 deleted
  - EC 3.4.23.12 nepenthesin
  - EC 3.4.23.13 deleted
  - EC 3.4.23.14 deleted
  - EC 3.4.23.15 renin
  - EC 3.4.23.16 HIV-1 retropepsin
  - EC 3.4.23.17 Pro-opiomelanocortin converting enzyme
  - EC 3.4.23.18 aspergillopepsin I
  - EC 3.4.23.19 aspergillopepsin II
  - EC 3.4.23.20 penicillopepsin
  - EC 3.4.23.21 rhizopuspepsin
  - EC 3.4.23.22 endothiapepsin
  - EC 3.4.23.23 mucorpepsin
  - EC 3.4.23.24 candidapepsin
  - EC 3.4.23.25 saccharopepsin
  - EC 3.4.23.26 rhodotorulapepsin
  - EC 3.4.23.27 physaropepsin
  - EC 3.4.23.28 acrocylindropepsin
  - EC 3.4.23.29 polyporopepsin
  - EC 3.4.23.30 pycnoporopepsin
  - EC 3.4.23.31 scytalidopepsin A
  - EC 3.4.23.32 scytalidopepsin B
  - EC 3.4.23.33 now EC 3.4.21.101
  - EC 3.4.23.34 cathepsin E
  - EC 3.4.23.35 barrierpepsin
  - EC 3.4.23.36 signal peptidase II
  - EC 3.4.23.37 now EC 3.4.21.100
  - EC 3.4.23.38 plasmepsin I
  - EC 3.4.23.39 plasmepsin II
  - EC 3.4.23.40 phytepsin
  - EC 3.4.23.41 yapsin 1
  - EC 3.4.23.42 thermopsin
  - EC 3.4.23.43 prepilin peptidase
  - EC 3.4.23.44 nodavirus endopeptidase
- EC 3.4.24 Metalloendopeptidases
  - EC 3.4.24.1 atrolysin A
  - EC 3.4.24.2 deleted
  - EC 3.4.24.3 microbial collagenase
  - EC 3.4.24.4 now covered by EC 3.4.24.25 to EC 3.4.24.32, EC 3.4.24.39 and EC 3.4.24.40
  - EC 3.4.24.5 now covered by EC 3.4.22.17 and EC 3.4.25.1
  - EC 3.4.24.6 leucolysin
  - EC 3.4.24.7 interstitial collagenase
  - EC 3.4.24.8 deleted, included in EC 3.4.24.3
  - EC 3.4.24.9 deleted
  - EC 3.4.24.10 deleted
  - EC 3.4.24.11 neprilysin
  - EC 3.4.24.12 envelysin
  - EC 3.4.24.13 IgA-specific metalloendopeptidase
  - EC 3.4.24.14 procollagen N-endopeptidase
  - EC 3.4.24.15 thimet oligopeptidase
  - EC 3.4.24.16 neurolysin
  - EC 3.4.24.17 stromelysin 1
  - EC 3.4.24.18 meprin A
  - EC 3.4.24.19 procollagen C-endopeptidase
  - EC 3.4.24.20 peptidyl-Lys metalloendopeptidase
  - EC 3.4.24.21 astacin
  - EC 3.4.24.22 stromelysin 2
  - EC 3.4.24.23 matrilysin
  - EC 3.4.24.24 gelatinase A
  - EC 3.4.24.25 vibriolysin
  - EC 3.4.24.26 pseudolysin
  - EC 3.4.24.27 thermolysin
  - EC 3.4 24.28 bacillolysin
  - EC 3.4.24.29 aureolysin
  - EC 3.4.24.30 coccolysin
  - EC 3.4.24.31 mycolysin
  - EC 3.4.24.32 b-lytic metalloendopeptidase
  - EC 3.4.24.33 peptidyl-Asp metalloendopeptidase
  - EC 3.4.24.34 neutrophil collagenase
  - EC 3.4.24.35 gelatinase B
  - EC 3.4.24.36 leishmanolysin
  - EC 3.4.24.37 saccharolysin
  - EC 3.4.24.38 gametolysin
  - EC 3.4.24.39 deuterolysin
  - EC 3.4.24.40 serralysin
  - EC 3.4.24.41 atrolysin B
  - EC 3.4.24.42 atrolysin C
  - EC 3.4.24.43 atroxase
  - EC 3.4.24.44 atrolysin E
  - EC 3.4.24.45 atrolysin F
  - EC 3.4.24.46 adamalysin
  - EC 3.4.24.47 horrilysin
  - EC 3.4.24.48 ruberlysin
  - EC 3.4.24.49 bothropasin
  - EC 3.4.24.50 bothrolysin
  - EC 3.4.24.51 ophiolysin
  - EC 3.4.24.52 trimerelysin I
  - EC 3.4.24.53 trimerelysin II
  - EC 3.4.24.54 mucrolysin
  - EC 3.4.24.55 pitrilysin
  - EC 3.4.24.56 insulysin

- EC 3.4.24.57 O-sialoglycoprotein endopeptidase
- EC 3.4.24.58 russellysin
- EC 3.4.24.59 mitochondrial intermediate peptidase
- EC 3.4.24.60 dactylysin
- EC 3.4.24.61 nardilysin
- EC 3.4.24.62 magnolysin
- EC 3.4.24.63 meprin B
- EC 3.4.24.64 mitochondrial processing peptidase
- EC 3.4.24.65 macrophage elastase
- EC 3.4.24.66 choriolysin L
- EC 3.4.24.67 choriolysin H
- EC 3.4.24.68 tentoxilysin
- EC 3.4.24.69 bontoxilysin
- EC 3.4.24.70 oligopeptidase A
- EC 3.4.24.71 endothelin-converting enzyme
- EC 3.4.24.72 fibrolase
- EC 3.4.24.73 jararhagin
- EC 3.4.24.74 fragilysin
- EC 3.4.24.75 lysostaphin
- EC 3.4.24.76 flavastacin
- EC 3.4.24.77 snapalysin

- EC 3.4.25 Threonine endopeptidases
  - EC 3.4.25.1 proteasome endopeptidase complex
- EC 3.4.99 Endopeptidases of unknown catalytic mechanism
  - EC 3.4.99.1 now EC 3.4.23.28
  - EC 3.4.99.2 deleted
  - EC 3.4.99.3 deleted
  - EC 3.4.99.4 now EC 3.4.23.12
  - EC 3.4.99.5 now EC 3.4.24.3
  - EC 3.4.99.6 now EC 3.4.24.21
  - EC 3.4.99.7 deleted
  - EC 3.4.99.8 deleted
  - EC 3.4.99.9 deleted
  - EC 3.4.99.10 now EC 3.4.24.56 (supplement 3)
  - EC 3.4.99.11 deleted
  - EC 3.4.99.12 deleted
  - EC 3.4.99.13 now EC 3.4.24.32
  - EC 3.4.99.14 deleted
  - EC 3.4.99.15 deleted
  - EC 3.4.99.16 deleted
  - EC 3.4.99.17 deleted
  - EC 3.4.99.18 deleted
  - EC 3.4.99.19 now EC 3.4.23.15
  - EC 3.4.99.20 deleted
  - EC 3.4.99.21 deleted
  - EC 3.4.99.22 now EC 3.4.24.29
  - EC 3.4.99.23 deleted
  - EC 3.4.99.24 deleted
  - EC 3.4.99.25 deleted, included in EC 3.4.23.21
  - EC 3.4.99.26 now covered by EC 3.4.21.73 and EC 3.4.21.68
  - EC 3.4.99.27 deleted
  - EC 3.4.99.28 now EC 3.4.21.60
  - EC 3.4.99.29 deleted
  - EC 3.4.99.30 deleted, included in EC 3.4.24.20
  - EC 3.4.99.31 deleted, included in EC 3.4.24.15
  - EC 3.4.99.32 now EC 3.4.24.20
  - EC 3.4.99.33 deleted
  - EC 3.4.99.34 deleted
  - EC 3.4.99.35 now EC 3.4.23.36 (supplement 2)
  - EC 3.4.99.36 now EC 3.4.21.89 (supplement 2)
  - EC 3.4.99.37 deleted
  - EC 3.4.99.38 now EC 3.4.23.17
  - EC 3.4.99.39 deleted
  - EC 3.4.99.40 deleted
  - EC 3.4.99.41 now EC 3.4.24.64 (supplement 2)
  - EC 3.4.99.42 deleted
  - EC 3.4.99.43 now EC 3.4.23.42 (supplement 6)
  - EC 3.4.99.44 now EC 3.4.24.55 (supplement 1)
  - EC 3.4.99.45 now EC 3.4.24.56 (supplement 1)
  - EC 3.4.99.46 now EC 3.4.25.1 (supplement 6)
- EC 3.5 Acting on Carbon-Nitrogen Bonds, other than Peptide Bonds
  - EC 3.5.1 In Linear Amides
    - EC 3.5.1.1 asparaginase
    - EC 3.5.1.2 glutaminase
    - EC 3.5.1.3 w-amidase
    - EC 3.5.1.4 amidase
    - EC 3.5.1.5 urease
    - EC 3.5.1.6 b-ureidopropionase
    - EC 3.5.1.7 ureidosuccinase
    - EC 3.5.1.8 formylaspartate deformylase
    - EC 3.5.1.9 arylformamidase
    - EC 3.5.1.10 formyltetrahydrofolate deformylase
    - EC 3.5.1.11 penicillin amidase
    - EC 3.5.1.12 biotinidase
    - EC 3.5.1.13 aryl-acylamidase
    - EC 3.5.1.14 aminoacylase
    - EC 3.5.1.15 aspartoacylase
    - EC 3.5.1.16 acetylornithine deacetylase
    - EC 3.5.1.17 acyl-lysine deacylase
    - EC 3.5.1.18 succinyl-diaminopimelate desuccinylase
    - EC 3.5.1.19 nicotinamidase
    - EC 3.5.1.20 citrullinase
    - EC 3.5.1.21 N-acetyl-b-alanine deacetylase
    - EC 3.5.1.22 pantothenase
    - EC 3.5.1.23 ceramidase
    - EC 3.5.1.24 choloylglycine hydrolase
    - EC 3.5.1.25 N-acetylglucosamine-6-phosphate deacetylase
    - EC 3.5.1.26 N4-(b-N-acetylglucosaminyl)-L-asparaginase
    - EC 3.5.1.27 N-formylmethionylaminoacyl-tRNA deformylase
    - EC 3.5.1.28 N-acetylmuramoyl-L-alanine amidase
    - EC 3.5.1.29 2-(acetamidomethylene)succinate hydrolase
    - EC 3.5.1.30 5-aminopentanamidase
    - EC 3.5.1.31 formylmethionine deformylase
    - EC 3.5.1.32 hippurate hydrolase
    - EC 3.5.1.33 N-acetylglucosamine deacetylase
    - EC 3.5.1.34 deleted, same as EC 3.4.13.5
    - EC 3.5.1.35 D-glutaminase
    - EC 3.5.1.36 N-methyl-2-oxoglutaramate hydrolase
    - EC 3.5.1.37 deleted, same as EC 3.5.1.26
    - EC 3.5.1.38 glutamin-(asparagin-)ase
    - EC 3.5.1.39 alkylamidase
    - EC 3.5.1.40 acylagmatine amidase
    - EC 3.5.1.41 chitin deacetylase
    - EC 3.5.1.42 nicotinamide-nucleotide amidase
    - EC 3.5.1.43 peptidyl-glutaminase
    - EC 3.5.1.44 protein-glutamine glutaminase
    - EC 3.5.1.45 now EC 6.3.4.6
    - EC 3.5.1.46 6-aminohexanoate-dimer hydrolase
    - EC 3.5.1.47 N-acetyldiaminopimelate deacetylase
    - EC 3.5.1.48 acetylspermidine deacetylase
    - EC 3.5.1.49 formamidase
    - EC 3.5.1.50 pentanamidase
    - EC 3.5.1.51 4-acetamidobutyryl-CoA deacetylase
    - EC 3.5.1.52 peptide-N4-(N-acetyl-b-glucosaminyl)asparagine amidase
    - EC 3.5.1.53 N-carbamoylputrescine amidase
    - EC 3.5.1.54 allophanate hydrolase
    - EC 3.5.1.55 long-chain-fatty-acyl-glutamate deacylase
    - EC 3.5.1.56 N,N-dimethylformamidase
    - EC 3.5.1.57 tryptophanamidase
    - EC 3.5.1.58 N-benzyloxycarbonylglycine hydrolase
    - EC 3.5.1.59 N-carbamoylsarcosine amidase
    - EC 3.5.1.60 N-(long-chain-acyl)ethanolamine deacylase
    - EC 3.5.1.61 mimosinase
    - EC 3.5.1.62 acetylputrescine deacetylase
    - EC 3.5.1.63 4-acetamidobutyrate deacetylase
    - EC 3.5.1.64 Na-benzyloxycarbonylleucine hydrolase
    - EC 3.5.1.65 theanine hydrolase
    - EC 3.5.1.66 2-(hydroxymethyl)-3-(acetamidomethylene)succinate hydrolase
    - EC 3.5.1.67 4-methyleneglutaminase
    - EC 3.5.1.68 N-formylglutamate deformylase
    - EC 3.5.1.69 glycosphingolipid deacylase
    - EC 3.5.1.70 aculeacin-A deacylase
    - EC 3.5.1.71 N-feruloylglycine deacylase
    - EC 3.5.1.72 D-benzoylarginine-4-nitroanilide amidase
    - EC 3.5.1.73 carnitinamidase
    - EC 3.5.1.74 chenodeoxycholoyltaurine hydrolase
    - EC 3.5.1.75 urethanase
    - EC 3.5.1.76 arylalkyl acylamidase
    - EC 3.5.1.77 N-carbamoyl-D-amino acid hydrolase
    - EC 3.5.1.78 glutathionylspermidine amidase
    - EC 3.5.1.79 phthalyl amidase
    - EC 3.5.1.80 deleted, identical to EC 3.5.1.25
    - EC 3.5.1.81 N-acyl-D-amino-acid deacylase
    - EC 3.5.1.82 N-acyl-D-glutamate deacylase
    - EC 3.5.1.83 N-acyl-D-aspartate deacylase
    - EC 3.5.1.84 biuret amidohydrolase
    - EC 3.5.1.85 (S)-N-acetyl-1-phenylethylamine hydrolase
    - EC 3.5.1.86 mandelamide amidase

    - EC 3.5.1.87 N-carbamoyl-L-amino-acid hydrolase
    - EC 3.5.1.88 peptide deformylase
    - EC 3.5.1.89 N-acetylglucosaminylphosphatidylinositol deacetylase
  - EC 3.5.2 In Cyclic Amides
    - EC 3.5.2.1 barbiturase
    - EC 3.5.2.2 dihydropyrimidinase
    - EC 3.5.2.3 dihydroorotase
    - EC 3.5.2.4 carboxymethylhydantoinase
    - EC 3.5.2.5 allantoinase
    - EC 3.5.2.6 b-lactamase
    - EC 3.5.2.7 imidazolonepropionase
    - EC 3.5.2.8 deleted, included in EC 3.5.2.6
    - EC 3.5.2.9 5-oxoprolinase (ATP-hydrolysing)
    - EC 3.5.2.10 creatininase
    - EC 3.5.2.11 L-lysine-lactamase
    - EC 3.5.2.12 6-aminohexanoate-cyclic-dimer hydrolase
    - EC 3.5.2.13 2,5-dioxopiperazine hydrolase
    - EC 3.5.2.14 N-methylhydantoinase (ATP-hydrolysing)
    - EC 3.5.2.15 cyanuric acid amidohydrolase
    - EC 3.5.2.16 maleimide hydrolase
  - EC 3.5.3 In Linear Amidines
    - EC 3.5.3.1 arginase
    - EC 3.5.3.2 guanidinoacetase
    - EC 3.5.3.3 creatinase
    - EC 3.5.3.4 allantoicase
    - EC 3.5.3.5 formiminoaspartate deiminase
    - EC 3.5.3.6 arginine deiminase
    - EC 3.5.3.7 guanidinobutyrase
    - EC 3.5.3.8 formimidoylglutamase
    - EC 3.5.3.9 allantoate deiminase
    - EC 3.5.3.10 D-arginase
    - EC 3.5.3.11 agmatinase
    - EC 3.5.3.12 agmatine deiminase
    - EC 3.5.3.13 formiminoglutamate deiminase
    - EC 3.5.3.14 amidinoaspartase
    - EC 3.5.3.15 protein-arginine deiminase
    - EC 3.5.3.16 methylguanidinase
    - EC 3.5.3.17 guanidinopropionase
    - EC 3.5.3.18 dimethylargininase
    - EC 3.5.3.19 ureidoglycolate hydrolase
    - EC 3.5.3.20 diguanidinobutanase
    - EC 3.5.3.21 methylenediurea deaminase
  - EC 3.5.4 In Cyclic Amidines
    - EC 3.5.4.1 cytosine deaminase
    - EC 3.5.4.2 adenine deaminase
    - EC 3.5.4.3 guanine deaminase
    - EC 3.5.4.4 adenosine deaminase
    - EC 3.5.4.5 cytidine deaminase
    - EC 3.5.4.6 AMP deaminase
    - EC 3.5.4.7 ADP deaminase
    - EC 3.5.4.8 aminoimidazolase
    - EC 3.5.4.9 methenyltetrahydrofolate cyclohydrolase
    - EC 3.5.4.10 IMP cyclohydrolase
    - EC 3.5.4.11 pterin deaminase
    - EC 3.5.4.12 dCMP deaminase
    - EC 3.5.4.13 dCTP deaminase
    - EC 3.5.4.14 deoxycytidine deaminase
    - EC 3.5.4.15 guanosine deaminase
    - EC 3.5.4.16 GTP cyclohydrolase I
    - EC 3.5.4.17 adenosine-phosphate deaminase
    - EC 3.5.4.18 ATP deaminase
    - EC 3.5.4.19 phosphoribosyl-AMP cyclohydrolase
    - EC 3.5.4.20 pyrithiamine deaminase
    - EC 3.5.4.21 creatinine deaminase
    - EC 3.5.4.22 1-pyrroline-4-hydroxy-2-carboxylate deaminase
    - EC 3.5.4.23 blasticidin-S deaminase
    - EC 3.5.4.24 sepiapterin deaminase
    - EC 3.5.4.25 GTP cyclohydrolase II
    - EC 3.5.4.26 diaminohydroxyphosphoribosylaminopyrimidine deaminase
    - EC 3.5.4.27 methenyltetrahydromethanopterin cyclohydrolase
    - EC 3.5.4.28 S-adenosylhomocysteine deaminase
  - EC 3.5.5 In Nitriles
    - EC 3.5.5.1 nitrilase
    - EC 3.5.5.2 ricinine nitrilase
    - EC 3.5.5.3 now EC 4.3.99.1
    - EC 3.5.5.4 cyanoalanine nitrilase
    - EC 3.5.5.5 arylacetonitrilase
    - EC 3.5.5.6 bromoxynil nitrilase
    - EC 3.5.5.7 aliphatic nitrilase
    - EC 3.5.5.8 thiocyanate hydrolase
  - EC 3.5.99 In Other Compounds
    - EC 3.5.99.1 riboflavinase
    - EC 3.5.99.2 thiaminase
    - EC 3.5.99.3 hydroxydechloroatrazine ethylaminohydrolase
    - EC 3.5.99.4 N-isopropylammelide isopropylaminohydrolase
    - EC 3.5.99.5 2-aminomuconate deaminase
    - EC 3.5.99.6 glucosamine-6-phosphate deaminase
    - EC 3.5.99.7 1-aminocyclopropane-1-carboxylate deaminase
- EC 3.6 Acting on Acid Anhydrides
  - EC 3.6.1 In Phosphorus-Containing Anhydrides
    - EC 3.6.1.1 inorganic diphosphatase
    - EC 3.6.1.2 trimetaphosphatase
    - EC 3.6.1.3 adenosinetriphosphatase
    - EC 3.6.1.4 deleted, included in EC 3.6.1.3
    - EC 3.6.1.5 apyrase
    - EC 3.6.1.6 nucleoside-diphosphatase
    - EC 3.6.1.7 acylphosphatase
    - EC 3.6.1.8 ATP diphosphatase
    - EC 3.6.1.9 nucleotide diphosphatase
    - EC 3.6.1.10 endopolyphosphatase
    - EC 3.6.1.11 exopolyphosphatase
    - EC 3.6.1.12 dCTP diphosphatase
    - EC 3.6.1.13 ADP-ribose diphosphatase
    - EC 3.6.1.14 adenosine-tetraphosphatase
    - EC 3.6.1.15 nucleoside-triphosphatase
    - EC 3.6.1.16 CDP-glycerol diphosphatase
    - EC 3.6.1.17 bis(5'-nucleosyl)-tetraphosphatase (asymmetrical)
    - EC 3.6.1.18 FAD diphosphatase
    - EC 3.6.1.19 nucleoside-triphosphate diphosphatase
    - EC 3.6.1.20 5'-acylphosphoadenosine hydrolase
    - EC 3.6.1.21 ADP-sugar diphosphatase
    - EC 3.6.1.22 NAD diphosphatase
    - EC 3.6.1.23 dUTP diphosphatase
    - EC 3.6.1.24 nucleoside phosphoacylhydrolase
    - EC 3.6.1.25 triphosphatase
    - EC 3.6.1.26 CDP-diacylglycerol diphosphatase
    - EC 3.6.1.27 undecaprenyl-diphosphatase
    - EC 3.6.1.28 thiamine-triphosphatase
    - EC 3.6.1.29 bis(5'-adenosyl)-triphosphatase
    - EC 3.6.1.30 m7G(5')pppN diphosphatase
    - EC 3.6.1.31 phosphoribosyl-ATP diphosphatase
    - EC 3.6.1.32 now EC 3.6.4.1
    - EC 3.6.1.33 now EC 3.6.4.2
    - EC 3.6.1.34 now EC 3.6.3.14
    - EC 3.6.1.35 now EC 3.6.3.6
    - EC 3.6.1.36 now EC 3.6.3.10
    - EC 3.6.1.37 now EC 3.6.3.9
    - EC 3.6.1.38 now EC 3.6.3.8
    - EC 3.6.1.39 thymidine-triphosphatase
    - EC 3.6.1.40 guanosine-5'-triphosphate,3'-diphosphate diphosphatase
    - EC 3.6.1.41 bis(5'-nucleosyl)-tetraphosphatase (symmetrical)
    - EC 3.6.1.42 guanosine-diphosphatase
    - EC 3.6.1.43 dolichyldiphosphatase
    - EC 3.6.1.44 oligosaccharide-diphosphodolichol diphosphatase
    - EC 3.6.1.45 UDP-sugar diphosphatase
    - EC 3.6.1.46 heterotrimeric G-protein GTPase
    - EC 3.6.1.47 small monomeric GTPase
    - EC 3.6.1.48 protein-synthesizing GTPase
    - EC 3.6.1.49 signal-recognition-particle GTPase
    - EC 3.6.1.50 dynamin GTPase
    - EC 3.6.1.51 tubulin GTPase
    - EC 3.6.1.52 diphosphoinositol-polyphosphate diphosphatase
  - EC 3.6.2 In Sulfonyl-Containing Anhydrides
    - EC 3.6.2.1 adenylylsulfatase
    - EC 3.6.2.2 phosphoadenylylsulfatase
  - EC 3.6.3 Acting on acid anhydrides; catalysing transmembrane movement of substances
    - EC 3.6.3.1 Mg2+-ATPase
    - EC 3.6.3.2 Mg2+-importing ATPase
    - EC 3.6.3.3 Cd2+-exporting ATPase
    - EC 3.6.3.4 Cu2+-exporting ATPase
    - EC 3.6.3.5 Zn2+-exporting ATPase
    - EC 3.6.3.6 H+-exporting ATPase
    - EC 3.6.3.7 Na+-exporting ATPase
    - EC 3.6.3.8 Ca2+-transporting ATPase
    - EC 3.6.3.9 Na+/K+-exchanging ATPase
    - EC 3.6.3.10 H+/K+-exchanging ATPase

        - EC 3.6.3.11 Cl–transporting ATPase
        - EC 3.6.3.12 K+-transporting ATPase
        - EC 3.6.3.13 deleted, identical to EC 3.6.3.1
        - EC 3.6.3.14 H+-transporting two-sector ATPase
        - EC 3.6.3.15 Na+-transporting two-sector ATPase
        - EC 3.6.3.16 arsenite-transporting ATPase
        - EC 3.6.3.17 monosaccharide-transporting ATPase
        - EC 3.6.3.18 oligosaccharide-transporting ATPase
        - EC 3.6.3.19 maltose-transporting ATPase
        - EC 3.6.3.20 glycerol-3-phosphate-transporting ATPase
        - EC 3.6.3.21 polar-amino-acid-transporting ATPase
        - EC 3.6.3.22 nonpolar-amino-acid-transporting ATPase
        - EC 3.6.3.23 oligopeptide-transporting ATPase
        - EC 3.6.3.24 nickel-transporting ATPase
        - EC 3.6.3.25 sulfate-transporting ATPase
        - EC 3.6.3.26 nitrate-transporting ATPase
        - EC 3.6.3.27 phosphate-transporting ATPase
        - EC 3.6.3.28 phosphonate-transporting ATPase
        - EC 3.6.3.29 molybdate-transporting ATPase
        - EC 3.6.3.30 Fe3+-transporting ATPase
        - EC 3.6.3.31 polyamine-transporting ATPase
        - EC 3.6.3.32 quaternary-amine-transporting ATPase
        - EC 3.6.3.33 vitamin B12-transporting ATPase
        - EC 3.6.3.34 iron-chelate-transporting ATPase
        - EC 3.6.3.35 manganese-transporting ATPase
        - EC 3.6.3.36 taurine-transporting ATPase
        - EC 3.6.3.37 guanine-transporting ATPase
        - EC 3.6.3.38 capsular-polysaccharide-transporting ATPase
        - EC 3.6.3.39 lipopolysaccharide-transporting ATPase
        - EC 3.6.3.40 teichoic-acid-transporting ATPase
        - EC 3.6.3.41 heme-transporting ATPase
        - EC 3.6.3.42 b-glucan-transporting ATPase
        - EC 3.6.3.43 peptide-transporting ATPase
        - EC 3.6.3.44 xenobiotic-transporting ATPase
        - EC 3.6.3.45 steroid-transporting ATPase
        - EC 3.6.3.46 cadmium-transporting ATPase
        - EC 3.6.3.47 fatty-acyl-CoA-transporting ATPase
        - EC 3.6.3.48 a-factor-transporting ATPase
        - EC 3.6.3.49 channel-conductance-controlling ATPase
        - EC 3.6.3.50 protein-secreting ATPase
        - EC 3.6.3.51 mitochondrial protein-transporting ATPase
        - EC 3.6.3.52 chloroplast protein-transporting ATPase
        - EC 3.6.3.53 Ag+-exporting ATPase
    - EC 3.6.4 Acting on acid anhydrides; involved in cellular and subcellular movement
        - EC 3.6.4.1 myosin ATPase
        - EC 3.6.4.2 dynein ATPase
        - EC 3.6.4.3 microtubule-severing ATPase
        - EC 3.6.4.4 plus-end-directed kinesin ATPase
        - EC 3.6.4.5 minus-end-directed kinesin ATPase
        - EC 3.6.4.6 vesicle-fusing ATPase
        - EC 3.6.4.7 peroxisome-assembly ATPase
        - EC 3.6.4.8 proteasome ATPase
        - EC 3.6.4.9 chaperonin ATPase
        - EC 3.6.4.10 non-chaperonin molecular chaperone ATPase
        - EC 3.6.4.11 nucleoplasmin ATPase
- EC 3.7 Acting on Carbon-Carbon Bonds
    - EC 3.7.1 In Ketonic Substances
        - EC 3.7.1.1 oxaloacetase
        - EC 3.7.1.2 fumarylacetoacetase
        - EC 3.7.1.3 kynureninase
        - EC 3.7.1.4 phloretin hydrolase
        - EC 3.7.1.5 acylpyruvate hydrolase
        - EC 3.7.1.6 acetylpyruvate hydrolase
        - EC 3.7.1.7 b-diketone hydrolase
        - EC 3.7.1.8 2,6-dioxo-6-phenylhexa-3-enoate hydrolase
        - EC 3.7.1.9 2-hydroxymuconate-semialdehyde hydrolase
        - EC 3.7.1.10 cyclohexane-1,3-dione hydrolase
- EC 3.8 Acting on Halide Bonds
    - EC 3.8.1 In C-Halide Compounds
        - EC 3.8.1.1 alkylhalidase
        - EC 3.8.1.2 2-haloacid dehalogenase
        - EC 3.8.1.3 haloacetate dehalogenase
        - EC 3.8.1.4 thyroxine deiodinase
        - EC 3.8.1.5 haloalkane dehalogenase
        - EC 3.8.1.6 4-chlorobenzoate dehalogenase
        - EC 3.8.1.7 4-chlorobenzoyl-CoA dehalogenase
        - EC 3.8.1.8 atrazine chlorohydrolase
    - EC 3.8.2 In P-Halide Compounds
        - EC 3.8.2.1 now EC 3.1.8.2
- EC 3.9 Acting on Phosphorus-Nitrogen Bonds
        - EC 3.9.1.1 phosphoamidase
- EC 3.10 Acting on Sulfur-Nitrogen Bonds
        - EC 3.10.1.1 N-sulfoglucosamine sulfohydrolase
        - EC 3.10.1.2 cyclamate sulfohydrolase
- EC 3.11 Acting on Carbon-Phosphorus Bonds
        - EC 3.11.1.1 phosphonoacetaldehyde hydrolase
        - EC 3.11.1.2 phosphonoacetate hydrolase
- EC 3.12 Acting on Sulfur-Sulfur Bonds
        - EC 3.12.1.1 trithionate hydrolase
- EC 3.13 Acting on Carbon-Sulfur Bonds
        - EC 3.13.1.1 UDPsulfoquinovose synthase

EC 4 Lyases

- EC 4.1 Carbon-Carbon Lyases
    - EC 4.1.1 Carboxy-Lyases
        - EC 4.1.1.1 pyruvate decarboxylase
        - EC 4.1.1.2 oxalate decarboxylase
        - EC 4.1.1.3 oxaloacetate decarboxylase
        - EC 4.1.1.4 acetoacetate decarboxylase
        - EC 4.1.1.5 acetolactate decarboxylase
        - EC 4.1.1.6 aconitate decarboxylase
        - EC 4.1.1.7 benzoylformate decarboxylase
        - EC 4.1.1.8 oxalyl-CoA decarboxylase
        - EC 4.1.1.9 malonyl-CoA decarboxylase
        - EC 4.1.1.10 deleted, included in EC 4.1.1.12
        - EC 4.1.1.11 aspartate 1-decarboxylase
        - EC 4.1.1.12 aspartate 4-decarboxylase
        - EC 4.1.1.13 deleted
        - EC 4.1.1.14 valine decarboxylase
        - EC 4.1.1.15 glutamate decarboxylase
        - EC 4.1.1.16 hydroxyglutamate decarboxylase
        - EC 4.1.1.17 ornithine decarboxylase
        - EC 4.1.1.18 lysine decarboxylase
        - EC 4.1.1.19 arginine decarboxylase
        - EC 4.1.1.20 diaminopimelate decarboxylase
        - EC 4.1.1.21 phosphoribosylaminoimidazole carboxylase
        - EC 4.1.1.21 phosphoribosylaminoimidazole carboxylase
        - EC 4.1.1.22 histidine decarboxylase
        - EC 4.1.1.23 orotidine-5'-phosphate decarboxylase
        - EC 4.1.1.24 aminobenzoate decarboxylase
        - EC 4.1.1.25 tyrosine decarboxylase
        - EC 4.1.1.26 deleted, included in EC 4.1.1.28
        - EC 4.1.1.27 deleted, included in EC 4.1.1.28
        - EC 4.1.1.28 aromatic-L-amino-acid decarboxylase
        - EC 4.1.1.29 sulfoalanine decarboxylase
        - EC 4.1.1.30 pantothenoylcysteine decarboxylase
        - EC 4.1.1.31 phosphoenolpyruvate carboxylase
        - EC 4.1.1.32 phosphoenolpyruvate carboxykinase (GTP)
        - EC 4.1.1.33 diphosphomevalonate decarboxylase
        - EC 4.1.1.34 dehydro-L-gulonate decarboxylase
        - EC 4.1.1.35 UDP-glucuronate decarboxylase
        - EC 4.1.1.36 phosphopantothenoylcysteine decarboxylase
        - EC 4.1.1.37 uroporphyrinogen decarboxylase
        - EC 4.1.1.38 phosphoenolpyruvate carboxykinase (diphosphate)
        - EC 4.1.1.39 ribulose-bisphosphate carboxylase
        - EC 4.1.1.40 hydroxypyruvate decarboxylase
        - EC 4.1.1.41 methylmalonyl-CoA decarboxylase
        - EC 4.1.1.42 carnitine decarboxylase
        - EC 4.1.1.43 phenylpyruvate decarboxylase
        - EC 4.1.1.44 4-carboxymuconolactone decarboxylase
        - EC 4.1.1.45 aminocarboxymuconate-semialdehyde decarboxylase
        - EC 4.1.1.46 o-pyrocatechuate decarboxylase
        - EC 4.1.1.47 tartronate-semialdehyde synthase
        - EC 4.1.1.48 indole-3-glycerol-phosphate synthase
        - EC 4.1.1.49 phosphoenolpyruvate carboxykinase (ATP)
        - EC 4.1.1.50 adenosylmethionine decarboxylase
        - EC 4.1.1.51 3-hydroxy-2-methylpyridine-4,5-dicarboxylate 4-decarboxylase
        - EC 4.1.1.52 6-methylsalicylate decarboxylase
        - EC 4.1.1.53 phenylalanine decarboxylase
        - EC 4.1.1.54 dihydroxyfumarate decarboxylase

- EC 4.1.1.55 4,5-dihydroxyphthalate decarboxylase
- EC 4.1.1.56 3-oxolaurate decarboxylase
- EC 4.1.1.57 methionine decarboxylase
- EC 4.1.1.58 orsellinate decarboxylase
- EC 4.1.1.59 gallate decarboxylase
- EC 4.1.1.60 stipitatonate decarboxylase
- EC 4.1.1.61 4-hydroxybenzoate decarboxylase
- EC 4.1.1.62 gentisate decarboxylase
- EC 4.1.1.63 protocatechuate decarboxylase
- EC 4.1.1.64 2,2-dialkylglycine decarboxylase (pyruvate)
- EC 4.1.1.65 phosphatidylserine decarboxylase
- EC 4.1.1.66 uracil-5-carboxylate decarboxylase
- EC 4.1.1.67 UDP-galacturonate decarboxylase
- EC 4.1.1.68 5-oxopent-3-ene-1,2,5-tricarboxylate decarboxylase
- EC 4.1.1.69 3,4-dihydroxyphthalate decarboxylase
- EC 4.1.1.70 glutaconyl-CoA decarboxylase
- EC 4.1.1.71 2-oxoglutarate decarboxylase
- EC 4.1.1.72 branched-chain-2-oxoacid decarboxylase
- EC 4.1.1.73 tartrate decarboxylase
- EC 4.1.1.74 indolepyruvate decarboxylase
- EC 4.1.1.75 5-guanidino-2-oxopentanoate decarboxylase
- EC 4.1.1.76 arylmalonate decarboxylase
- EC 4.1.1.77 4-oxalocrotonate decarboxylase
- EC 4.1.1.78 acetylenedicarboxylate decarboxylase
- EC 4.1.1.79 sulfopyruvate decarboxylase
- EC 4.1.1.80 4-hydroxyphenylpyruvate decarboxylase
- EC 4.1.2 Aldehyde-Lyases
  - EC 4.1.2.1 deleted, included in EC 4.1.3.16
  - EC 4.1.2.2 ketotetrose-phosphate aldolase
  - EC 4.1.2.3 deleted
  - EC 4.1.2.4 deoxyribose-phosphate aldolase
  - EC 4.1.2.5 threonine aldolase
  - EC 4.1.2.6 deleted
  - EC 4.1.2.7 deleted, included in EC 4.1.2.13
  - EC 4.1.2.8 deleted
  - EC 4.1.2.9 phosphoketolase
  - EC 4.1.2.10 mandelonitrile lyase
  - EC 4.1.2.11 hydroxymandelonitrile lyase
  - EC 4.1.2.12 ketopantoaldolase
  - EC 4.1.2.13 fructose-bisphosphate aldolase
  - EC 4.1.2.14 2-dehydro-3-deoxy-phosphogluconate aldolase
  - EC 4.1.2.15 now EC 2.5.1.54
  - EC 4.1.2.16 now EC 2.5.1.55
  - EC 4.1.2.17 L-fuculose-phosphate aldolase
  - EC 4.1.2.18 2-dehydro-3-deoxy-L-pentonate aldolase
  - EC 4.1.2.19 rhamnulose-1-phosphate aldolase
  - EC 4.1.2.20 2-dehydro-3-deoxyglucarate aldolase
  - EC 4.1.2.21 2-dehydro-3-deoxy-6-phosphogalactonate aldolase
  - EC 4.1.2.22 fructose-6-phosphate phosphoketolase
  - EC 4.1.2.23 3-deoxy-D-manno-octulosonate aldolase
  - EC 4.1.2.24 dimethylaniline-N-oxide aldolase
  - EC 4.1.2.25 dihydroneopterin aldolase
  - EC 4.1.2.26 phenylserine aldolase
  - EC 4.1.2.27 sphinganine-1-phosphate aldolase
  - EC 4.1.2.28 2-dehydro-3-deoxy-D-pentonate aldolase
  - EC 4.1.2.29 5-dehydro-2-deoxyphosphogluconate aldolase
  - EC 4.1.2.30 17α-hydroxyprogesterone aldolase
  - EC 4.1.2.31 deleted, included in EC 4.1.3.16
  - EC 4.1.2.32 trimethylamine-oxide aldolase
  - EC 4.1.2.33 fucosterol-epoxide lyase
  - EC 4.1.2.34 4-(2-carboxyphenyl)-2-oxobut-3-enoate aldolase
  - EC 4.1.2.35 propioin synthase
  - EC 4.1.2.36 lactate aldolase
  - EC 4.1.2.37 acetone-cyanhydrin lyase
  - EC 4.1.2.38 benzoin aldolase
  - EC 4.1.2.39 hydroxynitrilase
  - EC 4.1.2.40 tagatose-bisphosphate aldolase
  - EC 4.1.2.41 vanillin synthase
- EC 4.1.3 Oxo-Acid-Lyases
  - EC 4.1.3.1 isocitrate lyase
  - EC 4.1.3.2 now EC 2.3.3.9
  - EC 4.1.3.3 N-acetylneuraminate lyase
  - EC 4.1.3.4 hydroxymethylglutaryl-CoA lyase
  - EC 4.1.3.5 now EC 2.3.3.10
  - EC 4.1.3.6 citrate (pro-3S)-lyase
  - EC 4.1.3.7 now EC 2.3.3.1
  - EC 4.1.3.8 now EC 2.3.3.8
  - EC 4.1.3.9 now EC 2.3.3.11
  - EC 4.1.3.10 now EC 2.3.3.7
  - EC 4.1.3.11 now EC 2.3.3.12
  - EC 4.1.3.12 now EC 2.3.3.13
  - EC 4.1.3.13 oxalomalate lyase
  - EC 4.1.3.14 3-hydroxyaspartate aldolase
  - EC 4.1.3.15 now EC 2.2.1.5
  - EC 4.1.3.16 4-hydroxy-2-oxoglutarate aldolase
  - EC 4.1.3.17 4-hydroxy-4-methyl-2-oxoglutarate aldolase
  - EC 4.1.3.18 now EC 2.2.1.6
  - EC 4.1.3.19 now EC 2.5.1.56
  - EC 4.1.3.20 now EC 2.5.1.57
  - EC 4.1.3.21 now EC 2.3.3.14
  - EC 4.1.3.22 citramalate lyase
  - EC 4.1.3.23 now EC 2.3.3.2
  - EC 4.1.3.24 malyl-CoA lyase
  - EC 4.1.3.25 citramalyl-CoA lyase
  - EC 4.1.3.26 3-hydroxy-3-isohexenylglutaryl-CoA lyase
  - EC 4.1.3.27 anthranilate synthase
  - EC 4.1.3.28 now EC 2.3.3.3
  - EC 4.1.3.29 now EC 2.3.3.4
  - EC 4.1.3.30 methylisocitrate lyase
  - EC 4.1.3.31 now EC 2.3.3.5
  - EC 4.1.3.32 2,3-dimethylmalate lyase
  - EC 4.1.3.33 now EC 2.3.3.6
  - EC 4.1.3.34 citryl-CoA lyase
  - EC 4.1.3.35 (1-hydroxycyclohexan-1-yl)acetyl-CoA lyase
  - EC 4.1.3.36 naphthoate synthase
  - EC 4.1.3.37 now EC 2.2.1.7
- EC 4.1.99 Other Carbon-Carbon Lyases
  - EC 4.1.99.1 tryptophanase
  - EC 4.1.99.2 tyrosine phenol-lyase
  - EC 4.1.99.3 deoxyribodipyrimidine photo-lyase
  - EC 4.1.99.4 now EC 3.5.99.7
  - EC 4.1.99.5 octadecanal decarbonylase
  - EC 4.1.99.6 now EC 4.2.3.6
  - EC 4.1.99.7 now EC 4.2.3.9
  - EC 4.1.99.8 now EC 4.2.3.14
  - EC 4.1.99.9 now EC 4.2.3.15
  - EC 4.1.99.10 now EC 4.2.3.16
  - EC 4.1.99.11 benzylsuccinate synthase
- EC 4.2 Carbon-Oxygen Lyases
  - EC 4.2.1 Hydro-Lyases
    - EC 4.2.1.1 carbonate dehydratase
    - EC 4.2.1.2 fumarate hydratase
    - EC 4.2.1.3 aconitate hydratase
    - EC 4.2.1.4 citrate dehydratase
    - EC 4.2.1.5 arabinonate dehydratase
    - EC 4.2.1.6 galactonate dehydratase
    - EC 4.2.1.7 altronate dehydratase
    - EC 4.2.1.8 mannonate dehydratase
    - EC 4.2.1.9 dihydroxy-acid dehydratase
    - EC 4.2.1.10 3-dehydroquinate dehydratase
    - EC 4.2.1.11 phosphopyruvate hydratase
    - EC 4.2.1.12 phosphogluconate dehydratase
    - EC 4.2.1.13 now EC 4.3.1.17
    - EC 4.2.1.14 now EC 4.3.1.18
    - EC 4.2.1.15 now EC 4.4.1.1
    - EC 4.2.1.16 now EC 4.3.1.19
    - EC 4.2.1.17 enoyl-CoA hydratase
    - EC 4.2.1.18 methylglutaconyl-CoA hydratase
    - EC 4.2.1.19 imidazoleglycerol-phosphate dehydratase
    - EC 4.2.1.20 tryptophan synthase
    - EC 4.2.1.21 now EC 4.2.1.22
    - EC 4.2.1.22 cystathionine b-synthase
    - EC 4.2.1.23 deleted
    - EC 4.2.1.24 porphobilinogen synthase
    - EC 4.2.1.25 L-arabinonate dehydratase
    - EC 4.2.1.26 now EC 4.3.1.21
    - EC 4.2.1.27 malonate-semialdehyde dehydratase
    - EC 4.2.1.28 propanediol dehydratase
    - EC 4.2.1.29 indoleacetaldoxime dehydratase
    - EC 4.2.1.30 glycerol dehydratase
    - EC 4.2.1.31 maleate hydratase
    - EC 4.2.1.32 L(+)-tartrate dehydratase
    - EC 4.2.1.33 3-isopropylmalate dehydratase
    - EC 4.2.1.34 (S)-2-methylmalate dehydratase
    - EC 4.2.1.35 (R)-2-methylmalate dehydratase
    - EC 4.2.1.36 homoaconitate hydratase

- EC 4.2.1.37 now EC 3.3.2.4
- EC 4.2.1.38 now EC 4.3.1.20
- EC 4.2.1.39 gluconate dehydratase
- EC 4.2.1.40 glucarate dehydratase
- EC 4.2.1.41 5-dehydro-4-deoxyglucarate dehydratase
- EC 4.2.1.42 galactarate dehydratase
- EC 4.2.1.43 2-dehydro-3-deoxy-L-arabinonate dehydratase
- EC 4.2.1.44 myo-inosose-2 dehydratase
- EC 4.2.1.45 CDP-glucose 4,6-dehydratase
- EC 4.2.1.46 dTDP-glucose 4,6-dehydratase
- EC 4.2.1.47 GDP-mannose 4,6-dehydratase
- EC 4.2.1.48 D-glutamate cyclase
- EC 4.2.1.49 urocanate hydratase
- EC 4.2.1.50 pyrazolylalanine synthase
- EC 4.2.1.51 prephenate dehydratase
- EC 4.2.1.52 dihydrodipicolinate synthase
- EC 4.2.1.53 oleate hydratase
- EC 4.2.1.54 lactoyl-CoA dehydratase
- EC 4.2.1.55 3-hydroxybutyryl-CoA dehydratase
- EC 4.2.1.56 itaconyl-CoA hydratase
- EC 4.2.1.57 isohexenylglutaconyl-CoA hydratase
- EC 4.2.1.58 crotonoyl-[acyl-carrier-protein] hydratase
- EC 4.2.1.59 3-hydroxyoctanoyl-[acyl-carrier-protein] dehydratase
- EC 4.2.1.60 3-hydroxydecanoyl-[acyl-carrier-protein] dehydratase
- EC 4.2.1.61 3-hydroxypalmitoyl-[acyl-carrier-protein] dehydratase
- EC 4.2.1.62 5a-hydroxysteroid dehydratase
- EC 4.2.1.63 now EC 3.3.2.3
- EC 4.2.1.64 now EC 3.3.2.3
- EC 4.2.1.65 3-cyanoalanine hydratase
- EC 4.2.1.66 cyanide hydratase
- EC 4.2.1.67 D-fuconate dehydratase
- EC 4.2.1.68 L-fuconate dehydratase
- EC 4.2.1.69 cyanamide hydratase
- EC 4.2.1.70 pseudouridylate synthase
- EC 4.2.1.71 acetylenecarboxylate hydratase
- EC 4.2.1.72 now EC 4.1.1.78
- EC 4.2.1.73 protoaphin-aglucone dehydratase (cyclizing)
- EC 4.2.1.74 long-chain-enoyl-CoA hydratase
- EC 4.2.1.75 uroporphyrinogen-III synthase
- EC 4.2.1.76 UDP-glucose 4,6-dehydratase
- EC 4.2.1.77 trans-L-3-hydroxyproline dehydratase
- EC 4.2.1.78 (S)-norcoclaurine synthase
- EC 4.2.1.79 2-methylcitrate dehydratase
- EC 4.2.1.80 2-oxopent-4-enoate hydratase
- EC 4.2.1.81 D(-)-tartrate dehydratase
- EC 4.2.1.82 xylonate dehydratase
- EC 4.2.1.83 4-oxalmesaconate hydratase
- EC 4.2.1.84 nitrile hydratase
- EC 4.2.1.85 dimethylmaleate hydratase
- EC 4.2.1.86 16-dehydroprogesterone hydratase
- EC 4.2.1.87 octopamine dehydratase
- EC 4.2.1.88 synephrine dehydratase
- EC 4.2.1.89 carnitine dehydratase
- EC 4.2.1.90 L-rhamnonate dehydratase
- EC 4.2.1.91 carboxycyclohexadienyl dehydratase
- EC 4.2.1.92 hydroperoxide dehydratase
- EC 4.2.1.93 ATP-dependent H4NAD(P)OH dehydratase
- EC 4.2.1.94 scytalone dehydratase
- EC 4.2.1.95 kievitone hydratase
- EC 4.2.1.96 4a-hydroxytetrahydrobiopterin dehydratase
- EC 4.2.1.97 phaseollidin hydratase
- EC 4.2.1.98 16a-hydroxyprogesterone dehydratase
- EC 4.2.1.99 2-methylisocitrate dehydratase
- EC 4.2.1.100 cyclohexa-1,5-dienecarbonyl-CoA hydratase
- EC 4.2.1.101 trans-feruloyl-CoA hydratase
- EC 4.2.1.102 now EC 4.2.1.100
- EC 4.2.1.103 cyclohexyl-isocyanide hydratase
- EC 4.2.1.104 cyanate hydratase
- EC 4.2.2 Acting on Polysaccharides
  - EC 4.2.2.1 hyaluronate lyase
  - EC 4.2.2.2 pectate lyase
  - EC 4.2.2.3 poly(b-D-mannuronate) lyase
  - EC 4.2.2.4 chondroitin ABC lyase
  - EC 4.2.2.5 chondroitin AC lyase
  - EC 4.2.2.6 oligogalacturonide lyase
  - EC 4.2.2.7 heparin lyase
  - EC 4.2.2.8 heparin-sulfate lyase
  - EC 4.2.2.9 pectate disaccharide-lyase
  - EC 4.2.2.10 pectin lyase
  - EC 4.2.2.11 poly(a-L-guluronate) lyase
  - EC 4.2.2.12 xanthan lyase
  - EC 4.2.2.13 exo-(1 4)-a-D-glucan lyase
  - EC 4.2.2.14 glucuronan lyase
- EC 4.2.3 Acting on phosphates
  - EC 4.2.3.1 threonine synthase
  - EC 4.2.3.2 ethanolamine-phosphate phospho-lyase
  - EC 4.2.3.3 methylglyoxal synthase
  - EC 4.2.3.4 3-dehydroquinate synthase
  - EC 4.2.3.5 chorismate synthase
  - EC 4.2.3.6 trichodiene synthase
  - EC 4.2.3.7 pentalenene synthase
  - EC 4.2.3.8 casbene synthase
  - EC 4.2.3.9 aristolochene synthase
  - EC 4.2.3.10 (-)-endo-fenchol synthase
  - EC 4.2.3.11 sabinene-hydrate synthase
  - EC 4.2.3.12 6-pyruvoyltetrahydropterin synthase
  - EC 4.2.3.13 (+)-d-cadinene synthase
  - EC 4.2.3.14 pinene synthase
  - EC 4.2.3.15 myrcene synthase
  - EC 4.2.3.16 (-)-(4S)-limonene synthase
  - EC 4.2.3.17 taxadiene synthase
  - EC 4.2.3.18 abietadiene synthase
  - EC 4.2.3.19 ent-kaurene synthase
- EC 4.2.99 Other Carbon-Oxygen Lyases
  - EC 4.2.99.1 now EC 4.2.2.2
  - EC 4.2.99.2 now EC 4.2.3.1
  - EC 4.2.99.3 now EC 4.2.2.2
  - EC 4.2.99.4 now EC 4.2.2.3
  - EC 4.2.99.5 deleted
  - EC 4.2.99.6 deleted, included in EC 4.2.2.4 and EC 4.2.2.5
  - EC 4.2.99.7 now EC 4.2.3.2
  - EC 4.2.99.8 now EC 2.5.1.47
  - EC 4.2.99.9 now EC 2.5.1.48
  - EC 4.2.99.10 now EC 2.5.1.49
  - EC 4.2.99.11 now EC 4.2.3.3
  - EC 4.2.99.12 carboxymethyloxysuccinate lyase
  - EC 4.2.99.13 now EC 2.5.1.50
  - EC 4.2.99.14 now EC 2.5.1.51
  - EC 4.2.99.15 now EC 2.5.1.52
  - EC 4.2.99.16 now EC 2.5.1.53
  - EC 4.2.99.17 now EC 4.2.99.14
  - EC 4.2.99.18 DNA-(apurinic or apyrimidinic site) lyase
  - EC 4.2.99.19 2-hydroxypropyl-CoM lyase
- EC 4.3 Carbon-Nitrogen Lyases
  - EC 4.3.1 Ammonia-Lyases
    - EC 4.3.1.1 aspartate ammonia-lyase
    - EC 4.3.1.2 methylaspartate ammonia-lyase
    - EC 4.3.1.3 histidine ammonia-lyase
    - EC 4.3.1.4 formiminotetrahydrofolate cyclodeaminase
    - EC 4.3.1.5 phenylalanine ammonia-lyase
    - EC 4.3.1.6 b-alanyl-CoA ammonia-lyase
    - EC 4.3.1.7 ethanolamine ammonia-lyase
    - EC 4.3.1.8 hydroxymethylbilane synthase
    - EC 4.3.1.9 glucosaminate ammonia-lyase
    - EC 4.3.1.10 serine-sulfate ammonia-lyase
    - EC 4.3.1.11 dihydroxyphenylalanine ammonia-lyase
    - EC 4.3.1.12 ornithine cyclodeaminase
    - EC 4.3.1.13 carbamoyl-serine ammonia-lyase
    - EC 4.3.1.14 3-aminobutyryl-CoA ammonia-lyase
    - EC 4.3.1.15 diaminopropionate ammonia-lyase
    - EC 4.3.1.16 threo-3-hydroxyaspartate ammonia-lyase
    - EC 4.3.1.17 L-serine ammonia-lyase
    - EC 4.3.1.18 D-serine ammonia-lyase
    - EC 4.3.1.19 threonine ammonia-lyase
    - EC 4.3.1.20 erythro-3-hydroxyaspartate ammonia-lyase
  - EC 4.3.2 Amidine-Lyases
    - EC 4.3.2.1 argininosuccinate lyase
    - EC 4.3.2.2 adenylosuccinate lyase
    - EC 4.3.2.3 ureidoglycolate lyase
    - EC 4.3.2.4 purine imidazole-ring cyclase
    - EC 4.3.2.5 peptidylamidoglycolate lyase
  - EC 4.3.3 Amine-Lyases
    - EC 4.3.3.1 3-ketovalidoxylamine C-N-lyase
    - EC 4.3.3.2 strictosidine synthase
    - EC 4.3.3.3 deacetylisoipecoside synthase
    - EC 4.3.3.4 deacetylipecoside synthase

- EC 4.3.99 Other Carbon-Nitrogen Lyases
    - EC 4.3.99.1 now EC 4.2.1.104
- EC 4.4 Carbon-Sulfur Lyases
    - EC 4.4.1.1 cystathionine g-lyase
    - EC 4.4.1.2 homocysteine desulfhydrase
    - EC 4.4.1.3 dimethylpropiothetin dethiomethylase
    - EC 4.4.1.4 alliin lyase
    - EC 4.4.1.5 lactoylglutathione lyase
    - EC 4.4.1.6 S-alkylcysteine lyase
    - EC 4.4.1.7 deleted, included in EC 2.5.1.18
    - EC 4.4.1.8 cystathionine b-lyase
    - EC 4.4.1.9 L-3-cyanoalanine synthase
    - EC 4.4.1.10 cysteine lyase
    - EC 4.4.1.11 methionine g-lyase
    - EC 4.4.1.12 sulfoacetaldehyde lyase
    - EC 4.4.1.13 cysteine-S-conjugate b-lyase
    - EC 4.4.1.14 1-aminocyclopropane-1-carboxylate synthase
    - EC 4.4.1.15 D-cysteine desulfhydrase
    - EC 4.4.1.16 selenocysteine lyase
    - EC 4.4.1.17 holocytochrome-c synthase
    - EC 4.4.1.18 now EC 1.8.3.5
- EC 4.5 Carbon-Halide Lyases
    - EC 4.5.1.1 DDT-dehydrochlorinase
    - EC 4.5.1.2 3-chloro-D-alanine dehydrochlorinase
    - EC 4.5.1.3 dichloromethane dehalogenase
    - EC 4.5.1.4 L-2-amino-4-chloropent-4-enoate dehydrochlorinase
    - EC 4.5.1.5 S-carboxymethylcysteine synthase
- EC 4.6 Phosphorus-Oxygen Lyases
    - EC 4.6.1.1 adenylate cyclase
    - EC 4.6.1.2 guanylate cyclase
    - EC 4.6.1.3 now EC 4.2.3.4
    - EC 4.6.1.4 now EC 4.2.3.5
    - EC 4.6.1.5 now EC 4.2.3.7
    - EC 4.6.1.6 cytidylate cyclase
    - EC 4.6.1.7 now EC 4.2.3.8
    - EC 4.6.1.8 now EC 4.2.3.10
    - EC 4.6.1.9 now EC 4.2.3.11
    - EC 4.6.1.10 now EC 4.2.3.12
    - EC 4.6.1.11 now EC 4.2.3.13
    - EC 4.6.1.12 2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase
    - EC 4.6.1.13 phosphatidylinositol diacylglycerol-lyase
    - EC 4.6.1.14 glycosylphosphatidylinositol diacylglycerol-lyase
    - EC 4.6.1.15 FAD-AMP lyase (cyclizing)
- EC 4.99 Other Lyases
    - EC 4.99.1.1 ferrochelatase
    - EC 4.99.1.2 alkylmercury lyase
- **EC 5 Isomerases**
- EC 5.1 Racemases and Epimerases
    - EC 5.1.1 Acting on Amino Acids and Derivatives
        - EC 5.1.1.1 alanine racemase
        - EC 5.1.1.2 methionine racemase
        - EC 5.1.1.3 glutamate racemase
        - EC 5.1.1.4 proline racemase
        - EC 5.1.1.5 lysine racemase
        - EC 5.1.1.6 threonine racemase
        - EC 5.1.1.7 diaminopimelate epimerase
        - EC 5.1.1.8 4-hydroxyproline epimerase
        - EC 5.1.1.9 arginine racemase
        - EC 5.1.1.10 amino-acid racemase
        - EC 5.1.1.11 phenylalanine racemase (ATP-hydrolysing)
        - EC 5.1.1.12 ornithine racemase
        - EC 5.1.1.13 aspartate racemase
        - EC 5.1.1.14 nocardicin-A epimerase
        - EC 5.1.1.15 2-aminohexano-6-lactam racemase
        - EC 5.1.1.16 protein-serine epimerase
        - EC 5.1.1.17 isopenicillin-N epimerase
    - EC 5.1.2 Acting on Hydroxy Acids and Derivatives
        - EC 5.1.2.1 lactate racemase
        - EC 5.1.2.2 mandelate racemase
        - EC 5.1.2.3 3-hydroxybutyryl-CoA epimerase
        - EC 5.1.2.4 acetoin racemase
        - EC 5.1.2.5 tartrate epimerase
        - EC 5.1.2.6 isocitrate epimerase
    - EC 5.1.3 Acting on Carbohydrates and Derivatives
        - EC 5.1.3.1 ribulose-phosphate 3-epimerase
        - EC 5.1.3.2 UDP-glucose 4-epimerase
        - EC 5.1.3.3 aldose 1-epimerase
        - EC 5.1.3.4 L-ribulose-phosphate 4-epimerase
        - EC 5.1.3.5 UDP-arabinose 4-epimerase
        - EC 5.1.3.6 UDP-glucuronate 4-epimerase
        - EC 5.1.3.7 UDP-N-acetylglucosamine 4-epimerase
        - EC 5.1.3.8 N-acylglucosamine 2-epimerase
        - EC 5.1.3.9 N-acylglucosamine-6-phosphate 2-epimerase
        - EC 5.1.3.10 CDP-abequose epimerase
        - EC 5.1.3.11 cellobiose epimerase
        - EC 5.1.3.12 UDP-glucuronate 5'-epimerase
        - EC 5.1.3.13 dTDP-4-dehydrorhamnose 3,5-epimerase
        - EC 5.1.3.14 UDP-N-acetylglucosamine 2-epimerase
        - EC 5.1.3.15 glucose-6-phosphate 1-epimerase
        - EC 5.1.3.16 UDP-glucosamine 4-epimerase
        - EC 5.1.3.17 heparosan-N-sulfate-glucuronate 5-epimerase
        - EC 5.1.3.18 GDP-mannose 3,5-epimerase
        - EC 5.1.3.19 chondroitin-glucuronate 5-epimerase
        - EC 5.1.3.20 ADP-glyceromanno-heptose 6-epimerase
        - EC 5.1.3.21 maltose epimerase
    - EC 5.1.99 Acting on Other Compounds
        - EC 5.1.99.1 methylmalonyl-CoA epimerase
        - EC 5.1.99.2 16-hydroxysteroid epimerase
        - EC 5.1.99.3 allantoin racemase
        - EC 5.1.99.4 a-methylacyl-CoA racemase
- EC 5.2 cis-trans-Isomerases
    - EC 5.2.1.1 maleate isomerase
    - EC 5.2.1.2 maleylacetoacetate isomerase
    - EC 5.2.1.3 retinal isomerase
    - EC 5.2.1.4 maleylpyruvate isomerase
    - EC 5.2.1.5 linoleate isomerase
    - EC 5.2.1.6 furylfuramide isomerase
    - EC 5.2.1.7 retinol isomerase
    - EC 5.2.1.8 peptidylprolyl isomerase
    - EC 5.2.1.9 farnesol 2-isomerase
    - EC 5.2.1.10 2-chloro-4-carboxymethylenebut-2-en-1,4-olide isomerase
    - EC 5.2.1.11 4-hydroxyphenylacetaldehyde-oxime isomerase
- EC 5.3 Intramolecular Oxidoreductases
    - EC 5.3.1 Interconverting Aldoses and Ketoses
        - EC 5.3.1.1 triose-phosphate isomerase
        - EC 5.3.1.2 deleted
        - EC 5.3.1.3 arabinose isomerase
        - EC 5.3.1.4 L-arabinose isomerase
        - EC 5.3.1.5 xylose isomerase
        - EC 5.3.1.6 ribose-5-phosphate isomerase
        - EC 5.3.1.7 mannose isomerase
        - EC 5.3.1.8 mannose-6-phosphate isomerase
        - EC 5.3.1.9 glucose-6-phosphate isomerase
        - EC 5.3.1.10 now EC 3.5.99.6
        - EC 5.3.1.11 deleted
        - EC 5.3.1.12 glucuronate isomerase
        - EC 5.3.1.13 arabinose-5-phosphate isomerase
        - EC 5.3.1.14 L-rhamnose isomerase
        - EC 5.3.1.15 D-lyxose ketol-isomerase
        - EC 5.3.1.16 1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino)imidazole-4-carboxamide isomerase
        - EC 5.3.1.17 4-deoxy-L-threo-5-hexosulose-uronate ketol-isomerase
        - EC 5.3.1.18 deleted
        - EC 5.3.1.19 now EC 2.6.1.16
        - EC 5.3.1.20 ribose isomerase
        - EC 5.3.1.21 corticosteroid side-chain-isomerase
        - EC 5.3.1.22 hydroxypyruvate isomerase
        - EC 5.3.1.23 5-methylthioribose-1-phosphate isomerase
        - EC 5.3.1.24 phosphoribosylanthranilate isomerase
        - EC 5.3.1.25 L-fucose isomerase
        - EC 5.3.1.26 galactose-6-phosphate isomerase
    - EC 5.3.2 Interconverting Keto- and Enol-Groups
        - EC 5.3.2.1 phenylpyruvate tautomerase
        - EC 5.3.2.2 oxaloacetate tautomerase
    - EC 5.3.3 Transposing C=C Bonds
        - EC 5.3.3.1 steroid D-isomerase
        - EC 5.3.3.2 isopentenyl-diphosphate D-isomerase
        - EC 5.3.3.3 vinylacetyl-CoA D-isomerase
        - EC 5.3.3.4 muconolactone D-isomerase
        - EC 5.3.3.5 cholestenol D-isomerase
        - EC 5.3.3.6 methylitaconate D-isomerase
        - EC 5.3.3.7 aconitate D-isomerase
        - EC 5.3.3.8 dodecenoyl-CoA D-isomerase
        - EC 5.3.3.9 prostaglandin-A1 D-isomerase
        - EC 5.3.3.10 5-carboxymethyl-2-hydroxymuconate D-isomerase
        - EC 5.3.3.11 isopiperitenone D-isomerase
        - EC 5.3.3.12 dopachrome isomerase

- EC 5.3.4 Transposing S-S Bonds
    - EC 5.3.4.1 protein disulfide-isomerase
- EC 5.3.99 Other Intramolecular Oxidoreductases
    - EC 5.3.99.1 deleted
    - EC 5.3.99.2 prostaglandin-D synthase
    - EC 5.3.99.3 prostaglandin-E synthase
    - EC 5.3.99.4 prostaglandin-I synthase
    - EC 5.3.99.5 thromboxane-A synthase
    - EC 5.3.99.6 allene-oxide cyclase
    - EC 5.3.99.7 styrene-oxide isomerase

EC 5.4 Intramolecular Transferases

- EC 5.4.1 Transferring Acyl Groups
    - EC 5.4.1.1 lysolecithin acylmutase
    - EC 5.4.1.2 precorrin-8X methylmutase
- EC 5.4.2 Phosphotransferases (Phosphomutases)
    - EC 5.4.2.1 phosphoglycerate mutase
    - EC 5.4.2.2 phosphoglucomutase
    - EC 5.4.2.3 phosphoacetylglucosamine mutase
    - EC 5.4.2.4 bisphosphoglycerate mutase
    - EC 5.4.2.5 phosphoglucomutase (glucose-cofactor)
    - EC 5.4.2.6 b-phosphoglucomutase
    - EC 5.4.2.7 phosphopentomutase
    - EC 5.4.2.8 phosphomannomutase
    - EC 5.4.2.9 phosphoenolpyruvate mutase
    - EC 5.4.2.10 phosphoglucosamine mutase
- EC 5.4.3 Transferring Amino Groups
    - EC 5.4.3.1 deleted
    - EC 5.4.3.2 lysine 2,3-aminomutase
    - EC 5.4.3.3 b-lysine 5,6-aminomutase
    - EC 5.4.3.4 D-lysine 5,6-aminomutase
    - EC 5.4.3.5 D-ornithine 4,5-aminomutase
    - EC 5.4.3.6 tyrosine 2,3-aminomutase
    - EC 5.4.3.7 leucine 2,3-aminomutase
    - EC 5.4.3.8 glutamate-1-semialdehyde 2,1-aminomutase
- EC 5.4.99 Transferring Other Groups
    - EC 5.4.99.1 methylaspartate mutase
    - EC 5.4.99.2 methylmalonyl-CoA mutase
    - EC 5.4.99.3 2-acetolactate mutase
    - EC 5.4.99.4 2-methyleneglutarate mutase
    - EC 5.4.99.5 chorismate mutase
    - EC 5.4.99.6 isochorismate synthase
    - EC 5.4.99.7 lanosterol synthase
    - EC 5.4.99.8 cycloartenol synthase
    - EC 5.4.99.9 UDP-galactopyranose mutase
    - EC 5.4.99.10 deleted, included in EC 5.4.99.11
    - EC 5.4.99.11 isomaltulose synthase
    - EC 5.4.99.12 tRNA-pseudouridine synthase I
    - EC 5.4.99.13 isobutyryl-CoA mutase
    - EC 5.4.99.14 4-carboxymethyl-4-methylbutenolide mutase
    - EC 5.4.99.15 (1,4)-a-D-glucan 1-a-D-glucosylmutase
    - EC 5.4.99.16 maltose a-D-glucosyltransferase
    - EC 5.4.99.17 squalene—hopene cyclase

EC 5.5 Intramolecular Lyases

- EC 5.5.1.1 muconate cycloisomerase
- EC 5.5.1.2 3-carboxy-cis,cis-muconate cycloisomerase
- EC 5.5.1.3 tetrahydroxypteridine cycloisomerase
- EC 5.5.1.4 inositol-3-phosphate synthase
- EC 5.5.1.5 carboxy-cis,cis-muconate cyclase
- EC 5.5.1.6 chalcone isomerase
- EC 5.5.1.7 chloromuconate cycloisomerase
- EC 5.5.1.8 geranyl-diphosphate cyclase
- EC 5.5.1.9 cycloeucalenol cycloisomerase
- EC 5.5.1.10 a-pinene-oxide decyclase
- EC 5.5.1.11 dichloromuconate cycloisomerase
- EC 5.5.1.12 copalyl diphosphate synthase
- EC 5.5.1.13 ent-copalyl diphosphate synthase

EC 5.99 Other Isomerases

- EC 5.99.1.1 thiocyanate isomerase
- EC 5.99.1.2 DNA topoisomerase
- EC 5.99.1.3 DNA topoisomerase (ATP-hydrolysing)

EC 6 Ligases

EC 6.1 Forming Carbon-Oxygen Bonds

- EC 6.1.1 Ligases Forming Aminoacyl-tRNA and Related Compounds
    - EC 6.1.1.1 tyrosine—tRNA ligase
    - EC 6.1.1.2 tryptophan—tRNA ligase
    - EC 6.1.1.3 threonine—tRNA ligase
    - EC 6.1.1.4 leucine—tRNA ligase
    - EC 6.1.1.5 isoleucine—tRNA ligase
    - EC 6.1.1.6 lysine—tRNA ligase
    - EC 6.1.1.7 alanine—tRNA ligase
    - EC 6.1.1.8 deleted
    - EC 6.1.1.9 valine—tRNA ligase
    - EC 6.1.1.10 methionine—tRNA ligase
    - EC 6.1.1.11 serine—tRNA ligase
    - EC 6.1.1.12 aspartate—tRNA ligase
    - EC 6.1.1.13 D-alanine-poly(phosphoribitol) ligase
    - EC 6.1.1.14 glycine—tRNA ligase
    - EC 6.1.1.15 proline—tRNA ligase
    - EC 6.1.1.16 cysteine—tRNA ligase
    - EC 6.1.1.17 glutamate—tRNA ligase
    - EC 6.1.1.18 glutamine—tRNA ligase
    - EC 6.1.1.19 arginine—tRNA ligase
    - EC 6.1.1.20 phenylalanine—tRNA ligase
    - EC 6.1.1.21 histidine—tRNA ligase
    - EC 6.1.1.22 asparagine—tRNA ligase
    - EC 6.1.1.23 aspartate—tRNAAsn ligase
    - EC 6.1.1.24 glutamate—tRNAGln ligase
    - EC 6.1.1.25 lysine—tRNAPyl ligase

EC 6.2 Forming Carbon-Sulfur Bonds

- EC 6.2.1 Acid-Thiol Ligases
    - EC 6.2.1.1 acetate—CoA ligase
    - EC 6.2.1.2 butyrate—CoA ligase
    - EC 6.2.1.3 long-chain-fatty-acid—CoA ligase
    - EC 6.2.1.4 succinate—CoA ligase (GDP-forming)
    - EC 6.2.1.5 succinate—CoA ligase (ADP-forming)
    - EC 6.2.1.6 glutarate—CoA ligase
    - EC 6.2.1.7 cholate—CoA ligase
    - EC 6.2.1.8 oxalate—CoA ligase
    - EC 6.2.1.9 malate—CoA ligase
    - EC 6.2.1.10 acid—CoA ligase (GDP-forming)
    - EC 6.2.1.11 biotin—CoA ligase
    - EC 6.2.1.12 4-coumarate—CoA ligase
    - EC 6.2.1.13 acetate—CoA ligase (ADP-forming)
    - EC 6.2.1.14 6-carboxyhexanoate—CoA ligase
    - EC 6.2.1.15 arachidonate—CoA ligase
    - EC 6.2.1.16 acetoacetate—CoA ligase
    - EC 6.2.1.17 propionate—CoA ligase
    - EC 6.2.1.18 citrate—CoA ligase
    - EC 6.2.1.19 long-chain-fatty-acid—luciferin-component ligase
    - EC 6.2.1.20 long-chain-fatty-acid—[acyl-carrier-protein] ligase
    - EC 6.2.1.21 covered by EC 6.2.1.30
    - EC 6.2.1.22 [citrate (pro-3S)-lyase] ligase
    - EC 6.2.1.23 dicarboxylate—CoA ligase
    - EC 6.2.1.24 phytanate—CoA ligase
    - EC 6.2.1.25 benzoate—CoA ligase
    - EC 6.2.1.26 o-succinylbenzoate—CoA ligase
    - EC 6.2.1.27 4-hydroxybenzoate—CoA ligase
    - EC 6.2.1.28 3a,7a-dihydroxy-5b-cholestanate—CoA ligase
    - EC 6.2.1.29 3a,7a,12a-trihydroxy-5b-cholestanate—CoA ligase
    - EC 6.2.1.30 phenylacetate—CoA ligase
    - EC 6.2.1.31 2-furoate—CoA ligase
    - EC 6.2.1.32 anthranilate—CoA ligase
    - EC 6.2.1.33 4-chlorobenzoate—CoA ligase
    - EC 6.2.1.34 trans-feruloyl-CoA synthase

EC 6.3 Forming Carbon-Nitrogen Bonds

- EC 6.3.1 Acid-Ammonia (or Amide) Ligases (Amide Synthases)
    - EC 6.3.1.1 aspartate—ammonia ligase
    - EC 6.3.1.2 glutamate—ammonia ligase
    - EC 6.3.1.3 now EC 6.3.4.13
    - EC 6.3.1.4 aspartate—ammonia ligase (ADP-forming)
    - EC 6.3.1.5 NAD synthase
    - EC 6.3.1.6 glutamate—ethylamine ligase
    - EC 6.3.1.7 4-methyleneglutamate—ammonia ligase
    - EC 6.3.1.8 glutathionylspermidine synthase
    - EC 6.3.1.9 trypanothione synthase
- EC 6.3.2 Acid-D-Amino-Acid Ligases (Peptide Synthases)
    - EC 6.3.2.1 pantoate—b-alanine ligase
    - EC 6.3.2.2 glutamate—cysteine ligase
    - EC 6.3.2.3 glutathione synthase
    - EC 6.3.2.4 D-alanine—D-alanine ligase
    - EC 6.3.2.5 phosphopantothenate—cysteine ligase
    - EC 6.3.2.6 phosphoribosylaminoimidazolesuccinocarboxamide synthase
    - EC 6.3.2.7 UDP-N-acetylmuramoyl-L-alanyl-D-glutamate—L-lysine ligase
    - EC 6.3.2.8 UDP-N-acetylmuramate—L-alanine ligase
    - EC 6.3.2.9 UDP-N-acetylmuramoylalanine—D-glutamate ligase
    - EC 6.3.2.10 UDP-N-acetylmuramoylalanyl-tripeptide—D-alanyl-D-alanine ligase

    - EC 6.3.2.11 carnosine synthase
    - EC 6.3.2.12 dihydrofolate synthase
    - EC 6.3.2.13 UDP-N-acetylmuramoylalanyl-D-glutamate—2,6-diamino-pimelate ligase
    - EC 6.3.2.14 2,3-dihydroxybenzoate—serine ligase
    - EC 6.3.2.15 deleted, due to EC 6.3.2.10
    - EC 6.3.2.16 D-alanine—alanyl-poly(glycerolphosphate) ligase
    - EC 6.3.2.17 tetrahydrofolylpolyglutamate synthase
    - EC 6.3.2.18 g-glutamylhistamine synthase
    - EC 6.3.2.19 ubiquitin—protein ligase
    - EC 6.3.2.20 indoleacetate—lysine synthetase
    - EC 6.3.2.21 ubiquitin—calmodulin ligase
    - EC 6.3.2.22 diphthine—ammonia ligase
    - EC 6.3.2.23 homoglutathione synthase
    - EC 6.3.2.24 tyrosine—arginine ligase
    - EC 6.3.2.25 tubulin—tyrosine ligase
    - EC 6.3.2.26 N-(5-amino-5-carboxypentanoyl)-L-cysteinyl-D-valine synthase
    - EC 6.3.2.27 aerobactin synthase
  - EC 6.3.3 Cyclo-Ligases
    - EC 6.3.3.1 phosphoribosylformylglycinamidine cyclo-ligase
    - EC 6.3.3.2 5-formyltetrahydrofolate cyclo-ligase
    - EC 6.3.3.3 dethiobiotin synthase
  - EC 6.3.4 Other Carbon-Nitrogen Ligases
    - EC 6.3.4.1 GMP synthase
    - EC 6.3.4.2 CTP synthase
    - EC 6.3.4.3 formate—tetrahydrofolate ligase
    - EC 6.3.4.4 adenylosuccinate synthase
    - EC 6.3.4.5 argininosuccinate synthase
    - EC 6.3.4.6 urea carboxylase
    - EC 6.3.4.7 ribose-5-phosphate—ammonia ligase
    - EC 6.3.4.8 imidazoleacetate—phosphoribosyldiphosphate ligase
    - EC 6.3.4.9 biotin—[methylmalonyl-CoA-carboxyltransferase] ligase
    - EC 6.3.4.10 biotin—[propionyl-CoA-carboxylase (ATP-hydrolysing)] ligase
    - EC 6.3.4.11 biotin—[methylcrotonoyl-CoA-carboxylase] ligase
    - EC 6.3.4.12 glutamate—methylamine ligase
    - EC 6.3.4.13 phosphoribosylamine—glycine ligase
    - EC 6.3.4.14 biotin carboxylase
    - EC 6.3.4.15 biotin—[acetyl-CoA-carboxylase] ligase
    - EC 6.3.4.16 carbamoyl-phosphate synthase (ammonia)
    - EC 6.3.4.17 formate—dihydrofolate ligase
  - EC 6.3.5 Carbon-Nitrogen Ligases with Glutamine as Amido-N-Donor
    - EC 6.3.5.1 NAD synthase (glutamine-hydrolysing)
    - EC 6.3.5.2 GMP synthase (glutamine-hydrolysing)
    - EC 6.3.5.3 phosphoribosylformylglycinamidine synthase
    - EC 6.3.5.4 asparagine synthase (glutamine-hydrolysing)
    - EC 6.3.5.5 carbamoyl-phosphate synthase (glutamine-hydrolysing)
    - EC 6.3.5.6 asparaginyl-tRNA synthase (glutamine-hydrolysing)
    - EC 6.3.5.7 glutaminyl-tRNA synthase (glutamine-hydrolysing)
- EC 6.4 Forming Carbon-Carbon Bonds
    - EC 6.4.1.1 pyruvate carboxylase
    - EC 6.4.1.2 acetyl-CoA carboxylase
    - EC 6.4.1.3 propionyl-CoA carboxylase
    - EC 6.4.1.4 methylcrotonoyl-CoA carboxylase
    - EC 6.4.1.5 geranoyl-CoA carboxylase
    - EC 6.4.1.6 acetone carboxylase
- EC 6.5 Forming Phosphoric Ester Bonds
    - EC 6.5.1.1 DNA ligase (ATP)
    - EC 6.5.1.2 DNA ligase (NAD)
    - EC 6.5.1.3 RNA ligase (ATP)
    - EC 6.5.1.4 RNA-3'-phosphate cyclase

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The genome of *Bacillus cereus* 14579: a local analysis (U)

4. AUTHORS (Last name, first name, middle initial. If military, show rank, e.g. Doe, Maj. John E.)

Berger, Bradley J.

5. DATE OF PUBLICATION (month and year of publication of document)

October 2003

6a. NO. OF PAGES (total containing information, include Annexes, Appendices, etc) 218

6b. NO. OF REFS (total cited in document) 28

7. DESCRIPTIVE NOTES (the category of the document, e.g. technical report, technical note or memorandum. If appropriate, enter the type of report, e.g. interim, progress, summary, annual or final. Give the inclusive dates when a specific reporting period is covered.)

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9a. PROJECT OR GRANT NO. (If appropriate, the applicable research and development project or grant number under which the document was written. Please specify whether project or grant.)

CBD-01-013

9b. CONTRACT NO. (If appropriate, the applicable number under which the document was written.)

10a. ORIGINATOR'S DOCUMENT NUMBER (the official document number by which the document is identified by the originating activity. This number must be unique to this document.)

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Due to its close genetic and biochemical identity to *Bacillus anthracis*, *B. cereus* can be used as a lower risk pathogen in order to model anthrax biochemistry. The recent sequencing of the *B. cereus* 14579 genome has assisted in this process. This report presents the results of a locally performed analysis and annotation of the *B. cereus* 14579 genome. 4885 putative open reading frames were detected, with 2946 of these identified through homology searching. These identified gene products were then used for metabolic reconstruction of the organism, with an emphasis on potential enzymes involved in regenerating methionine from methylthioadenosine. The present results demonstrate the ease and utility of local genome analysis as a tool for assisting in research studies at DRDC Suffield.

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Bacillus cereus, genome, rRNA genes, tRNA genes, protein-encoding genes, metabolic pathways, methionine recycling, partial genome alignment