For regulon reconstruction we started from collections of known TFs in *Escherichia coli* and *Shewanella* species and identification of their orthologs. Collections of TFs were obtained from RegulonDB (Gama-Castro, et al. 2016) for *E. coli* and the RegPrecise (Novichkov et al., 2013) for *Shewanella* spp. For subsequent reconstruction steps we used genomes from MicrobesOnline (Dehal, et al. 2010) database because the RegPredict platform for reconstruction of transcription regulation is linked with genomes in MicrobesOnline. In each taxonomic group, from 4 to 16 representative genomes were selected based on the MicrobesOnline species tree. Closely related strains were eliminated from our analysis to
avoid skews in the consistency check approach and to simplify the simultaneous analysis in the RegPredict web server. At that we preferably selected most well studied genome representative in each set of closely-related genomes. Next we searched for orthologous TFs in the selected genomes using the bidirectional best hits approach and protein BLAST server at NCBI (Altschul, et al. 1997).

For regulon reconstruction in each group of genomes possessing TF orthologs we used standard comparative genomics approach (Rodionov 2007) that consists of the next steps:

1. Obtain training set of potential TFBS;
2. Build positional weight matrix (PWM);
3. Whole-genomic search for additional TFBSs and regulon members;
4. False positive filtering;
5. PWM refinement and continue from step 2.

For collection of training sets we used two strategies. (i) For studied known regulons we collected upstream regions of known to be regulated genes with attention for more precise information about location of TFBSs (as electrophoretic mobility shift assay or DNase footprinting assay). (ii) For novel TF regulons, we used genomic context analysis where we predicted regulation of neighborhood genes by their conservative co-localization in one locus mapped to phylogenetic tree of TF. Another approach is functional analysis based on assumption that genes from one metabolic pathway or one process should be regulated simultaneously. Based on this approach we taken upstreams of genes from one process. Association of TF with regulation was made by conservative co-localization of TF gene with genes from this pathway.

Collected upstream regions were used to identify a common DNA motif using the Discover Profiles tool in the RegPredict platform (Novichkov et al., 2010). We searched for DNA motifs either palindromic or tandem repeat symmetry. Sequences of identified DNA motif sites were used to build PWM. The constructed PWMs were further used to search for additional potential TFBSs across upstreams of all genes in genomes using the RegPredict server. Typically we searched the regions beginning 400 nt upstream to and ending 50 nt downstream to the translational start of each gene. Typical threshold for site search procedure was selected as 10% less of the lowest site score from the training set.

The whole genomic searches in RegPredict result in construction of a set of CRONs (Clusters of co-Regulated Orthologous operoNs). Each CRONs in RegPredict was built by the following algorithm: 1) PWM found potential TFBSs above threshold; 2) operon predicted by taking gene with potential TFBS as the first gene of operon and prolong operon to all genes with the same direction and intergenic distance less than 200 nt; 3) identification of orthologs and paralogs for each gene in this operon based on Orthologous Groups in MicrobesOnline database; 4) steps 2 and 3 repeated until convergence. Automatic construction of CRONs and manual curation of the obtained CRONs in the RegPredict server allowed us to filter out false positive site predictions by utilizing the consistency check approach. The consistency check approach is based on the assumption that true sites are conserved in evolution. It should be noted that the cases of operon gene content rearrangement are also taken into consideration in the course of CRON analysis and curation. On next step, the identified true positive TFBSs were added to refine PWM and further repeat the genomic site searches.

At the final step of the manual regulon annotation, gene functions are assigned using the existing gene annotations in Genbank and SEED databases (Overbeek, et al. 2005), annotations of homologous proteins in SwissProt / UniProt database (UniProt 2015) and analysis of Pfam domains (Finn, et al. 2016). All reconstructed regulons were finally deposited in the latest release of the RegPecise database (http://regprecise.lbl.gov) (Novichkov, et al. 2013).
| TF        | α-proteobacteria | γ-proteobacteria | β-proteobacteria | δ-proteobacteria | TOTAL regulons |
|----------|------------------|------------------|------------------|------------------|----------------|
| ArgR     | +                | 12 10 9 16 9 6   | 0 0 0 0 0        | 0 0 0            | 6 62           |
| BirA     | +                | 12 10 9 16 9 6   | 11 8 0 3 0      | 8 0 0            | 7 10 11 94     |
| FabR     | +                | 12 10 8 16 9 4   | 6 8 2 3 0       | 0 0 0            | 0 0 3 8 10 78  |
| FadP     | -                | 0 0 0 0 0        | 0 0 0 0 6       | 8 11 0 0 0      | 0 0 2 25 3 25  |
| FadR     | +                | 12 10 9 16 9 5   | 0 0 0 0 0       | 0 0 0            | 0 0 6 61       |
| GlcC     | +                | 1 0 0 0 0       | 0 3 6 0 0       | 4 0 2 6 1       | 0 0 7 23       |
| HexR     | +                | 11 10 0 16 5 6   | 6 16 0 6 8 9 2  | 0 0 0            | 0 0 13 95      |
| HmgQ     | -                | 0 0 0 0 0       | 0 0 0 0 0       | 0 0 0            | 0 0 2 17       |
| HmgR     | -                | 0 0 0 0 0       | 0 0 0 0 0       | 0 0 0            | 0 0 1 5        |
| HmgS     | -                | 0 0 0 0 0       | 0 0 0 0 0       | 0 0 0            | 0 0 1 3        |
| HutC     | -                | 8 10 0 16 8 4    | 3 6 2 3 6 8 7 1 | 10 10 5 2        | 4 0 18 113     |
| Hypr     | -                | 1 1 0 16 3 3 2 1 | 1 0 0 1 3 0 6 8 | 1 0 0           | 0 0 13 46      |
| LiuQ     | -                | 0 0 0 0 0       | 0 0 0 0 0       | 0 0 0            | 0 0 3 14       |
| LiuR     | +                | 0 6 0 16 8 2     | 6 8 0 0 6 2     | 10 5 9 13 3 6 4 | 0 0 16 104     |
| LidR     | +                | 5 0 0 0 0       | 0 4 7 2 1       | 4 8 3 5 0 2 4 0 | 6 4 13 55      |
| MetJ     | +                | 12 10 9 16 9 6   | 0 0 0 0 0       | 0 0 0            | 0 0 6 62       |
| MetR     | +                | 12 10 8 16 4 5   | 12 8 0 3 6 7 5 8 | 0 13 0 0       | 0 0 14 117     |
| NadQ     | -                | 0 0 0 0 0       | 0 0 0 0 2       | 0 2 1 2 2 7 0 4 | 0 0 7 30       |
| NadR     | +                | 11 0 0 0 0      | 0 0 0 0 0       | 0 0 0            | 0 0 1 11       |
| NagC     | +                | 12 10 2 0 6    | 1 0 0 0 0       | 0 0 0            | 0 0 5 31       |
| NagQ     | -                | 0 0 0 0 0       | 0 3 2 0 2 1 7 0 | 1 7 4 1 0 3 0 0 | 0 0 10 31      |
| NagR     | -                | 0 0 0 15 3 0    | 3 0 0 4 0       | 0 0 0            | 0 0 4 25       |
| NrdR     | +                | 12 10 9 16 9 6   | 12 8 4 4 6 8 11 | 12 15 15 9 7 4 0 | 9 20 186      |
| NrtC     | -                | 1 4 0 3 0       | 3 2 4 2 0       | 0 0 4 2 2 1      | 0 0 11 28      |
| PdhR     | +                | 12 10 0 16 9 6   | 2 0 0 0 0       | 0 0 0            | 0 0 6 55       |
| PsrA     | -                | 8 0 0 16 4 3     | 8 8 0 3 6 8 0 5 | 3 0 0 4 0       | 0 0 12 76      |
| RutR     | +                | 7 2 0 0 5       | 1 8 20 2 0 4 7 | 0 0 9 13 1 0 2 0 | 0 0 17 81      |
| SahR     | -                | 0 0 0 0 0       | 0 9 8 0 0       | 0 0 0            | 0 0 10 2 7 7 4 | 9 6 9 62 |
| SamR     | -                | 0 0 0 0 0       | 0 0 0 4 0       | 0 0 0            | 0 0 0 0 0 0 1 4 |
| TrpR     | +                | 12 10 8 16 0 2 2 | 0 2 1 0 0       | 0 0 0            | 0 0 0 0 8 53   |
| TyrR     | +                | 12 10 9 16 9 4   | 0 7 0 0 0       | 0 0 0            | 0 0 0 0 8 67   |
| TOTAL regulons | 17 20 19 9 19 21 19 21 22 9 12 13 14 12 13 13 15 10 5 9 3 5 | 283 | 189 160 71 290 124 84 115 139 22 35 62 94 75 61 110 104 46 28 33 18 36 1896 |

Figure S52. Taxonomic distribution of studied TF regulons and regulogs in 21 taxonomic groups of Proteobacteria

21 TFs are present in E. coli and/or Shewanella spp. and are conserved in five or more taxonomic groups of Proteobacteria.

12 TFs that represent non-orthologous replacements of the initial set of TFs in some taxonomic groups are marked by asterisk (*).

Each cell represents a TF regulon; each number corresponds to the number of TF regulons per regulon.

Numbers in red font highlight TFs/taxonomic groups that have multiple regulogs represented by paralogous TFs.
**Figure S3.** Conservation of regulatory interactions in the reconstructed regulons. Core, Taxonomy-specific and Genome-specific groups are highlighted with red, green and blue color respectively. Regulon member names are connected with respective dots by dashes. Functional belonging of regulon members is listed in table S3.
Average conservation of regulatory interaction

Number of taxonomic groups with regulatory interaction

Conservation groups
- Core
- Taxonomy
- Genome

ArgR

BirA
Conservation groups
- Core
- Taxonomy
- Genome

Average conservation of regulatory interaction
Number of taxonomic groups with regulatory interaction

**LiuR**

**LldR**
Table S1. Studied genomes and taxonomic groups of Proteobacteria.

| Tax ID | Phylum / Class / Taxonomic collection / Genome | Number of genomes |
|--------|--------------------------------------------|-------------------|
| Phylum | Proteobacteria                               | 196               |
| Class  | Gammaproteobacteria                          | 90                |
|        | Enterobacteriales                            | 12                |
| 511145 | Escherichia coli str. K-12 substr. MG1655    |                   |
| 99287  | Salmonella typhimurium LT2                   |                   |
| 290338 | Citrobacter koseri ATCC BAA-895              |                   |
| 272620 | Klebsiella pneumoniae subsp. pneumoniae MGH 78578 |               |
| 399742 | Enterobacter sp. 638                         |                   |
| 716540 | Erwinia amylovora ATCC 49946                 |                   |
| 187410 | Erwinia amylovora ATCC 49946                 |                   |
| 399741 | Serratia proteamaculans 568                  |                   |
| 218491 | Erwinia carotovora subsp. atroseptica SCRI1043 |               |
| 498217 | Edwardsiella tarda EIB202                   |                   |
| 529507 | Proteus mirabilis HI4320                   |                   |
| 243265 | Photobacterium luminescens subsp. laumondii TTO1 |             |
| Pasteurellales |                           | 9                |
| 71421  | Haemophilus influenzae Rd KW20               |                   |
| 634176 | Aggregatibacter aphrophilus NJ8700           |                   |
| 272843 | Pasteurella multocida subsp. multocida str. Pm70 |              |
| 221988 | Mannheimia succiniciproducens MBEL55E       |                   |
| 339671 | Actinobacillus succinogenes 130Z            |                   |
| 228400 | Haemophilus hominis 2336                    |                   |
| 537457 | Actinobacillus pleuropneumoniae serovar 7 str. AP76 |         |
| 233412 | Haemophilus ducreyi 35000HP                 |                   |
| 557723 | Haemophilus parasuis SH0165                 |                   |
| Vibrionales |                           | 10               |
| 243277 | Vibrio cholerae O1 biovar eltor str. N16961 |                   |
| 216895 | Vibrio vulnificus CMCP6                     |                   |
| 338187 | Vibrio harveyi ATCC BAA-1116                |                   |
| 223926 | Vibrio parahaemolyticus RIMD 2210633       |                   |
| 391591 | Vibrio shilonii AK1                        |                   |
| 575788 | Vibrio splendidus LGP32                    |                   |
| 312309 | Vibrio fischeri ES114                      |                   |
| 316275 | Vibrio salmonicida LFI1238                 |                   |
| 314292 | Vibrio angustum S14                        |                   |
| 298386 | Photobacterium profundum SS9               |                   |
| Psychromonadaceae/Aeromonadales |                          | 6               |
| 357804 | Psychromonas ingrahamii 37                  |                   |
| 314282 | Psychromonas sp. CNPT3                      |                   |
| 58051  | Moritella sp. PE36                         |                   |
| 380703 | Aeromonas hydrophila subsp. hydrophila ATCC 7966 |             |
| 382245 | Aeromonas salmonicida subsp. salmonicida A449 |               |
| 595494 | Tolumonas auensis DSM 9187                 |                   |
| Shewanellaceae |                             | 16              |
| 211586 | Shewanella oneidensis MR-1                 |                   |
| 319224 | Shewanella putrefaciens CN-32              |                   |
| 351745 | Shewanella sp W3-18-1                      |                   |
94122  Shewanella sp ANA-3
60480  Shewanella sp MR-4
60481  Shewanella sp MR-7
325240 Shewanella baltica OS155
318161 Shewanella denitrificans OS217
318167 Shewanella frigidimarina NCIMB 400
326297 Shewanella amazonensis SB2B
323850 Shewanella loihica PV-4
398579 Shewanella pealeana ATCC 700345
458817 Shewanella halifaxensis HAW-EB4
225849 Shewanella piezotolerans WP3
425104 Shewanella sediminis HAW-EB3
392500 Shewanella woodyi ATCC 51908

**Alteromonadales**

9

342610 Pseudoalteromonas atlantica T6c
314275 Alteromonas macleodii 'Deep ecotype'
455436 Glaciecola sp. HTCC2999
167879 Colwellia psychrerythraea 34H
156578 Alteromonadales bacterium TW-7
326442 Pseudoalteromonas haloplanktis TAC125
87626 Pseudoalteromonas tunicata D2
314276 Idiomarina baltica OS145
283942 Idiomarina loihica L2TR

**Oceanospirillales/Alteromonadales**

12

349521 Hahella chejuensis KCTC 2396
351348 Marinobacter aqueolei
270374 Marinobacter sp. ELB17
207949 Oceanobacter sp. RED65
207954 Oceanospirillum sp. MED92
400668 Marinomonas sp. MWYL1
203122 Saccharophagus degradans 2-40
377629 Teredinibacter turnerae T7901
498211 Cellvibrio japonicus Ueda107
290398 Chromohalobacter salexigens DSM 3043
314283 Reinekea sp. MED297
393595 Alcanivorax borkumensis SK2

**Pseudomonadaceae**

8

208964 Pseudomonas aeruginosa PAO1
384676 Pseudomonas entomophila L48
160488 Pseudomonas putida KT2440
223283 Pseudomonas syringae pv. tomato str. DC3000
220664 Pseudomonas fluorescens Pf-5
399739 Pseudomonas mendocina ymp
379731 Pseudomonas stutzeri A1501
322710 Azotobacter vinelandii AvOP

**Moraxellaceae**

4

62977 Acinetobacter sp. ADP1
480119 Acinetobacter baumannii AB0057
259536 Psychrobacter arcticum 273-4
349106 Psychrobacter sp. PRwf-1

**Xanthomonadales**

4
Xylella fastidiosa 9a5c
Xanthomonas axonopodis pv. citri str. 306
Xanthomonas campestris pv. campestris ATCC 33913
Stenotrophomonas maltophilia K279a

**Class**  Betaproteobacteria  **37**

**Ralstonia**  **6**
- Ralstonia eutropha H16
- Cupriavidus taiwanensis
- Ralstonia metallidurans CH34
- Ralstonia eutropha JMP134
- Ralstonia solanacearum GMI1000
- Ralstonia pickettii 12J

**Burkholderia**  **8**
- Burkholderia pseudomallei K96243
- Burkholderia mallei ATCC 23344
- Burkholderia sp. 383
- Burkholderia cepacia AMMD (Burkholderia ambifaria AMMD)
- Burkholderia vietnamiensis G4
- Burkholderia glumae BGR1
- Burkholderia xenovorans LB400
- Burkholderia phymatum STM815

**Comamonaceae**  **11**
- Acidovorax avenae subsp. citrulli AAC00-1
- Acidovorax sp. JS42
- Comamonas testosteroni KF-1
- Delftia acidovorans SPH-1
- Polaromonas naphthalenivorans CJ2
- Polaromonas sp. JS666
- Rhodoferax ferrireducens DSM 15236
- Variovorax paradoxus S110
- Verminephrobacter eiseniae EF01-2
- Methylobium petroleiphilum PM1
- Leptothrix cholodnii SP-6

**Various betaproteobacteria**  **12**
- Azoarcus sp. EbN1
- Thauera sp. MZ1T
- Dechloromonas aromatica RCB
- Nitrosomonas europaea ATCC 19718
- Nitrosospira multiformis ATCC 25196
- Thiobacillus denitrificans
- Chromobacterium violaceum ATCC 12472
- Neisseria meningitidis MC58
- Laribacter hongkongensis HLHK9
- Methylobacillus flagellatus KT
- Methylotenera mobilis JLW8
- Methylphilales bacterium HTCC2181

**Class**  Alphaproteobacteria  **50**

**Rhizobiales**  **15**
- Sinorhizobium meliloti 1021
- Rhizobium sp. NGR234
- Rhizobium leguminosarum bv. viciae 3841
| Number  | Species                                    |
|---------|--------------------------------------------|
| 347834  | Rhizobium etli CFN 42                      |
| 176299  | Agrobacterium tumefaciens str. C58 (Cereon) |
| 266779  | Mesorhizobium sp. BNC1                     |
| 266835  | Mesorhizobium loti MAFF303099             |
| 224914  | Brucella melitensis 16M                    |
| 283165  | Bartonella quintana str. Toulouse          |
| 258594  | Rhodopseudomonas palustris CGA009           |
| 224911  | Bradyrhizobium japonicum USDA 110          |
| 288000  | Bradyrhizobium sp. BTAi1                   |
| 323098  | Nitrobacter winogradskyi Nb-255            |
| 438753  | Azorhizobium caulinodans ORS 571           |
| 78245   | Xanthobacter autotrophicus Py2             |
|         | **Rhodobacterales**                       |
| 272943  | Rhodobacter sphaeroides 2.4.1              |
| 318586  | Paracoccus denitrificans PD1222            |
| 290400  | Jannaschia sp. CCS1                       |
| 314271  | Rhodobacterales bacterium HTCC2654         |
| 314256  | Oceanicola granulosus HTCC2516             |
| 314232  | Loktanella vestfoldensis SKA53             |
| 252305  | Oceanicola batsensis HTCC2597              |
| 89187   | Roseovarius nubinhibens ISM                |
| 314264  | Roseovarius sp. 217                        |
| 52598   | Sulfitobacter sp. EE-36                    |
| 292414  | Silicibacter TM1040                        |
| 246200  | Silicibacter pomeroyi DSS-3                |
| 314262  | Roseobacter sp. MED193                     |
| 228405  | Hyphomonas neptunium ATCC 15444            |
| 314254  | Oceanicaulis alexandrii HTCC2633          |
|         | **Rhodospirillales**                       |
| 269796  | Rhodospirillum rubrum ATCC 11170           |
| 342108  | Magnetospirillum magneticum AMB-1           |
| 272627  | Magnetospirillum magnetotacticum MS-1       |
| 137722  | Azospirillum sp. B510                      |
| 414684  | Rhodospirillum centenum SW                 |
| 272568  | Gluconacetobacter diazotrophicus PAI 5     |
| 634452  | Acetobacter pasteurianus IFO 3283-01       |
| 290633  | Gluconobacter oxydans 621H                 |
| 391165  | Granulibacter bethesdensis CGDNIH1         |
|         | **Sphingomonadales**                       |
| 314225  | Erythrobacter litoralis HTCC2594           |
| 237727  | Erythrobacter sp. NAP1                     |
| 279238  | Novosphingobium aromaticivorans DSM 12444  |
| 317655  | Sphingopyxis alaskensis RB2256             |
| 452662  | Sphingobium japonicum UT265                |
| 392499  | Sphingomonas wittichii RW1                 |
| 264203  | Zymomonas mobilis subsp. mobilis ZM4       |
|         | **Caulobacterales**                        |
| 190650  | Caulobacter crescentus CB15                |
| 509190  | Caulobacter segnis ATCC 21756              |
| 366602  | Caulobacter sp. K31                       |
| 450851  | Phenyllobacterium zucineum HLK1            |
| Class               | Proteobacteria/Delta          | 19 |
|---------------------|------------------------------|----|
| **Desulfovibrionales** | 10                           |    |
| 882                 | Desulfovibrio vulgaris Hildenborough |    |
| 883                 | Desulfovibrio vulgaris str. Miyazaki F |    |
| 207559              | Desulfovibrio desulfuricans G20 |    |
| 525146              | Desulfovibrio desulfuricans subsp. desulfuricans str. ATCC 27774 |    |
| 411464              | Desulfovibrio piger ATCC 29098 |    |
| 526222              | Desulfovibrio salexigens DSM 2638 |    |
| 573370              | Desulfovibrio magneticus RS-1 |    |
| 363253              | Lawsonia intracellularis PHE/MN1-00 |    |
| 525897              | Desulfomicrobium baculatum DSM 4028 |    |
| 485915              | Desulfohalobium retbaense DSM 5692 |    |
| **Desulfuromonadales** | 9                           |    |
| 269799              | Geobacter metallireducens GS-15 |    |
| 243231              | Geobacter sulfurreducens PCA |    |
| 351605              | Geobacter uraniumreducens Rf4 |    |
| 316067              | Geobacter sp. FRC-32 |    |
| 443144              | Geobacter sp. M21 |    |
| 398767              | Geobacter lovleyi SZ |    |
| 338966              | Pelobacter propionicus DSM 2379 |    |
| 338963              | Pelobacter carbinolicus str. DSM 2380 |    |
| 281689              | Desulfuromonas acetoxidans DSM 684 |    |

1 Taxonomic collections are according to the standartized genomic collections in the RegPrecise database.
Table S2. Examples of experimentally studied TFs analyzed in this work.

| TF      | Genome                        | Reference                                                |
|---------|-------------------------------|----------------------------------------------------------|
| ArgR    | *Escherichia coli*             | (Tian et al., 1992; Caldara et al., 2007; Paul et al., 2007; Cho et al., 2015) |
|         | *Salmonella typhimurium*       | (Lu and Abdelal, 1999)                                    |
| BioR    | *Brucella melitensis*          | (Feng et al., 2013)                                      |
|         | *Paracoccus denitrificans*     | (Feng et al., 2015)                                      |
| BirA    | *Escherichia coli*             | (Bower et al., 1995; Xu et al., 1995)                    |
| FabR    | *Escherichia coli*             | (Zhang et al., 2002; Fujita et al., 2007)                |
| FadR    | *Escherichia coli*             | (Di Russo et al., 1992; Fujita et al., 2007)             |
| GlcC    | *Escherichia coli*             | (Pellicer et al., 1999)                                  |
| HexR    | *Shewanella oneidensis*        | (Leyn et al., 2011)                                      |
|         | *Pseudomonas putida*           | (del Castillo et al., 2008; Daddaoua et al., 2009)       |
| HmgR    | *Pseudomonas putida*           | (Arias-Barrau et al., 2004)                              |
| HucC    | *Salmonella typhimurium*       | (Hagen et al., 1975)                                     |
| HypR    | *Sinorhizobium meliloti*       | (White et al., 2012)                                     |
| LldR    | *Pseudomonas aeruginosa*       | (Gao et al., 2012)                                       |
|         | *Escherichia coli*             | (Agullera et al., 2008)                                  |
| MetJ    | *Escherichia coli*             | (Merlin et al., 2002)                                    |
| MetR    | *Escherichia coli*             | (Cai et al., 1989)                                       |
|         | *Vibrio cholerae*              | (Bogard et al., 2012)                                    |
| NadR    | *Salmonella typhimurium*       | (Foster et al., 1990)                                    |
| NagC    | *Escherichia coli*             | (Plumbridge, 1995; 2001)                                 |
| NagQ    | *Xanthomonas campestris*       | (Boulanger et al., 2010)                                 |
| NagR    | *Xanthomonas campestris*       | (Boulanger et al., 2010)                                 |
|         | *Shewanella oneidensis*        | (Rodionov et al., 2011)                                  |
| NrdR    | *Escherichia coli*             | (Torrents et al., 2007)                                  |
|         | *Salmonella typhimurium*       | (Panosa et al., 2010)                                    |
|         | *Pseudomonas aeruginosa*       | (Crespo et al., 2015)                                    |
| NrtR    | *Shewanella oneidensis*        | (Rodionov et al., 2008)                                  |
| NtrC    | *Escherichia coli*             | (Muse and Bender, 1998; Zimmer et al., 2000)             |
| PdhR    | *Escherichia coli*             | (Quail and Guest, 1995; Ogasawara et al., 2007)          |
| PsrA    | *Pseudomonas putida*           | (Kojic et al., 2002; Fonseca et al., 2014)               |
|         | *Pseudomonas aeruginosa*       | (Kang et al., 2009)                                      |
| RutR    | *Escherichia coli*             | (Shimada et al., 2007; Nguyen Ple et al., 2010; Nguyen Le Minh et al., 2015) |
| SahR    | *Desulfovibrio alaskensis*     | (Novichkov et al., 2014)                                 |
| TrpR    | *Escherichia coli*             | (Czernik et al., 1994; Jeeves et al., 1999)              |
| TyrR    | *Escherichia coli*             | (Camakaris and Pittard, 1982; Yang et al., 2002; Yang et al., 2004; Pittard et al., 2005) |
|         | *Enterobacter cloacae*         | (Coulson and Patten, 2015)                               |
| TyrR    | *Citrobacter freundii*         | (Smith and Somerville, 1997)                             |
| PhhR    | *Pseudomonas aeruginosa*       | (Palmer et al., 2010)                                    |
| PhhR    | *Pseudomonas putida*           | (Herrera et al., 2009; Herrera et al., 2010)             |
References:

Aguilera, L., Campos, E., Gimenez, R., Badia, J., Aguilar, J., and Baldoma, L. (2008). Dual role of LldR in regulation of the lldPRD operon, involved in L-lactate metabolism in Escherichia coli. *J Bacteriol* 190, 2997-3005.

Arias-Barrau, E., Olivera, E.R., Luengo, J.M., Fernandez, C., Galan, B., Garcia, J.L., Diaz, E., and Minambres, B. (2004). The homogentisate pathway: a central catabolic pathway involved in the degradation of L-phenylalanine, L-tyrosine, and 3-hydroxyphenylacetate in Pseudomonas putida. *J Bacteriol* 186, 5062-5077.

Bogard, R.W., Davies, B.W., and Mekalanos, J.J. (2012). MetR-regulated Vibrio cholerae metabolism is required for virulence. *MBio* 3.

Boulanger, A., Dejean, G., Lautier, M., Glories, M., Zischek, C., Amlal, M., and Lauber, E. (2010). Identification and regulation of the N-acetylglucosamine utilization pathway of the plant pathogenic bacterium Xanthomonas campestris pv. campestris. *J Bacteriol* 192, 1487-1497.

Bower, S., Perkins, J., Yocum, R.R., Serror, P., Sorokin, A., Rahaim, P., Howitt, C.L., Prasad, N., Ehrlich, S.D., and Pero, J. (1995). Cloning and characterization of the Bacillus subtilis birA gene encoding a repressor of the biotin operon. *J Bacteriol* 177, 2572-2575.

Cai, X.Y., Maxon, M.E., Redfield, B., Glass, R., Brot, N., and Weissbach, H. (1989). Methionine synthesis in Escherichia coli: effect of the MetR protein on metE and metH expression. *Proc Natl Acad Sci U S A* 86, 4407-4411.

Caldara, M., Minh, P.N., Bostoen, S., Massant, J., and Charlier, D. (2007). ArgR-dependent repression of arginine and histidine transport genes in Escherichia coli K-12. *J Mol Biol* 373, 251-267.

Camakaris, H., and Pittard, J. (1982). Autoregulation of the tyrR gene. *J Bacteriol* 150, 70-75.

Cho, S., Cho, Y.B., Kang, T.J., Kim, S.C., Palsson, B., and Cho, B.K. (2015). The architecture of ArgR-DNA complexes at the genome-scale in Escherichia coli. *Nucleic Acids Res* 43, 3079-3088.

Coulson, T.J., and Patten, C.L. (2015). The TyrR transcription factor regulates the divergent akr-ipdC operons of Enterobacter cloacae UW5. *PLoS One* 10, e0121241.

Crespo, A., Pedraz, L., and Torrents, E. (2015). Function of the Pseudomonas aeruginosa NrdR Transcription Factor: Global Transcriptomic Analysis and Its Role on Ribonucleotide Reductase Gene Expression. *PLoS One* 10, e0123571.

Czernik, P.J., Shin, D.S., and Hurlburt, B.K. (1994). Functional selection and characterization of DNA binding sites for trp repressor of Escherichia coli. *J Biol Chem* 269, 27869-27875.

Daddaoua, A., Krell, T., and Ramos, J.L. (2009). Regulation of glucose metabolism in Pseudomonas: the phosphorylative branch and entner-doudoroff enzymes are regulated by a repressor containing a sugar isomerase domain. *J Biol Chem* 284, 21360-21368.

Del Castillo, T., Duque, E., and Ramos, J.L. (2008). A set of activators and repressors control peripheral glucose pathways in Pseudomonas putida to yield a common central intermediate. *J Bacteriol* 190, 2331-2339.

Dirusso, C.C., Heimert, T.L., and Metzger, A.K. (1992). Characterization of FadR, a global transcriptional regulator of fatty acid metabolism in Escherichia coli. Interaction with the fadB promoter is prevented by long chain fatty acyl coenzyme A. *J Biol Chem* 267, 8685-8691.

Feng, Y., Kumar, R., Ravcheev, D.A., and Zhang, H. (2015). Paracoccus denitrificans possesses two BioR homologs having a role in regulation of biotin metabolism. *Microbiologyopen* 4, 644-659.

Feng, Y., Xu, J., Zhang, H., Chen, Z., and Srinivas, S. (2013). Brucella BioR regulator defines a complex regulatory mechanism for bacterial biotin metabolism. *J Bacteriol* 195, 3451-3467.

Fonseca, P., De La Pen, F., and Prieto, M.A. (2014). A role for the regulator PsrA in the polyhydroxyalkanoate metabolism of Pseudomonas putida KT2440. *Int J Biol Macromol* 71, 14-20.

Foster, J.W., Park, Y.K., Penfound, T., Fenger, T., and Spector, M.P. (1990). Regulation of NAD metabolism in Salmonella typhimurium: molecular sequence analysis of the bifunctional nadR regulator and the nadA-pnuC operon. *J Bacteriol* 172, 4187-4196.
Fujita, Y., Matsuoka, H., and Hirooka, K. (2007). Regulation of fatty acid metabolism in bacteria. *Mol Microbiol* 66, 829-839.

Gao, C., Hu, C., Zheng, Z., Ma, C., Jiang, T., Dou, P., Zhang, W., Che, B., Wang, Y., Lv, M., and Xu, P. (2012). Lactate utilization is regulated by the FadR-type regulator LldR in Pseudomonas aeruginosa. *J Bacteriol* 194, 2687-2692.

Hagen, D.C., Gerson, S.L., and Magasanik, B. (1975). Isolation of super-repressor mutants in the histidine utilization system of Salmonella typhimurium. *J Bacteriol* 121, 583-593.

Herrera, M.C., Duque, E., Rodriguez-Herva, J.J., Fernandez-Escamilla, A.M., and Ramos, J.L. (2010). Identification and characterization of the PhhR regulon in Pseudomonas putida. *Environ Microbiol* 12, 1427-1438.

Herrera, M.C., Krell, T., Zhang, X., and Ramos, J.L. (2009). PhhR binds to target sequences at different distances with respect to RNA polymerase in order to activate transcription. *J Mol Biol* 394, 576-586.

Jeeves, M., Evans, P.D., Parslow, R.A., Jaseja, M., and Hyde, E.I. (1999). Studies of the Escherichia coli Trp transcriptional regulator: a case study in Shewanella oneidensis. *J Biol Chem* 286, 35782-35794.

Kang, Y., Lunin, V.V., Skarina, T., Savchenko, A., Schurr, M.J., and Hoang, T.T. (2009). The long-chain fatty acid sensor, PsrA, modulates the expression of rpoS and the III secretion exsCEBA operon in Pseudomonas aeruginosa. *Mol Microbiol* 73, 120-136.

Kojic, M., Aguilar, C., and Venturi, V. (2002). TetR family member psrA directly binds the Pseudomonas rpoS and psrA promoters. *J Bacteriol* 184, 2324-2330.

Leyn, S.A., Li, X., Zheng, Q., Novichkov, P.S., Reed, S., Romine, M.F., Fredrickson, J.K., Yang, C., Osterman, A.L., and Rodionov, D.A. (2011). Control of proteobacterial central carbon metabolism by the HexR transcriptional regulator: a case study in Shewanella oneidensis. *J Biol Chem* 286, 35782-35794.

Lu, C.D., and Abdelal, A.T. (1999). Role of ArgR in activation of the ast operon, encoding enzymes of the arginine succinyltransferase pathway in Salmonella typhimurium. *J Bacteriol* 181, 1934-1938.

Merlin, C., Gardiner, G., Durand, S., and Masters, M. (2002). The Escherichia coli metD locus encodes an ABC transporter which includes Abc (MetN), YaeE (MetI), and YaeC (MetQ). *J Bacteriol* 184, 5513-5517.

Muse, W.B., and Bender, R.A. (1998). The nac (nitrogen assimilation control) gene from Escherichia coli. *J Bacteriol* 180, 1166-1173.

Nguyen Le Minh, P., De Cima, S., Bervoets, I., Maes, D., Rubio, V., and Charlier, D. (2015). Ligand binding specificity of RutR, a member of the TetR family of transcription regulators in Escherichia coli. *FEBS Open Bio* 5, 76-84.

Nguyen Ple, M., Bervoets, I., Maes, D., and Charlier, D. (2010). The protein-DNA contacts in RutR*carAB operator complexes. *Nucleic Acids Res* 38, 6286-6300.

Novichkov, P.S., Li, X., Kuehl, J.V., Deutschbauer, A.M., Arkin, A.P., Price, M.N., and Rodionov, D.A. (2014). Control of methionine metabolism by the SahR transcriptional regulator in Proteobacteria. *Environ Microbiol* 16, 1-8.

Ogasawara, H., Ishida, Y., Yamada, K., Yamamoto, K., and Ishihama, A. (2007). PdhR (pyruvate dehydrogenase complex regulator) controls the respiratory electron transport system in Escherichia coli. *J Bacteriol* 189, 5534-5541.

Palmer, G.C., Palmer, K.L., Jorth, P.A., and Whiteley, M. (2010). Characterization of the Pseudomonas aeruginosa transcriptional response to phenylalanine and tyrosine. *J Bacteriol* 192, 2722-2728.

Panosa, A., Rocia, I., and Gibert, I. (2010). Ribonucleotide reductases of Salmonella typhimurium: transcriptional regulation and differential role in pathogenesis. *PLoS One* 5, e11328.

Paul, L., Mishra, P.K., Blumenthal, R.M., and Matthews, R.G. (2007). Integration of regulatory signals through involvement of multiple global regulators: control of the Escherichia coli gltBDF operon by Lrp, IFF, Crp, and ArgR. *BMC Microbiol* 7, 2.

Pellicer, M.T., Fernandez, C., Badia, J., Aguilar, J., Lin, E.C., and Baldom, L. (1999). Cross-induction of glc and ace operons of Escherichia coli attributable to pathway intersection. Characterization of the glc promoter. *J Biol Chem* 274, 1745-1752.
Pittard, J., Camakaris, H., and Yang, J. (2005). The TyrR regulon. *Mol Microbiol* 55, 16-26.

Plumbridge, J. (1995). Co-ordinated regulation of amino sugar biosynthesis and degradation: the NagC repressor acts as both an activator and a repressor for the transcription of the glmUS operon and requires two separated NagC binding sites. *EMBO J* 14, 3958-3965.

Plumbridge, J. (2001). DNA binding sites for the Mlc and NagC proteins: regulation of nagE, encoding the N-acetylglicosamine-specific transporter in Escherichia coli. *Nucleic Acids Res* 14, 3958-3965.

Quail, M.A., and Guest, J.R. (1995). Purification, characterization and mode of action of PdhR, the transcriptional repressor of the pdhR-aceEF-lpd operon of Escherichia coli. *Mol Microbiol* 15, 519-529.

Rodionov, D.A., De Ingeniis, J., Mancini, C., CIMadmore, F., Zhang, H., Osterman, A.L., and Raffaelli, N. (2008). Transcriptional regulation of NAD metabolism in bacteria: NrtR family of Nudix-related regulators. *Nucleic Acids Res* 36, 2047-2059.

Shimada, T., Hirao, K., Kori, A., Yamamoto, K., and Ishihama, A. (2007). RutR is the uracil/thymine-sensing master regulator of a set of genes for synthesis and degradation of pyrimidines. *Mol Microbiol* 66, 744-757.

Smith, H.Q., and Somerville, R.L. (1997). The tpl promoter of Citrobacter freundii is activated by the TyrR protein. *J Bacteriol* 179, 5914-5921.

Xu, Y., Nenortas, E., and Beckett, D. (1995). Evidence for distinct ligand-bound conformational states of the multifunctional Escherichia coli repressor of biotin biosynthesis. *Biochemistry* 34, 16624-16631.

Yang, J., Camakaris, H., and Pittard, J. (2002). Molecular analysis of tyrosine-and phenylalanine-mediated repression of the tyrB promoter by the TyrR protein of Escherichia coli. *Mol Microbiol* 45, 1407-1419.

Yang, J., Hwang, J.S., Camakaris, H., Irawaty, W., Ishihama, A., and Pittard, J. (2004). Mode of action of the TyrR protein: repression and activation of the tyrP promoter of Escherichia coli. *Mol Microbiol* 52, 243-256.

Zhang, Y.M., Marrakchi, H., and Rock, C.O. (2002). The FabR (YijC) transcription factor regulates unsaturated fatty acid biosynthesis in Escherichia coli. *J Biol Chem* 277, 15558-15565.

Zimmer, D.P., Soupene, E., Lee, H.L., Wendisch, V.F., Khodursky, A.B., Peter, B.J., Bender, R.A., and Kustu, S. (2000). Nitrogen regulatory protein C-controlled genes of Escherichia coli: scavenging as a defense against nitrogen limitation. *Proc Natl Acad Sci U S A* 97, 14674-14679.
Table S3. Reconstructed regulatory interactions and functional annotations for the analyzed TF regulons of Proteobacteria.

| Regulon | Target gene | RI | Taxa | Functional role |
|---------|-------------|----|------|-----------------|
| ArgR    | argH        | 57 | 6    | Argininosuccinate lyase (EC 4.3.2.1) | Arginine biosynthesis |
| ArgR    | argB        | 54 | 6    | Acetylglutamate kinase (EC 2.7.2.8) | Arginine biosynthesis |
| ArgR    | argC        | 53 | 6    | N-acetyl-gamma-glutamyl-phosphate reductase (EC 1.2.1.38) | Arginine biosynthesis |
| ArgR    | argG        | 52 | 5    | Argininosuccinate synthase (EC 6.3.4.5) | Arginine biosynthesis |
| ArgR    | argF        | 52 | 5    | Ornithine carbamoyltransferase (EC 2.1.3.3) | Arginine biosynthesis |
| ArgR    | argA        | 51 | 6    | Arginine biosynthesis transcription regulator ArgR, ArgR family |
| ArgR    | argE        | 42 | 6    | Acetylornithine deacetylase (EC 3.5.1.16) | Arginine biosynthesis |
| ArgR    | artI        | 41 | 5    | Arginine ABC transporter, substrate-binding protein | Arginine transport |
| ArgR    | artQ        | 39 | 5    | Arginine ABC transporter, permease protein 1 | Arginine transport |
| ArgR    | artM        | 39 | 5    | Arginine ABC transporter, permease protein 2 | Arginine transport |
| ArgR    | astD        | 37 | 4    | Succinylglutamic semialdehyde dehydrogenase (EC 1.2.1.71) | Arginine degradation |
| ArgR    | astA        | 37 | 4    | Arginine N-succinyltransferase (EC 2.3.1.109) | Arginine degradation |
| ArgR    | astC        | 31 | 3    | Acetylornithine aminotransferase (EC 2.6.1.11) / N-succinyl-L,L-diaminopimelate aminotransferase (EC 2.6.1.81) | Arginine degradation |
| ArgR    | astB        | 21 | 2    | Succinylarginine dihydratase (EC 3.5.3.23) | Arginine degradation |
| ArgR    | artP        | 28 | 4    | Arginine ABC transporter, ATP-binding protein | Arginine transport |
| ArgR    | carA        | 25 | 4    | Carbamoyl-phosphate synthase small chain (EC 6.3.5.5) | Arginine and pyrimidine biosynthesis |
| ArgR    | carB        | 24 | 4    | Carbamoyl-phosphate synthase large chain (EC 6.3.5.5) | Arginine and pyrimidine biosynthesis |
| ArgR    | argD        | 22 | 3    | Acetylornithine aminotransferase (EC 2.6.1.11) | Arginine biosynthesis |
| ArgR    | gltB        | 34 | 3    | Glutamate synthase [NADPH] large chain (EC 1.4.1.13) | Glutamate biosynthesis |
| ArgR    | gltD        | 33 | 3    | Glutamate synthase [NADPH] small chain (EC 1.4.1.13) | Glutamate biosynthesis |
| ArgR    | argW        | 17 | 2    | Predicted arginine uptake transporter, COG3314 family | Arginine transport |
| ArgR    | SO0620      | 15 | 1    | Conserved hypothetical protein | |
| ArgR    | ilvM        | 14 | 1    | Acetolactate synthase small subunit (EC 2.2.1.6) | Branched-chain amino acid biosynthesis |
| ArgR    | SO3392      | 14 | 1    | NADH-dependent flavin oxidoreductase, Oye family | |
| ArgR    | ivG         | 14 | 1    | Acetolactate synthase large subunit (EC 2.2.1.6) | Branched-chain amino acid biosynthesis |
| ArgR    | ivD         | 14 | 1    | Dihydroxy-acid dehydratase (EC 4.2.1.9) | Branched-chain amino acid biosynthesis |
| ArgR    | ivA         | 14 | 1    | Threonine dehydratase biosynthetic (EC 4.3.1.19) | Branched-chain amino acid biosynthesis |
| ArgR    | artJ        | 10 | 1    | arginine ABC transporter, substrate-binding protein | Arginine transport |
| ArgR    | yfC         | 7  | 1    | Conserved hypothetical protein | |
| ArgR    | omp         | 14 | 1    | Toli-dependent outer membrane transporter | Arginine transport ? |
| ArgR    | oadA        | 12 | 1    | Oxaloacetate decarboxylase, alpha chain (EC 4.1.1.3) | Pyruvate metabolism |
| ArgR    | oadB        | 12 | 1    | Oxaloacetate decarboxylase, beta chain (EC 4.1.1.3) | Pyruvate metabolism |
| ArgR    | oadG        | 12 | 1    | Oxaloacetate decarboxylase gamma chain (EC 4.1.1.3) | Pyruvate metabolism |
| ArgR    | potF        | 12 | 1    | Putrescine ABC transporter, substrate-binding protein (TC 3.A.1.11.2) | Putrescine transport |
| ArgR    | potG        | 12 | 1    | Putrescine ABC transporter, ATP-binding protein (TC 3.A.1.11.2) | Putrescine transport |
| ArgR    | potH        | 12 | 1    | Putrescine ABC transporter, permease protein 1 (TC 3.A.1.11.2) | Putrescine transport |
| ArgR    | potI        | 12 | 1    | Putrescine ABC transporter, permease protein 2 (TC 3.A.1.11.2) | Putrescine transport |
| ArgR    | recN        | 12 | 1    | DNA repair protein RecN | DNA repair |
| ArgR    | aprE        | 11 | 1    | Alkaline serine protease | |
| ArgR    | SO0762      | 10 | 1    | Isochorismate hydratase (EC 3.3.2.2) | Arginine degradation |
| ArgR    | astE        | 7  | 2    | succinylglutamate desuccinylase | Arginine degradation |
| ArgR    | SO2753      | 9  | 1    | Prolyl endopeptidase (EC 3.4.21.26) | |
| ArgR    | arcA        | 5  | 1    | Arginine deiminase (EC 3.5.3.6) | Arginine degradation |
| ArgR    | arcB        | 1  | 1    | Ornithine carbamoyltransferase (EC 2.1.3.3), catabolic | Arginine degradation |
| ArgR    | arcC        | 1  | 1    | Carbamate kinase (EC 2.7.2.2) | Arginine degradation |
| ArgR  | Gene  | Description                                                                 | Function                              |
|------|-------|-----------------------------------------------------------------------------|---------------------------------------|
| ArgR | arcD  | 1 Arginine/ornithine antiporter                                              | Arginine degradation                  |
| ArgR | hisJ  | 6 histidine ABC transporter, substrate-binding protein                       | Histidine degradation                 |
| ArgR | hisM  | 6 histidine ABC transporter, inner membrane permease                        | Histidine transport                   |
| ArgR | hisP  | 6 histidine ABC transporter, ATP-binding protein                            | Histidine transport                   |
| ArgR | hisQ  | 6 histidine ABC transporter, permease protein                               | Histidine transport                   |
| ArgR | potE  | 8 Putrescine/ornithine antiporter                                            | Putrescine transport                  |
| ArgR | proV  | 3 Glycine betaine/L-proline ABC transporter, ATP-binding protein             | Proline transport                     |
| ArgR | proW  | 3 Glycine betaine/L-proline ABC transporter, permease protein               | Proline transport                     |
| ArgR | proX  | 3 Glycine betaine/L-proline ABC transporter, substrate-binding protein       | Proline transport                     |
| ArgR | SO0312| 8 Predicted outer membrane porin                                            |                                       |
| ArgR | ggt2  | 7 Gamma-glutamyltranspeptidase (EC 2.3.2.2)                                 | Glutathione metabolism                |
| ArgR | SO4732| 7 Conserved hypothetical protein                                             |                                       |
| ArgR | mcp   | 6 Methyl-accepting chemotaxis protein                                        |                                       |
| ArgR | aprE2 | 5 Cold-active alkaline serine protease (EC 3.4.21.62)                        | Branch-chor amino acid biosynthesis   |
| ArgR | ilvE  | 5 Branched-chain amino acid aminotransferase (EC 2.6.1.42)                  | Branch-chor amino acid biosynthesis   |
| ArgR | ECA3537| 3 amino acid-binding protein                                                 |                                       |
| ArgR | ECA3538| 3 polar amino acid ABC transporter, inner membrane subunit                   |                                       |
| ArgR | ECA3539| 3 amino acid ABC transporter, ATP-binding protein                           |                                       |
| ArgR | hisA  | 4 Histidinol-phosphatase (EC 3.1.3.15) / Imidazole glycerol-phosphate dehydratase (EC 4.2.1.19) | Histidine biosynthesis                |
| ArgR | hisB  | 4 Histidinol-phosphate aminotransferase (EC 2.6.1.9)                        | Histidine biosynthesis                |
| ArgR | hisC  | 4 Histidinol dehydrogenase (EC 1.1.1.23)                                    | Histidine biosynthesis                |
| ArgR | hisD  | 4 Imidazole glycerol phosphate synthase cyclase subunit (EC 4.1.3.-)         | Histidine biosynthesis                |
| ArgR | hisF  | 4 ATP phosphoribosyltransferase (EC 2.4.2.17)                               | Histidine biosynthesis                |
| ArgR | hisG  | 4 Imidazole glycerol phosphate synthase amidotransferase subunit (EC 2.4.2.-) | Histidine biosynthesis                |
| ArgR | hisH  | 4 Phosphoribosyl-AMP cyclohydrolase (EC 3.5.4.19) / Phosphoribosyl-ATP pyrophosphatase (EC 3.6.1.31) | Histidine biosynthesis                |
| ArgR | hisI  | 4 Histidinol-phosphate aminotransferase (EC 2.6.1.9)                        | Histidine biosynthesis                |
| ArgR | pbpG  | 4 D-alanyl-D-alanine endopeptidase                                            |                                       |
| ArgR | Swoo_0949| 4 Peptidase U32                                                             |                                       |
| ArgR | ybgH  | 3 Amino acid/peptide transporter                                             |                                       |
| ArgR | SQ1443| 3 Conserved hypothetical protein                                             |                                       |
| ArgR | SQ1915| 3 Serine protease, subtilase family                                          |                                       |
| ArgR | SQ2306| 3 Cell division protein FtsK                                                 |                                       |
| ArgR | marC  | 1 Membrane protein, MarC family                                              |                                       |
| ArgR | speF  | 1 Ornithine decarboxylase (EC 4.1.1.17)                                      | Putrescine metabolism                 |
| BioR | bioB  | 12 Biotin synthase (EC 2.8.1.6)                                              | Biotin biosynthesis                   |
| BioR | bioR  | 10 Biotin metabolism regulatory protein BioR, GntR family                    | Transcription regulation              |
| BioR | bioY  | 8 Substrate-specific component BioY of biotin ECF transporter                | Biotin transport                      |
| BioR | bioF  | 7 B-aminoo-7-oxononanoate synthase (EC 2.3.1.47)                             | Biotin biosynthesis                   |
| BioR | bioD  | 7 Dethiobiotin synthetase (EC 6.3.3.3)                                       | Biotin biosynthesis                   |
| BioR | bioA  | 7 Adenosylmethionine-8-aminoo-7-oxononanoate aminotransferase (EC 2.6.1.62) | Biotin biosynthesis                   |
| BioR | bioZ  | 3 Biotin synthesis protein BioZ                                               | Biotin biosynthesis                   |
| BioR | bioM  | 1 ATPase component BioM of energizing module of biotin ECF transporter       | Biotin transport                      |
| BioR | bioG  | 1 Biotin synthesis protein BioG                                              | Biotin biosynthesis                   |
| BioR | bioN  | 1 Transmembrane component BioN of energizing module of biotin ECF transporter | Biotin transport                      |
| BioR | bioC  | 1 Biotin synthesis protein BioC                                              | Biotin biosynthesis                   |
| BioR | panD  | 1 Aspartate alpha-decarboxylase                                              | Pantothenate biosynthesis              |
| BirA | bioB  | 93 Biotin synthase (EC 2.8.1.6)                                              | Biotin biosynthesis                   |
| BirA | bioF  | 86 B-aminoo-7-oxononanoate synthase (EC 2.3.1.47)                            | Biotin biosynthesis                   |
| Protein | Accession | Exon | Location |
|---------|-----------|------|----------|
| BirA bioD | 83 10 | Biotin synthesis protein BioD |
| BirA bioC | 84 10 | Biotin synthesis protein BioC |
| BirA bioA | 65 8 | Adenosylmethionine-8-amino-7-oxononanoate aminotransferase (EC 2.6.1.62) |
| BirA bioH | 33 5 | Biotin synthesis protein BioH |
| BirA COG1040 | 23 4 | Competence protein F |
| BirA fabF | 3 1 | 3-oxoacyl-[acyl-carrier-protein] synthase, KASII (EC 2.3.1.41) |
| BirA birA | 3 1 | Biotin-protein ligase (EC 6.3.4.15) / Biotin operon repressor |
| BirA fabG | 3 1 | 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) |
| BirA DVU2560 | 3 1 | Conserved domain protein |
| BirA acpP | 3 1 | Acyl carrier protein, putative |
| BirA Dde_2651 | 2 1 | Hypothetical thioesterase domain protein |
| BirA XAC0384 | 2 1 | Putative short chain dehydrogenase |
| BirA XAC0386 | 2 1 | Hypothetical protein |
| BirA bioHC | 3 1 | Biotin synthesis protein BioH / Biotin synthesis protein BioC |
| BirA yigM | 3 1 | Predicted biotin transporter YigM |
| BirA CV3478 | 1 1 | Phosphatidylethanolamine N-methyltransferase (EC 2.1.1.17) |
| FabR fabA | 62 8 | 3-hydroxydecanoyl-[acyl-carrier-protein] dehydratase (EC 4.2.1.60) |
| FabR hyll | 30 6 | COG172: Predicted membrane protein hemolysin III homolog |
| FabR OLE1 | 38 5 | Fatty acid desaturase (EC 1.14.19.1) |
| FabR pIIc | 30 6 | 1-acyl-sn-glycerol-3-phosphate acyltransferase (EC 2.3.1.51) |
| FabR desB | 13 6 | Acyl-CoA delta-9-desaturase, DesB |
| FabR desC | 13 6 | Flavodoxin reductases (ferredoxin-NADPH reductases) family 1 |
| FabR iccH | 25 5 | Putative long-chain-fatty-acid--CoA ligase (EC 6.2.1.3) |
| FabR fabR | 26 3 | Unsaturated fatty acid biosynthesis repressor FabR, TetR family |
| FabR fabD | 25 3 | Long-chain fatty acid transport protein |
| FabR fabR2 | 5 2 | Unsaturated fatty acid biosynthesis repressor FabR, TetR family |
| FabR fabB | 20 4 | 3-oxoacyl-[acyl-carrier-protein] synthase, KASI (EC 2.3.1.41) |
| FabR rraB | 17 2 | Ribonuclease E inhibitor RraB |
| FabR lcE | 16 1 | Long-chain-fatty-acid--CoA ligase (EC 6.2.1.3) |
| FabR hyll | 17 2 | COG172: Predicted membrane protein hemolysin III homolog |
| FabR Maqu_3149 | 2 1 | AraC family transcriptional regulator |
| FabR pfA | 7 2 | Omega-3 unsaturated fatty acid synthase subunit, PfA |
| FabR pfB | 7 2 | Omega-3 unsaturated fatty acid synthase subunit, PfB |
| FabR COG2030 | 6 1 | Putative acyl dehydrogenase, COG2030 |
| FabR pfaR | 6 1 | Transcriptional regulator for synthesis of eicosapentaenoic acid, PfaR |
| FabR pfaC | 6 1 | Omega-3 unsaturated fatty acid synthase subunit, PfaC |
| FabR faeA | 1 1 | Fatty acid desaturase (EC 1.14.99.9) |
| FabR desE | 5 1 | Acyl-CoA dehydrogenase, short-chain specific (EC 1.3.99.2) |
| FabR pfaD | 4 1 | Enoyl-[acyl-carrier-protein] reductase [FMN] (EC 1.3.1.9), inferred for PFA pathway |
| FabR psaA | 2 1 | Predicted transcriptional regulator for fatty acid degradation PsaA, TetR family |
| FabR faeE | 1 1 | Acyl-CoA dehydrogenase, short-chain specific (EC 1.3.99.2) |
| FabR COG2072 | 3 2 | Probable flavin-containing monooxygenase, COG2072 |
| FabR COG0300 | 2 1 | Probable short-chain dehydrogenase, COG0300 |
| FadP fadP | 24 3 | Predicted transcriptional regulator for fatty acid degradation FadP, TetR family |
| FadP etfA | 23 3 | Electron transfer flavoprotein alpha subunit |
| FadP etfB | 23 3 | Electron transfer flavoprotein, beta subunit |
| FadP acdH | 23 3 | Acyl-CoA dehydrogenase (EC 1.3.99.3) |
| FadP fadA | 22 3 | 3-ketoacyl-CoA thiolase (EC 2.3.1.16) |
Enoyl-CoA hydratase (EC 4.2.1.17) / Delta(3)-cis-delta(2)-trans-enoyl-CoA isomerase (EC 5.3.3.8) / 3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35) / 3-hydroxybutyryl-CoA epimerase (EC 5.1.2.3)
Fatty acid degradation

Enoyl-CoA hydratase (EC 4.2.1.17) / 1,2-trans-enoyl-CoA isomerase (EC 5.3.3.8) / 3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35)
Fatty acid degradation

Electron transfer flavoprotein-ubiquinone oxidoreductase (EC 1.5.5.1)
Electron transfer chain for fatty acid degradation

3-ketoacyl-CoA thiolase (EC 2.3.1.16) @ Acetyl-CoA acetyltransferase (EC 2.3.1.9)
Fatty acid degradation

Acyl-CoA dehydrogenase domain protein
Fatty acid degradation

Fatty acid degradation
| **FadR** | **plsB** | 8 | 1 | Glycerol-3-phosphate acyltransferase (EC 2.3.1.15) | Glycerolipid metabolism |
| **FadR** | **iclR** | 8 | 1 | Acetate operon transcriptional repressor, IclR family | Transcription regulation |
| **FadR** | **fadM** | 8 | 1 | Long-chain acyl-CoA thioesterase FadM (EC=3.1.2.1) | Fatty acid degradation |
| **FadR** | **yebV** | 8 | 1 | hypothetical protein | 
| **FadR** | **VC2105** | 6 | 1 | Thioesterase/thiol ester dehydrase-isomerase | 
| **FadR** | **tesB** | 4 | 1 | Acyl-CoA thioesterase | Fatty acid degradation |
| **FadR** | **acdB** | 2 | 1 | Acyl-CoA dehydrogenase (EC 1.3.99.3) | Fatty acid degradation |
| **FadR** | **COG0596** | 1 | 1 | Predicted hydrolase/acyltransferase | 
| **GlcC** | **glcE** | 23 | 7 | Glycolate dehydrogenase (EC 1.1.99.14), FAD-binding subunit GlcE | Glycolate utilization |
| **GlcC** | **glcF** | 22 | 7 | Glycolate dehydrogenase (EC 1.1.99.14), iron-sulfur subunit GlcF | Glycolate utilization |
| **GlcC** | **glcD** | 7 | 7 | Glycolate dehydrogenase (EC 1.1.99.14), subunit GlcD | Glycolate utilization |
| **GlcC** | **glcC** | 22 | 6 | Glycolate utilization operon transcriptional activator GlcC | Transcription regulation |
| **GlcC** | **glcG** | 13 | 4 | Hypothetical protein GlcG in glycolate utilization operon | Glycolate utilization |
| **GlcC** | **glcB** | 8 | 3 | Malate synthase G (EC 2.3.3.9) | Tricarboxylic acid cycle |
| **GlcC** | **glcA** | 1 | 1 | Glycolate permease | Glycolate transport |
| **GlcC** | **lldD** | 4 | 1 | L-lactate dehydrogenase (EC 1.1.2.3) | Lactate utilization |
| **GlcC** | **mln6914** | 4 | 1 | uncharacterized conserved membrane protein | 
| **GlcC** | **lyrR** | 3 | 1 | Transcriptional regulator, LyrR family, in glycolate utilization operon | Transcription regulation |
| **GlcC** | **lldG** | 1 | 1 | L-lactate dehydrogenase, subunit LldG | Lactate utilization |
| **GlcC** | **lldE** | 1 | 1 | L-lactate dehydrogenase, Fe-S oxidoreductase subunit LldE | Lactate utilization |
| **GlcC** | **glcQ** | 1 | 1 | Predicted TRAP-type glycolate transport system, small permease component | Glycolate transport |
| **GlcC** | **glcM** | 1 | 1 | Predicted TRAP-type glycolate transport system, large permease component | Glycolate transport |
| **GlcC** | **lldP** | 2 | 1 | L-lactate permease | Lactate utilization |
| **GlcC** | **lldF** | 1 | 1 | L-lactate dehydrogenase, Iron-sulfur cluster-binding subunit LldF | Lactate utilization |
| **GlcC** | **glcP** | 1 | 1 | Predicted TRAP-type glycolate transport system, periplasmic component | Glycolate transport |
| **GlcC** | **NGR_c03940** | 1 | 1 | hypothetical protein | 
| **GlcC** | **ykgE** | 1 | 1 | L-lactate dehydrogenase, Fe-S oxidoreductase subunit YkgE | Lactate utilization |
| **GlcC** | **ykgF** | 1 | 1 | L-lactate dehydrogenase, Iron-sulfur cluster-binding subunit YkgF | Lactate utilization |
| **GlcC** | **ykgG** | 1 | 1 | L-lactate dehydrogenase, hypothetical protein subunit YkgG | Lactate utilization |
| **HexR** | **hexR** | 74 | 9 | Central carbohydrate metabolism transcription regulator HexR, RpiR family | Transcription regulation |
| **HexR** | **zwf** | 72 | 9 | Glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49) | Pentose phosphate pathway |
| **HexR** | **edd** | 55 | 9 | 2-keto-3-deoxy-D-arabino-heptulosonate-7-phosphate synthase I alpha (EC 2.5.1.54) # AroA I alpha | Entner-Doudoroff pathway |
| **HexR** | **eda** | 53 | 9 | Entner-Doudoroff pathway | 
| **HexR** | **pgi** | 53 | 8 | 6-phosphogluconolactonase (EC 3.1.1.31), eukaryotic type | Pentose phosphate pathway |
| **HexR** | **gk** | 33 | 7 | Glucokinase (EC 2.7.1.2) | Glycolysis |
| **HexR** | **pykA** | 40 | 7 | Pyruvate kinase (EC 2.7.1.40) | Glycolysis |
| **HexR** | **gapA** | 28 | 5 | NAD-dependent glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) | Glycolysis |
| **HexR** | **pgi** | 31 | 5 | Glucose-6-phosphate isomerase (EC 5.3.1.1) | Glycolysis |
| **HexR** | **ppc** | 20 | 4 | Phosphoenolpyruvate carboxylase (EC 4.1.1.31) | Glycolysis |
| **HexR** | **tal** | 23 | 5 | Transaldolase (EC 2.2.1.2) | Pentose phosphate pathway |
| **HexR** | **ppA** | 20 | 3 | Phosphoenolpyruvate synthase (EC 2.7.9.2) | Gluconeogenesis |
| **HexR** | **aceB** | 25 | 3 | Malate synthase (EC 2.3.3.9) | Tricarboxylic acid cycle |
| **HexR** | **aceA** | 21 | 4 | Isocitrate lyase (EC 4.1.3.1) | Tricarboxylic acid cycle |
| **HexR** | **gapB** | 19 | 3 | NADPH-dependent glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.13) | Glycolysis |
| **HexR** | **pfIA** | 12 | 3 | Pyruvate formate-lyase activating enzyme (EC 1.97.1.4) | Fermentation |
| **HexR** | **aceE** | 10 | 2 | Pyruvate dehydrogenase E1 component (EC 1.2.4.1) | Pyruvate metabolism |
| **HexR** | **aceF** | 10 | 2 | Dihydropilloamide acetyltransferase component of pyruvate dehydrogenase complex (EC 2.3.3.12) | Pyruvate metabolism |
| **HexR** | **gpmM** | 12 | 2 | 2,3-bisphosphoglycerate-independent phosphoglycerate mutase (EC 5.4.2.1) | Glycolysis |
| **HexR** | **adhE** | 18 | 3 | Alcohol dehydrogenase (EC 1.1.1.1) | Fermentation |
HexR  pckA  10  4  Phosphoenolpyruvate carboxykinase [ATP] (EC 4.1.1.49)  Gluconeogenesis
HexR  grcA  12  2  Autonomous glycol radical cofactor
HexR  gldD  12  2  Glutamate synthase [NADPH] small chain (EC 1.4.1.13)  Glutamate biosynthesis
HexR  gldB  12  2  Glutamate synthase [NADPH] large chain (EC 1.4.1.13)  Glutamate biosynthesis
HexR  aldE  7  4  Aldose 1-epimerase  Glycolysis
HexR  tpiA  11  2  Triosephosphate isomerase (EC 5.3.1.1)  Glycolysis
HexR  pntB  11  2  NAD(P) transhydrogenase subunit beta (EC 1.6.1.2)  NAD metabolism
HexR  ptsG  8  2  PTS system, glucose-specific IIB component (EC 2.7.1.69)  PTS system, glucose-specific IIC component (EC 2.7.1.69)  Glucose transport
HexR  mtaA  10  2  PTS system, mannitol-specific IIB component (EC 2.7.1.69)  Mannitol utilization
HexR  pntA  10  2  NAD(P) transhydrogenase alpha subunit (EC 1.6.1.2)  NAD metabolism
HexR  pflB  7  2  Pyruvate formate-lyase (EC 2.3.1.54)  Fermentation
HexR  ptsI  7  2  Phosphoenolpyruvate-protein phosphotransferase of PTS system (EC 2.7.3.9)  Glucose transport
HexR  focA  7  2  Formate efflux transporter (TC 2.A.44 family)  Fermentation
HexR  ptsH  7  2  Phosphocarrier protein of PTS system  Glucose transport
HexR  mltD  9  2  Mannitol-1-phosphate 5-dehydrogenase (EC 1.1.1.17)  Mannitol utilization
HexR  ptsL  9  2  Mannitol operon repressor  Transcription regulation
HexR  crr  7  2  PTS system, glucose-specific IIA component (EC 2.7.1.69)  Glucose transport
HexR  phk  16  1  Xylose-5-phosphate phosphoketolase (EC 4.1.2.9)  Pentose phosphate pathway
HexR  hexR1  8  1  Central carbohydrate metabolism transcription regulator HexR, RpiR family  Transcription regulation
HexR  gapA2  16  1  glyceraldehyde-3-phosphate dehydrogenase, type I  Glycolysis
HexR  ybA  10  1  Putative exported protein
HexR  pepD  9  1  Aminoacyl-histidine dipeptidase (Peptidase D) (EC 3.4.13.3)  Nucleoside metabolism
HexR  gnd  14  1  6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44)  Pentose phosphate pathway
HexR  nqrD  14  1  NqrD  Electron transport chain
HexR  nqrC  14  1  NADH:ubiquinone oxidoreductase, Na translocating, gamma subunit  Electron transport chain
HexR  gltR  7  1  DNA-binding response regulator GltR, controls specific porins for the entry of glucose  Transcription regulation
HexR  nqrE  14  1  NqrE  Electron transport chain
HexR  nqrB  14  1  NADH:ubiquinone oxidoreductase, Na translocating, hydrophobic membrane protein  Electron transport chain
HexR  gcvT  12  1  Aminomethyltransferase (glycine cleavage system T protein) (EC 2.4.2.1)  Glycine cleavage system
HexR  gcvP  12  1  Glycine dehydrogenase [decarboxylating] (glycine cleavage system P protein) (EC 1.4.4.2)  Glycine cleavage system
HexR  nupC  12  1  Nucleoside transporter, NupC family  Nucleoside metabolism
HexR  gcvH  12  1  Glycine cleavage system H protein  Glycine cleavage system
HexR  nirB  7  1  Nitrite reductase [NAD(P)H] large subunit (EC 1.7.1.4)  Nitrogen metabolism
HexR  nirD  7  1  Nitrite reductase [NAD(P)H] small subunit (EC 1.7.1.4)  Nitrogen metabolism
HexR  pta  4  1  Phosphate acetyltransferase (EC 2.3.1.8)  Fermentation
HexR  mgsA  2  1  Methylglyoxal synthase (EC 4.2.3.3)  Methylglyoxal metabolism
HexR  gta  2  1  Citrate synthase (s) (EC 2.3.3.1)  Tricarboxylic acid cycle
| Gene  | Accession | Description                                                                 | Function                          |
|-------|-----------|------------------------------------------------------------------------------|-----------------------------------|
| HexR  | ackA      | Acetate kinase (EC 2.7.2.1)                                                   | Fermentation                      |
| HexR  | PF00248   | Putative aldo/keto reductase                                                  |                                   |
| HexR  | SO1118    | hypothetical protein                                                          |                                   |
| HexR  | cdd       | Cytidine deaminase                                                            | Nucleoside metabolism             |
| HexR  | glgX      | Glycogen debranching enzyme (EC 2.7.2.1)                                     | Glycogen utilization              |
| HexR  | pgk       | Phosphoglycerate kinase (EC 2.7.2.3)                                         | Glycolysis                        |
| HexR  | giPA      | Glycogen synthase, ADP-glucose transglycosylase (EC 2.4.1.2)                 | Glycogen utilization              |
| HexR  | adhB      | Alcohol dehydrogenase II                                                      | Fermentation                      |
| HexR  | ldhA      | D-lactate dehydrogenase (EC 1.1.1.28)                                        | Fermentation                      |
| HexR  | gntU      | Low-affinity gluconate/H+ symporter GntU                                     | Gluconate utilization             |
| HexR  | giGC      | Glucose-1-phosphate adenyltransferase (EC 2.7.7.27)                           | Glycogen utilization              |
| HexR  | mglB      | Galactose/methyl galactoside ABC transport system, D-galactose-binding periplasmic protein MglB (TC 3.A.1.2.3) | Galactose transport               |
| HexR  | pgk       | Phosphoglycerate kinase (EC 2.7.2.3)                                         | Glycolysis                        |
| HexR  | glgA      | Glycogen synthase, ADP-glucose transglycosylase (EC 2.4.1.2)                 | Glycogen utilization              |
| HexR  | adhB      | Alcohol dehydrogenase II                                                      | Fermentation                      |
| HexR  | ldhA      | D-lactate dehydrogenase (EC 1.1.1.28)                                        | Fermentation                      |
| HexR  | gntU      | Low-affinity gluconate/H+ symporter GntU                                     | Gluconate utilization             |
| HexR  | giGC      | Glucose-1-phosphate adenyltransferase (EC 2.7.7.27)                           | Glycogen utilization              |
| HexR  | mglB      | Galactose/methyl galactoside ABC transport system, D-galactose-binding periplasmic protein MglB (TC 3.A.1.2.3) | Galactose transport               |
| HexR  | mcp1      | 1 methyl-accepting chemotaxis protein                                         |                                   |
| HexR  | ptsHI     | PTS system, glucose-specific IIA component (EC 2.7.1.69) / Phosphocarrier protein of PTS system / Phosphoenolpyruvate-protein phosphotransferase of PTS system (EC 2.7.3.9) | Glucose transport                |
| HexR  | gntK      | Glucokinase (EC 2.7.1.12)                                                     | Gluconate utilization             |
| HexR  | mglA      | Galactose/methyl galactoside ABC transport system, ATP-binding protein MglA (EC 3.6.3.17) | Galactose transport               |
| HexR  | mglC      | Galactoside transport system permease protein mglC (TC 3.A.1.2.3)             | Galactose transport               |
| HexR  | cpsA      | Capsular polysaccharide synthesis enzyme CpsA, sugar transferase              |                                   |
| HexR  | giGP      | Glycogen phosphorylase (EC 2.4.1.1)                                          | Glycogen utilization              |
| HexR  | prpB      | Carboxyphosphoenolpyruvate phosphomutase (EC 2.7.8.23)                       |                                   |
| HexR  | oxIT      | Putative oxalate:formate antiporter                                           | Tricarboxylic acid cycle          |
| HexR  | uggC      | SN-glycerol-3-phosphate transport ATP-binding protein UggC (TC 3.A.1.1.3)     | Glycerol-3-phosphate transport    |
| HexR  | giPT      | Glycerol-3-phosphate transporter                                              | Glycerol-3-phosphate transport    |
| HexR  | pyKF      | Pyruvate kinase (EC 2.7.1.40)                                                 | Glycolysis                        |
| HexR  | icIP      | L-Lactate permease                                                            | Lactate utilization               |
| HexR  | gapN      | NADP-dependent glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.9)          | Glycolysis                        |
| HexR  | fba       | Fructose-biphosphate aldolase class II (EC 4.1.2.13)                          | Glycolysis                        |
| HexR  | manC      | Mannose-1-phosphate guanylyltransferase (GDP) (EC 2.7.7.22)                    | Mannose utilization               |
| HexR  | bkdA2     | Branched-chain alpha-keto acid dehydrogenase, E1 component, beta subunit (EC 1.2.4.4) | Branched-chain amino acid degradation |
| HexR  | bkdB      | Branched-chain alpha-keto acid dehydrogenase complex (EC 2.3.1.168)           | Branched-chain amino acid degradation |
| HexR  | bkdA1     | Branched-chain alpha-keto acid dehydrogenase, E1 component, alpha subunit (EC 1.2.4.4) | Branched-chain amino acid degradation |
| HexR  | nupC2     | Putative nucleoside transporter, NupC family                                  | Nucleoside metabolism             |
| HexR  | mcp2      | Methyl-accepting chemotaxis sensory transducer                                |                                   |
| HexR  | PST_3493  | Aldo/keto reductase                                                           |                                   |
| HexR  | dld       | D-Lactate dehydrogenase (EC 1.1.2.5)                                          | Lactate utilization               |
| HmgQ  | hpd       | 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)                           | Tyrosine degradation              |
| HmgQ  | hmgA      | Homogentisate 1,2-dioxygenase (EC 1.13.11.5)                                  | Tyrosine degradation              |
| HmgQ  | hmgB      | Maleylacetate isomerase (EC 5.2.1.2)                                          | Tyrosine degradation              |
| HmgQ  | hmgC      | Fumarylacetate isomerase (EC 3.7.1.2)                                         | Tyrosine degradation              |
| HmgQ  | gloA      | Predicted homogentisate dioxygenase, GloA family                             | Tyrosine degradation              |
| HmgQ  | hmgQ      | Tyrosine degradation transcriptional regulator, LysR family                    | Transcription regulation          |
| HmgR  | hpd       | 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27)                           | Tyrosine degradation              |
| HmgR  | hmgA      | Homogentisate 1,2-dioxygenase (EC 1.13.11.5)                                  | Tyrosine degradation              |
| HmgR  | hmgB      | Maleylacetate isomerase (EC 5.2.1.2)                                          | Tyrosine degradation              |
| HmgR  | hmgC      | Fumarylacetate isomerase (EC 3.7.1.2)                                         | Tyrosine degradation              |
| HmgR  | COG2814   | Predicted tyrosine transporter, COG2814 family                               | Tyrosine transport                |
| Gene    | Accession | Description                                                                 | Function                  |
|---------|-----------|------------------------------------------------------------------------------|---------------------------|
| HmgR    | hmgR      | Tyrosine degradation transcriptional regulator, IclR family                   | Transcription regulation  |
| HmgA    | hmgA      | Homogentisate 1,2-dioxygenase (EC 1.13.11.5)                                 | Tyrosine degradation      |
| HmgB    | hmgB      | Maleylacetate isomerase (EC 5.2.1.2)                                         | Tyrosine degradation      |
| HmgS    | hmgS      | Tyrosine degradation transcriptional regulator, MarR family                   | Transcription regulation  |
| HutC    | hutU      | Urocanate hydratase (EC 4.2.1.49)                                            | Histidine degradation     |
| HutC    | hutH      | Histidine ammonia-lyase (EC 4.3.1.3)                                         | Histidine degradation     |
| HutC    | hutI      | Imidazolonepropionase (EC 3.5.2.7)                                           | Histidine degradation     |
| HutC    | hutC      | Histidine utilization repressor, GntR family                                 | Transcription regulation  |
| HutC    | hutF      | Formiminoglutamic iminohydrolase (EC 3.5.3.13)                               | Histidine degradation     |
| HutC    | hutG      | N-formylglutamate deformylase (EC 3.5.1.68)                                  | Histidine degradation     |
| HutC    | hutD      | Conserved hypothetical protein related to histidine degradation             | Histidine degradation     |
| HutC    | hutG2     | Formiminoglutamase (EC 3.5.3.8)                                             | Histidine degradation     |
| HutC    | hisT      | Histidine transport protein (permease)                                       | Histidine transport       |
| HutC    | hutH2     | Histidine ammonia-lyase (EC 4.3.1.3)                                         | Histidine degradation     |
| HutC    | COG3314   | Predicted histidine uptake transporter                                       | Histidine transport       |
| HutC    | COG1457   | Permease, cysteine/purines, uracil, thiamine, allantoin family protein       | Transport                 |
| HutC    | hutX      | Histidine ABC transporter, histidine-binding protein (TC 3.A.1)              | Histidine transport       |
| HutC    | hutW      | Histidine ABC transporter, permease protein (TC 3.A.1)                       | Histidine transport       |
| HutC    | hutV      | Histidine ABC transporter, ATP-binding protein (TC 3.A.1)                    | Histidine transport       |
| HutC    | COG834    | ABC amino acid transporter, periplasmic binding protein                      | Histidine transport       |
| HutC    | hisC      | Histidinol-phosphate aminotransferase                                        | Histidine biosynthesis    |
| HutC    | COG1126   | ABC amino acid transporter, ATPase component                                 | Histidine transport       |
| HutC    | COG765    | ABC amino acid transporter, permease component                               | Histidine transport       |
| HutC    | hisX      | Putative histidine ABC transporter, substrate binding protein                | Histidine transport       |
| HutC    | hisY      | Putative histidine ABC transporter, permease protein                         | Histidine transport       |
| HutC    | hisZ      | Putative histidine ABC transporter, ATPase protein                            | Histidine transport       |
| HutC    | Caul_2357 | Optional hypothetical component of omp transporter                           | Transport                 |
| HutC    | omp       | TonB-dependent outer membrane transporter                                    | Histidine transport?      |
| HutC    | COG5285   | Phytanoyl-CoA dioxygenase                                                     | Transport                 |
| HutC    | COG4160   | ABC amino acid transporter, permease component                               | Transport                 |
| HutC    | COG2777   | FAD linked oxidase domain protein                                             | Transport                 |
| HutC    | COG1125   | ABC proline/glycine/betaine transporter, ATPase component                    | Transport                 |
| HutC    | COG1174   | ABC proline/glycine/betaine transporter, permease component                 | Transport                 |
| HutC    | COG1732   | ABC proline/glycine/betaine transporter, periplasmic binding domain          | Transport                 |
| HutC    | COG2423   | Predicted ornithine cycleoaminase, mu-crystallin homolog (EC 4.3.1.12)      | Transport                 |
| HutC    | COG3221   | ABC phosphate/phosphonate transporter, periplasmic binding component         | Transport                 |
| HutC    | hisD      | Histidinol dehydrogenase (EC 1.1.1.23)                                       | Histidine biosynthesis    |
| HutC    | hisI      | ABC amino acid transporter, permease component                               | Transport                 |
| HutC    | hisG      | ATP phosphoribosyltransferase (EC 2.4.2.17)                                  | Histidine biosynthesis    |
| HutC    | hisF      | Imidazole glycerol phosphate synthase cyclase subunit (EC 4.1.3.-)          | Histidine biosynthesis    |
| HutC    | hisA      | Phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase (EC 5.3.1.16) | Histidine biosynthesis    |
| HutC    | hisH      | Imidazole glycerol phosphate synthase amidotransferase subunit (EC 2.4.2.-) | Histidine biosynthesis    |
| HutC    | hisB      | Histidinol-phosphate (EC 3.1.3.15) / Imidazoleglycerol-phosphate dehydratase (EC 4.2.1.19) | Histidine biosynthesis    |
| HutC    | COG2814   | Putative histidine permease, major facilitator superfamily                  | Histidine transport       |
| HutC    | hisP      | Histidine ABC transporter, ATP-binding protein HisP (TC 3.A.1.3.1)           | Histidine transport       |
| HutC    | hisP2     | Histidine ABC transporter, ATP-binding protein HisP (TC 3.A.1.3.1)           | Histidine transport       |
| HutC    | COG1960   | Acyl-CoA dehydrogenase, short-chain specific (EC 1.3.99.2)                   | Histidine transport       |
| HutC    | COG1804   | CAIB/BAIF family protein                                                      | Histidine transport       |
| HypR  | Gene  | Description                                                                 | Function                                                                 |
|-------|-------|----------------------------------------------------------------------------|--------------------------------------------------------------------------|
| HypR  | hypC  | Putative hydroxylases or acyltransferases (alpha/beta hydrolase superfamily)| TCA cycle                                                               |
| HypR  | hypD  | 1-pyrroline-4-hydroxy-2-carboxylate deaminase (EC 3.5.4.22) # predicted   | Hydroxypoline/proline degradation                                        |
| HypR  | hypE  | Proline racemase /4-hydroxyproline epimerase (EC 5.1.1.8)                  | Hydroxypoline/proline degradation                                        |
| HypR  | hypH  | Ketoglutarate semialdehyde dehydrogenase (EC 1.2.1.26) # hydroxy-L-proline-inducible | Hydroxypoline/proline degradation                                        |
| HypR  | hypP  | Predicted hydroxypoline ABC transporter, permease protein                   | Hydroxypoline/proline transport                                          |
| HypR  | hypQ  | Predicted hydroxypoline ABC transporter, ATP-binding protein               | Hydroxypoline/proline transport                                          |
| HypR  | hypX  | Predicted citrate/succinate isomerase or aconitase # predicted from clustering to proline racemase | TCA cycle                                                               |
| HypR  | hypD' | 1-pyrroline-4-hydroxy-2-carboxylate deaminase (EC 3.5.4.22) # predicted   | Hydroxypoline/proline degradation                                        |
| HypR  | hypH' | Ketoglutarate semialdehyde dehydrogenase (EC 1.2.1.26) # hydroxy-L-proline-inducible | Hydroxypoline/proline degradation                                        |
| HypR  | hypH'-2| Predictive ketoglutarate semialdehyde dehydrogenase (EC 1.2.1.26) # hydroxy-L-proline-inducible | Hydroxypoline/proline degradation                                        |
| HypR | hypT  | 1  | 1 | Putative hydroxyproline transporter | Hydroxyproline transport |
|------|-------|----|---|-------------------------------------|-------------------------|
| HypR | hypZ  | 1  | 1 | OsmC/Ohr family protein             |                         |
| HypR | COG531 (PotE) | 1 | 1 | Putative proline/hydroxyproline permease, PotE family | Hydroxyproline/proline transport |
| HypR | colA1 | 7  | 1 | Microbial collagenase, secreted [EC 3.4.24.3] | Collagen degradation |
| HypR | pdtP  | 6  | 1 | Predicted proline dipeptide/tripeptide permease, MFS family | Proline transport |
| HypR | ATW7_13133 | 1 | 1 | hypothetical protein                 |                         |
| HypR | ypfF  | 1  | 1 | Aminopeptidase YpfF (MP-, MA-, MS-, AP-, NP- specific) | Collagen degradation |
| HypR | hypA  | 1  | 1 | Predicted hydroxyproline TRAP-type transport system, small permease component | Hydroxyproline transport |
| HypR | hypB  | 1  | 1 | Predicted hydroxyproline TRAP-type transport system, large permease component | Hydroxyproline transport |
| HypR | hypC  | 1  | 1 | Predicted hydroxyproline TRAP-type transport system, periplasmic component | Hydroxyproline transport |
| HypR | colA3 | 4  | 1 | Microbial collagenase, secreted [EC 3.4.24.3] | Collagen degradation |
| HypR | omp2  | 1  | 1 | TonB-dependent receptor              |                         |
| LiuQ | liuD  | 14 | 3 | Methylcrotonyl-CoA carboxylase carboxyl transferase subunit [EC 6.4.1.4] | Branched_chain amino acid degradation |
| LiuQ | liuB  | 14 | 3 | Methylcrotonyl-CoA carboxylase biotin-containing subunit [EC 6.4.1.4] | Branched_chain amino acid degradation |
| LiuQ | liuQ  | 12 | 3 | Predicted branched-chain amino acid degradation regulator LiuQ, TetR family | Branched_chain amino acid degradation |
| LiuQ | liuA  | 11 | 3 | Isovaleryl-CoA dehydrogenase [EC 1.3.99.10] | Branched_chain amino acid degradation |
| LiuQ | liuC  | 11 | 3 | Methylglutaryl-CoA hydratase [EC 4.2.1.18] | Branched_chain amino acid degradation |
| LiuQ | aacS  | 4  | 1 | AMP-dependent synthetase and ligase | Branched_chain amino acid degradation |
| LiuQ | liuE  | 2  | 2 | Hydroxymethylglutaryl-CoA lyase [EC 4.1.3.4] | Branched_chain amino acid degradation |
| LiuQ | ivd2  | 1  | 1 | Isovaleryl-CoA dehydrogenase [EC 1.3.99.10] | Branched_chain amino acid degradation |
| LiuQ | liuQ2 | 1  | 1 | Predicted transcriptional regulator LiuQ of leucine degradation pathway, TetR family | Transcription regulation |
| LiuQ | atuB  | 1  | 1 | Short-chain dehydrogenase/reductase SDR |                         |
| LiuQ | liuQ1 | 1  | 1 | Predicted transcriptional regulator LiuQ of leucine degradation pathway, TetR family | Transcription regulation |
| LiuQ | acsA  | 1  | 1 | Acetyl-coenzyme A synthetase [EC 6.2.1.1] | Acetyl-coenzyme A synthetase |
| LiuR | etfA  | 49 | 10| Electron transfer flavoprotein, alpha subunit | Electron transfer chain for branched-chain amino acid degradation |
| LiuR | etfB  | 48 | 9 | Electron transfer flavoprotein, beta subunit | Electron transfer chain for branched-chain amino acid degradation |
| LiuR | ivdA  | 54 | 10| Acetyl-CoA C-acyltransferase [EC 2.3.1.16] \& Acetyl-CoA acetyltransferase [EC 2.3.1.9] | Branched-chain amino acid degradation |
| LiuR | ivdC  | 47 | 9 | Branched-chain acyl-CoA dehydrogenase [EC 1.3.99.12] | Branched-chain amino acid degradation |
| LiuR | liuA  | 65 | 11| Isovaleryl-CoA dehydrogenase [EC 1.3.99.10]; Butyryl-CoA dehydrogenase [EC 1.3.99.2] | Branched-chain amino acid degradation |
| LiuR | liuB  | 55 | 10| Methylcrotonyl-CoA carboxylase biotin-containing subunit [EC 6.4.1.4] | Branched-chain amino acid degradation |
| LiuR | liuC  | 54 | 10| Methylglutaryl-CoA hydratase [EC 4.2.1.18] | Branched-chain amino acid degradation |
| LiuR | liuD  | 46 | 9 | Methylcrotonyl-CoA carboxylase carboxyl transferase subunit [EC 6.4.1.4] | Branched-chain amino acid degradation |
| LiuR | liuE  | 49 | 9 | Hydroxymethylglutaryl-CoA lyase [EC 4.1.3.4] | Branched-chain amino acid degradation |
| LiuR | liuR  | 90 | 13| Predicted transcriptional regulator LiuR of leucine degradation pathway, MerR family | Transcriptional regulator |
| LiuR | acsS2 | 1  | 1 | Acetoacetyl-CoA synthetase [EC 6.2.1.16] \& Long-chain-fatty-acid--CoA ligase [EC 6.2.1.3] | Branched-chain amino acid degradation |
| LiuR | acdA2 | 2  | 2 | 3-ketoacyl-CoA thiolase [EC 2.3.1.16] \& Acetyl-CoA acetyltransferase [EC 2.3.1.9] | Branched-chain amino acid degradation |
| LiuR | acdA3 | 6  | 2 | 3-ketoacyl-CoA thiolase [EC 2.3.1.16] \& Acetyl-CoA acetyltransferase [EC 2.3.1.9] | Branched-chain amino acid degradation |
| LiuR | acdA2 | 1  | 1 | Enoyl-CoA hydratase [EC 4.2.1.17] | Branched-chain amino acid degradation |
| LiuR | acdA3 | 1  | 1 | Enoyl-CoA hydratase [EC 4.2.1.17] | Branched-chain amino acid degradation |
| LiuR | acdA4 | 2  | 1 | Enoyl-CoA hydratase [valine degradation] [EC 4.2.1.17] | Branched-chain amino acid degradation |
| LiuR | acdA5 | 1  | 1 | Enoyl-CoA hydratase [EC 4.2.1.17] | Branched-chain amino acid degradation |
| LiuR | acdH3 | 3  | 1 | Acyl-CoA dehydrogenase, short-chain specific [EC 1.3.99.2] | Branched-chain amino acid degradation |
| LiuR | acdH4 | 1  | 1 | Acyl-CoA dehydrogenase [EC 1.3.99.3] | Branched-chain amino acid degradation |
| LiuR | acdH5 | 1  | 1 | Acyl-CoA dehydrogenase, short-chain specific [EC 1.3.99.2] | Branched-chain amino acid degradation |
| LiuR | Gene ID | Description                                                                 | Functional Category                                |
|------|---------|------------------------------------------------------------------------------|---------------------------------------------------|
| aceA | 1       | isocitrate lyase                                                              | Tricarboxylic acid cycle                           |
| acs  | 2       | acyl-CoA synthase                                                             | Acyl-coenzyme A synthetase                         |
| acsA | 2       | Acyl-coenzyme A synthetases/AMP-(fatty) acid ligases                          | Acyl-coenzyme A synthetase                         |
| ahpD | 2       | alkylhydroperoxidase AhpD family core domain protein                           |                                                  |
| badI | 1       | 2-ketocyclohexanecarboxyl-CoA hydrolase (EC 4.1.3.36)                         |                                                  |
| csgA | 1       | Short-chain dehydrogenase/reductase SDR (EC:1.1.1.184)                         |                                                  |
| Dai_5984 | 1 | Alpha/beta Hydrolase fold                                                    |                                                  |
| dcp  | 2       | Peptidyl-dipeptidase dcp (EC 3.4.15.5)                                        |                                                  |
| ebA6516 | 1 | Enoyl-CoA hydrolase (EC 4.2.1.17)                                             | Enoyl-CoA hydrolase                              |
| etfB | 1       | Electron transfer flavoprotein, beta subunit                                  | Electron transfer chain for branched-chain amino acid degradation |
| etfD1 | 1      | Electron transfer flavoprotein-ubiquinone oxidoreductase (EC 1.5.5.1)         | Electron transfer chain for branched-chain amino acid degradation |
| etfD2 | 1      | Electron transfer flavoprotein-ubiquinone oxidoreductase (EC 1.5.5.1)         | Electron transfer chain for branched-chain amino acid degradation |
| fabG | 2       | 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100)                      |                                                  |
| fadA | 1       | acetyl-CoA acyltransferase                                                     | Fatty acid biosynthesis                            |
| fadB | 1       | 3-hydroxyacyl-CoA dehydrogenase                                               | Fatty acid degradation                             |
| fadL | 1       | Long-chain fatty acid transport protein                                        | Fatty acid degradation                             |
| fpr  | 1       | Flavodoxin reductases (ferredoxin-NADPH reductases) family 1                   |                                                  |
| h16_A0164 | 1 | Metallo-beta-lactamase family protein                                          | Dehydrogenases with different specificities (related to short-chain alcohol dehydrogenases) |
| h16_A0171 | 1 | 2-Hydroxychromene-2-carboxylate isomerase                                      |                                                  |
| h16_A0173 | 1 | Putative phosphatase YieH                                                      |                                                  |
| h16_A0174 | 1 | Dienenalactone hydrolase or related enzyme                                     |                                                  |
| h16_A0175 | 1 | Dienenalactone hydrolase or related enzyme                                     |                                                  |
| h16_A0176 | 1 | Maleylacetate isomerase (EC 5.2.1.2) / Glutathione S-transferase               |                                                  |
| h16_A0178 | 1 | Maleylacetate isomerase (EC 5.2.1.2) / Glutathione S-transferase               |                                                  |
| hit  | 3       | Bis(5'-nucleosyl)-tetraphosphatase (asymmetrical) (EC 3.6.1.17)               |                                                  |
| IL0880 | 2  | Sensory box/GGDEF family protein                                               |                                                  |
| ivdA1 | 1      | 3-ketoacyl-CoA thiola (isoleucine degradation) (EC 2.3.1.16)                   | Branched-chain amino acid degradation              |
| ivdA2 | 1      | 3-ketoacyl-CoA thiola (isoleucine degradation) (EC 2.3.1.16)                   | Branched-chain amino acid degradation              |
| ivdB1 | 1      | Methylmalonate-semialdehyde dehydrogenase (EC 1.2.1.27)                       | Branched-chain amino acid degradation              |
| ivdB2 | 1      | Methylmalonate-semialdehyde dehydrogenase (EC 1.2.1.27)                       | Branched-chain amino acid degradation              |
| ivdC1 | 1      | Branched-chain acyl-CoA dehydrogenase (EC 1.3.99.12)                          | Branched-chain amino acid degradation              |
| ivdC2 | 1      | Branched-chain acyl-CoA dehydrogenase (EC 1.3.99.12)                          | Branched-chain amino acid degradation              |
| ivdD1 | 1      | 3-hydroxyisobutyryl-CoA hydrolase (EC 3.1.2.4)                                 | Branched-chain amino acid degradation              |
| ivdD2 | 1      | 3-hydroxyisobutyryl-CoA hydrolase (EC 3.1.2.4)                                 | Branched-chain amino acid degradation              |
| ivdE1 | 1      | Enoyl-CoA hydratase (valine degradation) (EC 4.2.1.17) / Enoyl-CoA hydratase (isoleucine degradation] (EC 4.2.1.17) | Branched-chain amino acid degradation              |
| ivdE2 | 1      | Enoyl-CoA hydratase (valine degradation) (EC 4.2.1.17) / Enoyl-CoA hydratase (isoleucine degradation] (EC 4.2.1.17) | Branched-chain amino acid degradation              |
| ivdG1 | 1      | 3-hydroxyacyl-CoA dehydrogenase (isoleucine degradation) (EC 1.1.1.35)         | Branched-chain amino acid degradation              |
| ivdG2 | 1      | 3-hydroxyacyl-CoA dehydrogenase (isoleucine degradation) (EC 1.1.1.35)         | Branched-chain amino acid degradation              |
| lc6A | 1      | Long-chain fatty acid-CoA ligase (EC 6.2.1.3)                                  | Fatty acid degradation                             |
| livF  | 4      | Branched-chain amino acid transport ATP-binding protein LivF (TC 3.A.1.4.1)     | Branched-chain amino acid transport                |
| livG  | 4      | Branched-chain amino acid transport ATP-binding protein LivG (TC 3.A.1.4.1)     | Branched-chain amino acid transport                |
| livH  | 4      | Branched-chain amino acid transport permease protein LivH (TC 3.A.1.4.1)       | Branched-chain amino acid transport                |
| livK  | 6      | Branched-chain amino acid transport substrate-binding protein LivK (TC 3.A.1.4.1) | Branched-chain amino acid transport                |
| livM  | 4      | Branched-chain amino acid transport system permease protein LivM (TC 3.A.1.4.1) | Branched-chain amino acid transport                |
| mmgB | 1      | 3-hydroxybutyryl-CoA dehydrogenase (EC 1.1.1.157)                              | Branched-chain amino acid degradation              |
| mmgC | 1      | Acyl-CoA dehydrogenase, short-chain specific (EC 1.3.99.2)                    | Branched-chain amino acid degradation              |
LiuR  paaG  2  2  Enoyl-CoA hydratase/isomerase
LiuR  paaH1  3  1  3-hydroxybutyryl-CoA dehydrogenase (EC 1.1.1.157)  Branched-chain amino acid degradation
LiuR  paaI  10  3  Phenylacetic acid degradation-related protein
LiuR  paaK  2  2  Phenylacetate-coenzyme A ligase (EC 6.2.1.30)
LiuR  Rsu_A1944  1  1  2-hydroxychromene-2-carboxylate isomerase (EC 5.3.99.-)
LiuR  RSc0258  1  1  Protein of unknown function
LiuR  RSc0259  1  1  Beta-lactamase domain protein
LiuR  RSc0281  1  1  Metallo-beta-lactamase family protein
LiuR  serA  2  1  D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95)  Serine biosynthesis
LiuR  SMc00041  5  1  hypothetical protein
LiuR  tyrP  1  1  Tyrosine-specific transport protein (HAAAP family)
LiuR  tyrR  7  1  aromatic amino acid biosynthesis/transport transcriptional regulator  Transcriptional regulator
LiuR  yciK  3  1  Oxidoreductase, short-chain dehydrogenase/reductase family
LiuR  acdA  28  5  Acetoacetyl-CoA synthetase [leucine] (EC 6.2.1.16)  Branched-chain amino acid degradation
LiuR  acdB  27  5  3-ketoacyl-CoA thiolase (EC 2.3.1.16) @ Acetyl-CoA acetyltransferase (EC 2.3.1.9)  Branched-chain amino acid degradation
LiuR  acdH  43  8  Acyl-CoA dehydrogenase (EC 1.3.99.3)  Branched-chain amino acid degradation
LiuR  acdH2  14  4  Acyl-CoA dehydrogenase (EC 1.3.99.3)  Branched-chain amino acid degradation
LiuR  acdL  7  4  Acyl-CoA dehydrogenase, long-chain specific, mitochondrial precursor (EC 1.3.99.13)  Branched-chain amino acid degradation
LiuR  acdL2  6  3  Acyl-CoA dehydrogenase, long-chain specific, mitochondrial precursor (EC 1.3.99.13)  Branched-chain amino acid degradation
LiuR  acdP  4  1  Acyl-CoA dehydrogenase family protein
LiuR  acdQ  4  1  Acyl-CoA dehydrogenases  Branched-chain amino acid degradation
LiuR  aceB  16  1  malate synthase A  Tricarboxylic acid cycle
LiuR  aceK  17  3  Isocitrate dehydrogenase phosphatase (EC 2.7.11.5)/kinase (EC 3.1.3.-)  Tricarboxylic acid cycle
LiuR  attC  1  1  Geranyl-CoA carboxylase carboxyl transferase subunit
LiuR  attD  1  1  Isovaleryl-CoA dehydrogenase (EC 1.3.99.10)  Branched-chain amino acid degradation
LiuR  attE  1  1  Isohexenylglutaconyl-CoA hydratase  Branched-chain amino acid degradation
LiuR  attF  1  1  Methylcrotonyl-CoA carboxylase biotin-containing subunit (EC 6.4.1.4)  Branched-chain amino acid degradation
LiuR  bkdA1  25  3  Branched-chain alpha-keto acid dehydrogenase, E1 component, alpha subunit (EC 1.2.4.4)  Branched-chain amino acid degradation
LiuR  bkdA2  25  3  Branched-chain alpha-keto acid dehydrogenase, E1 component, beta subunit (EC 1.2.4.4)  Branched-chain amino acid degradation
LiuR  bkdB  25  3  Dihydrolipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex (EC 2.3.1.168)  Branched-chain amino acid degradation
LiuR  cah  19  4  Carbonic anhydrase (EC 4.2.1.1)  Carbonic anhydrase
LiuR  echH  7  1  Enoyl-CoA hydratase (EC 4.2.1.17)  Branched-chain amino acid degradation
LiuR  etfD  23  5  Electron transfer flavoprotein-ubiquinone oxidoreductase (EC 1.5.5.1)  Electron transfer chain for branched-chain amino acid degradation
LiuR  fadA  9  4  Long-chain-fatty acid--CoA ligase (EC 6.2.1.3)  Fatty acid degradation
LiuR  gldB  18  2  Glutamate synthase [NADPH] large chain (EC 1.4.1.13)  Glutamate biosynthesis
LiuR  gldD  18  2  Glutamate synthase [NADPH] small chain (EC 1.4.1.13)  Glutamate biosynthesis
LiuR  hbdA  6  1  3-hydroxybutyryl-CoA dehydrogenase (EC 1.1.1.157)  Branched-chain amino acid degradation
LiuR  ivdA  28  5  Methylmalonate-semialdehyde dehydrogenase (EC 1.2.1.27)  Branched-chain amino acid degradation
LiuR  ivdB  27  5  3-hydroxyisobutyryl-CoA hydratase (EC 3.1.2.4)  Branched-chain amino acid degradation
LiuR  ivdE  31  6  Enoyl-CoA hydratase [valine degradation] (EC 4.2.1.17)  Branched-chain amino acid degradation
LiuR  ivdF  32  6  3-hydroxyisobutyrate dehydrogenase (EC 1.1.1.31)  Branched-chain amino acid degradation
LiuR  ivdG  31  6  3-hydroxybutyryl-CoA dehydrogenase (EC 1.1.1.157)  Branched-chain amino acid degradation
LiuR  ldh  21  3  Leucine dehydrogenase (EC 1.4.1.9)  Branched-chain amino acid degradation
LiuR  liuF  19  2  Succinyl-CoA 3-ketoacid-coenzyme A transferase subunit A (EC 2.8.3.5)  Branched-chain amino acid degradation
LiuR  liuG  19  2  Succinyl-CoA 3-ketoacid-coenzyme A transferase subunit B (EC 2.8.3.5)  Branched-chain amino acid degradation
| LiuR | liuR1 | 10 | 2 | Predicted transcriptional regulator LiuR of leucine degradation pathway, MerR family |
| LiuR | liuR2 | 5 | 4 | Predicted transcriptional regulator LiuR of leucine degradation pathway, MerR family |
| LiuR | mcma | 9 | 2 | Methylmalonyl-CoA mutase (EC 5.4.99.2) |
| LiuR | mdh | 9 | 1 | Malate dehydrogenase (EC 1.1.1.137) |
| LiuR | paaH | 17 | 4 | 3-hydroxybutyryl-CoA dehydrogenase (EC 1.1.1.157) |
| LiuR | PF03060 | 6 | 1 | Dioxygenases related to 2-nitropropane dioxygenase |
| LiuR | PF04828 | 11 | 1 | Glutathione S-transferase, unnamed subgroup (EC 2.5.1.18) |
| LiuR | PF09917 | 6 | 1 | Protein of unknown function, PF09917 |
| LiuR | prpB | 2 | 1 | Methylisocitrate lyase (EC 4.1.3.30) |
| LiuR | prpC | 2 | 1 | 2-methylcitrate synthase (EC 2.3.3.5) |
| LiuR | prpD | 2 | 1 | 2-methylcitrate dehydratase (EC 4.2.1.79) |
| LiuR | Rfer_2814 | 1 | 1 | protein of unknown function DUF849 |
| LiuR | sucA | 9 | 1 | 2-oxoglutarate dehydrogenase E1 component (EC 1.2.4.2) |
| LiuR | sucB | 8 | 1 | Tricarboxylic acid cycle |
| LiuR | succ | 9 | 1 | Succinyl-CoA ligase [ADP-forming] beta chain (EC 6.2.1.5) |
| LiuR | succD | 9 | 1 | Succinyl-CoA ligase [ADP-forming] alpha chain (EC 6.2.1.5) |
| LiuR | thrA | 15 | 1 | Threonine biosynthesis |
| LiuR | thrB | 15 | 1 | Threonine biosynthesis |
| LiuR | thrC | 15 | 1 | Threonine biosynthesis |
| LldR | lldR | 54 | 13 | Lactate-responsive regulator LldR, GntR family |
| LldR | lldP | 41 | 12 | L-lactate permease |
| LldR | lldD | 23 | 8 | L-lactate dehydrogenase (EC 1.1.2.5) |
| LldR | lldG | 29 | 9 | L-lactate dehydrogenase, hypothetical protein subunit LldG |
| LldR | lldE | 21 | 7 | L-lactate dehydrogenase (EC 1.1.2.3) |
| LldR | lldE | 26 | 8 | L-lactate dehydrogenase, Fe-S oxidoreductase subunit |
| LldR | lldF | 25 | 8 | L-lactate dehydrogenase, iron-sulfur cluster-binding subunit |
| LldR | glcF | 5 | 2 | Glycolate dehydrogenase (EC 1.1.99.14), iron-sulfur subunit GlcF |
| LldR | glcD | 5 | 2 | Glycolate dehydrogenase (EC 1.1.99.14), subunit GlcD |
| LldR | glcE | 4 | 1 | L-lactate dehydrogenase, iron-sulfur cluster-binding subunit LldE |
| LldR | lldD | 5 | 1 | predicted lactate permease, DUF81 family |
| LldR | glcE | 1 | 1 | Glycolate dehydrogenase (EC 1.1.99.14), FAD-binding subunit GlcE |
| LldR | glcG | 1 | 1 | Hypothetical protein GlcG in glycolate utilization operon |
| LldR | glcB | 1 | 1 | Malate synthase G (EC 2.3.3.9) |
| MetJ | metA | 50 | 5 | Methionine biosynthesis |
| MetJ | metB | 46 | 6 | Methionine biosynthesis |
| MetJ | metE | 44 | 6 | S-methyltetrahydropteroyltriglutamate–homocysteine methyltransferase (EC 2.1.1.14) |
| MetJ | metF | 43 | 6 | 5,10-methyleneetahydrofolate reductase (EC 1.5.1.20) |
| MetJ | metH | 36 | 4 | S-methyltetrahydrofolate–homocysteine methyltransferase (EC 2.1.1.13) |
| MetJ | metI | 36 | 4 | Methionine ABC transporter permease protein |
| MetJ | metJ | 59 | 6 | S-adenosylmethionine-responsive transcriptional repressor MetJ |
| MetJ | metK | 55 | 6 | S-adenosylmethionine synthetase (EC 2.5.1.6) |
| MetJ | metL | 48 | 5 | Aspartokinase (EC 2.7.2.4) / Homoserine dehydrogenase (EC 1.1.1.3) |
| MetJ | metN | 37 | 4 | Methionine ABC transporter ATP-binding protein |
| MetJ | metQ | 38 | 4 | Methionine ABC transporter substrate-binding protein |
| MetJ | metR | 44 | 5 | Methionine-responsive transcriptional regulator of methionine metabolism, LysR family |
| MetJ | metT | 32 | 4 | Methionine transporter MetT, NhaC antiporter family |
| MetJ | ahpC | 5 | 1 | Alkyl hydroperoxide reductase protein C (EC 1.6.4.-) |
| Gene | Function | Description |
|------|----------|-------------|
| ahpF | Alkyl hydroperoxide reductase protein F | EC 1.6.4.- |
| ASA_2534 | Erythronate-4-phosphate dehydrogenase | (EC 1.1.1.290) |
| asd | Aspartate-semialdehyde dehydrogenase | EC 1.2.1.11 |
| btuB | TonB-dependent outer membrane transporter for vitamin B12 | |
| btuC | Vitamin B12 ABC transporter, permease component | |
| btuD | Vitamin B12 ABC transporter, ATPase component | |
| btuF | Vitamin B12 ABC transporter, B12-binding component | |
| CKO_03982 | Hypothetical protein | |
| COG0235 | Ribulose-5-phosphate 4-epimerase and related epimerases and aldolases | |
| COG4948 | L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily | |
| COG5276 | Hypothetical protein, COG5276 family | |
| folE | GTP cyclohydrolase I | Type 1 |
| mccA | Cystathionine beta-synthase | EC 4.2.1.22 |
| mccB | Cystathionine gamma-lyase | EC 4.4.1.11 |
| metC | Cystathionine beta-lyase | EC 4.4.1.8 |
| metE | Methionine synthase II, vitamin-B12 independent | |
| metF-II | 5,10-methylenetetrahydrofolate reductase, non-orthologous isozyme | |
| metF | Methionine ABC transporter substrate-binding protein | |
| mmuM | Homocysteine S-methyltransferase | EC 2.1.1.10 |
| mmuP | S-methylmethionine transporter | |
| mtnA | Methylthioribose-1-phosphate dehydratase | EC 4.2.1.10 |
| mtnB | 2,3-diketo-5-methylthiopentyl-1-phosphate enolase-phosphatase | |
| mtnC | 1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase | |
| mtnD | Methionine aminotransferase | |
| mtnE | Methylthioribose recycling | |
| mtnF | Predicted methylthioribose ABC transporter, substrate-binding protein | |
| mtnG | Predicted methylthioribose ABC transporter, ATP-binding protein | |
| mtnH | Predicted methylthioribose ABC transporter, permease protein | |
| mtnI | Methylthioribose recycling | |
| mtnJ | Putative ZOG-Fe(II) oxygenase | |
| mtnK | Homoserine/homoserine lactone efflux protein | |
| mtnL | Cob(II)alamin adenosyltransferase | EC 2.5.1.17 |
| pduO | Protein of unknown function | DU1852 |
| serA | D-3-phosphoglycerate dehydrogenase | EC 1.1.1.95 |
| thrA | Aspartokinase | EC 2.7.2.4 / Homoserine dehydrogenase | EC 1.1.1.3 |
| thrB | Homoserine kinase | EC 2.7.1.39 |
| thrC | Threonine synthase | EC 4.2.3.1 |
| ybdH | Uncharacterized oxidoreductase | |
| btuB | TonB-dependent outer membrane transporter for vitamin B12 | |
| COG3126 | Homoserine/lactone efflux protein | |
| csd | Cysteine desulfurase | EC 2.8.1.7 |
| metX | Homoserine O-acethyltransferase | EC 2.3.1.31 |
| metY | O-acetylhomoserine sulfhydrylase | / O-succinylhomoserine sulfhydrylase | |
| mtsA | Substrate-specific component | |
| mtsB | Duplicated ATPase component | |
| mtsC | Transmembrane component | |

**Gene Functions:**
- **Methionine biosynthesis:**
- **Vitamin B12 transport:**
- **Methionine metabolism:**
- **Threonine biosynthesis:**
- **Serine biosynthesis:**
- **Threonine biosynthesis:**
- **Vitamin B12 transport:**
- **Methionine metabolism:**
- **Methionine metabolism:**
- **Methionine transport:**
- **Methionine transport:**
- **Methionine transport:**
- **Protein of unknown function:**
- **Protein of unknown function:**
- **Lipoprotein-related protein:**
- **Cysteine desulfurase:**
- **Homoserine O-acetyltransferase:**
- **O-acetylhomoserine sulfhydrylase:**
- **O-succinylhomoserine sulfhydrylase:**
- **Substrate-specific component:**
- **Duplicated ATPase component:**
- **Transmembrane component:**
| Gene | Description |
|------|-------------|
| metR | Homocysteine-responsive transcriptional regulator of methionine metabolism, LysR family |
| metE | 5-methyltetrahydropteroylglutamate--homocysteine methyltransferase (EC 2.1.1.14) |
| metE2 | Methionine synthase II, vitamin-B12 independent (EC 2.1.1.14) |
| metF | 5,10-methylenetetrahydrofolate reductase (EC 1.5.1.20) |
| glyA | Serine hydroxymethyltransferase (EC 2.1.2.1) |
| PF08908 | Protein of unknown function DUF1852 |
| metH | 5-methyltetrahydrofolate--homocysteine methyltransferase (EC 2.1.1.13) |
| luxS | S-ribosylhomocysteine lyase (EC 4.4.1.21) / Autoinducer-2 production protein LuxS |
| metA | Homoserine O-succinyltransferase (EC 2.3.1.46) |
| metE2-2 | Methionine synthase II, vitamin-B12 independent (EC 2.1.1.14) |
| PF03358 | NADPH-dependent FMN reductase |
| ilvI | Acetolactate synthase large subunit (EC 2.2.1.6) |
| ilvH | Acetolactate synthase small subunit (EC 2.2.1.6) |
| hmp | Flavohemoprotein (Hemoglobin-like protein) (Flavohemoglobin) (Nitric oxide dioxygenase) (EC 1.14.12.17) |
| metF-II | 5,10-methylenetetrahydrofolate reductase, non-orthologous isozyme (EC 1.5.1.20) |
| metC | Cystathionine beta-lyase (EC 4.4.1.8) |
| HI0736 | Methionine gamma-lyase (EC 4.4.1.11) |
| PF0613 | Hypothetical sodium-dependent transporter |
| PF02677 | Protein of unknown function DUF208 |
| pfI | Pyruvate formate-lyase (EC 2.3.1.54) |
| dsbC | Thiol-disulfide interchange protein DsbC |
| metQ2 | Methionine ABC transporter substrate-binding protein |
| thrC | Threonine synthase (EC 4.2.3.1) |
| hom | Homoserine dehydrogenase (EC 1.1.1.3) |
| metF2 | 5,10-methylenetetrahydrofolate reductase (EC 1.5.1.20) |
| metH2 | 5-methyltetrahydrofolate--homocysteine methyltransferase (EC 2.1.1.13) |
| metR2 | Homocysteine-responsive transcriptional regulator of methionine metabolism, LysR family |
| gcvP | Glycine dehydrogenase [decarboxylating] (glycine cleavage system P protein) (EC 1.4.4.2) |
| gcvH | Glycine cleavage system H protein |
| mdeA | Methionine gamma-lyase (EC 4.4.1.11) |
| bhmT | Betaine--homocysteine S-methyltransferase (EC 2.1.1.5) |
| nadA | Quinolinate synthetase (EC 4.1.99.-) |
| nadC | Quinolinate phosphoribosyltransferase [decarboxylating] (EC 2.4.2.19) |
| nadE | Nicotinate phosphoribosyltransferase (EC 2.4.2.11) |
| nadB | L-aspartate oxidase (EC 1.4.3.16) |
| nadR | Transcriptional regulator of NAD metabolism / Nicotinamide-nucleotide adenylyltransferase, NadR family (EC 2.7.7.1) / Ribosylnicotinamide kinase (EC 2.7.1.22) |
| niaA | Niacin transporter, MFS family |
| nadA | Quinolinate synthetase (EC 4.1.99.-) |
| nadC | Quinolinate phosphoribosyltransferase [decarboxylating] (EC 2.4.2.19) |
| nadB | L-aspartate oxidase (EC 1.4.3.16) |
| nadE | Nicotinate-nucleotide adenylyltransferase, NadE family (EC 6.3.1.5) / Glutamine amidotransferase chain of NAD synthetase |
| nadQ | Transcriptional regulator of NAD metabolism, COG4111 family |
| nadD | Nicotinate-nucleotide adenylyltransferase (EC 2.7.7.18) ## bacterial NadD family |
| proA | Gamma-glutamyl phosphate reductase (EC 1.2.1.41) |
| Protein | Gene Symbol | Description | Function |
|---------|-------------|-------------|----------|
| NadQ    | HNE_0691    | Hypothetical protein | |
| NadQ    | nadC2       | Quinolinate phosphoribosyltransferase [decarboxylating] (EC 2.4.2.19) | NAD biosynthesis |
| NadQ    | nadA1       | Quinolinate synthetase (EC 4.1.99.-) | NAD biosynthesis |
| NadQ    | nadA2       | Quinolinate synthetase (EC 4.1.99.-) | NAD biosynthesis |
| NadQ    | nadB2       | L-aspartate oxidase (EC 1.4.3.16) | NAD biosynthesis |
| NadQ    | nadB1       | L-aspartate oxidase (EC 1.4.3.16) | NAD biosynthesis |
| NagC    | nagC        | PTS system, N-acetylglucosamine-specific II B component (EC 2.7.1.69) / PTS system, glucose-specific II C component (EC 2.7.1.69) | N-acetylglucosamine utilization |
| NagC    | nagE        | N-acetylglucosamine-6-phosphate deacetylase (EC 3.5.1.25) | N-acetylglucosamine utilization |
| NagC    | nagC        | N-acetylglucosamine-6 phosphate deaminase (EC 3.5.99.6) | N-acetylglucosamine utilization |
| NagC    | ptsI        | Phosphoenolpyruvate-protein phosphotransferase of PTS system (EC 2.7.3.9) | Sugar transport |
| NagC    | ptsH        | Phosphocarrier protein of PTS system | Sugar transport |
| NagC    | crr         | PTS system, glucose-specific III A component (EC 2.7.1.69) | Sugar transport |
| NagC    | nagA        | N-acetylglucosamine-6-phosphate deacetylase (EC 3.5.1.25) | N-acetylglucosamine utilization |
| NagC    | nagB        | N-acetylglucosamine-6 phosphate deaminase (EC 3.5.99.6) | N-acetylglucosamine utilization |
| NagC    | ptsI        | Phosphoenolpyruvate-protein phosphotransferase of PTS system (EC 2.7.3.9) | Sugar transport |
| NagC    | ptsH        | Phosphocarrier protein of PTS system | Sugar transport |
| NagC    | crr         | PTS system, glucose-specific III A component (EC 2.7.1.69) | Sugar transport |
| NagC    | mcp         | N-acetylglucosamine regulated methyl-accepting chemotaxis protein | Chemotaxis |
| NagC    | mcp2        | N-acetylglucosamine regulated methyl-accepting chemotaxis protein | Chemotaxis |
| NagC    | glmU        | N-acetylglucosamine-1-phosphate uridylyltransferase (EC 2.7.7.23) / Glucosamine-1-phosphate N-acetyltransferase (EC 2.3.1.157) | N-acetylglucosamine utilization |
| NagC    | hex         | Beta-hexosaminidase (EC 3.2.1.52) | Chitin degradation |
| NagC    | rpmE1       | SOS ribosomal protein L31 | |
| NagC    | znuA        | Zinc ABC transporter, periplasmic-binding protein ZnuA | |
| NagC    | pyrG        | CTP synthase (EC 6.3.4.2) | Glycolysis |
| NagC    | eno         | Enolase (EC 4.2.1.11) | Glycolysis |
| NagC    | tfoX        | DNA transformation protein TfoX | |
| NagC    | tfoX1       | DNA transformation protein TfoX1 (Sxy) | |
| NagC    | ptsG        | PTS system, glucose-specific III B component (EC 2.7.1.69) / PTS system, glucose-specific III C component (EC 2.7.1.69) | Mannose and glucose transport |
| NagC    | fbaA        | Fructose-biphosphate aldolase class II (EC 4.1.2.13) | Glycolysis |
| NagC    | pgk         | Phosphoglycerate kinase (EC 2.7.2.3) | Glycolysis |
| NagC    | chiA        | Chitinase (EC 3.2.1.14) | Chitin degradation |
| NagC    | manX        | PTS system, mannose-specific IIIA B component | Mannose and glucose transport |
| NagC    | glmS        | Glucosamine-fructose-6-phosphate aminotransferase [isomerizing] (EC 2.6.1.16) | N-acetylglucosamine utilization |
| NagC    | manZ        | PTS system, mannose-specific III D component | Mannose and glucose transport |
| NagC    | manY        | PTS system, mannose-specific III C component | Mannose and glucose transport |
| NagC    | negE2       | N-acetylglucosamine-specific III A component (EC 2.7.1.69) / PTS system, N-acetylglucosamine-specific III C component (EC 2.7.1.69) | N-acetylglucosamine utilization |
| NagC    | aldE        | Aldose 1-epimerase | |
| NagC    | chi         | Chitinase (EC 3.2.1.14) | Chitin degradation |
| NagC    | nagD        | Phosphatase NagD predicted to act in N-acetylglucosamine utilization subsystem | N-acetylglucosamine utilization |
| NagC    | nagE1       | N-acetylglucosamine-specific III B component (EC 2.7.1.69) / PTS system, N-acetylglucosamine-specific III C component (EC 2.7.1.69) | N-acetylglucosamine utilization |
| NagC    | gapA        | NAD-dependent glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) | Glycolysis |
| NagC    | chbR        | Chitobiose-specific regulator ChbR, AraC family | Transcription regulation |
| NagC    | chbB        | Chitobiose-specific III B component (EC 2.7.1.69) | Chitobiose utilization |
| NagC    | gdhA        | NADP-specific glutamate dehydrogenase (EC 1.4.1.14) | Glutamate degradation |
| NagC    | rpmJ1       | Ribosomal protein L36 | |
| Gene  | Description                                                                 | Function/Location                                               |
|-------|-------------------------------------------------------------------------------|-----------------------------------------------------------------|
| chbA  | N,N'-diacetylchitobiose-specific PTS system, EIIA component                   | Chitobiose utilization                                          |
| exbD  | Biopolymer transport protein ExbD/TolR                                        |                                                                  |
| tonB  | Periplasmic binding protein TonB                                                |                                                                  |
| chbC  | PTS system, chitobiose-specific IIC component (EC 2.7.1.69)                   | Chitobiose utilization                                          |
| exbB  | Biopolymer transport protein ExbB                                              |                                                                  |
| chbG  | Cellulobiose phosphotransferase system YdjC-like protein                      |                                                                  |
| chbF  | Chitobiose-specific 6-phospho-beta-glucosidase ChbF (EC 3.2.1.86)             | Chitobiose utilization                                          |
| ybFM  | N-acetylglucosamine-regulated outer membrane porin                             | Chitobiose utilization                                          |
| chbG  | PTS system, chitobiose-specific IIC component (EC 2.7.1.69)                   | Chitobiose utilization                                          |
| chbF  | Chitobiose-specific 6-phospho-beta-glucosidase ChbF (EC 3.2.1.86)             | Chitobiose utilization                                          |
| glpA  | Glycogen synthase, ADP-glucose transglycosylase (EC 2.4.1.21)                 | Glycogen metabolism                                            |
| glpC  | Glucose-1-phosphate adenyltransferase (EC 2.7.7.27)                           | Glycogen metabolism                                            |
| omC   | Predicted OmpC-like chitoporin                                                 | Chitobiose utilization                                          |
| adh   | Alcohol dehydrogenase (EC 1.1.1.1); Acetaldehyde dehydrogenase (EC 1.2.1.10) | Chitobiose utilization                                          |
| gltA  | Citrate synthase (u) (EC 2.3.3.1)                                              | Tricarboxylic acid cycle                                       |
| chiS  | Chitin catabolic cascade sensor histidine kinase ChiS                           |                                                                  |
| epd   | D-erythrose-4-phosphate dehydrogenase (EC 1.2.1.72)                          |                                                                  |
| galP  | D-galactose transporter                                                        |                                                                  |
| chi1  | Chitinase (EC 3.2.1.14)                                                        | Chitin degradation                                              |
| VP1029| Hypothetical protein                                                           |                                                                  |
| ompU  | Outer membrane protein OmpU                                                    |                                                                  |
| VC1591| Oxidoreductase, short-chain dehydrogenase/reductase family                    |                                                                  |
| aldC  | Alpha-acetolactate decarboxylase (EC 4.1.1.5)                                 |                                                                  |
| budB  | Acetolactate synthase, catabolic (EC 2.2.1.6)                                 |                                                                  |
| alsR  | Transcriptional regulator of alpha-acetolactate operon alsR                   | Transcription regulation                                        |
| nanM  | N-acetylneuraminic acid-induced hypothetical transmembrane protein             | N-acetylneuraminic acid transport                               |
| nanC  | N-acetylneuraminic acid outer membrane channel protein NanC                   | N-acetylneuraminic acid transport                               |
| nagQ  | Predicted transcriptional regulator of N-Acetylglucosamine utilization, GntR family | Transcription regulation                                        |
| nagA  | N-acetylglucosamine-6-phosphate deacetylase (EC 3.5.1.25)                     | N-acetylglucosamine utilization                                 |
| nagB2 | Glucosamine-6-phosphate deaminase [isomerizing], alternative (EC 3.5.99.6)   | N-acetylglucosamine utilization                                 |
| nagE  | PTS system, N-acetylglucosamine-specific IIB component (EC 2.7.1.69) / PTS system, N-acetylglucosamine-specific IIC component (EC 2.7.1.69) | N-acetylglucosamine utilization                                 |
| ptsI  | PTS system, glucose-specific II8 component (EC 2.7.1.69) / Phosphocarrier protein of PTS system / Phosphoenolpyruvate-protein phosphotransferase of PTS system (EC 2.7.3.9) | Sugar transport |
| nagK  | N-acetylglucosamine kinase of eukaryotic type (EC 2.7.1.59)                   | N-acetylglucosamine utilization                                 |
| mruQ  | N-acetyluramic acid 6-phosphate etherase (EC 4.2.-.-)                          | N-acetyluramic acid utilization                                 |
| nagT  | N-Acetyl-D-glucosamine ABC transport system, sugar-binding protein             | N-acetylglucosamine utilization                                 |
| nagV  | N-Acetyl-D-glucosamine ABC transport system, permease protein 2                | N-acetylglucosamine utilization                                 |
| nagU  | N-Acetyl-D-glucosamine ABC transport system, permease protein 1                | N-acetylglucosamine utilization                                 |
| nagW  | N-Acetyl-D-glucosamine ABC transport system, ATP-binding component             | N-acetylglucosamine utilization                                 |
| hex   | Beta-hexosaminidase (EC 3.2.1.52)                                              | N-acetylglucosamine utilization                                 |
| chiA  | Chitinase (EC 3.2.1.14)                                                        | Chitin degradation                                              |
| cdxA  | Chitodextrinase precursor (EC 3.2.1.14)                                        | Chitin degradation                                              |
| omp_nag| Hypothetical oxidoreductase related to N-acetylglucosamine utilization        |                                                                  |
| nagD  | Hypothetical oxidoreductase related to N-acetylglucosamine utilization        |                                                                  |
| nagZ  | Beta N-acetyl-glucosaminidase (EC 3.2.1.52)                                   | Chitin degradation                                              |
| Gene   | Accession | Description                                                                 | Function                                      |
|--------|-----------|------------------------------------------------------------------------------|-----------------------------------------------|
| NagQ   | nagB      | Glucosamine-6-phosphate deaminase (EC 3.5.99.6)                              | N-acetylglucosamine utilization              |
| NagQ   | nagR      | Transcriptional regulator of N-acetylglucosamine utilization, Lact family     | Transcription regulation                      |
| NagQ   | wecA      | Undecaprenyl-phosphate N-acetylglucosaminyl 1-phosphate transferase (EC 2.7.8.-) | Chitin degradation                            |
| NagQ   | hex2      | N-Acetyl-D-glucosamine ABC transport system ATP-binding protein              |                                              |
| NagQ   | cga       | Glucoamylase (EC 3.2.1.3)                                                    | Chitin degradation                            |
| NagQ   | ybM       | N-acetylglucosamine-regulated outer membrane porin                          | Chitin degradation                            |
| NagQ   | cbp21     | Chitin binding protein                                                        | Chitin degradation                            |
| NagQ   | chiC      | Chitinase (EC 3.2.1.14)                                                      | Chitin degradation                            |
| NagQ   | chi       | Chitinase (EC 3.2.1.14)                                                      | Chitin degradation                            |
| NagQ   | nagP      | N-acetylglucosamine transporter, NagP                                         | N-acetylmuramic acid utilization              |
| NagQ   | omp1      | Outer membrane protein (porin)                                               | Chitobiose utilization                        |
| NagQ   | CC0542    | Predicted periplasmic phosphohydrolase                                        |                                              |
| NagQ   | MED297_05914 | Hypothetical protein                                                          |                                              |
| NagQ   | nagX      | N-acetylglucosamine related transporter, NagX                                  | N-acetylmuramic acid utilization              |
| NagQ   | anaG      | Alpha-N-acetylglucosaminidase (EC 3.2.1.50)                                   | Alpha-N-acetylglucosaminidase                |
| NagQ   | mrl4776   | Hypothetical protein                                                          |                                              |
| NagQ   | nagM      | Predicted N-Acetylglucosamine ABC transporter, inner membrane subunit         | N-acetylmuramic acid utilization              |
| NagQ   | nagO      | Predicted N-Acetylglucosamine ABC transporter, periplasmic sugar-binding protein | N-acetylmuramic acid utilization          |
| NagQ   | nagN      | Predicted N-Acetylglucosamine ABC transporter, permease protein               | N-acetylmuramic acid utilization              |
| NagQ   | nagK2     | N-acetylglucosamine kinase (EC 2.7.1.59), ROX family                         | N-acetylmuramic acid utilization              |
| NagQ   | nagD1     | Probable oxidoreductase                                                       |                                              |
| NagQ   | nagL      | Predicted N-Acetylglucosamine ABC transporter, ATP-binding protein            | N-acetylmuramic acid utilization              |
| NagR   | omp_nag   | N-acetylglucosamine-regulated TonB-dependent outer membrane receptor          | Chitobiose utilization                        |
| NagR   | trpX      | Tryptophan halogenase                                                         |                                              |
| NagR   | nagA      | N-acetylglucosamine-6-phosphate deacetylase (EC 3.5.1.25)                    | N-acetylglucosamine utilization              |
| NagR   | nagP      | PTS system, N-acetylglucosamine-specific IIIB component (EC 2.7.1.69)         | N-acetylmuramic acid utilization              |
| NagR   | nagK      | PTS system, N-acetylglucosamine-specific IIC component (EC 2.7.1.69)          | N-acetylmuramic acid utilization              |
| NagR   | nagX      | N-acetylglucosamine related transporter, NagX                                  | N-acetylmuramic acid utilization              |
| NagR   | hex       | Beta-hexosaminidase (EC 3.2.1.52)                                             | Chitobiose utilization                        |
| NagR   | nagB2     | Glucosamine-6-phosphate deaminase [isomerizing], alternative (EC 3.5.99.6)    | N-acetylmuramic acid utilization              |
| NagR   | nagK2     | Predicted N-acetylglucosamine kinase, glucokinase-like (EC 2.7.1.59)          | N-acetylmuramic acid utilization              |
| NagR   | nagR      | Transcriptional regulator of N-acetylglucosamine utilization, Lact family      | Transcription regulation                      |
| NagR   | nagB      | Glucosamine-6-phosphate deaminase (EC 3.5.99.6)                              | N-acetylmuramic acid utilization              |
| NagR   | chiA      | Chitinase (EC 3.2.1.14)                                                       | Chitin degradation                            |
| NagR   | nixC      | N-acetylglucosamine-regulated TonB-dependent outer membrane receptor          | Chitobiose utilization                        |
| NagR   | naxA      | N-acetylglucosamine-regulated TonB-dependent outer membrane receptor          | Chitobiose utilization                        |
| NagR   | cbp       | Chitin and N-acetylglucosamine-binding protein A                              | Chitin degradation                            |
| NagR   | pckA      | Phosphoenolpyruvate carboxykinase [ATP] (EC 4.1.1.49)                          | Gluconeogenesis                               |
| NagR   | chiD      | Chitodextrinase (EC 3.2.1.14)                                                 | Chitin degradation                            |
| NagR   | pgii2     | Glucose-6-phosphate isomerase (EC 5.3.1.9)                                    | Glycolysis                                    |
| NagR   | sapC      | Peptide transport system permease protein sapC (TC 3.A.1.5.5)                 |                                              |
| NagR   | mcp_nag   | N-acetylglucosamine regulated methyl-accepting chemotaxis protein             | Chemotaxis                                    |
| NagR   | nixD      | N-acetylglucosamine-regulated TonB-dependent outer membrane receptor          | Chitobiose utilization                        |
| NagR   | nixB      | N-acetylglucosamine-regulated TonB-dependent outer membrane receptor          | Chitobiose utilization                        |
| NagR   | pilIM     | Homolog of type IV pilus assembly protein PilIM                                |                                              |
| NagR   | duf81     | Protein of unknown function DUF81                                             |                                              |
| NagR   | nagS2     | Putative sulfatase (EC 3.1.6.-)                                               |                                              |
| NagR   | SO0851    | Preplin-type cleavage/methylation-like protein                                 |                                              |
| Gene     | Accession | Start | End | Description                                                                                     |
|----------|-----------|-------|-----|-------------------------------------------------------------------------------------------------|
| NagR     | CPS_2383  | 1     | 1   | Putative surface protein                                                                        |
| NagR     | SO0852    | 5     | 1   | Type IV fimbrial biogenesis protein PilV                                                        |
| NagR     | ATW7_01305| 1     | 1   | Pass1-related protein                                                                          |
| NagR     | bgIX      | 1     | 1   | Beta-glucosidase (EC 3.2.1.21)                                                                  |
| NagR     | SO0850    | 5     | 1   | Type IV fimbrial biogenesis protein PilX                                                        |
| NagR     | SO0854    | 4     | 1   | Type IV pilus biogenesis protein PilE                                                           |
| NagR     | SO0853    | 4     | 1   | Type IV fimbrial biogenesis protein FimT                                                         |
| NagR     | nixA      | 1     | 1   | N-acetylglucosamine-regulated TonB-dependent outer membrane receptor                             |
| NagR     | cbp2      | 2     | 1   | putative chitin-binding protein, exported                                                       |
| NagR     | cdxA      | 2     | 1   | Chitodextrinase precursor (EC 3.2.1.14)                                                         |
| NagR     | pdaA      | 1     | 1   | Peptidoglycan N-acetylglucosamine deacetylase                                                   |
| NagR     | omp_nag2  | 1     | 1   | N-acetylglucosamine-regulated TonB-dependent outer membrane receptor                             |
| NagR     | chiA3     | 1     | 1   | Chitodextrinase                                                                                 |
| NrdR     | nrdA      | 126   | 19  | Ribonucleotide reductase of class la (aerobic), alpha subunit (EC 1.17.4.1)                     |
| NrdR     | nrdB      | 117   | 19  | Ribonucleotide reductase of class la (aerobic), beta subunit (EC 1.17.4.1)                      |
| NrdR     | nrdD      | 70    | 12  | Ribonucleotide reductase of class III (anaerobic), large subunit (EC 1.17.4.2)                   |
| NrdR     | nrdE      | 63    | 12  | Ribonucleotide reductase of class III (anaerobic), activating protein (EC 1.97.1.4)             |
| NrdR     | yfAe      | 40    | 7   | Ferredoxin                                                                                      |
| NrdR     | nrdJa     | 21    | 4   | Ribonucleotide reductase of class II (coenzyme B12-dependent)                                   |
| NrdR     | trxA      | 4     | 1   | Thioredoxin                                                                                    |
| NrdR     | topA      | 8     | 1   | DNA topoisomerase I (EC 5.99.1.2)                                                               |
| NrtR     | nrtR      | 24    | 10  | Nudix-related transcriptional regulator NrtR                                                    |
| NrtR     | nrtX      | 7     | 6   | NrtR-regulated hypothetical OrfX, Band 7 protein domain                                          |
| NrtR     | pncB      | 15    | 5   | Nicotinate phosphoribosyltransferase (EC 2.4.2.11)                                              |
| NrtR     | pncA      | 13    | 5   | Nicotinamidase (EC 3.5.1.19)                                                                   |
| NrtR     | nadV      | 7     | 4   | Nicotinamide phosphoribosyltransferase (EC 2.4.2.12)                                            |
| NrtR     | prs       | 6     | 3   | Ribose-phosphate pyrophosphokinase (EC 2.7.6.1)                                                |
| NrtR     | nadE      | 8     | 4   | NAD synthetase (EC 6.3.1.5)                                                                    |
| NrtR     | nadD      | 4     | 3   | Nicotinate-nucleotide adenyltransferase (EC 2.7.7.18)                                           |
| NrtR     | nadM      | 4     | 2   | NAD metabolism                                                                                 |
| Gene | Accession | Days | | Description | Function |
|------|-----------|------|------|-----------------|----------|
| NrtR | pmuC      | 1    |     | Ribosyl nicotinamide transporter, PmuC-like | NAD metabolism |
| NrtR | nadR      | 1    |     | Nicotinamide-nucleotide adenylyltransferase, NadR family (EC 2.7.7.1) / Ribosynicotinamide kinase (EC 2.7.1.22) | NAD metabolism |
| NtrC | glnA      | 163  | 19  | Glutamine synthetase type I (EC 6.3.1.2) | Glutamine biosynthesis |
| NtrC | ntrC      | 157  | 19  | Nitrogen regulation protein NR(I) | Transcription regulation |
| NtrC | ntrB      | 157  | 19  | Nitrogen regulation protein NR(II) (EC 2.7.3.7) | Nitrogen metabolism regulation proteins |
| NtrC | amtB      | 134  | 17  | Ammonium transporter | Nitrogen source transport |
| NtrC | glnK      | 107  | 13  | Nitrogen regulatory protein P-II | Nitrogen metabolism regulation proteins |
| NtrC | glnB      | 66   | 7   | Nitrogen regulatory protein P-II | Nitrogen metabolism regulation proteins |
| NtrC | nifR3     | 41   | 5   | Nitrogen assimilation transcriptional regulator NtrX, Fis family | Nitrogen metabolism regulation proteins |
| NtrC | nasD      | 34   | 8   | Nitrite reductase, large subunit (EC 1.7.1.4) | Nitrogen metabolism |
| NtrC | nasE      | 33   | 8   | Nitrite reductase, small subunit (EC 1.7.1.4) | Nitrogen metabolism |
| NtrC | ntrY      | 30   | 4   | Nitrogen regulation protein NtrY, sensor kinase (EC 2.7.3.7) | Nitrogen metabolism |
| NtrC | amtB2     | 30   | 8   | Ammonium transporter | Nitrogen source transport |
| NtrC | narK      | 23   | 6   | Nitrate/nitrite antiporter | Nitrogen source transport |
| NtrC | ntrX      | 24   | 3   | Nitrogen assimilation transcriptional regulator NtrX, Fis family | Nitrogen metabolism |
| NtrC | ntrZ      | 23   | 3   | Conserved hypothetical signal peptide protein | Nitrogen metabolism |
| NtrC | nasA      | 23   | 7   | Assimilatory nitrate reductase, large subunit (EC 1.7.99.4) | Nitrogen metabolism |
| NtrC | nrtC      | 22   | 4   | Nitrate ABC transporter, ATP-binding component | Nitrogen source transport |
| NtrC | nrtB      | 21   | 4   | Nitrate ABC transporter, permease component | Nitrogen source transport |
| NtrC | nrtA      | 21   | 4   | Nitrate ABC transporter, substrate-binding component | Nitrogen source transport |
| NtrC | urtB      | 22   | 3   | Urea ABC transporter, permease component 2 | Nitrogen source transport |
| NtrC | gdhA      | 13   | 3   | NADP-specific glutamate dehydrogenase (EC 1.4.1.4) | Nitrogen metabolism |
| NtrC | ureD      | 20   | 3   | Urease accessory protein, UreD | Nitrogen metabolism |
| NtrC | ureA      | 20   | 3   | Urease, gamma subunit (EC 3.5.1.5) | Nitrogen metabolism |
| NtrC | ureB      | 19   | 3   | Urease, beta subunit (EC 3.5.1.5) | Nitrogen metabolism |
| NtrC | ureC      | 19   | 3   | Urease, alpha subunit (EC 3.5.1.5) | Nitrogen metabolism |
| NtrC | urtA      | 18   | 3   | Urea ABC transporter, substrate-binding component | Nitrogen source transport |
| NtrC | urtD      | 16   | 3   | Urea ABC transporter, ATP-binding component 1 | Nitrogen source transport |
| NtrC | CHP02001  | 12   | 2   | Conserved hypothetical protein CHP02001 | Nitrogen source transport |
| NtrC | dppC      | 10   | 2   | Dipeptide ABC transporter, permease component 2 | Nitrogen source transport |
| NtrC | dppA      | 10   | 2   | Dipeptide ABC transporter, substrate-binding component | Nitrogen source transport |
| NtrC | dppB      | 10   | 2   | Dipeptide ABC transporter, permease component 1 | Nitrogen source transport |
| NtrC | ureE      | 15   | 2   | Urease accessory protein, UreE | Nitrogen metabolism |
| NtrC | ureG      | 15   | 2   | Urease accessory protein, UreG | Nitrogen metabolism |
| NtrC | ureF      | 15   | 2   | Urease accessory protein, UreF | Nitrogen metabolism |
| NtrC | cydG      | 10   | 4   | Uroporphyrinogen-III methyltransferase (EC 2.1.1.107) | Porphyrin biosynthesis |
| NtrC | urtE      | 15   | 3   | Urea ABC transporter, ATP-binding component 1 | Nitrogen source transport |
| NtrC | glnK2     | 12   | 3   | Nitrogen regulatory protein P-II | Nitrogen metabolism |
| NtrC | nasB      | 8    | 1   | Assimilatory nitrate reductase, large and small subunits protein fusion (EC 1.7.99.4) | Nitrogen metabolism |
| NtrC | dat       | 4    | 1   | D-alanine aminotransferase (EC 2.6.1.21) | Proline degradation |
| NtrC | nasA      | 8    | 2   | Assimilatory nitrate reductase, small subunit (EC 1.7.99.4) | Nitrogen metabolism |
| NtrC | glutI     | 11   | 1   | Glutamate-aspartate ABC transporter, transmembrane component 1 | Nitrogen source transport |
| NtrC | glutK     | 11   | 1   | Glutamate-aspartate ABC transporter, transmembrane component 2 | Nitrogen source transport |
| NtrC | glutL     | 11   | 1   | Glutamate-aspartate ABC transporter, ATP-binding component | Nitrogen source transport |
| NtrC | glutI     | 11   | 1   | Glutamate-aspartate ABC transporter, substrate-binding component | Nitrogen source transport |
| NtrC | dppD      | 5    | 5   | Dipeptide ABC transporter, ATP-binding component 1 | Nitrogen source transport |
| NtrC | dppF      | 5    | 5   | Dipeptide ABC transporter, ATP-binding component 2 | Nitrogen source transport |
| NtrC | ntrXY     | 5    | 1   | Nitrogen assimilation transcriptional regulator NtrX, Fis family | Transcription regulation |
| NtrC | nifR      | 7    | 1   | Predicted oxidoreductase, FAD binding | Nitrogen metabolism |
| Gene   | Type              | Function                                                      |
|--------|-------------------|--------------------------------------------------------------|
| urtC   | Carboxylate-amine ligase | Urea transporter, permease component 2                      |
| ybdK   | Conserved hypothetical protein | Nitrogen source transport                                    |
| PF04168| Conserved hypothetical protein | Nitrogen source transport                                    |
| gltB   | Glutamate synthase, large chain (EC 1.4.1.13) | Glutamate biosynthesis                                      |
| gltD   | Glutamate synthase, small chain (EC 1.4.1.13) | Glutamate biosynthesis                                      |
| nraA2  | Nitrate ABC transporter, substrate-binding component | Nitrogen source transport                                    |
| nifEN  | Nitrogenase FeMo-cofactor scaffold and assembly protein | Nitrogen metabolism                                          |
| Gmet_0693 | Conserved hypothetical protein | Nitrogen source transport                                    |
| PF01841| Transglutaminase-like protein | Nitrogen source transport                                    |
| rutG   | Uracl permease     | Nitrogen source transport                                    |
| hisM   | Histidine ABC transporter, transmembrane component 2 | Nitrogen source transport                                    |
| rutC   | Aminoacylate peracid reductase | Pyrimidine Degradation                                      |
| rutA   | Pyrimidine oxygenase | Pyrimidine Degradation                                      |
| glnP   | Glutamine ABC transporter, transmembrane component | Nitrogen source transport                                    |
| hisP   | Histidine ABC transporter, ATP-binding component | Nitrogen source transport                                    |
| glnH   | Glutamine ABC transporter, substrate-binding component | Nitrogen source transport                                    |
| hisQ   | Histidine ABC transporter, transmembrane component 1 | Nitrogen source transport                                    |
| rutB   | Peroxoyureidocarboxyl/ureidocarboxyl amido hydrolase | Nitrogen source transport                                    |
| rutF   | Flavin reductase | Pyrimidine Degradation                                      |
| hisJ   | Histidine ABC transporter | Nitrogen source transport                                    |
| astD   | Succinylglutamic semialdehyde dehydrogenase (EC 1.2.1.71) | Arginine degradation                                       |
| glnQ   | Glutamine ABC transporter, ATP-binding component | Nitrogen source transport                                    |
| astB   | Succinylarginine dihydroase (EC 3.5.3.23) | Arginine degradation                                       |
| astA   | Arginine N-succinyltransferase (EC 2.3.1.109) | Arginine degradation                                       |
| nac    | Nitrogen assimilation transcriptional regulator, LysR family | Transcription regulation                                    |
| astC   | Succinylornithine transaminase (EC 2.6.1.81) | Arginine degradation                                       |
| astE   | Succinylglutamate dessuccinylase (EC 3.5.1.96) | Arginine degradation                                       |
| uctA   | Urea carboxylase-related ABC transporter, substrate-binding component | Nitrogen source transport                                    |
| COG0733| Predicted sodium dependent transporter | Nitrogen source transport                                    |
| glnK1  | Nitrogen regulatory protein P-II | Nitrogen metabolism                                          |
| uctB   | Urea carboxylase-related ABC transporter, permease component | Nitrogen source transport                                    |
| nasT   | Nitrogen assimilation attenuator protein NasT | Transcription regulation                                    |
| uctC   | Urea carboxylase-related ABC transporter, ATP-binding component | Nitrogen source transport                                    |
| ureJ   | Urease accessory protein, UreI | Nitrogen metabolism                                          |
| alsT   | Predicted alanin/sodium symporter | Nitrogen source transport                                    |
| ansA   | L-asparaginase I (EC 3.5.1.1) | Asparagine degradation                                      |
| dppDE  | Dipeptide ABC transporter, ATP-binding component | Nitrogen source transport                                    |
| hmp    | Nitric oxide dioxygenase | Nitrogen stress response                                     |
| uahA   | Urea carboxylase (EC 6.3.4.6) | Nitrogen metabolism                                          |
| uahB   | Urea carboxylase-related aminomethyltransferase (EC 2.1.2.10) | Nitrogen metabolism                                          |
| uahC   | Urea carboxylase-related aminomethyltransferase (EC 2.1.2.10) | Nitrogen metabolism                                          |
| EAM_0873| Predicted ABC transporter, permease component 1 | Nitrogen source transport                                    |
| EAM_0875| Predicted ABC transporter, ATP-binding component | Nitrogen source transport                                    |
| potG   | Putrescine ABC transporter, ATP-binding component | Nitrogen source transport                                    |
| potI   | Putrescine ABC transporter, transmembrane component 1 | Nitrogen source transport                                    |
| rutD   | Aminoacylate hydrolase | Pyrimidine Degradation                                      |
| PF09694| Conserved hypothetical protein, nitrogen assimilation associated | Nitrogen assimilation metabolism                              |
| ygG    | Putrescine aminotransferase (EC 2.6.1.82) | Putrescine metabolism                                       |
| EAM_0872| Predicted ABC transporter, substrate-binding component | Nitrogen assimilation metabolism                              |
| EAM_0874| Predicted ABC transporter, permease component 2 | Nitrogen source transport                                    |
| Gene   | Accession | Count | Description                                                                 | Function                          |
|--------|-----------|-------|------------------------------------------------------------------------------|-----------------------------------|
| NtrC   | potH      | 4     | Putrescine ABC transporter, transmembrane component 2                        | Nitrogen source transport         |
| NtrC   | nasB2     | 4     | Assimilatory nitrate reductase, large subunit (EC:1.7.99.4)                  | Nitrogen metabolism              |
| NtrC   | nirA      | 4     | Ferredoxin–nitrite reductase [EC 1.7.7.1]                                    | Nitrogen metabolism              |
| NtrC   | ddpC      | 3     | Dipeptide ABC transporter, transmembrane component 2 [TC 3.A.1.5.2]          | Nitrogen source transport         |
| NtrC   | amaB      | 3     | N-carbamoyl-L-amino acid hydrolase                                           |                                   |
| NtrC   | potC      | 2     | Putrescine ABC transporter, transmembrane component 2 [TC 3.A.1.11.1]        | Nitrogen source transport         |
| NtrC   | pucG      | 3     | Serine–pyruvate aminotransferase [EC 2.6.1.51] / L-alanine:glyoxylate aminotransferase [EC 2.6.1.44] | Amino acid degradation           |
| NtrC   | rutE      | 3     | 3-hydroxy propionic acid dehydrogenase                                       | Pyrimidine Degradation            |
| NtrC   | ddpA      | 3     | Dipeptide ABC transporter, substrate-binding component [TC 3.A.1.5.2]         | Nitrogen source transport         |
| NtrC   | potA      | 2     | Putrescine ABC transporter, ATP-binding component [TC 3.A.1.11.1]            | Nitrogen source transport         |
| NtrC   | ddpX      | 3     | D-alanyl-D-alanine dipeptidase [EC 3.4.13.1]                                  |                                   |
| NtrC   | ddpB      | 3     | Dipeptide ABC transporter, transmembrane component 1 [TC 3.A.1.5.2]          | Nitrogen source transport         |
| NtrC   | rutE2     | 1     | 3-hydroxy propionic acid dehydrogenase                                       | Pyrimidine Degradation            |
| NtrC   | potB      | 2     | Putrescine ABC transporter, transmembrane component 1 [TC 3.A.1.11.1]        | Nitrogen source transport         |
| NtrC   | rutR      | 1     | Pyrimidine catabolism transcriptional regulator RutR, TetR family             | Transcription regulation          |
| NtrC   | potD      | 2     | Putrescine ABC transporter, substrate-binding component [TC 3.A.1.11.1]      | Nitrogen source transport         |
| NtrC   | ddpD      | 3     | Dipeptide ABC transporter, transmembrane component 3 [TC 3.A.1.5.2]          | Nitrogen source transport         |
| NtrC   | ddpF      | 3     | Dipeptide ABC transporter, ABC-binding component [TC 3.A.1.5.2]              | Nitrogen source transport         |
| NtrC   | ybiB      | 2     | Conserved hypothetical protein                                               |                                   |
| NtrC   | CKO_01526 | 2     | Predicted transcriptional regulator, RpiR family                             | Transcription regulation          |
| NtrC   | TM1040_0383| 2     | Conserved hypothetical protein                                               |                                   |
| NtrC   | CDG0547   | 2     | Glycyl transferase, family 3                                                 |                                   |
| NtrC   | atzF      | 2     | Allophanate hydrolyase [EC 3.5.1.54]                                         | Nitrogen metabolism              |
| NtrC   | atzF2     | 2     | Allophanate hydrolyase [EC 3.5.1.54]                                         | Nitrogen metabolism              |
| NtrC   | Jann_1753 | 2     | Conserved hypothetical protein                                               |                                   |
| NtrC   | iSBma2    | 1     | Transposase, IS4                                                             |                                   |
| NtrC   | nrtB3     | 1     | Nitrate ABC transporter, permease component                                   | Nitrogen source transport         |
| NtrC   | nrtC3     | 1     | Nitrate ABC transporter, ATP-binding component                                | Nitrogen source transport         |
| NtrC   | nrtA3     | 1     | Nitrate ABC transporter, substrate-binding component                           | Nitrogen source transport         |
| NtrC   | Daro_0818 | 1     | Hypothetical protein                                                         |                                   |
| NtrC   | pkn       | 1     | Probable serine/threonine-protein kinase SCO3848                             |                                   |
| NtrC   | PF00262    | 1     | Putative alkylhydroperoxidase                                                 |                                   |
| NtrC   | QB2597_07045 | 1     | Conserved hypothetical protein                                               |                                   |
| NtrC   | QB2597_07055 | 1     | Hypothetical protein                                                          |                                   |
| NtrC   | Xaut_1081 | 1     | Hypothetical protein                                                          |                                   |
| NtrC   | NGR_b03860 | 1     | Hypothetical protein                                                          |                                   |
| NtrC   | speB      | 1     | Agmatinase [EC 3.5.3.11]                                                     | Putrescine metabolism            |
| NtrC   | Jann_1751 | 1     | Hypothetical protein                                                         |                                   |
| PdhR   | aceE      | 55    | Pyruvate dehydrogenase E1 component [EC 1.2.4.1]                             | Pyruvate metabolism              |
| PdhR   | pdhR      | 55    | Transcriptional repressor for pyruvate dehydrogenase complex                 | Transcription regulation          |
| PdhR   | aceF      | 54    | Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase complex [EC 2.3.1.12] | Transcription regulation         |
| PdhR   | lpdA      | 49    | Dihydrolipoamide dehydrogenase of pyruvate dehydrogenase complex [EC 1.8.1.4] | Pyruvate metabolism              |
| PdhR   | oadB      | 19    | Oxaloacetate decarboxylase beta chain [EC 4.1.1.3]                            | Pyruvate metabolism              |
| PdhR   | oadA      | 19    | Oxaloacetate decarboxylase alpha chain [EC 4.1.1.3]                           | Pyruvate metabolism              |
| PdhR   | oadG      | 18    | Oxaloacetate decarboxylase gamma chain [EC 4.1.1.3]                           | Pyruvate metabolism              |
| PdhR   | pfA       | 16    | Pyruvate formate-lyase activating enzyme [EC 1.97.1.4]                        | Formate metabolism               |
| PdhR   | pfB       | 16    | Pyruvate formate-lyase [EC 2.3.1.54]                                          | Formate metabolism               |
| PdhR   | aceB      | 14    | Malate synthase [EC 2.3.3.9]                                                  | Tricarboxylic acid cycle         |
PdhR  aceA  12  1  Iso citrate lyase (EC 4.1.3.1)  Tricarboxylic acid cycle
PdhR  pfIX  11  1  pyruvate formate lyase-related hypothetical transporter
PdhR  ndh  8  1  NADH dehydrogenase  NAD metabolism
PdhR  hemL  6  1  Glutamate-1-semialdehyde aminotransferase (EC 5.4.3.8)  Porphyrin biosynthesis
PdhR  focA  6  1  formate transporter
PdhR  yfdD  4  1  stress-induced alternate pyruvate formate-lyase subunit
PdhR  deaD  5  1  Cold-shock DEAD-box protein A
PdhR  cyoC  3  2  Cytochrome O ubiquinol oxidase subunit III (EC 1.10.3.-)  Electron transfer chain
PdhR  cyoE  3  2  Heme O synthase, protoheme IX farnesyltransferase (EC 2.5.1.-) COX10-CtaB  Porphyrin biosynthesis
PdhR  cyoD  3  2  Cytochrome O ubiquinol oxidase subunit IV (EC 1.10.3.-)  Electron transfer chain
PdhR  cyoB  3  2  Cytochrome O ubiquinol oxidase subunit I (EC 1.10.3.-)  Electron transfer chain
PdhR  cyoA  3  2  Cytochrome O ubiquinol oxidase subunit II (EC 1.10.3.-)  Electron transfer chain
PdhR  dld  2  1  Predicted D-lactate dehydrogenase, Fe-S protein, FAD/FMN-containing  Lactate metabolism
PdhR  lldP  2  1  L-lactate permease  Lactate metabolism
PdhR  grcA  1  1  stress-induced alternate pyruvate formate-lyase subunit  Pyruvate metabolism
PdhR  glcB  1  1  Malate synthase G (EC 2.3.3.9)  Glycolate utilization
PdhR  glcD  1  1  Glycolate dehydrogenase (EC 1.1.99.14), subunit GlcD  Glycolate utilization
PdhR  glcG  1  1  Hypothetical protein GlcG in glycolate utilization operon  Glycolate utilization
PdhR  glcE  1  1  Glycolate dehydrogenase (EC 1.1.99.14), FAD-binding subunit GlcE  Glycolate utilization
PdhR  glcF  1  1  Glycolate dehydrogenase (EC 1.1.99.14), iron-sulfur subunit GlcF  Glycolate utilization
PdhR  SO0273  1  1  protein of unknown function DUF1439
PdhR  sdhC  1  1  succinate dehydrogenase, cytochrome b556 subunit  Tricarboxylic acid cycle
PdhR  gltA  1  1  citrate synthase  Tricarboxylic acid cycle
PdhR  ppc  1  1  Phosphoenolpyruvate carboxylase (EC 4.1.1.31)  Pyruvate metabolism
PdhR  sdhA  1  1  succinate dehydrogenase, flavoprotein subunit  Tricarboxylic acid cycle
PdhR  sdhB  1  1  succinate dehydrogenase, hydrophobic membrane anchor protein  Tricarboxylic acid cycle
PsrA  psrA  69  12  Predicted transcriptional regulator for fatty acid degradation PsrA, TetR family  Transcription regulation
PsrA  fadA  56  10  3-ketoacyl-CoA thiolase (EC 2.3.1.16)  Fatty acid degradation
PsrA  fadB  55  9  Enoyl-CoA hydratase (EC 4.2.1.17)  Fatty acid degradation
PsrA  fadD  25  5  Long-chain-fatty-acid--CoA ligase (EC 6.2.1.3)  Fatty acid degradation
PsrA  acdH  26  4  Acyl-CoA dehydrogenase (EC 1.3.99.3)  Fatty acid degradation
PsrA  fadH  31  6  2,4-dienoyl-CoA reductase [NADPH] (EC 1.3.1.34)  Fatty acid degradation
PsrA  etfD  31  6  Electron transfer flavoprotein-ubiquinone oxidoreductase (EC 1.5.5.1)  Electron transfer chain for fatty acid degradation
PsrA  fadJ  27  3  3-ketoacyl-CoA thiolase (EC 2.3.1.16) @ Acetyl-CoA acetyltransferase (EC 2.3.1.9)  Fatty acid degradation
PsrA  fadI  27  3  3-ketoacyl-CoA thiolase (EC 2.3.1.16) @ Acetyl-CoA acetyltransferase (EC 2.3.1.9)  Fatty acid degradation
PsrA  etfA  27  5  electron transfer flavoprotein, alpha subunit  Electron transfer chain for fatty acid degradation
PsrA  etfB  27  5  electron transfer flavoprotein, beta subunit  Electron transfer chain for fatty acid degradation
PsrA  fadE  17  5  Acyl-CoA dehydrogenase, short-chain specific (EC 1.3.99.2)  Fatty acid degradation
PsrA  fadE1  21  3  Acyl-CoA dehydrogenase, short-chain specific (EC 1.3.99.2)  Fatty acid degradation
PsrA  fabG  16  2  3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100)  Fatty acid biosynthesis
PsrA  fabF  14  3  3-oxoacyl-[acyl-carrier-protein] synthase, KASII (EC 2.3.1.41)  Fatty acid biosynthesis
PsrA  fadD2  18  4  Long-chain-fatty-acid--CoA ligase (EC 6.2.1.3)  Fatty acid degradation
PsrA  echH  20  3  Enoyl-CoA hydratase [valine degradation] (EC 4.2.1.17)  Fatty acid degradation
PsrA  fadL  9  3  Long-chain fatty acid transport protein  Fatty acid degradation
PsrA  scp  13  3  Sterol-binding domain protein
PsrA  fabH  12  2  3-oxoacyl-[acyl-carrier-protein] synthase, KASIII (EC 2.3.1.41)  Fatty acid biosynthesis
PsrA  fabD  12  2  Malonyl CoA-acyl carrier protein transacylase (EC 2.3.1.39)  Fatty acid biosynthesis
| Gene   | Description                                                                 | Function                                      |
|--------|-----------------------------------------------------------------------------|-----------------------------------------------|
| acpP   | Acyl carrier protein                                                        | Fatty acid degradation                        |
| acdH1  | Acyl-CoA dehydrogenase (EC 1.3.99.3)                                        | Fatty acid degradation                        |
| fadE2  | Acyl-CoA dehydrogenase, short-chain specific (EC 1.3.99.2)                  | Fatty acid degradation                        |
| fadD1  | Long-chain fatty acid-CoA ligase (EC 6.2.1.3)                                | Fatty acid degradation                        |
| sdhC   | Succinate dehydrogenase, cytochrome b556 subunit                            | Tricarboxylic acid cycle                      |
| g7A    | Citrate synthase                                                             | Tricarboxylic acid cycle                      |
| aroQ   | 3-dehydroquinate dehydratase II (EC 4.2.1.10)                               | Aromatic amino acid biosynthesis              |
| SO2935 | Oxidoreductase, short-chain dehydrogenase/reductase family                   | Tricarboxylic acid cycle                      |
| sdhA   | Succinate dehydrogenase, flavoprotein subunit                               | Tricarboxylic acid cycle                      |
| rpoS   | RNA polymerase sigma factor RpoS                                             | Transcription                                 |
| aceB   | Malate synthase A                                                           | Tricarboxylic acid cycle                      |
| sdhD   | Succinate dehydrogenase subunit D                                           | Tricarboxylic acid cycle                      |
| acdB   | Enoyl-CoA hydratase (EC 4.2.1.17) / 3,2-trans-enoyl-CoA dehydrogenase (EC 1.1.1.35) | Fatty acid degradation                        |
| sdhB   | Succinate dehydrogenase, iron-sulfur protein                                | Tricarboxylic acid cycle                      |
| bccP   | Biotin carboxyl carrier protein of acetyl-CoA carboxylase                    |                                              |
| accC   | Biotin carboxylase of acetyl-CoA carboxylase (EC 6.3.4.14)                  |                                              |
| acdA   | 3-ketoacyl-CoA thiolase (EC 2.3.1.16) @ Acetyl-CoA acetyltransferase (EC 2.3.1.9) | Fatty acid degradation                        |
| acdH2  | Acyl-CoA dehydrogenase (EC 1.3.99.3)                                        | Fatty acid degradation                        |
| SO0881 | Conserved hypothetical protein                                               |                                              |
| SO0882 | Oxidoreductase, GMC family                                                   |                                              |
| paal   | Phenylacetic acid degradation protein paal                                   |                                              |
| algQ   | Regulator of RNA polymerase sigma(70) subunit, Rsd/AlgQ                      | Transcription                                 |
| phhB   | Pterin-4-alpha-carbinolamine dehydrogenase (EC 4.2.1.96)                    |                                              |
| fabL   | ENOYL-[ACYL-CARRIER-PROTEIN] REDUCTASE (FabL) (NADPH) (EC 1.3.1.9)            | Fatty acid biosynthesis                       |
| aceA   | Isocitrate lyase                                                            | Tricarboxylic acid cycle                      |
| SO0080 | Thioesterase superfamily protein                                             |                                              |
| mdh    | Malate synthase (EC 2.3.3.9)                                                | Tricarboxylic acid cycle                      |
| ldh    | Leucine dehydrogenase (EC 1.4.1.9)                                          | Branched-chain amino acid biosynthesis        |
| fadH1  | 2,4-dienoyl-CoA reductase [NADPH] (EC 1.3.1.34)                              | Fatty acid degradation                        |
| fadE3  | Acyl-CoA dehydrogenase                                                       | Fatty acid degradation                        |
| acdH3  | Acyl-CoA dehydrogenase (EC 1.3.99.3)                                        | Fatty acid degradation                        |
| paal2  | Phenylacetic acid degradation protein paal                                   |                                              |
| Sbal_0657 | Hypothetical protein                                                       |                                              |
| fabK   | Enoyl-[acyl-carrier-protein] reductase (FMN) (EC 1.3.1.9)                    | Fatty acid biosynthesis                       |
| SO3908 | Enoyl-CoA hydratase (EC 4.2.1.17)                                           | Fatty acid degradation                        |
| acdH4  | Acyl-CoA dehydrogenase (EC 1.3.99.3)                                        | Fatty acid degradation                        |
| fadL2  | Long-chain fatty acid transport protein                                      | Fatty acid degradation                        |
| fadD3  | Long-chain-fatty acid-CoA ligase                                             | Fatty acid degradation                        |
| rutR   | Transcriptional regulator RutR of pyrimidine catabolism, TetR family         | Transcription regulation                      |
| rutB   | Peroxyreioacylase / ureidoacylacte amido hydrolase                          | Pyrimidine degradation                        |
| rutA   | Pyrimidine oxygenase                                                         | Pyrimidine degradation                        |
| xdhC   | XdhC protein (assists in molybdopterin insertion into xanthine dehydrogenase) | Purine degradation                            |
| xdhA   | Xanthine dehydrogenase, iron-sulfur cluster and FAD-binding subunit A (1.17.1.4) | Purine degradation                            |
| xdhB   | Xanthine dehydrogenase, molybdenum binding subunit (EC 1.17.1.4)            | Purine degradation                            |
| guaD   | Guanine deaminase (EC 3.5.4.3)                                              | Purine degradation                            |
| rutC   | Aminoacylase peracid reductase                                               | Pyrimidine degradation                        |
| rutD   | Aminoacylase hydrolase                                                       | Pyrimidine degradation                        |
| pydC   | Beta-ureidopropionase (EC 3.5.1.6)                                           | Pyrimidine degradation                        |
| Gene   | Description                                                                 | Function                          |
|--------|-----------------------------------------------------------------------------|-----------------------------------|
| pydX   | Pyridine nucleotide-disulphide oxidoreductase associated with reductive pyrimidine catabolism | Pyrimidine degradation            |
| pydA   | Dihydropyrimidine dehydrogenase [NADP+] (EC 1.3.1.2)                         | Pyrimidine degradation            |
| rutF   | Flavin reductase                                                             | Pyrimidine degradation            |
| pydB   | Dihydropyrimidinase (EC 3.5.2.2)                                            | Pyrimidine degradation            |
| pbuT   | Xanthine/urate permease                                                      | Nucleoside transport              |
| pucL   | Uracilase (EC 1.7.3.3)                                                       | Pyrimidine degradation            |
| COG3748| hypothetical protein, COG3748                                                |                                   |
| pydA   | Dihydropyrimidine dehydrogenase [NADP+] (EC 1.3.1.2)                         | Pyrimidine degradation            |
| rutR2  | Transcriptional regulator RutR of pyrimidine catabolism, TetR family        | Transcription regulation          |
| codA   | Cytosine deaminase (EC 3.5.4.1)                                             | Pyrimidine degradation            |
| pydP   | 3-hydroxy propionic acid dehydrogenase                                       | Pyrimidine degradation            |
| pucM   | Hydroxysisurate hydrolase (EC 3.5.2.17)                                      | Pyrimidine degradation            |
| upp    | Uracil phosphoribosyltransferase (EC 2.4.2.9)                                | Pyrimidine degradation            |
| ppuD   | Predicted ABC transporter, inner membrane protein precursor                  | Nucleoside transport              |
| ppuC   | Predicted ABC transporter, permease protein                                   | Nucleoside transport              |
| ppuA   | Predicted ABC transporter, ATP-binding protein                               | Nucleoside transport              |
| aIA    | Ureidoglycolate hydrolase (EC 3.5.3.19)                                      | Purine degradation                |
| COG7026| putative polysaccharide deacetylase family protein                           | Nucleoside-binding outer membrane protein |
| tsx    | Xanthine deaminase (EC 3.5.4.5)                                             | Pyrimidine degradation            |
| cdd    | Cytidine deaminase (EC 3.5.4.5)                                             | Pyrimidine degradation            |
| pbuT2  | Xanthine/urate permease                                                      | Nucleoside transport              |
| deoA   | Thymidine phosphorylase (EC 2.4.2.4)                                         | Pyrimidine degradation            |
| pntB   | Predicted nucleoside ABC transporter, permease protein 1                     | Nucleoside transport              |
| pntC   | Predicted nucleoside ABC transporter, permease protein 2                     | Nucleoside transport              |
| pntA   | Predicted nucleoside ABC transporter, ATP-binding protein                    | Nucleoside transport              |
| rutG   | Uracil permease                                                              | Pyrimidine transport              |
| rutG2  | Uracil permease                                                              | Pyrimidine transport              |
| gat    | Xanthine-guanine phosphoribosyltransferase (EC 2.4.2.22)                     | Purine degradation                |
| xpt    | Xanthine phosphoribosyltransferase (EC 2.4.2.22)                             | Purine degradation                |
| PF07958| Conserved hypothetical protein                                               |                                   |
| ribA2  | GTP cyclohydrolase II (EC 3.5.4.25) homolog                                  |                                   |
| pntD   | Predicted nucleoside ABC transporter, substrate-binding protein              | Nucleoside transport              |
| pytD   | Predicted pyrimidine ABC transporter, permease protein 1                     | Pyrimidine transport              |
| pytM   | Predicted pyrimidine ABC transporter, substrate-binding protein              | Pyrimidine transport              |
| pytN   | Predicted pyrimidine ABC transporter, ATP-binding protein                    | Pyrimidine transport              |
| pytQ   | Predicted pyrimidine ABC transporter, permease protein 2                     | Pyrimidine transport              |
| allC   | Allantoicase (EC 3.5.4.3)                                                    | Purine degradation                |
| ppuB   | Predicted ABC transporter, substrate-binding protein precursor               |                                   |
| pytC   | Pyrimidine ABC transporter, permease protein 2                              | Pyrimidine transport              |
| pytB   | Pyrimidine ABC transporter, permease protein 1                               | Pyrimidine transport              |
| deoC   | Decoxyribose-phosphate aldolase (EC 4.1.2.4)                                 | Pyrimidine degradation            |
| pytA   | Pyrimidine ABC transporter, ATP-binding protein                              | Pyrimidine transport              |
| carA   | Carbamoyl-phosphate synthase small chain (EC 6.3.5.5)                        | Arginine and pyrimidine biosynthesis |
| carB   | Carbamoyl-phosphate synthase large chain (EC 6.3.5.5)                       | Arginine and pyrimidine biosynthesis |
| pytD   | Pyrimidine ABC transporter, substrate-binding protein                        | Pyrimidine transport              |
| deoD   | Purine nucleoside phosphorylase (EC 2.4.2.1)                                 | Purine degradation                |
| nupX   | Nucleoside permease                                                          | Nucleoside transport              |
| udk    | Uridine kinase (EC 2.7.1.48)                                                 | Pyrimidine metabolism             |
| COG1739| hypothetical protein, COG1739                                                |                                   |
| Gene   | NCBI  | Function                                                                                       |
|--------|-------|-----------------------------------------------------------------------------------------------|
| RutR   | ald   | Aldehyde dehydrogenase (EC 1.2.1.3)                                                          |
| RutR   | add   | Adenosine deaminase (EC 3.5.4.4)                                                              |
| RutR   | allB  | Allantoinase (EC 3.5.2.5)                                                                    |
| RutR   | omp1  | putative TonB-dependent outer membrane transporter                                             |
| RutR   | omp2  | putative TonB-dependent outer membrane transporter                                             |
| RutR   | pbuT3 | Xanthine/uracil permease                                                                     |
| RutR   | ssnA  | Predicted chlorohydrolase/aminohydrolase                                                      |
| RutR   | pytH  | Predicted hydrolase                                                                          |
| RutR   | praX  | Omega-amino acid--pyruvate aminotransferase (EC 2.6.1.18)                                     |
| RutR   | tsx2  | Cytosine permease                                                                            |
| RutR   | codB  | Predicted purine nucleoside permease                                                          |
| RutR   | nupP  | Adenosine deaminase (EC 3.5.4.4)                                                              |
| RutR   | add2  | Hypoxanthine-guanine phosphoribosyltransferase (EC 2.4.2.8)                                   |
| RutR   | deoB  | Phosphopentomutase (EC 5.4.2.7)                                                               |
| RutR   | RL3717| Hypothetical protein                                                                         |
| RutR   | RSP_1242 | Predicted lyase                                                                             |
| RutR   | tsx3  | Xanthine/uracil permease                                                                     |
| RutR   | pbuT4 | Xanthine/uracil permease                                                                     |
| RutR   | urA   | Uracil permease                                                                               |
| RutR   | rutR3 | Transcriptional regulator RutR of pyrimidine catabolism, TetR family                          |
| RutR   | Meso_2056| Hypothetical protein                                                                          |
| RutR   | Atu2387| NTP pyrophosphohydrolase, MutT family                                                          |
| RutR   | mll1644| Predicted methyltransferase                                                                    |
| RutR   | OG2516_07987| Conserved hypothetical protein                                                               |
| RutR   | Jann_2708| Hypothetical protein                                                                          |
| RutR   | Jann_2706| Hypothetical protein                                                                          |
| RutR   | MED193_05504| Hypothetical protein                                                                         |
| RutR   | MED193_05494| Hypothetical protein                                                                         |
| RutR   | Jann_0788| Hypothetical protein                                                                          |
| RutR   | Jann_0787| Hypothetical protein                                                                          |
| RutR   | Jann_2704| Hypothetical protein                                                                          |
| RutR   | RSP_0188| DedA family integral membrane protein                                                          |
| RutR   | OB2597_04350| Hypothetical protein                                                                         |
| RutR   | SKA53_10669| Hypothetical protein                                                                         |
| RutR   | RB2654_14945| Hypothetical protein                                                                         |
| RutR   | OG2516_10896| Hypothetical protein                                                                         |
| RutR   | amiC  | Predicted amidase                                                                             |
| SahR   | sahR  | Predicted regulator of methionine metabolism, ArsR family                                     |
| SahR   | ahyY  | Adenosylhomocysteine (EC 3.3.1.1)                                                              |
| SahR   | metF  | 5,10-methylene tetrahydrofolate reductase (EC 1.5.1.20)                                       |
| SahR   | metK  | 5-adenosylmethionine synthetase (EC 2.5.1.6)                                                   |
| SahR   | metH  | 5-methyltetrahydrofolate--homocysteine methyltransferase (EC 2.1.1.13)                        |
| SahR   | metH2 | 5-methyltetrahydrofolate--homocysteine methyltransferase (EC 2.1.1.13)                        |
| SahR   | betE  | 4-Benzoyl-DL-homocysteine methyltransferase (EC 2.1.1.14)                                      |
| SahR   | panC  | Pantoate--beta-alanine ligase (EC 6.3.2.1)                                                    |

**Transcription Regulation**

- **Aldehyde dehydrogenase (EC 1.2.1.3)**
- **Adenosine deaminase (EC 3.5.4.4)**
- **Allantoinase (EC 3.5.2.5)**
- **Putative TonB-dependent outer membrane transporter**
- **Xanthine/uracil permease**
- **Predicted chlorohydrolase/aminohydrolase**
- **Predicted hydrolase**
- **Omega-amino acid--pyruvate aminotransferase (EC 2.6.1.18)**
- **Cytosine permease**
- **Predicted purine nucleoside permease**
- **Hypoxanthine-guanine phosphoribosyltransferase (EC 2.4.2.8)**
- **Phosphopentomutase (EC 5.4.2.7)**
- **Hypothetical protein**
- **Conserved hypothetical protein**
- **Hypothetical protein**
- **Hypothetical protein**
- **Hypothetical protein**
- **Hypothetical protein**
- **Hypothetical protein**
- **DedA family integral membrane protein**
- **Hypothetical protein**
- **Hypothetical protein**
- **Hypothetical protein**
- **Hypothetical protein**
- **Hypothetical protein**
- **Hypothetical protein**
- **Hypothetical protein**
- **Hypothetical protein**
- **Predicted amidase**

**Methionine Metabolism**

- **Adenosylhomocysteine (EC 3.3.1.1)**
- **5,10-methylene tetrahydrofolate reductase (EC 1.5.1.20)**
- **5-adenosylmethionine synthetase (EC 2.5.1.6)**
- **5-methyltetrahydrofolate--homocysteine methyltransferase (EC 2.1.1.13)**
- **5-methyltetrahydrofolate--homocysteine methyltransferase (EC 2.1.1.13)**
- **4-Benzoyl-DL-homocysteine methyltransferase (EC 2.1.1.14)**
- **Pantoate--beta-alanine ligase (EC 6.3.2.1)**

**Methionine Biosynthesis**

- **Metabolism**
- **Methionine metabolism**
- **Methionine biosynthesis**
- **Methionine biosynthesis**
- **Methionine biosynthesis**

**Alanine Metabolism**

- **Methionine biosynthesis**
|  |  | Description | Metabolism | Notes |
|---|---|---|---|---|
| SahR | metB | Cystathionine gamma-synthase (EC 2.5.1.48) | Methionine biosynthesis |  |
| SahR | metX2 | Homoserine O-acetyltransferase (EC 2.3.1.31) | Methionine biosynthesis |  |
| SahR | hom | Homoserine dehydrogenase (EC 1.1.1.3) | Methionine biosynthesis |  |
| SahR | metE2 | Methionine synthase | Methionine biosynthesis |  |
| SahR | DUF1852 | Protein of unknown function DUF1852 |  |  |
| SahR | ddl | D-alanine--D-alanine ligase B (EC 6.3.2.4) | Alanine metabolism |  |
| SahR | Caul_3406 | PIN domain protein |  |  |
| SahR | metT | Methionine transporter MetT | Methionine transport |  |
| SamR | metE | 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase (EC 2.1.1.14) | Methionine biosynthesis |  |
| SamR | metF2 | 5,10-methylenetetrahydrofolate reductase (EC 1.5.1.20) | Methionine biosynthesis |  |
| SamR | metX2 | Homoserine O-acetyltransferase (EC 2.3.1.31) | Methionine biosynthesis |  |
| SamR | hom | Cystathionine gamma-synthase (EC 2.5.1.48) | Methionine biosynthesis |  |
| SamR | metK | 5-methyltetrahydrofolate--homocysteine methyltransferase (EC 2.1.1.13) | Methionine biosynthesis |  |
| SamR | samR | Transcriptional regulator of methionine metabolism, ArsR family | Transcription regulation |  |
| SamR | metH1 | 5-methyltetrahydrofolate--homocysteine methyltransferase (EC 2.1.1.13) | Methionine biosynthesis |  |
| SamR | metH2 | 5-methyltetrahydrofolate--homocysteine methyltransferase (EC 2.1.1.13) | Methionine biosynthesis |  |
| TrpR | trpE | Anthranilate synthase, aminase component (EC 4.1.3.27) | Tryptophan biosynthesis |  |
| TrpR | trpR | Trp operon repressor | Transcription regulation |  |
| TrpR | trpG | Anthranilate synthase, amidotransferase component (EC 4.1.3.27) | Tryptophan biosynthesis |  |
| TrpR | trpB | Tryptophan synthase beta chain (EC 4.2.1.20) | Tryptophan biosynthesis |  |
| TrpR | trpC | Indole-3-glycerol phosphate synthase (EC 4.1.1.48) | Tryptophan biosynthesis |  |
| TrpR | trpA | Tryptophan synthase alpha chain (EC 4.2.1.20) | Tryptophan biosynthesis |  |
| TrpR | mtr | Tryptophan-specific transport protein | Tryptophan transport |  |
| TrpR | trpD | Anthranilate phosphoribosyltransferase (EC 2.4.2.18) | Tryptophan biosynthesis |  |
| TrpR | trpD_a | Anthranilate synthase, amidotransferase component (EC 4.1.3.27) | Tryptophan biosynthesis |  |
| TrpR | trpD_b | Anthranilate phosphoribosyltransferase (EC 2.4.2.18) | Tryptophan biosynthesis |  |
| TrpR | tyrA | Chorismate mutase I (EC 5.4.99.5) / Prephenate dehydrogenase (EC 5.4.99.5.1.12) | Tyrosine & Phenylalanine biosynthesis |  |
| TrpR | COG1541 | Coenzyme F390 synthetase | Aromatic amino acid biosynthesis |  |
| TrpR | aroF | 2-keto-3-deoxy-D-arabino-heptulosonate-7-phosphate synthase (EC 2.5.1.54) | Aromatic amino acid biosynthesis |  |
| TrpR | SSF55729 | Acyl-CoA N-acyltransferase |  |  |
| TrpR | COG0733(Trp) | Predicted tryptophan transporter, SNF family | Tryptophan transport |  |
| TrpR | aroG | 2-keto-3-deoxy-D-arabino-heptulosonate-7-phosphate synthase (EC 2.5.1.54) | Aromatic amino acid biosynthesis |  |
| TrpR | aroH | 2-keto-3-deoxy-D-arabino-heptulosonate-7-phosphate synthase (EC 2.5.1.54) | Aromatic amino acid biosynthesis |  |
| TrpR | aroM | AroM family protein | Aromatic amino acid biosynthesis |  |
| TrpR | aroL | Shikimate kinase III (EC 2.7.1.71) | Aromatic amino acid biosynthesis |  |
| TrpR | yaiA | Putative cytoplasmic protein |  |  |
| TrpR | aroA | 5-Enolpyruvylshikimate-3-phosphate synthase (EC 2.5.1.19) | Aromatic amino acid biosynthesis |  |
| TrpR | COG4221 | Short-chain alcohol dehydrogenase of unknown specificity | Tryptophan biosynthesis |  |
| TrpR | HI1388 | Anthranilate synthase, amidotransferase component (EC 4.1.3.27) | Tryptophan biosynthesis |  |
| TrpR | tnaB | Tryptophan-specific transport protein | Tryptophan transport |  |
| TrpR | aroF2 | 2-keto-3-deoxy-D-arabino-heptulosonate-7-phosphate synthase (EC 2.5.1.54) | Aromatic amino acid biosynthesis |  |
| TrpR | HAPS_1139 | ABC transporter, inner-membrane component |  |  |
| TrpR | HAPS_0395 | ABC transporter, substrate binding component |  |  |
| TrpR | HAPS_1138 | ABC transporter, ATP-binding protein |  |  |
| TrpR | tnaA | Tryptophanase (EC 4.1.99.3) | Tryptophan utilization |  |
| TrpR | trpB2 | Tryptophan synthase beta chain like (EC 4.2.1.20) | Tryptophan utilization |  |
| TyrR | phhA | Phenylalanine-4-hydroxylase (EC 1.14.16.1) | Phenylalanine degradation |  |
| TyrR | phhB | Pterin-4-alpha-carbinolamine dehydratase (EC 4.2.1.96) | Phenylalanine degradation |  |
| **YrSR** | **Name** | **Location** | **Function** |
|-------|-------|------------|-------------|
| TyrR  | tyrA  | 39 5 | Chorismate mutase I (EC 5.4.99.5) / Prephenate dehydrogenase (EC 5.4.99.5 1.3.1.12) | Tyrosine & Phenylalanine biosynthesis |
| TyrR  | tyrR  | 45 6 | Transcriptional regulator of aromatic amino acid biosynthesis | |
| TyrR  | aroF  | 35 5 | 2-keto-3-deoxy-D-arabino-heptulosonate-7-phosphate synthase (EC 2.5.1.54) | Aromatic amino acid biosynthesis |
| TyrR  | COG2814 | 7 1 | Predicted tyrosine transporter, COG2814 family | Tyrosine transport |
| TyrR  | emrD  | 9 1 | Multidrug resistance protein D | |
| TyrR  | pepD  | 9 1 | Aminoacyl-histidine dipeptidase (Peptidase D) (EC 3.4.13.5) | |
| TyrR  | putA  | 9 1 | 2-keto-3-deoxy-D-arabino-heptulosonate-7-phosphate synthase I alpha (EC 2.5.1.54) | Aromatic amino acid biosynthesis |
| TyrR  | COG1284 | 4 1 | Hypothetical protein | |
| TyrR  | SfrI_3409 | 6 1 | Hypothetical protein | |
| TyrR  | aprE  | 6 1 | Alkaline serine protease | |
| TyrR  | SfrI_3410 | 6 1 | Transcriptional regulator, XRE family protein | |
| TyrR  | ompF  | 4 1 | Outer membrane porin F | Tyrosine degradation |
| TyrR  | ipdC  | 7 2 | Indole-3-pyruvate decarboxylase (EC 4.1.1.14) | Tryptophan degradation |
| TyrR  | plpC  | 4 1 | Oligopeptidase A (EC 3.4.24.70) | Tryptophan degradation |
| TyrR  | pep1  | 3 1 | Alkaline serine exoprotease A precursor (EC 3.4.21.-) | |
| TyrR  | aprE2 | 3 1 | Cold-active alkaline serine protease (EC 3.4.21.62) | |
| TyrR  | omp2  | 3 1 | Putative TonB-dependent outer membrane receptor | |
| TyrR  | tpi  | 3 2 | Tyrosine phenol-lyase (EC 4.1.99.2) | |
| TyrR  | folA  | 1 1 | Dihydrofolate reductase (EC 1.5.1.1) | Tetrahydrofolate biosynthesis |
| TyrR  | pep2  | 1 1 | Peptidase M4 thermolysin | |
| TyrR  | omp1  | 1 1 | TonB-dependent receptor | |
| TyrR  | pep4  | 1 1 | Prolyl oligopeptidase family protein | |
| TyrR  | tyrP  | 32 5 | Tyrosine-specific transport protein | Tyrosine transporter |
| TyrR  | hmgB  | 29 5 | Maleylacetacetate isomerase (EC 5.2.1.2) | Tyrosine degradation |
| TyrR  | hmgC  | 29 5 | Fumarylacetacetase (EC 3.7.1.2) | Tyrosine degradation |
| TyrR  | hpd  | 14 4 | 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27) | Tyrosine degradation |
| TyrR  | hmgA  | 13 4 | Homogentisate 1,2-dioxygenase (EC 1.13.11.5) | Tyrosine degradation |
| TyrR  | aceA  | 12 1 | Isocitrate lyase (EC 4.1.1.1) | Tricarboxylic acid cycle |
| TyrR  | aceB  | 16 1 | Malate synthase (EC 2.3.3.9) | Tricarboxylic acid cycle |
| TyrR  | acsA  | 8 1 | Acetoacetyl-CoA synthetase (EC 6.2.1.16) | Acetyl-coenzyme A synthetase |
| TyrR  | aroA  | 14 1 | 5-Enolpyruvylshikimate-3-phosphate synthase (EC 2.5.1.19) | Aromatic amino acid biosynthesis |
| TyrR  | aroL  | 10 1 | Shikimate kinase III (EC 2.7.1.71) | Aromatic amino acid biosynthesis |
| TyrR  | aroP  | 11 1 | Aromatic amino acid transport protein AroP | Aromatic amino acid transport |
| TyrR  | bkdA1 | 16 1 | Branched-chain alpha-keto acid dehydrogenase, E1 component, alpha subunit (EC 1.2.4.4) | Branched-chain amino acid degradation |
| TyrR  | bkdA2 | 16 1 | Branched-chain alpha-keto acid dehydrogenase, E1 component, beta subunit (EC 1.2.4.4) | Branched-chain amino acid degradation |
| TyrR  | bkdB | 16 1 | Dihydrolipoamide acetyltransferase component of branched-chain alpha-keto acid dehydrogenase complex (EC 2.3.1.168) | Branched-chain amino acid degradation |
| TyrR  | brnQ  | 16 1 | Branched-chain amino acid transport system carrier protein | Branched-chain amino acid transport |
| TyrR  | COG0733[Tyr] | 13 2 | Predicted tyrosine transporter, SNF family | |
| TyrR  | tyrR2 | 2 1 | Tyrosine and phenylalanine degradation transcriptional activator, TyrR family | Transcription regulation |
| TyrR  | ivdA | 16 1 | 3-ketoacyl-CoA thiolase [isoleucine degradation] (EC 2.3.1.16) | Branched-chain amino acid degradation |
| TyrR | Genomic Position | Description                                                                 | Pathway                        |
|------|------------------|------------------------------------------------------------------------------|--------------------------------|
| ivdB | 16               | Methylmalonate-semialdehyde dehydrogenase (EC 1.2.1.27)                    | Branched_chain amino acid degradation |
| ivdC | 16               | Branched-chain acyl-CoA dehydrogenase (EC 1.3.99.12)                       | Branched_chain amino acid degradation |
| ivdD | 16               | Enoyl-CoA hydratase [valine degradation] (EC 4.2.1.17) / Enoyl-CoA hydratase [isoleucine degradation] (EC 4.2.1.17) | Branched_chain amino acid degradation |
| ivdE | 16               | 3-hydroxoisobutyryl-CoA hydrolase (EC 3.1.2.4)                              | Branched_chain amino acid degradation |
| ivdF | 16               | 3-hydroxoisobutyrate dehydrogenase (EC 1.1.1.31)                           | Branched_chain amino acid degradation |
| ivdG | 16               | 3-hydroxyacyl-CoA dehydrogenase [isoleucine degradation] (EC 1.1.1.35)      | Branched_chain amino acid degradation |
| ldh  | 16               | Leucine dehydrogenase (EC 1.4.1.9)                                          | Branched_chain amino acid degradation |
| liuA | 14               | Isovaleryl-CoA dehydrogenase (EC 1.3.99.10)                                 | Branched_chain amino acid degradation |
| liuB | 14               | Methylcrotonyl-CoA carboxylase carboxyl transferase subunit (EC 6.4.1.4)    | Branched_chain amino acid degradation |
| liuC | 14               | Methylglutaconyl-CoA hydratase (EC 4.2.1.18)                                | Branched_chain amino acid degradation |
| liuD | 16               | Methylcrotonyl-CoA carboxylase biotin-containing subunit (EC 6.4.1.4)       | Branched_chain amino acid degradation |
| liuE | 14               | Hydroxymethylglutaryl-CoA lyase (EC 4.1.3.4)                                | Branched_chain amino acid degradation |
| liuF | 13               | Succinyl-CoA:3-ketoacid-coenzyme A transferase subunit A (EC 2.8.3.5)       | Branched_chain amino acid degradation |
| liuG | 13               | Succinyl-CoA:3-ketoacid-coenzyme A transferase subunit B (EC 2.8.3.5)       | Branched_chain amino acid degradation |
| liuR | 14               | Predicted transcriptional regulator LiuR of leucine degradation pathway, MerR family | Transcription regulation |
| mdeA | 14               | Methionine gamma-lyase (EC 4.4.1.11)                                         | Methionine degradation          |
| pep3 | 14               | Peptidase, M13 family                                                        |                                 |
| phhC | 5                | Aromatic-amino-acid aminotransferase (EC 2.6.1.57)                          | Phenylalanine degradation       |
| phhR | 7                | Phenylalanine degradation transcriptional activator, TyrR family            | Transcription regulation        |
| tyrB | 16               | Tyrosine aminotransferase (EC 2.6.1.42)                                     | Tyrosine biosynthesis / Tyrosine degradation |

1 Number of regulatory interactions  
2 Number of taxa with regulation
Table S4. Metabolic and gene content of reconstructed TF regulons in Proteobacteria classified by conservation of regulatory interactions.

| TF name | TF regulon members | Assigned metabolic pathway or process | Major function | TF effector |
|---------|-------------------|---------------------------------------|----------------|------------|
| **ArgR** | Core | ArgH, argB, argC, argG, argF, argA, argE | Arginine biosynthesis | Arginine | metabolism |
|        | argR | Transcription regulation | | | |
|        | artL, artQ, artM, artP | Arginine transport | | | |
|        | astD, astA | Arginine degradation | | | |
|        | carA, carB | Arginine and pyrimidine biosynthesis | | | |
|        | **Taxonomy-specific** | argD | Arginine biosynthesis | | |
|        | argW, artJ, omp | Arginine transport | | | |
|        | gltB, gltD | Glutamate biosynthesis | | | |
|        | ilvM, ilvG, ilvD, ilvA | Branched-chain amino acid biosynthesis | | | |
|        | potF, potG, potH, potI | Putrescine transport | | | |
|        | recN | DNA repair | | | |
|        | oadA, oadB, oadG | Pyruvate metabolism | | | |
|        | astC, astB | Arginine degradation | | | |
|        | **Genome-specific** | ilvE | Branched-chain amino acid biosynthesis | | |
|        | hisJ, hisM, hisP, hisQ | Histidine transport | | | |
|        | arcA, arcB, arcC, arcD, astE | Arginine degradation | | | |
|        | hisA, hisB, hisC, hisD, hisF, hisG, hisH, hisI | Histidine biosynthesis | | | |
|        | proV, proW, proX | Proline transport | | | |
|        | speF, potE | Putrescine metabolism | | | |
| **BioR** | All target genes | bioY, bioM, bioN | Biotin transport | | |
|        | bioB, bioF, bioD, bioA, bioZ, bioG, bioC | Biotin biosynthesis | | | |
|        | bioR | Transcription regulation | | | |
| **BirA** | Core | bioB, bioF, bioD, bioC, bioA | Biotin biosynthesis | | |
|        | **Taxonomy-specific** | bioH | Biotin biosynthesis | | |
|        | birA | Transcription regulation | | | |
|        | fabF, fabG | Fatty acid biosynthesis | | | |
|        | **Genome-specific** | yigM | Biotin transport | | |
|        | bioW | Biotin biosynthesis | | | |
| **FabR** | Core | OLE1 (desA) | Unsaturated fatty acid biosynthesis | | |
|        | fabA, fabB, lcfH | Fatty acid biosynthesis | | | |
|        | plsC | Glycerolipid metabolism | | | |
|        | hyll | Fatty acid metabolism | | | |
|        | **Taxonomy-specific** | desB, desC | Unsaturated fatty acid biosynthesis | | |
|        | fabL, lcfE | Fatty acid biosynthesis | | | |
|        | fabR, fabR2 | Transcription regulation | | | |
|        | **Genome-specific** | pfaA, pfaB, pfaC, pfaD | Unsaturated fatty acid biosynthesis | | |
|        | pfaR, psrA | Transcription regulation | | | |
|        | fadE | Fatty acid degradation | | | |
### FadP

| Genes/Proteins | Function                           | Type                          |
|---------------|------------------------------------|-------------------------------|
| fadA, fadB, acdA, acdB, acdH, echH, acdP, acdQ, fadD | Fatty acid degradation          | Unknown                       |
| etfA, etfB, etfD | Electron transfer chain for fatty acid degradation |                              |
| pncA          | Nicotinate biosynthesis            |                              |
| fadP          | Transcription regulation           |                              |

**Taxonomy-specific and Genome-specific**

| Genes/Proteins | Function                           | Type                          |
|---------------|------------------------------------|-------------------------------|
| acsA          | Acetyl-coenzyme A synthetase       |                              |
| BPSL1236      | Glycolysis                         |                              |
| liuR          | Transcription regulation           |                              |
| paaI, paaG4, paaH1, bktB, alkK | Fatty acid degradation            |                              |

### FadR

| Genes/Proteins | Function                           | Type                          |
|---------------|------------------------------------|-------------------------------|
| fadL, fadI, fadJ, fadE | Fatty acid degradation          | Unknown                       |

**Taxonomy-specific**

| Genes/Proteins | Function                           | Type                          |
|---------------|------------------------------------|-------------------------------|
| fabA, fabB    | Fatty acid biosynthesis            |                              |
| plsB          | Glycerolipid metabolism            |                              |
| fadA, fadD, fadH, fadb, fadM, SO0572 | Fatty acid degradation          |                              |
| fadr, iclR    | Transcription regulation           |                              |

**Genome-specific**

| Genes/Proteins | Function                           | Type                          |
|---------------|------------------------------------|-------------------------------|
| acdB, tesB    | Fatty acid degradation             |                              |

### GlcC

| Genes/Proteins | Function                           | Type                          |
|---------------|------------------------------------|-------------------------------|
| glcE, glcF, glcD, glcG | Glycolate utilization          |                              |
| glcC          | Transcription regulation           |                              |

**Taxonomy-specific**

| Genes/Proteins | Function                           | Type                          |
|---------------|------------------------------------|-------------------------------|
| glcB          | Tricarboxylic acid cycle           |                              |
| glcA          | Glycolate transport                |                              |
| lldD          | Lactate utilization                |                              |

**Genome-specific**

| Genes/Proteins | Function                           | Type                          |
|---------------|------------------------------------|-------------------------------|
| glcQ, glcM, glcP | Glycolate transport          |                              |
| lldG, lldE, lldF, ykgE, ykgF, ykgG, lldP | Lactate utilization |                              |
| lysR          | Transcription regulation           |                              |

### HexR

| Genes/Proteins | Function                           | Type                          |
|---------------|------------------------------------|-------------------------------|
| glk, pykA     | Glycolysis                         |                              |
| edd, eda      | Entner-Doudoroff pathway           |                              |
| zwf, pgl      | Pentose phosphate pathway          |                              |
| hexR          | Transcription regulation           |                              |

**Taxonomy-specific**

| Genes/Proteins | Function                           | Type                          |
|---------------|------------------------------------|-------------------------------|
| nqrD, nqrC, nqrF, nqrA, nqrE, nqrB | Pentose phosphate pathway          |                              |
| adhE, pflA, pflB, ackA, pta, focA | Electron transport chain          |                              |
| ppsA          | Fermentation                       |                              |
| ptsI, ptsH, ptsG, crr | Gluconeogenesis          |                              |
| gldD, gldB    | Glucose transport                  |                              |
| gcvT, gcVP, gcvH | Glutamate biosynthesis          |                              |
| gapA, pgi, ppc, tiA, gapB, gpmM | Glycine cleavage system          |                              |
| mtlA, mtlD    | Glycolysis                         |                              |
| pntB, pntA    | Mannitol utilization               |                              |
| nirB, nirD    | NAD metabolism                     |                              |
| deoD, deoA, deoB, nupC | Nitrogen metabolism          |                              |
| mtlR, gltR, gltS | Transcription regulation         |                              |
| Genes (or Proteins) | Pathway | Function |
|---------------------|----------|----------|
| aceB, aceA          | Tricarboxylic acid cycle |
| **Genome-specific** |          |
| bkdA2, bkdB, bkdA1  | Branched-chain amino acid degradation |
| adhB, ldhA          | Fermentation |
| mglA, mglB, mglC    | Galactose transport |
| gntU, gntK          | Gluconate utilization |
| pckA                | Gluconeogenesis |
| ptsHI               | Glucose transport |
| glpT                | Glycerol-3-phosphate transport |
| glgX, glgA, glgC, glgP | Glycogen utilization |
| gapN, eno, pgk, fba, aldE | Glycolysis |
| lctP, cld          | L-lactate utilization |
| manC                | Mannose utilization |
| cdd                 | Nucleoside metabolism |

| HmgQ | All target genes | Tyrosine degradation | Unknown |
|------|------------------|----------------------|---------|
| hmgA, hmgB, hmgC, hpd, gloA | Tyrosine degradation |
| hmgQ  | Transcription regulation |

| HmgR | All target genes | Tyrosine degradation | Homogentisate |
|------|------------------|----------------------|--------------|
| hmgA, hmgB, hmgC, hpd COG2814 | Tyrosine degradation |
| hmgR  | Tyrosine transport |
|       | Transcription regulation |

| HmgS | All target genes | Tyrosine degradation | Unknown |
|------|------------------|----------------------|---------|
| hmgA, hmgB | Tyrosine degradation |
| hmgS  | Transcription regulation |

| HutC | Core | Histidine utilization | Urocanate |
|------|------|-----------------------|----------|
| hutU, hutH, hutL, hutD, hutF, hutG, hutG2 | Histidine degradation |
| hutC  | Transcription regulation |
| **Taxonomy-specific** |          |
| hisT, hisX, hisY, hisZ, hisP, hisQ, hisM, hisJ, COG2814, omp | Histidine transport |

| HypR | Core | Proline and 4-hydroxyproline utilization | Proline; 4-hydroxyproline |
|------|------|----------------------------------------|---------------------------|
| hypD, hypE, hypH, hypO | Hydroxyproline/proline degradation |
| hypR  | Transcription regulation |
| **Taxonomy-specific** |          |
| hypY, hypH', 2 | Hydroxyproline/proline degradation |
| putA, prdP, ampP | Proline degradation |
| hypP, hypM, hypN, hypQ, COG531, omp | Hydroxyproline transport |
| hypX, hypS | Hydroxyproline/proline transport |
| colA2  | TCA cycle |
|       | Collagen degradation |
| **Genome-specific** |          |
| pdtp  | Proline transport |
| hypA, hypB, hypC, hypT | Hydroxyproline transport |
| **LiuQ** | Core | Taxonomy-specific and Genome-specific | Branched-chain amino acid degradation | Unknown |
|---|---|---|---|---|
| liuA, liuB, liuC, liuD | liuQ | liuA, liuB, liuC, liuD, ivdA, ivdC, acdH | Branched-chain amino acid degradation | Unknown |
| | liuQ | liuE, aacS, ivd2, acsA | Branched-chain amino acid degradation | Acyl-coenzyme A synthetase |
| **LiuR** | Core | Taxonomy-specific | Branched-chain amino acid degradation | Unknown |
| liuA, liuB, liuC, liuD, liuE, ivdA, ivdC, acdH | liuR, etfA, etfB | aacS, acdA, acdB, acdP, bkdA, bkdB, hbdA, ivdA, ivdB, ivdD, ivdE, ivdF, ivdG, ldh, liuF, liuG, mcm, paaH, echH | Branched-chain amino acid degradation | Electron transfer chain for branched-chain amino acid degradation |
| etfD | atuC, atuD, atuE, atuF | gltB, gltD | Acyclic terpenes degradation | Fatty acid degradation |
| prpB, prpC, prpD | fadD | aceB, mdh, sucA, sucB, sucC, sucD, aceK | Glutamate biosynthesis | Propionate metabolism |
| fadD | aceB, mdh, sucA, sucB, sucC, sucD, aceK | thrA, thrB, thrC | Fatty acid degradation | Threonine biosynthesis |
| cah | cah | | Fatty acid degradation | Carbonic anhydrase |
| **LidR** | Core | Taxonomy-specific | Lactate utilization | Lactate |
| dld, llD, llDl, llDf, llDg | lidP, lidD | llDl, llDf, llDg | Lactate utilization | Lactate |
| lidP | lidR | | Lactate transport | Lactate transport |
| **MetJ** | Core | Genome-specific | Methionine metabolism | S-adenosyl-methionine |
| metI, metN, metQ, metT | glcE, glcG | metI, metN, metQ, metT | Methionine transport | Methionine biosynthesis |
| metJ, metR | glcB | metJ, metR | Transcription regulation | Transcription regulation |
| metA, metB, metE, metF, metH, metK, metL | | metA, metB, metE, metF, metH, metK, metL | Methionine transport | Methionine biosynthesis |
|                | Vitamin B12 transport | Methionine transport | Methionine biosynthesis | Methionine metabolism |Metionine biosynthesis | Metionine transport | Methionine transport | Methionine transport | Vitamin B12 biosynthesis | Serine biosynthesis | Threonine biosynthesis |
|----------------|------------------------|----------------------|-------------------------|-----------------------|-----------------------|----------------------|----------------------|----------------------|------------------------|----------------------|------------------------|
| **btuB**       |                        |                      |                         |                       |                       |                      |                      |                      |                        |                      |                        |
| **Taxonomy-specific** |                        |                      |                         |                       |                       |                      |                      |                      |                        |                      |                        |
| mtsA, mtsB, mtsC |                        |                      |                         |                       |                       |                      |                      |                      |                        |                      |                        |
| metX, metY      |                        |                      |                         |                       |                       |                      |                      |                      |                        |                      |                        |
| msrA, csd       |                        |                      |                         |                       |                       |                      |                      |                      |                        |                      |                        |
| **Genome-specific** |                        |                      |                         |                       |                       |                      |                      |                      |                        |                      |                        |
| btuC, btuD, btuF |                        |                      |                         |                       |                       |                      |                      |                      |                        |                      |                        |
| asd, mccA, mccB, mdeA2, metC, metF-II, mmuM |                        |                      |                         |                       |                       |                      |                      |                      |                        |                      |                        |
| mmuP            |                        |                      |                         |                       |                       |                      |                      |                      |                        |                      |                        |
| mtnA, mtnB, mtnC, mtnD, mtnE, mtnK, mtnX, mtnY, mtnZ |                        |                      |                         |                       |                       |                      |                      |                      |                        |                      |                        |
| pduO            |                        |                      |                         |                       |                       |                      |                      |                      |                        |                      |                        |
| serA            |                        |                      |                         |                       |                       |                      |                      |                      |                        |                      |                        |
| thrA, thrB, thrC |                        |                      |                         |                       |                       |                      |                      |                      |                        |                      |                        |

|                | Methionine metabolism | Homocysteine |
|----------------|------------------------|--------------|
| **MetR**       |                        |              |
| metE           |                        | Methionine biosynthesis |
| metR           |                        | Transcription regulation |
| **Taxonomy-specific** |                        |              |
| metF, glyA, metH, metA, metF-II |                        | Methionine biosynthesis |
| luxS            |                        | SAM recycling |
| hmp             |                        | Nitric oxide cell defense |
| ilvI, ilvH      |                        | Branched-chain amino acid biosynthesis |
| **Genome-specific** |                        |              |
| gcvP, gcvH      |                        | Glycine cleavage system |
| metQ2           |                        | Methionine transport |
| thrC            |                        | Threonine biosynthesis |
| metC, hom, mdeA, bhmT |                        | Methionine biosynthesis |

|                | NAD metabolism | NAD |
|----------------|----------------|-----|
| **NadR**       |                |     |
| pnuC, niaP      |                | Niacin or Ribosyl nicotinamide transport (NAD salvage) |
| nadA, nadB      |                | NAD biosynthesis |
| nadR, pncB      |                | NAD salvage |

|                | NAD metabolism | Unknown |
|----------------|----------------|---------|
| **NadQ**       |                |         |
| nadA, nadC, nadB |            | NAD biosynthesis |
| **Taxonomy-specific** |            |         |
| nadE, nadD      |            | NAD biosynthesis |
| proA            |            | Proline biosynthesis |
| nadQ            |            | Transcription regulation |

|                | N-acetylglucosamine utilization | N-acetylglucosamine |
|----------------|---------------------------------|---------------------|
| **NagC**       |                                  |                     |
| nagA, nagB, nagE |                                | N-acetylglucosamine utilization |
| ptsI, ptsH, crr |                                | Sugar transport |
| nagC            |                                | Transcription regulation |
| **Taxonomy-specific** |                                |                     |
| eno, pgk, fbaA  |                                | Glycolysis |
| omp, glmU, glmS, nagD, nagF |                                | N-acetylglucosamine utilization |
| manX, manZ, manY, ptsG |                                | Mannose and glucose transport |
| chiA, hex       |                                | Chitin degradation |
| mcp             |                                | Chemotaxis protein (toward chitin?) |
| **Genome-specific** |                                |                     |
| chbB, chbA, chbC, chbF, chiP, ompC, ybfM |                                | Chitobiose utilization |
| chi, cbp, chiD, chi1 |                                | Chitin degradation |
| Protein | Function |
|--------|----------|
| galP, gapA, gapB, chbR, chiS, alsR, glgA, glgC, gdhA, gtlA, nanM, nanC | Galactose transport, Glycolysis, Glycogen metabolism, Glutamate degradation, Tricarboxylic acid cycle, N-acetylmuramic acid transport |
| NagQ | N-acetylglucosamine utilization, Transcription regulation |
| NagR | N-acetylglucosamine utilization, N-acetylglucosamine-6-phosphate |
| NrdR | Deoxyribonucleotide biosynthesis, NAD metabolism, Adenosine diphosphate ribose |
| NrtR | Transcription regulation |

### NagQ
- **Core**
  - nagA, nagB2, nagE, nagQ
  - N-acetylglucosamine utilization
  - Transcription regulation

- **Taxonomy-specific**
  - chiA, cdxA, cbp21, chiC, chi, hex
  - NagB, nagK, nagZ, nagT, nagV, nagU, nagW, nagP
  - ybfM, omp_nag, omp1
  - murQ
  - ptsI
  - nagR
  - Chitin degradation
  - N-acetylglucosamine utilization
  - Chitobiose utilization
  - N-acetylmuramic acid utilization
  - Sugar transport
  - Transcription regulation

- **Genome-specific**
  - nagX, nagM, nagO, nagN, nagL, nagK2, anaG
  - N-acetylglucosamine utilization
  - Alpha-N-acetylglucosaminidase

### NagR
- **Core**
  - nagA, nagK, nagB, nagB2, nagP, nagX, hex, omp_nag, chiA, nagR
  - N-acetylglucosamine utilization
  - Chitobiose utilization
  - Chitin degradation
  - Transcription regulation

- **Taxonomy-specific**
  - nagK2, chiD, nixC, naxA, pgi2, pckA
  - N-acetylglucosamine utilization
  - Chitin degradation
  - Chitobiose utilization
  - Glycolysis
  - Gluconeogenesis

- **Genome-specific**
  - cbp, cbp2, cdxA, chiA3, nixD, nixB, nixA, omp_nag2, bglX, SO0852, SO0850, SO0854, SO0853, pdA, mcp
  - Chitin degradation
  - Chitobiose utilization
  - Glucosides utilization
  - Fimbriae biogenesis
  - N-acetylglucosamine utilization
  - Chemotaxis protein (toward chitin?)

### NrdR
- **Taxonomy-specific**
  - ndA, ndB, ndD, ndG
  - Deoxyribonucleotide biosynthesis

### NrtR
- **Taxonomy- and Genome-specific**
  - pncB, pncA, nadV, nadE, nadD, nadM, nadR, pnuC, prs
  - NAD biosynthesis; NAD salvage
| NtrC | Core | Nitrogen assimilation | Phosphorylated NtrB |
|------|------|----------------------|---------------------|
|      |      | Glutamine biosynthesis | Nitrogen source transport | Nitrogen metabolism regulation proteins | Transcription regulation |
| glnA |      |                      |                     |                                  |
| amtB |      |                      |                     |                                  |
| ntrB, glnB, glnK |      |                      |                     |                                  |
| ntrC |      |                      |                     |                                  |
|      | **Taxonomy-specific** |                      |                     |                                  |
| dat  |      | Proline degradation  |                     |                                  |
| narK, nrtC, nrtB, nrtA, gltK, gltI, gltI, dppC, dppA, dppB, dppD, dppF |      | Nitrogen source transport |                      |                                  |
| ntrXY |      | Transcription regulation |                     |                                  |
| nasD, nasE, ntrY, ntrX, nasA, gdhA, nasBA, nasB, nifEN |      | Nitrogen metabolism |                     |                                  |
|      | **Genome-specific** |                      |                     |                                  |
| ureD, ureA, ureB, ureC, ureE, ureG, ureF, ureJ |      | Nitrogen metabolism |                     |                                  |
| hmp, uahA, uahB, uahC, nirA, atzF |      |                     |                     |                                  |
| hisQ, hisJ, hisM, glnH, glnQ, uctA, uctB, uctC, alsT, potG, potI, potH, potA, potB, potC, potD, gltB, gltD |      |                     |                     |                                  |
| speB, ygjG |      | Glutamate biosynthesis |                     |                                  |
| astD, astB, astA, astC, astE |      | Putrescine metabolism |                     |                                  |
| rucC, rucA, rucF, rucD, rucE, rucE2 |      | Arginine degradation |                     |                                  |
| ansA |      | Pyrimidine degradation |                     |                                  |
| hmp |      | Asparagine degradation |                     |                                  |
| nac, nasT, rutR |      | Nitrogen stress response |                     |                                  |
|      | **Transcription regulation** |                      |                     |                                  |
|      |      |                      |                     |                                  |
| PdhR | Core | Nitrogen assimilation | Pyruvate metabolism | Pyruvate |
|      |      | Pyruvate utilization |                      |                     |
| aceE, aceF, lpdA |      |                      |                     |                     |
| pdhR |      | Transcription regulation |                     |                     |
|      | **Taxonomy-specific** |                      |                     |                                  |
| ndh  |      | NAD metabolism       |                      |                                  |
| aceB, aceA |      | Tricarboxylic acid cycle |                     |                                  |
| oadB, oadA, oadG |      | Pyruvate metabolism |                      |                                  |
| pflA, pflB |      | Formate metabolism |                      |                                  |
|      | **Genome-specific** |                      |                     |                                  |
| sdhC, gltA, sdhA, sdhD, sdhB |      | Tricarboxylic acid cycle |                     |                                  |
| cyoC, cyoD, cyoB, cyoA |      | Electron transfer chain |                     |                                  |
| ldpD, did |      | Lactate metabolism |                      |                                  |
| ppc, grcA |      | Pyruvate metabolism |                      |                                  |
| hemL, cyoE |      | Porphyrin biosynthesis |                     |                                  |
| glcB, glcD, glcG, glcE, glcF |      | Glycolate utilization |                     |                                  |
|      | **Transcription regulation** |                      |                     |                                  |
|      |      |                      |                     |                                  |
| PsrA | Core | Nitrogen assimilation | Fatty acid degradation | Oleate |
|      |      | Fatty acid degradation |                      |                     |
| fadA, fadB |      |                      |                     |                     |
| psrA |      | Transcription regulation |                     |                     |
|      | **Taxonomy-specific** |                      |                     |                                  |
| fabG, fabF, fabH, fabD, fabL |      | Fatty acid degradation |                      |                     |
| aceA, aceB, gltA, sdhA, sdhB, sdhC, sdhD |      | Fatty acid biosynthesis |                     |                                  |
| etfD, etfA, etfB |      | Tricarboxylic acid cycle |                     |                                  |
| rpoS, algQ |      | Electron transfer chain for fatty acid degradation |                     |                                  |
| aroQ |      | Transcription |                     |                                  |
|      | **Genome-specific** |                      |                     |                                  |
| ldh |      | Aromatic amino acid biosynthesis |                     |                                  |
|      |      |                      |                     |                                  |
|      |      |                      |                     |                                  |
| Genes | Function |
|-------|----------|
| mdh | Tricarboxylic acid cycle |
| SO3908 | Fatty acid degradation |
| fabK | Fatty acid biosynthesis |

### RutR

| Genes | Function |
|-------|----------|
| rutB, rutA, rutC, rutD | Pyrimidine degradation |
| rutR | Transcription regulation |

| Genes | Function |
|-------|----------|
| carA, carB | Arginine and pyrimidine biosynthesis |
| rutG, pydP | Pyrimidine transport |
| xdhC, xdhA, xdhB, guaD, gpt, xpt, deoD | Purine degradation |
| rutF, pydC, pydX, pydA, pydB, rutE, codA, upp, cdd, deoA, pucM, pucL | Pyrimidine degradation |
| pbuT, pntB, pntC, pntA, ppuD, ppuC, pntD | Nucleoside transport |

### Taxonomy-specific

| Genes | Function |
|-------|----------|
| pytO, pytM, pytN, pytQ, pytC, pytB, pytA, pytD | Pyrimidine transport |
| add, allB, allA, allC, hpt, deoB | Purine degradation |
| deoC | Pyrimidine degradation |

### Genome-specific

| Genes | Function |
|-------|----------|
| pytO, pytM, pytN, pytQ, pytC, pytB, pytA, pytD | Pyrimidine transport |

### SahR

| Genes | Function |
|-------|----------|
| ahy | Methionine metabolism |
| metF, metH | Methionine biosynthesis |
| sahR | Transcription regulation |
| metK | Methionine metabolism |

| Genes | Function |
|-------|----------|
| metE, metH2 | Methionine biosynthesis |

### Taxonomy-specific

| Genes | Function |
|-------|----------|
| metT | Methionine transport |
| bhmT, metB, metX, hom | Methionine biosynthesis |

### Genome-specific

| Genes | Function |
|-------|----------|
| metT | Methionine transport |
| bhmT, metB, metX, hom | Methionine biosynthesis |

### SamR

| Genes | Function |
|-------|----------|
| metE, metF2, metX2, metB, metH, hom | Methionine biosynthesis |
| samR | Transcription regulation |
| metK | SAM biosynthesis |

### TyrR

| Genes | Function |
|-------|----------|
| aroF | Chorismate biosynthesis |
| tyrA | Tyrosine & Phenylalanine biosynthesis |
| phhA, phhB | Phenylalanine degradation |
| hmgB, hmgC, hpd, hmgA | Tyrosine degradation |
| tyrP | Tyrosine transporter |
| tyrR (phhR) | Transcription regulation |

| Genes | Function |
|-------|----------|
| brnQ | Branched-chain amino acid transport |
| mdeA | Methionine degradation |
| putA | Proline degradation |
| bkdA, bkdB, ivdA, ivdB, ivdC, ivdD, ivdE, ivdF, ivdG, ldh, liuA, liuB, liuC, liuD, liuE, liuF, liuG | Branched-chain amino acid degradation |
| hmgR, liuR | Transcription regulation |
| tyrB | Tyrosine biosynthesis / Tyrosine degradation |
| aceA, aceB | Tricarboxylic acid cycle |
| aroA, aroL | Chorismate biosynthesis |
| Gene   | Function                                           |
|--------|----------------------------------------------------|
| aroP   | Aromatic amino acid transport                      |
| acsA   | Acetyl-coenzyme A synthetase                       |
| phhC   | Phenylalanine degradation                          |
| COG0733| Tyrosine transport                                 |
| **Genome-specific** |                                      |
| aroM, aroG | Chorismate biosynthesis                       |
| kyn, tdo, ipdC | Tryptophan degradation                       |
| mtr    | Tryptophan transport                               |
| tpl    | Tyrosine degradation                               |
| COG2814| Tyrosine transport                                 |
| folA   | Tetrahydrofolate biosynthesis                      |

| Gene   | Function                                           |
|--------|----------------------------------------------------|
| trpE   | Tryptophan biosynthesis                            |
| trpR   | Transcription regulation                           |
| **Taxonomy-specific** |                                      |
| aroF, aroG | Chorismate biosynthesis                       |
| trpG, trpB, trpC, trpA, trpD | Tryptophan biosynthesis                       |
| tyrA   | Tyrosine biosynthesis                              |
| mtr, COG0733 | Tryptophan transport                       |
| **Genome-specific** |                                      |
| aroH, aroM, arol, aroA | Chorismate biosynthesis                       |
| tnaA, tnaB | Tryptophan transport and degradation               |

*annotated gene functions and metabolic pathways are listed in Table S3. This table excludes functionally unassigned genes.*
| Gamma-proteobacteria | TyrR | TyrA | TyrB | TyrP | HpdC | HmgA | HmgB | HmgC | HmgD | HmgE | HmgF | TyrR regulon |
|-----------------------|------|------|------|------|------|------|------|------|------|------|------|----------------|
| Alteromonadales        |      |      |      |      |      |      |      |      |      |      |      |                |
| Alteromonadales bacterium TW-7 | +   | +   | -    | -    | +    | +    | +    | +    | +    | -    | +    | tyrR, HpdA, HpdB, rib-kyne, hmgAB, hmgB, hmgC, hmgD, hmgE, hmgF, tyrR, tyrA, tyrB, tyrP, rib-kyne, hmgAB, hmgB, hmgC, hmgD, hmgE, hmgF, tyrR, tyrA, tyrB, tyrP, rib-kyne, hmgAB, hmgB, hmgC, hmgD, hmgE, hmgF, tyrR, tyrA, tyrB, tyrP, rib-kyne, hmgAB, hmgB, hmgC, hmgD, hmgE, hmgF, tyrR, tyrA, tyrB, tyrP, rib-kyne, hmgAB, hmgB, hmgC, hmgD, hmgE, hmgF, tyrR, tyrA, tyrB, tyrP, rib-kyne, hmgAB, hmgB, hmgC, hmgD, hmgE, hmgF, tyrR, tyrA, tyrB, tyrP, rib-kyne, hmgAB, hmgB, hmgC, hmgD, hmgE, hmgF, tyrR, tyrA, tyrB, tyrP, rib-kyne, hmgAB, hmgB, hmgC, hmgD, hmgE, hmgF, tyrR, tyrA, tyrB, tyrP, rib-kyne, hmgAB, hmgB, hmgC, hmgD, hmgE, hmgF, tyrR, tyrA, tyrB, tyrP, rib-kyne, hmgAB, hmgB, hmgC, hmgD, hmgE, hmgF, tyrR, tyrA, tyrB, tyrP, rib-kyne, hmgAB, hmgB, hmgC, hmgD, hmgE, hmgF, tyrR, tyrA, tyrB, tyrP, rib-kyne, hmgAB, hmgB, hmgC, hmgD, hmgE, hmgF, tyrR, tyrA, tyrB, tyrP, rib-kyne, hmgAB, hmgB, hmgC, hmgD, hmgE, hmgF, tyrR, tyrA, tyrB, tyrP, rib-kyne, hmgAB, hmgB, hmgC, hmgD, hmgE, hmgF, tyrR, tyrA, tyrB, tyrP, rib-kyne, hmgAB, hmgB, hmgC, hmgD, hmgE, hmgF, tyrR, tyrA, tyrB, tyrP, rib-kyne, hmgAB, hmgB, hmgC, hmgD, hmgE, hmgF, tyrR, tyrA, tyrB, tyrP, rib-kyne, hmgAB, hmgB, hmgC, hmgD, hmgE, hmgF, tyrR, tyrA, tyrB, tyrP, rib-kyne, hmgAB, hmgB, hmgC, hmgD, hmgE, hmgF, tyrR, tyrA, tyrB, tyrP, rib-kyne, hmgAB, hmgB, hmgC, hmgD, hmgE, hmgF, tyrR, tyrA, tyrB, tyrP, rib-kyne, hmgAB, hmgB, hmgC, hmgD, hmgE, hmgF, tyrR, tyrA, tyrB, tyrP, rib-kyne, hmgAB, hmgB, hmgC, hmgD, hmgE, hmgF, tyrR, tyrA, tyrB, tyrP, rib-kyne, hmgAB, hmgB, hmgC, hmgD, hmgE, hmgF, tyrR, tyrA, tyrB, tyrP, rib-kyne, hmgAB, hmgB, hmgC, hmgD, hmgE, hmgF, tyrR, tyrA, tyrB, tyrP, rib-kyne, hmgAB, hmgB, hmgC, hmgD, hmgE, hmgF, tyrR, tyrA, tyrB, tyrP, rib-kyne, hmgAB, hmgB, hmgC, hmgD, hmgE, hmgF, tyrR, tyrA, tyrB, tyrP, rib-kyne, hmgAB, hmgB, hmgC, hmgD, hmgE, hmgF, tyrR, tyrA, tyrB, tyrP, rib-kyne, hmgAB, hmgB, hmgC, hmgD, hmgE, hmgF, tyrR, tyrA, tyrB, tyrP, rib-kyne, hmgAB, hmgB, hmgC, hmgD, hmgE, hmgF, tyrR, tyrA, tyrB, tyrP, rib-kyne, hmgAB, hmgB, hmgC, hmgD, hmgE, hmgF, tyrR, tyrA, tyrB, tyrP, rib-kyne, hmgAB, hmgB, hmgC, hmgD, hmgE, hmgF, tyrR, tyrA, tyrB, tyrP, rib-kyne, hmgAB, hmgB, hmgC, hmgD, hmgE, hmgF, tyrR, tyrA, tyrB, tyrP, rib-kyne, hmgAB, hmgB, hmgC, hmgD, hmgE, hmgF, tyrR, tyrA, tyrB, tyrP, rib-kyne, hmgAB, hmgB, hmgC, hmgD, hmgE, hmgF, tyrR, tyrA, tyrB, tyrP, rib-kyne, hmgAB, hmgB, hmgC, hmgD, hmgE, hmgF, tyrR, tyrA, tyrB, tyrP, rib-kyne, hmgAB, hmgB, hmgC, hmgD, hmgE, hmgF, tyrR, tyrA, tyrB, tyrP, rib-kyne, hmgAB, hmgB, hmgC, hmgD, hmgE, hmgF, tyrR, tyrA, tyrB, tyrP, rib-kyne, hmgAB, hmgB, hmgC, hmgD, hmgE, hmgF, tyrR, tyrA, tyrB, tyrP, rib-kyne, hmgAB, hmgB, hmgC, hmgD, hmgE, hmgF, tyrR, tyrA, tyrB, tyrP, rib-kyne, hmgAB, hmgB, hmgC, hmgD, hmgE, hmgF, tyrR, tyrA, tyrB, tyrP, rib-kyne, hmgAB, hmgB, hmgC, hmgD, hmgE, hmgF, tyrR, tyrA, tyrB, tyrP, rib-kyne, hmgAB, hmgB, hmgC, hmgD, hmgE, hmgF, tyrR, tyrA, tyrB, tyrP, rib-kyne, hmgAB, hmgB, hmgC, hmgD, hmgE, hmgF, tyrR, tyrA, tyrB, tyrP, rib-kyne, hmgAB, hmgB, hmgC, hmgD, hmgE, hmgF, tyrR, tyrA, tyrB, tyrP, rib-kyne, hmgAB, hmgB, hmgC, hmgD, hmgE, hmgF, tyrR, tyrA, tyrB, tyrP, rib-kyne, hmgAB, hmgB, hmgC, hmgD, hmgE, hmgF, tyrR, tyrA, tyrB, tyrP, rib-kyne, hmgAB, hmgB, hmgC, hmgD, hmgE, hmgF, tyrR, tyrA, tyrB, tyrP, rib-kyne, hmgAB, hmgB, hmgC, hmgD, hmgE, hmgF, tyrR, tyrA, tyrB, tyrP, rib-kyne, hmgAB, hmgB, hmgC, hmgD, hmgE, hmgF, tyrR, tyrA, tyrB, tyrP, rib-kyne, hmgAB, hmgB, hmgC, hmgD, hmgE, hmgF, tyrR, tyrA, tyrB, tyrP, rib-kyne, hmgAB, hmgB, hmgC, hmgD, hmgE, hmgF, tyrR, tyrA, tyrB, tyrP, rib-kyne, hmgAB, hmgB, hmgC, hmgD, hmgE, hmgF, tyrR, tyrA, tyrB, tyrP, rib-kyne, hmgAB, hmgB, hmgC, hmgD, hmgE, hmgF, tyrR, tyrA, tyrB, tyrP, rib-kyne, hmgAB, hmgB, hmgC, hmgD, hmgE, hmgF, tyrR, tyrA, tyrB, tyrP, rib-kyne, hmgAB, hmgB, hmgC, hmgD, hmgE, hmgF, tyrR, tyrA, tyrB, tyrP, rib-kyne, hmgAB, hmgB, hmgC, hmgD, hmgE, hmgF, tyrR, tyrA, tyrB, tyrP, rib-kyne, hmg
| Genus/Species                          | TyrR | AroL | AroH | AroG | AroF | TyrA | TyrB | Hpd  | HmgA | HmgB | HmgC | PhhAB | PhhR | Other Genes |
|---------------------------------------|------|------|------|------|------|------|------|------|------|------|------|-------|------|-------------|
| **Psychromonas spp. (2 genomes)**    |      |      |      |      |      |      |      |      |      |      |      |       |      |             |
| Psychromonas sp. F136                 |      |      |      |      |      |      |      |      |      |      |      |       |      |             |
| Aeromonas hydrophila ATCC 7966        |      |      |      |      |      |      |      |      |      |      |      |       |      |             |
| Aeromonas salmonicida M449            |      |      |      |      |      |      |      |      |      |      |      |       |      |             |
| Tolomona auensis DSM 1817             |      |      |      |      |      |      |      |      |      |      |      |       |      |             |
| **Moritella sp. PE36**                 |      |      |      |      |      |      |      |      |      |      |      |       |      |             |
| **Aeromonas hydrophila ATCC 7966**     |      |      |      |      |      |      |      |      |      |      |      |       |      |             |
| **Aeromonas salmonicida M449**         |      |      |      |      |      |      |      |      |      |      |      |       |      |             |
| **Tolumona auensis DSM 1817**          |      |      |      |      |      |      |      |      |      |      |      |       |      |             |
| **Oceanospirillales/Alteromonadales**  |      |      |      |      |      |      |      |      |      |      |      |       |      |             |
| Hahella chejuensis KCTC 21906          |      |      |      |      |      |      |      |      |      |      |      |       |      |             |
| Marinobacter aquaeolii                 |      |      |      |      |      |      |      |      |      |      |      |       |      |             |
| Marinobacter sp. ELB13                 |      |      |      |      |      |      |      |      |      |      |      |       |      |             |
| Oceanobacter sp. RED65                 |      |      |      |      |      |      |      |      |      |      |      |       |      |             |
| Oceanospirillum sp. MED92              |      |      |      |      |      |      |      |      |      |      |      |       |      |             |
| Marinomonas sp. MWYL1                  |      |      |      |      |      |      |      |      |      |      |      |       |      |             |
| Saccharophaga degradans 2-40           |      |      |      |      |      |      |      |      |      |      |      |       |      |             |
| Tereutilacter turnerae T901            |      |      |      |      |      |      |      |      |      |      |      |       |      |             |
| Cellvibrio japonicus Ueda107           |      |      |      |      |      |      |      |      |      |      |      |       |      |             |
| Chromohalobacter salexigens DSM 3043   |      |      |      |      |      |      |      |      |      |      |      |       |      |             |
| Reinekeia sp. MED207                   |      |      |      |      |      |      |      |      |      |      |      |       |      |             |
| Akkai vibrio berkemensis SK2            |      |      |      |      |      |      |      |      |      |      |      |       |      |             |
| **Pseudomonadaceae**                   |      |      |      |      |      |      |      |      |      |      |      |       |      |             |
| Pseudomonas aeruginosa PA01            |      |      |      |      |      |      |      |      |      |      |      |       |      |             |
| Pseudomonas entomophila I48            |      |      |      |      |      |      |      |      |      |      |      |       |      |             |
| Pseudomonas putida KT2440              |      |      |      |      |      |      |      |      |      |      |      |       |      |             |
| Pseudomonas syringae DC3000             |      |      |      |      |      |      |      |      |      |      |      |       |      |             |
| Pseudomonas fluorescens IF-5            |      |      |      |      |      |      |      |      |      |      |      |       |      |             |
| Pseudomonas mendocina ymp               |      |      |      |      |      |      |      |      |      |      |      |       |      |             |
| **Acetobacter sp. met33**               |      |      |      |      |      |      |      |      |      |      |      |       |      |             |
| **Acinetobacter sp. A0139**            |      |      |      |      |      |      |      |      |      |      |      |       |      |             |
| Acinetobacter baumannii AB0057          |      |      |      |      |      |      |      |      |      |      |      |       |      |             |
| Psychrobacter arcticus 775             |      |      |      |      |      |      |      |      |      |      |      |       |      |             |
| **Psychrobacter arcticus 775**          |      |      |      |      |      |      |      |      |      |      |      |       |      |             |
| **Xanthomonadiales**                   |      |      |      |      |      |      |      |      |      |      |      |       |      |             |
| Xylella fastidiosa Belfri               |      |      |      |      |      |      |      |      |      |      |      |       |      |             |
| Xanthomonas axonopodis 306              |      |      |      |      |      |      |      |      |      |      |      |       |      |             |
| Xanthomonas campestris ATCC 33913       |      |      |      |      |      |      |      |      |      |      |      |       |      |             |
| Stenotrophomonas maltophilia K279a     |      |      |      |      |      |      |      |      |      |      |      |       |      |             |
| **Unclassified**                       |      |      |      |      |      |      |      |      |      |      |      |       |      |             |
| **TyR (PhhR) regulon**                 |      |      |      |      |      |      |      |      |      |      |      |       |      |             |
| **Chorismate biosynthesis genes**      |      |      |      |      |      |      |      |      |      |      |      |       |      |             |
| **Tyr biosynthesis pathway genes**     |      |      |      |      |      |      |      |      |      |      |      |       |      |             |
| **Tyr transporter genes**              |      |      |      |      |      |      |      |      |      |      |      |       |      |             |
| **Tyr degradation genes**              |      |      |      |      |      |      |      |      |      |      |      |       |      |             |

The presence or absence of gene orthologs is shown by ‘+’/-’ signs. Colored ‘+’ signs (red, purple, green, blue) indicate that the gene belong to TyrR(PhhR), HmgR, HmgQ, HmgS regulons, respectively. Column shows the list of all corresponding operons from reconstructed regulons. Additional member of TyrR regulons that are not involved in aromatic amino acid metabolism are not included.

Color code for genes in the table:

- **TyR (PhhR) regulator gene**
- **Chorismate biosynthesis genes**
- **Tyr biosynthesis pathway genes**
- **Tyr transporter genes**
- **Tyr degradation genes**