Supplementary materials for:

Curvibacter soli sp. nov., Extensimonas soli sp. nov., Pseudarthrobacter

napthalenicus sp. nov., and Terripilifer ovatus gen. nov., sp. nov., four new species

isolated from polluted soil

Ze-Shen Liu¹, Ke-Huan Wang¹, Xiao-Kang Wang¹, Man Cai¹, Mei-Ling Yang¹,

Wen-Ke Yang¹, De-Feng Li*¹, Shuang-Jiang Liu*^{1,2}

1. State Key Laboratory of Microbial Resources, Institute of Microbiology, Chinese

Academy of Sciences, Beijing 100101, China.

2. State Key Laboratory of Microbial Biotechnology, Shandong University, Qingdao

266237, China.

*Corresponding authors:

De-Feng Li (lidefeng@im.ac.cn) & Shuang-Jiang Liu (liusj@im.ac.cn)

Postal address: Institute of Microbiology, Chinese Academy of Sciences, No. 1

Beichen West Road, Chaoyang District, Beijing 100101, China

Telephone number: +86-010-64807423

Table S1. Cellular fatty acid compositions of strains H3Y2-7^T, H3SJ34-1^T, and their closely related species.

| Strains | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 |
|---------------------------------|------|------|------|------|------|------|------|------|
| C _{12:0} | ND | / | / | ND | 1.1 | / | / | / |
| $C_{14:0}$ | 1.3 | 1.4 | 1.7 | 2.3 | 4.0 | / | / | / |
| $C_{16:0}$ | 2.8 | 6.1 | 8.1 | 9.2 | 27.9 | 8.7 | 11.4 | 9.3 |
| $C_{18:0}$ | / | / | / | / | 9.1 | / | / | ND |
| iso-C _{15:0} | 15.3 | 10.6 | 7.1 | 9.0 | / | / | / | / |
| iso-C _{16:0} | 4.0 | 5.2 | 7.2 | 6.2 | ND | / | / | / |
| iso-C _{17:0} | 1.0 | / | / | 2.7 | ND | / | / | / |
| iso-C _{19:0} | / | / | / | / | 1.3 | / | / | / |
| anteiso-C _{15:0} | 59.5 | 52.2 | 51.5 | 46.1 | / | / | / | / |
| anteiso-C _{17:0} | 9.0 | 14.8 | 12.7 | 16.5 | / | / | / | / |
| anteiso-C _{17:1} ω9c | 2.4 | / | / | 2.4 | ND | / | / | / |
| C _{15:0} 3-OH | ND | / | / | ND | 6.1 | / | / | / |
| C _{16:0} 3-OH | ND | / | / | ND | 3.7 | / | 3.1 | / |
| cyclo-C _{19:0} ω8c | ND | / | / | ND | ND | / | / | 38.9 |
| 11-methyl-C _{18:1} ω7c | ND | / | / | ND | 4.2 | / | / | / |
| C _{16:1} ω7c | ND | / | / | ND | ND | 45.4 | 46.8 | / |
| C _{18:1} ω7c | / | / | / | / | 8.9 | 42.2 | 35.0 | 26.3 |
| C _{18:1} ω9c | ND | / | / | ND | 2.2 | / | / | / |
| C _{20:1} ω9c | ND | / | / | ND | 1.4 | / | / | / |
| Summed feature 2 | ND | / | / | ND | 3.9 | / | / | / |
| Summed feature 3 | / | 2.3 | 1.2 | 2.9 | 4.1 | / | / | / |
| Summed feature 7 | ND | / | / | ND | 14.4 | / | / | / |

Strains: 1, H3Y2-7^T; 2, Pseudarthrobacter psychrotolerans YJ56^T [1]; 3, Pseudarthrobacter sulfonivorans ALL^T [1, 2]; 4, Pseudarthrobacter polychromogenes JCM 2523^T (this study); 5, H3SJ34-1^T; 6, Rhodoblastus sphagnicola DSM 16996^T [3]; 7, Rhodoblastus acidophilus DSM 137^T [3, 4]; 8, Roseiarcus fermentans Pf56^T [5]. Data for the strains in column 1, 4, and 5 are derived from this study, while data for other strains are referenced from previous studies as indicated. Fatty acids with content proportion \geq 1.0% are shown, and those \geq 5.0% are considered as major component and indicated in bold. /, not reported; ND, not detected. Summed features are fatty acids that cannot be resolved reliably from another fatty acid using the chromatographic conditions chosen. The MIDI system groups these fatty acids together as one feature with a single percentage of the total. Summed feature 2 represents C_{14:0} 3-OH and/or iso-C_{16:1} I; summed feature 3 represents C_{16:1} ω 7c and/or C_{16:1} ω 6c; summed feature 7 represents C_{19:1} ω 7c and/or C_{19:1} ω 6c.

Table S2. Cellular fatty acid compositions of strains H3M7-6^T, H39-3-26^T, and their closely related species.

| Strains | 1 | 2 | 3 | 4 | 5 | 6 |
|-----------------------------------|------|------|------|------|------|------|
| C _{12:0} | 2.9 | 2.6 | 4.0 | 2.1 | 3.2 | 3.6 |
| $C_{16:0}$ | 34.8 | 35.7 | 29.1 | 34.9 | 34.2 | 16.9 |
| C _{17:0} | 2.0 | 2.1 | / | / | / | ND |
| C _{10:0} 3-OH | 4.7 | 4.5 | 4.6 | / | ND | ND |
| C _{12:0} 2-OH | ND | ND | / | 5.3 | ND | / |
| C _{14:0} 2-OH | 1.9 | / | ND | / | ND | ND |
| C _{16:0} 2-OH | / | 1.3 | 1.3 | 1.2 | ND | / |
| C _{16:1} 2-OH | 1.5 | / | 2.5 | 3.7 | ND | / |
| C _{18:1} 2-OH | / | 1.1 | / | / | ND | / |
| C _{18:1} ω7c | 11.4 | 13.3 | / | 6.6 | 12.9 | 35.5 |
| iso-C _{17:0} 3-OH | ND | / | ND | 1.0 | ND | ND |
| anteiso-C _{17:1} ω9c | 1.5 | 1.2 | ND | 1.2 | / | ND |
| cyclo-C _{17:0} | 13.1 | 11.9 | 24.8 | 14.3 | 9.7 | ND |
| cyclo-C _{19:0} ω8c | / | 3.3 | 2.9 | / | ND | / |
| 11-methyl- $C_{18:1}$ ω 7c | ND | 1.4 | ND | ND | / | ND |
| Summed feature 3 | 20.2 | 15.5 | 26.9 | 25.0 | 32.9 | 41.9 |
| Summed feature 7 | ND | 1.9 | 1.4 | ND | 3.2 | / |

Strains: 1, H3M7-6^T; 2, Extensimonas vulgaris JCM 17803^T (this study); 3, 'Extensimonas perlucida' HX2-24 [6]; 4, H39-3-26^T; 5, Curvibacter gracilis JCM 21496^T (this study); 6, Curvibacter lanceolatus ATCC 14669^T [7, 8]. Data for the strains in column 1, 2, 4, and 5 are derived from this study, while data for other strains are referenced from previous studies as indicated. Fatty acids with content proportion \geq 1.0% are shown, and those \geq 5.0% are considered as major component and indicated in bold. /, not reported; ND, not detected. Summed features are fatty acids that cannot be resolved reliably from another fatty acid using the chromatographic conditions chosen. The MIDI system groups these fatty acids together as one feature with a single percentage of the total. Summed feature 3 represents $C_{16:1} \omega 7c$ and/or $C_{16:1} \omega 6c$; summed feature 7 represents $C_{19:1} \omega 7c$ and/or $C_{19:1} \omega 6c$.

Table S3. Genomic features of the four novel species isolated from polluted soil.

| Genome features | H3Y2-7 ^T | H3SJ34-1 ^T | H3M7-6 ^T | H39-3-26 ^T |
|---|---------------------|-----------------------|---------------------|-----------------------|
| Genome Size (kbp) | 4559.1 | 7197.9 | 3438.2 | 3359.1 |
| G+C comtent (mol %) | 65.2 | 62.3 | 65.3 | 67.2 |
| Completeness (%) | 99.1 | 99.7 | 99.3 | 98.9 |
| Coverage of the genome (%) | 99.9 | 99.8 | 99.6 | 96.3 |
| Gene number | 4287 | 6730 | 3144 | 3126 |
| Contamination (%) | 0.05 | 0.73 | 0 | 0.47 |
| Number of contigs | 90 | 86 | 50 | 99 |
| N50 of contigs (kbp) | 178.6 | 279.2 | 181.9 | 82.2 |
| Largest contig (kbp) | 452.1 | 568.8 | 529.4 | 177.6 |
| Number of tRNA | 52 | 49 | 46 | 49 |
| Number of 5S rRNA | 3 | 1 | 1 | 1 |
| Number of 23S rRNA | 1 | 1 | 1 | 1 |
| Number of 16SrRNA | 1 | 1 | 1 | 1 |
| Number of sRNA | 1 | 8 | 3 | 4 |
| Plasimid size (Kbp) | 299.7 | 1024.1 | 215.1 | 71 |
| Identity between 16S rRNA gene sequences obtained from genome and Sanger sequencing | 99.8 | 99.7 | 99.7 | 100.0 |

Table S4. Annotated gene number related to antibiotics resistance, carbohydrates and amino acids metabolism, and prophage based on the genomes of the four novel species.

| Strains | $H3Y2-7^T$ | H3SJ34-1 ^T | $H3M7-6^{T}$ | H39-3-26 ^T |
|---------------------------------|------------|-----------------------|--------------|-----------------------|
| Resistance to antibiotics | | | | |
| Anti fluoroquinolones | 2 | 3 | 2 | 2 |
| Beta-lactamase | 1 | 1 | - | 1 |
| Carbohydrates metabolism | | | | |
| Central carbohydrate metabolism | 139 | 113 | 81 | 73 |
| Monosaccharides | 59 | 9 | 2 | 2 |
| Di- and oligo-saccharides | 35 | 24 | 2 | 3 |
| Aminosugars | 6 | - | - | - |
| Organic acids | 28 | 8 | 10 | 6 |
| Amino acids and derivatives | 309 | 357 | 284 | 256 |
| Prophage | - | 17 | 32 | 20 |
| Head protein | - | 3 | 5 | 5 |
| Tail protein | - | 2 | 5 | 1 |
| Portal protein | - | - | 1 | 2 |
| Fiber protein | - | 1 | - | - |
| Plate protein | - | 3 | - | - |
| Regulatory protein | - | - | 1 | - |
| Phage-like protein | - | 3 | 6 | 4 |
| Protease | - | - | | 1 |
| Integrase | - | - | 1 | 1 |
| Terminase | - | - | 1 | 1 |
| Hypothetical protein | - | 5 | 12 | 5 |

The genomes were annotated using RAST engine. -, no related genes were annotated. Prophage sequences were predicted and annotated with PHAEST program.

Table S5. Annotated gene number related to heavy metal resistance and aromatic compound metabolism based on the genomes of the four novel species.

| Strains | H3Y2-7 ^T | H3SJ34-1 ^T | H3M7-6 ^T | H39-3-26 ^T |
|----------------------------------|---------------------|-----------------------|---------------------|-----------------------|
| Enymes for arsenic resistance | | | | |
| ArsA | 1 | - | - | 1 |
| ArsB | 1 | 2 | - | 1 |
| Enymes for chromium resistance | | | | |
| ChrB | - | 1 | - | - |
| ChrR | 1 | 3 | 1 | - |
| Chromate transporter | - | 7 | 2 | 1 |
| Enymes for aromatic compounds | | | | |
| metabolism | | | | |
| Naphthalene 1,2-dioxygenase | - | 2 | 5 | 4 |
| Cytochrome P450 | 4 | 2 | 2 | 1 |
| Peripheral pathways for aromatic | 10 | 20 | 26 | _ |
| compound catabolism | 12 | 28 | 26 | 5 |
| Metabolism of central aromatic | 42 | 75 | 7 | 0 |
| intermediates | 42 | 75 | 7 | 9 |

The genomes were annotated on the Global Catalogue of Type Strain (gcType) Platform. -, no related genes were annotated.

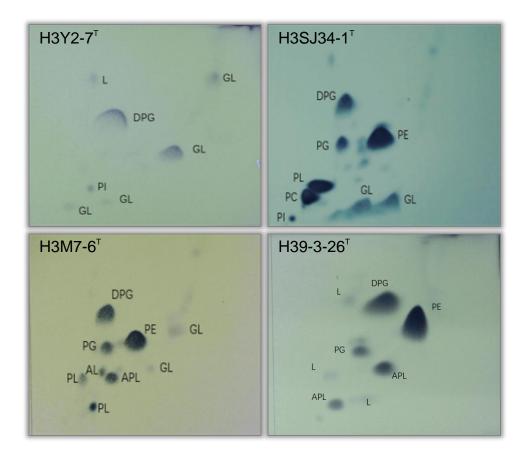


Fig. S1. Polar lipid profiles after separation by two-dimensional thin layer chromatography of the four strains. DPG, diphosphatidylglycerol; PG, phosphatidylglycerol; PE, phosphatidylethanolamine; APL, unknown aminophospholipid; PL, phospholipid; GL, glycolipid; AL, aminolipid; L, unknown lipid; PC, phosphatidylcholine; PI, phosphatidylinositols.

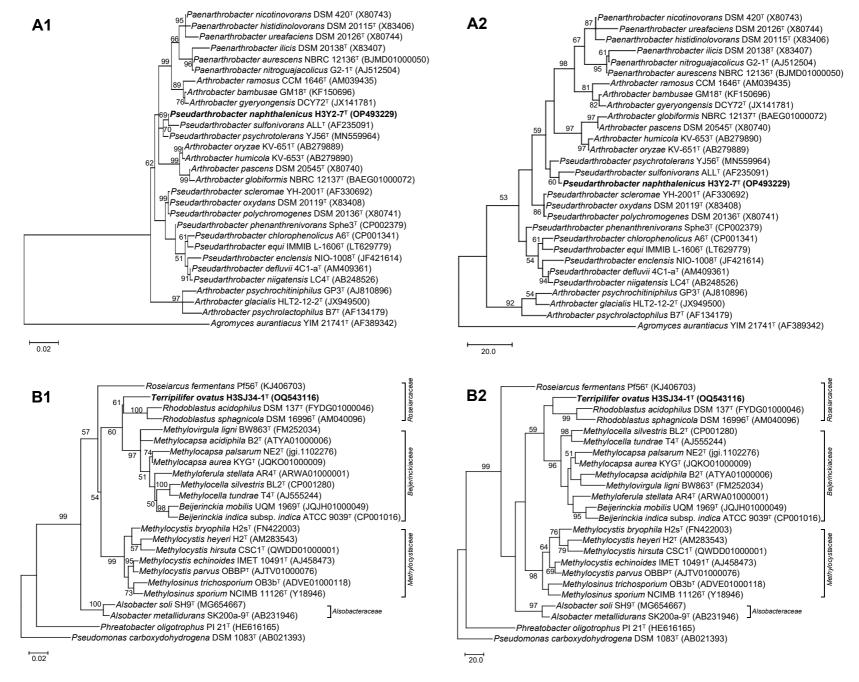


Fig. S2. Maximum-likelihood (A1, B1) and maximum parsimony (A2, B2) phylogenetic trees based on 16S rRNA gene sequences show the relationship between strains H3Y2-7^T and H3SJ34-1^T and their closely related microorganisms. A, strain H3Y2-7^T and its closely related species in the family *Micrococcaceae*. The sequence of *Agromyces aurantiacus* YIM 21741^T (AF389342) was used as an outgroup; B, strain H3SJ34-1^T and its closely related species in the families *Roseiarcaceae*, *Beijerinckiaceae*, *Methylocystaceae* and *Alsobacteraceae*. The sequence of *Pseudomonas carboxydohydrogena* DSM 1083^T (AB021393) and *Phreatobacter oligotrophus* PI 21^T (HE616165) were used as outgroup. GenBank accession numbers are given in parentheses. Bootstrap percentages (>50%) based on 1,000 replicates are shown at the nodes. Bar, 0.02 substitutions per nucleotide position for A1 and B1; Bar, 20.0 substitutions per nucleotide position for A2, B2.

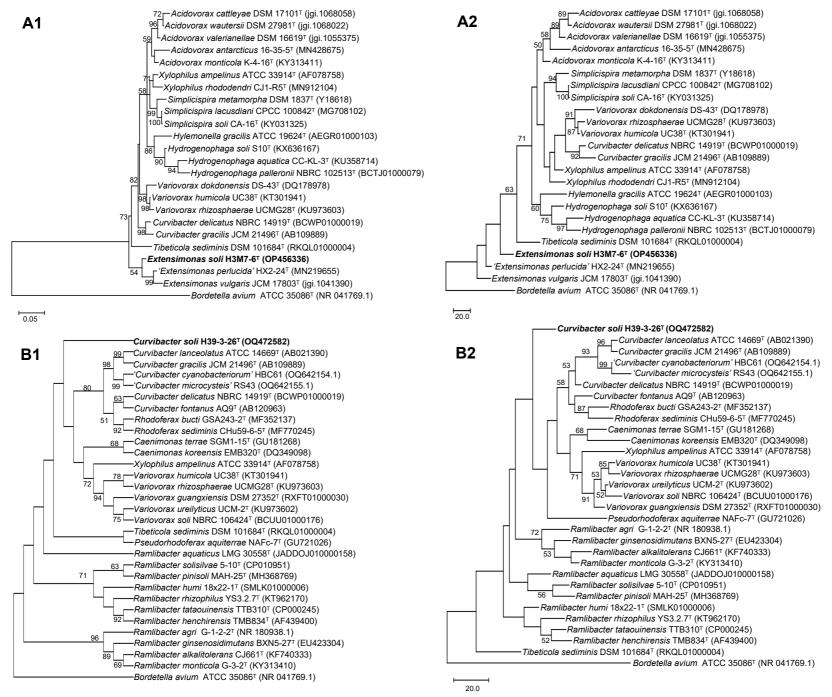


Fig. S3. Maximum-likelihood (A1, B1) and maximum parsimony (A2, B2) phylogenetic trees based on 16S rRNA gene sequences show the relationship between strains H3M7-6^T and H39-3-26^T and their closely related microorganisms. A, strain H3M7-6^T and its closely related species in the family *Comamonadaceae*. The sequence of *Bordetella avium* ATCC 35086^T (NR 041769.1) was used as outgroup; B, strain H39-3-26^T and its closely related species in the family *Comamonadaceae*. The sequence of *Bordetella avium* ATCC 35086^T (NR 041769.1) was used as outgroup. GenBank accession numbers are given in parentheses. Bootstrap percentages (>50%) based on 1,000 replicates are shown at the nodes. Bar, 0.05 substitutions per nucleotide position for A1; Bar, 20.0 substitutions per nucleotide position for A2, B2.

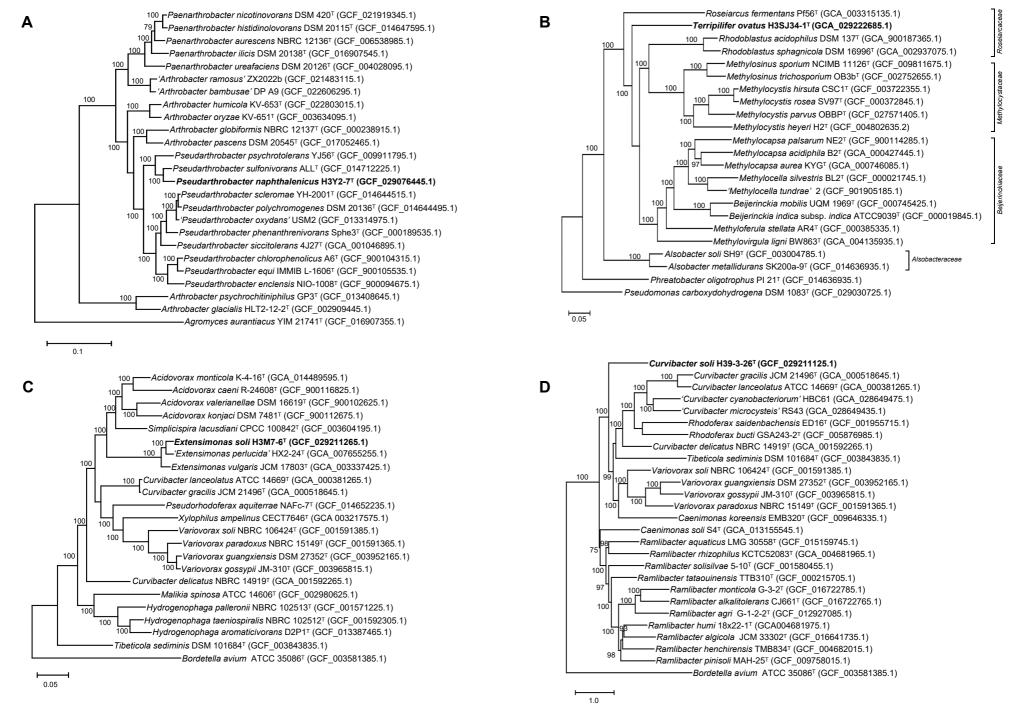


Fig. S4. Phylogenomic trees reconstructed with IPGA based on genome sequences. **A**, strain H3Y2-7^T and its closely related species; **B**, strain H3SJ34-1^T and its closely related species; **C**, strain H3M7-6^T and its closely related species; **D**, strain H39-3-26^T and its closely related species. Bootstrap percentages (>50%) based on 1,000 replicates are shown at the nodes. Bar, 0.1 substitutions per nucleotide position for **A** and **D**; Bar, 0.05 substitutions per nucleotide position for **B** and **C**. The IPGA program was developed by Liu *et al.*, 2022 [9].

References

- 1. Shin Y, Lee BH, Lee KE, Park W. Pseudarthrobacter psychrotolerans sp. nov., a cold-adapted bacterium isolated from Antarctic soil. Int J Syst Evol Microbiol 2020; 70:6106-6114.
- 2. **Borodina E, Kelly DP, Schumann P, Rainey FA, Ward-Rainey NL, et al.** Enzymes of dimethylsulfone metabolism and the phylogenetic characterization of the facultative methylotrophs *Arthrobacter sulfonivorans* sp. nov., *Arthrobacter methylotrophus* sp. nov., and *Hyphomicrobium sulfonivorans* sp. nov. *Arch Microbiol* 2002; 177:173-183.
- 3. Kulichevskaya IS, Guzev VS, Gorlenko VM, Liesack W, Dedysh SN. *Rhodoblastus sphagnicola* sp. nov., a novel acidophilic purple non-sulfur bacterium from *Sphagnum* peat bog. *Int J Syst Evol Microbiol* 2006; 56:1397-1402.
- 4. **Imhoff JF.** Transfer of *Rhodopseudomonas acidophila* to the new genus *Rhodoblastus* as *Rhodoblastus acidophilus* gen. nov., comb. nov. *Int J Syst Evol Microbiol* 2001; 51:1863-1866.
- 5. **Kulichevskaya IS, Danilova OV, Tereshina VM, Kevbrin VV, Dedysh SN.** Descriptions of *Roseiarcus fermentans* gen. nov., sp. nov., a bacteriochlorophyll a-containing fermentative bacterium related phylogenetically to alphaproteobacterial methanotrophs, and of the family *Roseiarcaceae* fam. nov. *Int J Syst Evol Microbiol* 2014; 64:2558-2565.
- 6. **Peng Q, Sheng M, Yang Z, Ni H, Li Q, et al.** Extensimonas perlucida sp. nov., a novel bacterium isolated from sludge. *Curr Microbiol* 2020; 77:1316-1320.
- 7. **Ding L, Yokota A.** *Curvibacter fontana* sp. nov., a microaerobic bacteria isolated from well water. *J Gen Appl Microbiol* 2010; 56:267-271.
- 8. **Ding L, Yokota A.** Proposals of *Curvibacter gracilis* gen. nov., sp. nov. and *Herbaspirillum putei* sp. nov. for bacterial strains isolated from well water and reclassification of [Pseudomonas] huttiensis, [Pseudomonas] lanceolata, [Aquaspirillum] delicatum and [Aquaspirillum] autotrophicum as Herbaspirillum huttiense comb. nov., Curvibacter lanceolatus comb. nov., Curvibacter delicatus comb. nov. and Herbaspirillum autotrophicum comb. nov. Int J Syst Evol Microbiol 2004; 54:2223-2230.
- 9. **Dongmei L, Yifei ZH, Guomei F, Dingzhong S, Xingjiao ZH, et al.** IPGA: a handy integrated prokaryotes genome and pan-genome analysis web service. iMeta 2022; 1:e55.

Supplementary information about the genomic annotation

The annotated genes from the genome of strain H3Y2-7^T involving in metabolizaton of carbohydrates, amino acids, and aromatic compounds and resistance to antibiotics and heavy metals.

| Category | Subcategory | Subsystem | Annotated genes and its roles |
|---------------|---------------------------------|---|--|
| Carbohydrates | Central carbohydrate metabolism | Pentose phosphate pathway | Glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49) |
| Carbohydrates | Central carbohydrate metabolism | Pentose phosphate pathway | Transketolase, C-terminal section (EC 2.2.1.1) |
| Carbohydrates | Central carbohydrate metabolism | Pentose phosphate pathway | Xylulose-5-phosphate phosphoketolase (EC 4.1.2.9) |
| Carbohydrates | Central carbohydrate metabolism | Pentose phosphate pathway | Fructose-6-phosphate phosphoketolase (EC 4.1.2.22) |
| Carbohydrates | Central carbohydrate metabolism | Pentose phosphate pathway | 6-phosphogluconolactonase (EC 3.1.1.31), eukaryotic type |
| Carbohydrates | Central carbohydrate metabolism | Pentose phosphate pathway | Ribulose-phosphate 3-epimerase (EC 5.1.3.1) |
| Carbohydrates | Central carbohydrate metabolism | Pentose phosphate pathway | Transaldolase (EC 2.2.1.2) |
| Carbohydrates | Central carbohydrate metabolism | Pentose phosphate pathway | Transketolase (EC 2.2.1.1) |
| Carbohydrates | Central carbohydrate metabolism | Pentose phosphate pathway | 6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44) |
| Carbohydrates | Central carbohydrate metabolism | Pentose phosphate pathway | Ribose-phosphate pyrophosphokinase (EC 2.7.6.1) |
| Carbohydrates | Central carbohydrate metabolism | Pentose phosphate pathway | Transketolase, N-terminal section (EC 2.2.1.1) |
| Carbohydrates | Central carbohydrate metabolism | Dihydroxyacetone kinases | DHA-specific phosphocarrier protein HPr |
| Carbohydrates | Central carbohydrate metabolism | Dihydroxyacetone kinases | Putative dihydroxyacetone kinase (EC 2.7.1.29), ADP-binding subunit |
| Carbohydrates | Central carbohydrate metabolism | Dihydroxyacetone kinases | DHA-specific IIA component |
| Carbohydrates | Central carbohydrate metabolism | Dihydroxyacetone kinases | Phosphoenolpyruvate-dihydroxyacetone phosphotransferase (EC 2.7.1.121), subunit DhaM |
| Carbohydrates | Central carbohydrate metabolism | Dihydroxyacetone kinases | Phosphoenolpyruvate-dihydroxyacetone phosphotransferase (EC 2.7.1.121), ADP-binding subunit DhaL |
| Carbohydrates | Central carbohydrate metabolism | Dihydroxyacetone kinases | Dihydroxyacetone kinase, ATP-dependent (EC 2.7.1.29) |
| , | ř | , , | Phosphoenolpyruvate-dihydroxyacetone phosphotransferase (EC 2.7.1.121), dihydroxyacetone |
| Carbohydrates | Central carbohydrate metabolism | Dihydroxyacetone kinases | binding subunit DhaK |
| Carbohydrates | Central carbohydrate metabolism | Pyruvate Alanine Serine Interconversions | L-serine dehydratase, beta subunit (EC 4.3.1.17) |
| Carbohydrates | Central carbohydrate metabolism | Pyruvate Alanine Serine Interconversions | Alanine dehydrogenase (EC 1.4.1.1) |
| Carbohydrates | Central carbohydrate metabolism | Pyruvate Alanine Serine Interconversions | Alanine racemase (EC 5.1.1.1) |
| Carbohydrates | Central carbohydrate metabolism | Pyruvate Alanine Serine Interconversions | L-serine dehydratase, alpha subunit (EC 4.3.1.17) |
| Carbohydrates | Central carbohydrate metabolism | Pyruvate Alanine Serine Interconversions | D-serine/D-alanine/glycine transporter |
| Carbohydrates | Central carbohydrate metabolism | Pyruvate Alanine Serine Interconversions | Branched-chain amino acid aminotransferase (EC 2.6.1.42) |
| Carbohydrates | Central carbohydrate metabolism | Pyruvate metabolism I: anaplerotic reactions, PEP | Phosphoenolpyruvate carboxykinase [GTP] (EC 4.1.1.32) |
| Carbohydrates | Central carbohydrate metabolism | Pyruvate metabolism I: anaplerotic reactions, PEP | Phosphoenolpyruvate carboxylase (EC 4.1.1.31) |
| Carbohydrates | Central carbohydrate metabolism | Pyruvate metabolism I: anaplerotic reactions, PEP | Phosphoenolpyruvate synthase (EC 2.7.9.2) |
| Carbohydrates | Central carbohydrate metabolism | Pyruvate metabolism I: anaplerotic reactions, PEP | NADP-dependent malic enzyme (EC 1.1.1.40) |
| Carbohydrates | Central carbohydrate metabolism | Pyruvate metabolism I: anaplerotic reactions, PEP | Pyruvate kinase (EC 2.7.1.40) |
| Carbohydrates | Central carbohydrate metabolism | Pyruvate metabolism I: anaplerotic reactions, PEP | NAD-dependent malic enzyme (EC 1.1.1.38) |
| Carbohydrates | Central carbohydrate metabolism | Glyoxylate bypass | Citrate synthase (si) (EC 2.3.3.1) |
| Carbohydrates | Central carbohydrate metabolism | Glyoxylate bypass | Isocitrate lyase (EC 4.1.3.1) |
| Carbohydrates | Central carbohydrate metabolism | Glyoxylate bypass | Malate synthase (EC 2.3.3.9) |
| Carbohydrates | Central carbohydrate metabolism | Glyoxylate bypass | Aconitate hydratase (EC 4.2.1.3) |
| Carbohydrates | Central carbohydrate metabolism | Dehydrogenase complexes | Branched-chain alpha-keto acid dehydrogenase, E1 component, beta subunit (EC 1.2.4.4) |
| Carbohydrates | Central carbohydrate metabolism | Dehydrogenase complexes | 2-oxoglutarate dehydrogenase E1 component (EC 1.2.4.2) |
| Carbohydrates | Central carbohydrate metabolism | Dehydrogenase complexes | Pyruvate dehydrogenase E1 component (EC 1.2.4.1) |
| Carbohydrates | Central carbohydrate metabolism | Dehydrogenase complexes | Cytosol aminopeptidase PepA (EC 3.4.11.1) |
| | | | |

| | | | Dihydrolipoamide succinyltransferase component (E2) of 2-oxoglutarate dehydrogenase complex |
|---------------|---------------------------------|--|---|
| Carbohydrates | Central carbohydrate metabolism | Dehydrogenase complexes | (EC 2.3.1.61) |
| Carbohydrates | Central carbohydrate metabolism | Dehydrogenase complexes | Branched-chain alpha-keto acid dehydrogenase, E1 component, alpha subunit (EC 1.2.4.4) |
| Carbohydrates | Central carbohydrate metabolism | Dehydrogenase complexes | Dihydrolipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex (EC 2.3.1.168) |
| Carbohydrates | Central carbohydrate metabolism | Dehydrogenase complexes | Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase complex (EC 2.3.1.12) |
| Carbohydrates | Central carbohydrate metabolism | Glycolate, glyoxylate interconversions | Glycolate dehydrogenase (EC 1.1.99.14), subunit GlcD |
| Carbohydrates | Central carbohydrate metabolism | Glycolate, glyoxylate interconversions | Phosphoglycolate phosphatase (EC 3.1.3.18) |
| Carbohydrates | Central carbohydrate metabolism | Glycolysis and Gluconeogenesis | Glucose-6-phosphate isomerase (EC 5.3.1.9) |
| Carbohydrates | Central carbohydrate metabolism | Glycolysis and Gluconeogenesis | Fructose-1,6-bisphosphatase, GlpX type (EC 3.1.3.11) |
| Carbohydrates | Central carbohydrate metabolism | Glycolysis and Gluconeogenesis | Fructose-bisphosphate aldolase class II (EC 4.1.2.13) |
| Carbohydrates | Central carbohydrate metabolism | Glycolysis and Gluconeogenesis | Phosphoenolpyruvate synthase (EC 2.7.9.2) |
| Carbohydrates | Central carbohydrate metabolism | Glycolysis and Gluconeogenesis | Putative phosphoenolpyruvate synthase/pyruvate phosphate dikinase, N-terminal domain |
| Carbohydrates | Central carbohydrate metabolism | Glycolysis and Gluconeogenesis | Glucokinase (EC 2.7.1.2) |
| Carbohydrates | Central carbohydrate metabolism | Glycolysis and Gluconeogenesis | Phosphoglycerate kinase (EC 2.7.2.3) |
| Carbohydrates | Central carbohydrate metabolism | Glycolysis and Gluconeogenesis | Enolase (EC 4.2.1.11) |
| Carbohydrates | Central carbohydrate metabolism | Glycolysis and Gluconeogenesis | Pyruvate kinase (EC 2.7.1.40) |
| Carbohydrates | Central carbohydrate metabolism | Glycolysis and Gluconeogenesis | Putative phosphoenolpyruvate synthase/pyruvate phosphate dikinase, C-terminal domain |
| Carbohydrates | Central carbohydrate metabolism | Glycolysis and Gluconeogenesis | NAD-dependent glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) |
| Carbohydrates | Central carbohydrate metabolism | Glycolysis and Gluconeogenesis | 6-phosphofructokinase (EC 2.7.1.11) |
| Carbohydrates | Central carbohydrate metabolism | Glycolysis and Gluconeogenesis | Triosephosphate isomerase (EC 5.3.1.1) |
| Carbohydrates | Central carbohydrate metabolism | Glycolysis and Gluconeogenesis | Phosphoglycerate mutase (EC 5.4.2.1) |
| Carbohydrates | Central carbohydrate metabolism | Glycolysis and Gluconeogenesis | Polyphosphate glucokinase (EC 2.7.1.63) |
| Carbohydrates | Central carbohydrate metabolism | Entner-Doudoroff Pathway | Pyruvate kinase (EC 2.7.1.40) |
| Carbohydrates | Central carbohydrate metabolism | Entner-Doudoroff Pathway | Phosphoglycerate kinase (EC 2.7.2.3) |
| Carbohydrates | Central carbohydrate metabolism | Entner-Doudoroff Pathway | Enolase (EC 4.2.1.11) |
| Carbohydrates | Central carbohydrate metabolism | Entner-Doudoroff Pathway | Glucokinase (EC 2.7.1.2) |
| Carbohydrates | Central carbohydrate metabolism | Entner-Doudoroff Pathway | Gluconokinase (EC 2.7.1.12) |
| Carbohydrates | Central carbohydrate metabolism | Entner-Doudoroff Pathway | 6-phosphogluconolactonase (EC 3.1.1.31), eukaryotic type |
| Carbohydrates | Central carbohydrate metabolism | Entner-Doudoroff Pathway | OpcA, an allosteric effector of glucose-6-phosphate dehydrogenase, actinobacterial |
| Carbohydrates | Central carbohydrate metabolism | Entner-Doudoroff Pathway | Glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49) |
| Carbohydrates | Central carbohydrate metabolism | Entner-Doudoroff Pathway | Glucose 1-dehydrogenase (EC 1.1.1.47) |
| Carbohydrates | Central carbohydrate metabolism | Entner-Doudoroff Pathway | Polyphosphate glucokinase (EC 2.7.1.63) |
| Carbohydrates | Central carbohydrate metabolism | Entner-Doudoroff Pathway | Gluconate dehydratase (EC 4.2.1.39) |
| Carbohydrates | Central carbohydrate metabolism | Entner-Doudoroff Pathway | Phosphoglycerate mutase (EC 5.4.2.1) |
| Carbohydrates | Central carbohydrate metabolism | Entner-Doudoroff Pathway | 2-dehydro-3-deoxyphosphogluconate aldolase (EC 4.1.2.14) |
| Carbohydrates | Central carbohydrate metabolism | Entner-Doudoroff Pathway | NAD-dependent glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) |
| • | • | Pyruvate metabolism II: acetyl-CoA, acetogenesis from | Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase complex (EC |
| Carbohydrates | Central carbohydrate metabolism | pyruvate | 2.3.1.12) |
| Carbohydrates | Central carbohydrate metabolism | Pyruvate metabolism II: acetyl-CoA, acetogenesis from pyruvate | Aldehyde dehydrogenase (EC 1.2.1.3) |
| | | | |

| Carbohydrates | Central carbohydrate metabolism | Pyruvate metabolism II: acetyl-CoA, acetogenesis from pyruvate | Acetate kinase (EC 2.7.2.1) |
|---------------|---------------------------------|--|---|
| Carbohydrates | Central carbohydrate metabolism | Pyruvate metabolism II: acetyl-CoA, acetogenesis from pyruvate | Pyruvate dehydrogenase E1 component (EC 1.2.4.1) |
| Carbohydrates | Central carbohydrate metabolism | Pyruvate metabolism II: acetyl-CoA, acetogenesis from pyruvate | Dihydrolipoamide dehydrogenase of pyruvate dehydrogenase complex (EC 1.8.1.4) |
| Carbohydrates | Central carbohydrate metabolism | Pyruvate metabolism II: acetyl-CoA, acetogenesis from pyruvate | NAD-dependent protein deacetylase of SIR2 family |
| Carbohydrates | Central carbohydrate metabolism | Pyruvate metabolism II: acetyl-CoA, acetogenesis from pyruvate | Acetyl-CoA synthetase (ADP-forming) alpha and beta chains, putative |
| Carbohydrates | Central carbohydrate metabolism | Pyruvate metabolism II: acetyl-CoA, acetogenesis from pyruvate | Phosphate acetyltransferase (EC 2.3.1.8) |
| Carbohydrates | Central carbohydrate metabolism | TCA Cycle | Succinyl-CoA ligase [ADP-forming] alpha chain (EC 6.2.1.5) |
| Carbohydrates | Central carbohydrate metabolism | TCA Cycle | Fumarate hydratase class II (EC 4.2.1.2) |
| Carbohydrates | Central carbohydrate metabolism | TCA Cycle | Aconitate hydratase (EC 4.2.1.3) |
| 6 1 1 1 1 | | TOLO | Dihydrolipoamide succinyltransferase component (E2) of 2-oxoglutarate dehydrogenase complex |
| Carbohydrates | Central carbohydrate metabolism | TCA Cycle | (EC 2.3.1.61) |
| Carbohydrates | Central carbohydrate metabolism | TCA Cycle | Citrate synthase (si) (EC 2.3.3.1) |
| Carbohydrates | Central carbohydrate metabolism | TCA Cycle | Isocitrate dehydrogenase [NADP] (EC 1.1.1.42) |
| Carbohydrates | Central carbohydrate metabolism | TCA Cycle | Succinyl-CoA ligase [ADP-forming] beta chain (EC 6.2.1.5) |
| Carbohydrates | Central carbohydrate metabolism | TCA Cycle | Malate:quinone oxidoreductase (EC 1.1.5.4) |
| Carbohydrates | Central carbohydrate metabolism | TCA Cycle | Dihydrolipoamide dehydrogenase of pyruvate dehydrogenase complex (EC 1.8.1.4) |
| Carbohydrates | Central carbohydrate metabolism | TCA Cycle | 2-oxoglutarate dehydrogenase E1 component (EC 1.2.4.2) |
| Carbohydrates | Monosaccharides | D-galactarate, D-glucarate and D-glycerate catabolism - gjo | 2-hydroxy-3-oxopropionate reductase (EC 1.1.1.60) |
| Carbohydrates | Monosaccharides | D-galactarate, D-glucarate and D-glycerate catabolism - gjo | Predicted D-glucarate or D-galactorate regulator, GntR family |
| Carbohydrates | Monosaccharides | D-galactarate, D-glucarate and D-glycerate catabolism - gjo | Glycerate kinase (EC 2.7.1.31) |
| Carbohydrates | Monosaccharides | D-galactarate, D-glucarate and D-glycerate catabolism - gjo | 5-dehydro-4-deoxyglucarate dehydratase (EC 4.2.1.41) |
| Carbohydrates | Monosaccharides | D-galactarate, D-glucarate and D-glycerate catabolism - gjo | Glucarate dehydratase (EC 4.2.1.40) |
| Carbohydrates | Monosaccharides | D-Galacturonate and D-Glucuronate Utilization | Uronate isomerase (EC 5.3.1.12) |
| Carbohydrates | Monosaccharides | D-Galacturonate and D-Glucuronate Utilization | D-mannonate oxidoreductase (EC 1.1.1.57) |
| Carbohydrates | Monosaccharides | D-Galacturonate and D-Glucuronate Utilization | Glucuronide transporter UidB |
| Carbohydrates | Monosaccharides | D-Galacturonate and D-Glucuronate Utilization | 5-dehydro-4-deoxyglucarate dehydratase (EC 4.2.1.41) |
| Carbohydrates | Monosaccharides | D-Galacturonate and D-Glucuronate Utilization | Mannonate dehydratase (EC 4.2.1.8) |
| Carbohydrates | Monosaccharides | D-Galacturonate and D-Glucuronate Utilization | Alpha-glucosidase (EC 3.2.1.20) |
| Carbohydrates | Monosaccharides | D-Galacturonate and D-Glucuronate Utilization | 2-dehydro-3-deoxyphosphogluconate aldolase (EC 4.1.2.14) |
| Carbohydrates | Monosaccharides | Mannose Metabolism | Phosphomannomutase (EC 5.4.2.8) |
| Carbohydrates | Monosaccharides | Mannose Metabolism | Mannose-6-phosphate isomerase (EC 5.3.1.8) |
| Carbohydrates | Monosaccharides | D-gluconate and ketogluconates metabolism | Gluconokinase (EC 2.7.1.12) |
| | | | |

| Controlondon | Managadagidaa | Delegants and leater becomes mostly lines | 5 bets Disharat 5 m herter (EC 1.1.1.60) |
|--------------------------------|------------------------------------|--|--|
| Carbohydrates | Monosaccharides Monosaccharides | D-gluconate and ketogluconates metabolism | 5-keto-D-gluconate 5-reductase (EC 1.1.1.69) |
| Carbohydrates Carbohydrates | Monosaccharides | D-gluconate and ketogluconates metabolism D-gluconate and ketogluconates metabolism | Gluconate dehydratase (EC 4.2.1.39) L-idonate 5-dehydrogenase (EC 1.1.1.264) |
| Carbonydrates Carbohydrates | | D-gluconate and ketogluconates metabolism D-gluconate and ketogluconates metabolism | , , , |
| • | Monosaccharides | | 6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44) |
| Carbohydrates | Monosaccharides Monosaccharides | D-gluconate and ketogluconates metabolism | Glucose 1-dehydrogenase (EC 1.1.1.47) |
| Carbohydrates | | D-gluconate and ketogluconates metabolism | Low-affinity gluconate/H+ symporter GntU |
| Carbohydrates | Monosaccharides | D-gluconate and ketogluconates metabolism | Gluconate transporter family protein |
| Carbohydrates | Monosaccharides | Deoxyribose and Deoxynucleoside Catabolism | Deoxyribose-phosphate aldolase (EC 4.1.2.4) |
| Carbohydrates | Monosaccharides | Deoxyribose and Deoxynucleoside Catabolism | Purine nucleoside phosphorylase (EC 2.4.2.1) |
| Carbohydrates | Monosaccharides | Deoxyribose and Deoxynucleoside Catabolism | Ribokinase (EC 2.7.1.15) |
| Carbohydrates | Monosaccharides | Deoxyribose and Deoxynucleoside Catabolism | Pyrimidine-nucleoside phosphorylase (EC 2.4.2.2) |
| Carbohydrates | Monosaccharides | D-ribose utilization | Ribokinase (EC 2.7.1.15) |
| Carbohydrates | Monosaccharides | D-galactarate, D-glucarate and D-glycerate catabolism | Predicted D-glucarate or D-galactorate regulator, GntR family |
| Carbohydrates | Monosaccharides | D-galactarate, D-glucarate and D-glycerate catabolism | 2-hydroxy-3-oxopropionate reductase (EC 1.1.1.60) |
| Carbohydrates | Monosaccharides | D-galactarate, D-glucarate and D-glycerate catabolism | Glucarate dehydratase (EC 4.2.1.40) |
| Carbohydrates | Monosaccharides | D-galactarate, D-glucarate and D-glycerate catabolism | Glycerate kinase (EC 2.7.1.31) |
| Carbohydrates | Monosaccharides | D-galactarate, D-glucarate and D-glycerate catabolism | 5-dehydro-4-deoxyglucarate dehydratase (EC 4.2.1.41) |
| Carbohydrates | Monosaccharides | Fructose utilization | 1-phosphofructokinase (EC 2.7.1.56) |
| Carbohydrates | Monosaccharides | Fructose utilization | Phosphotransferase system, phosphocarrier protein HPr |
| Carbohydrates | Monosaccharides | Fructose utilization | Transcriptional repressor of the fructose operon, DeoR family |
| Carbohydrates | Monosaccharides | Fructose utilization | Fructokinase (EC 2.7.1.4) |
| Carbohydrates | Monosaccharides | Fructose utilization | Phosphoenolpyruvate-protein phosphotransferase of PTS system (EC 2.7.3.9) |
| Carbohydrates | Monosaccharides | Fructose utilization | Transaldolase (EC 2.2.1.2) |
| Carbohydrates | Di- and oligosaccharides | Maltose and Maltodextrin Utilization | Neopullulanase (EC 3.2.1.135) |
| Carbohydrates | Di- and oligosaccharides | Maltose and Maltodextrin Utilization | Beta-phosphoglucomutase (EC 5.4.2.6) |
| Carbohydrates | Di- and oligosaccharides | Maltose and Maltodextrin Utilization | Maltose phosphorylase (EC 2.4.1.8) |
| Carbohydrates | Di- and oligosaccharides | Maltose and Maltodextrin Utilization | Alpha-amylase (EC 3.2.1.1) |
| Carbohydrates | Di- and oligosaccharides | Maltose and Maltodextrin Utilization | Malto-oligosyltrehalose synthase (EC 5.4.99.15) |
| Carbohydrates | Di- and oligosaccharides | Maltose and Maltodextrin Utilization | 4-alpha-glucanotransferase (amylomaltase) (EC 2.4.1.25) |
| Carbohydrates | Di- and oligosaccharides | Maltose and Maltodextrin Utilization | Glycogen phosphorylase (EC 2.4.1.1) |
| Carbohydrates | Di- and oligosaccharides | Maltose and Maltodextrin Utilization | Alpha-glucosidase (EC 3.2.1.20) |
| Carbohydrates | Di- and oligosaccharides | Maltose and Maltodextrin Utilization | Glucoamylase (EC 3.2.1.3) |
| Carbohydrates | Di- and oligosaccharides | Trehalose Uptake and Utilization | Trehalose phosphorylase (EC 2.4.1.64) |
| Carbohydrates | Di- and oligosaccharides | Trehalose Uptake and Utilization | Glucose/mannose:H+ symporter GlcP |
| Carbohydrates | Di- and oligosaccharides | Trehalose Uptake and Utilization | Beta-phosphoglucomutase (EC 5.4.2.6) |
| Carbohydrates | Di- and oligosaccharides | Trehalose Biosynthesis | Alpha-amylase (EC 3.2.1.1) |
| Carbohydrates | Di- and oligosaccharides | Trehalose Biosynthesis | Malto-oligosyltrehalose synthase (EC 5.4.99.15) |
| Carbohydrates | Di- and oligosaccharides | Trehalose Biosynthesis | 1,4-alpha-glucan (glycogen) branching enzyme, GH-13-type (EC 2.4.1.18) |
| Carbohydrates | Di- and oligosaccharides | Trehalose Biosynthesis | Trehalose synthase (EC 5.4.99.16) |
| Carbohydrates | Di- and oligosaccharides | Trehalose Biosynthesis | Putative glucanase glgE (EC 3.2.1) |
| Carbohydrates | Di- and oligosaccharides | Trehalose Biosynthesis | Glucoamylase (EC 3.2.1.3) |
| Carbohydrates | Di- and oligosaccharides | Trehalose Biosynthesis | Trehalose-6-phosphate phosphatase (EC 3.1.3.12) |
| Carbohydrates | Di- and oligosaccharides | Trehalose Biosynthesis | Trehalose phosphorylase (EC 2.4.1.64) |
| | | | |

| Carbohydrates | Di- and oligosaccharides | Trehalose Biosynthesis | Malto-oligosyltrehalose trehalohydrolase (EC 3.2.1.141) |
|-----------------|------------------------------|--|---|
| Carbohydrates | Di- and oligosaccharides | Lactose and Galactose Uptake and Utilization | UDP-glucose 4-epimerase (EC 5.1.3.2) |
| Carbohydrates | Di- and oligosaccharides | Lactose and Galactose Uptake and Utilization | Galactokinase (EC 2.7.1.6) |
| Carbohydrates | Di- and oligosaccharides | Lactose and Galactose Uptake and Utilization | Galactose-1-phosphate uridylyltransferase (EC 2.7.7.10) |
| Carbohydrates | Aminosugars | Chitin and N-acetylglucosamine utilization | Predicted transcriptional regulator of N-Acetylglucosamine utilization, GntR family |
| Carbohydrates | Aminosugars | Chitin and N-acetylglucosamine utilization | N-acetylglucosamine-6-phosphate deacetylase (EC 3.5.1.25) |
| Carbohydrates | Aminosugars | Chitin and N-acetylglucosamine utilization | N-acetylglucosamine kinase of eukaryotic type (EC 2.7.1.59) |
| Carbohydrates | Aminosugars | Chitin and N-acetylglucosamine utilization | Chitinase (EC 3.2.1.14) |
| Carbohydrates | Aminosugars | Chitin and N-acetylglucosamine utilization | Glucosamine-6-phosphate deaminase (EC 3.5.99.6) |
| Carbohydrates | Polysaccharides | Glycogen metabolism | 4-alpha-glucanotransferase (amylomaltase) (EC 2.4.1.25) |
| Carbohydrates | Polysaccharides | Glycogen metabolism | Glycogen phosphorylase (EC 2.4.1.1) |
| Carbohydrates | Polysaccharides | Glycogen metabolism | Glucose-1-phosphate adenylyltransferase (EC 2.7.7.27) |
| Carbohydrates | Polysaccharides | Glycogen metabolism | Predicted glycogen synthase, ADP-glucose transglucosylase (EC 2.4.1.21), Actinobacterial type |
| Carbohydrates | Polysaccharides | Glycogen metabolism | 1,4-alpha-glucan (glycogen) branching enzyme, GH-13-type (EC 2.4.1.18) |
| Carbohydrates | Organic acids | Glycerate metabolism | 2-hydroxy-3-oxopropionate reductase (EC 1.1.1.60) |
| Carbohydrates | Organic acids | Glycerate metabolism | Hydroxypyruvate isomerase (EC 5.3.1.22) |
| Carbohydrates | Organic acids | Glycerate metabolism | Pyruvate kinase (EC 2.7.1.40) |
| Carbohydrates | Organic acids | Glycerate metabolism | Glyoxylate carboligase (EC 4.1.1.47) |
| Carbohydrates | Organic acids | Glycerate metabolism | Glycerate kinase (EC 2.7.1.31) |
| Carbohydrates | Organic acids | Propionate-CoA to Succinate Module | 2-methylcitrate dehydratase (EC 4.2.1.79) |
| Carbohydrates | Organic acids | Propionate-CoA to Succinate Module | 2-methylaconitate isomerase |
| Carbohydrates | Organic acids | Propionate-CoA to Succinate Module | Methylisocitrate lyase (EC 4.1.3.30) |
| Carbohydrates | Organic acids | Propionate-CoA to Succinate Module | 2-methylisocitrate dehydratase (EC 4.2.1.99) |
| Carbohydrates | Organic acids | Propionate-CoA to Succinate Module | Aconitate hydratase (EC 4.2.1.3) |
| Carbohydrates | Organic acids | Propionate-CoA to Succinate Module | 2-methylcitrate synthase (EC 2.3.3.5) |
| Carbohydrates | Organic acids | Lactate utilization | Predicted L-lactate dehydrogenase, Iron-sulfur cluster-binding subunit YkgF |
| Carbohydrates | Organic acids | Lactate utilization | L-lactate permease |
| Carbohydrates | Organic acids | Lactate utilization | Predicted L-lactate dehydrogenase, hypothetical protein subunit YkgG |
| Carbohydrates | Organic acids | Lactate utilization | Lactate-responsive regulator LldR in Actinobacteria, GntR family |
| Carbohydrates | Organic acids | Lactate utilization | Predicted D-lactate dehydrogenase, Fe-S protein, FAD/FMN-containing |
| Carbohydrates | Organic acids | Lactate utilization | Predicted L-lactate dehydrogenase, Fe-S oxidoreductase subunit YkgE |
| Carbohydrates | Organic acids | Methylcitrate cycle | 2-methylcitrate synthase (EC 2.3.3.5) |
| Carbohydrates | Organic acids | Methylcitrate cycle | 2-methylisocitrate dehydratase (EC 4.2.1.99) |
| Carbohydrates | Organic acids | Methylcitrate cycle | Methylisocitrate lyase (EC 4.1.3.30) |
| Carbohydrates | Organic acids | Methylcitrate cycle | 2-methylaconitate isomerase |
| Carbohydrates | Organic acids | Methylcitrate cycle | 2-methylcitrate dehydratase (EC 4.2.1.79) |
| Amino Acids and | | Al 1 11 di 1 | D 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 |
| Derivatives | Alanine, serine, and glycine | Alanine biosynthesis | Branched-chain amino acid aminotransferase (EC 2.6.1.42) |
| Amino Acids and | | Al Colombia | O (1 15 (FO2017) |
| Derivatives | Alanine, serine, and glycine | Alanine biosynthesis | Cysteine desulfurase (EC 2.8.1.7) |
| Amino Acids and | Alanina and a data | Alexino Lierando eia | Alwin manner (FC 5 1 1 1) |
| Derivatives | Alanine, serine, and glycine | Alanine biosynthesis | Alanine racemase (EC 5.1.1.1) |
| | | | |

| Amino Acids and Derivatives | Alanine, serine, and glycine | Alanine biosynthesis | Ferredoxin, 2Fe-2S |
|--------------------------------|------------------------------|--------------------------------|--|
| Amino Acids and Derivatives | Alanine, serine, and glycine | Serine Biosynthesis | Phosphoserine aminotransferase (EC 2.6.1.52) |
| Amino Acids and Derivatives | Alanine, serine, and glycine | Serine Biosynthesis | Serine hydroxymethyltransferase (EC 2.1.2.1) |
| Amino Acids and Derivatives | Alanine, serine, and glycine | Serine Biosynthesis | Phosphoserine phosphatase (EC 3.1.3.3) |
| Amino Acids and Derivatives | Alanine, serine, and glycine | Serine Biosynthesis | D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95) |
| Amino Acids and Derivatives | Alanine, serine, and glycine | Glycine cleavage system | Glycine dehydrogenase [decarboxylating] (glycine cleavage system P protein) (EC 1.4.4.2) |
| Amino Acids and Derivatives | Alanine, serine, and glycine | Glycine cleavage system | Glycine cleavage system H protein |
| Amino Acids and Derivatives | Alanine, serine, and glycine | Glycine cleavage system | Aminomethyltransferase (glycine cleavage system T protein) (EC 2.1.2.10) |
| Amino Acids and Derivatives | Alanine, serine, and glycine | Glycine and Serine Utilization | Serine hydroxymethyltransferase (EC 2.1.2.1) |
| Amino Acids and Derivatives | Alanine, serine, and glycine | Glycine and Serine Utilization | L-serine dehydratase, alpha subunit (EC 4.3.1.17) |
| Amino Acids and Derivatives | Alanine, serine, and glycine | Glycine and Serine Utilization | Phosphoserine phosphatase (EC 3.1.3.3) |
| Amino Acids and Derivatives | Alanine, serine, and glycine | Glycine and Serine Utilization | Aminomethyltransferase (glycine cleavage system T protein) (EC 2.1.2.10) |
| Amino Acids and Derivatives | Alanine, serine, and glycine | Glycine and Serine Utilization | Phosphoserine aminotransferase (EC 2.6.1.52) |
| Amino Acids and Derivatives | Alanine, serine, and glycine | Glycine and Serine Utilization | Seryl-tRNA synthetase (EC 6.1.1.11) |
| Amino Acids and Derivatives | Alanine, serine, and glycine | Glycine and Serine Utilization | Glycine cleavage system H protein |
| Amino Acids and Derivatives | Alanine, serine, and glycine | Glycine and Serine Utilization | Cystathionine beta-synthase (EC 4.2.1.22) |
| Amino Acids and Derivatives | Alanine, serine, and glycine | Glycine and Serine Utilization | D-serine/D-alanine/glycine transporter |
| Amino Acids and Derivatives | Alanine, serine, and glycine | Glycine and Serine Utilization | Cystathionine gamma-lyase (EC 4.4.1.1) |
| Amino Acids and | Alanine, serine, and glycine | Glycine and Serine Utilization | L-serine dehydratase, beta subunit (EC 4.3.1.17) |
| Derivatives Amino Acids and | Alanine, serine, and glycine | Glycine and Serine Utilization | 2-amino-3-ketobutyrate coenzyme A ligase (EC 2.3.1.29) |
| Derivatives Amino Acids and | Alanine, serine, and glycine | Glycine and Serine Utilization | Glycerate kinase (EC 2.7.1.31) |
| Derivatives | | • | • |

| Amino Acids and Derivatives | Alanine, serine, and glycine | Glycine and Serine Utilization | L-serine dehydratase, (PLP)-dependent (EC 4.3.1.17) |
|--------------------------------|----------------------------------|--------------------------------|--|
| Amino Acids and Derivatives | Alanine, serine, and glycine | Glycine and Serine Utilization | D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95) |
| Amino Acids and Derivatives | Alanine, serine, and glycine | Glycine and Serine Utilization | Threonine dehydratase, catabolic (EC 4.3.1.19) |
| Amino Acids and Derivatives | Alanine, serine, and glycine | Glycine and Serine Utilization | Glycine dehydrogenase [decarboxylating] (glycine cleavage system P protein) (EC 1.4.4.2) |
| Amino Acids and Derivatives | Alanine, serine, and glycine | Glycine Biosynthesis | L-threonine 3-dehydrogenase (EC 1.1.1.103) |
| Amino Acids and Derivatives | Alanine, serine, and glycine | Glycine Biosynthesis | 2-amino-3-ketobutyrate coenzyme A ligase (EC 2.3.1.29) |
| Amino Acids and Derivatives | Alanine, serine, and glycine | Glycine Biosynthesis | Serine hydroxymethyltransferase (EC 2.1.2.1) |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Urease subunits | Urease accessory protein UreE |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Urease subunits | Urease accessory protein UreF |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Urease subunits | Urease beta subunit (EC 3.5.1.5) |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Urease subunits | Urease alpha subunit (EC 3.5.1.5) |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Urease subunits | Urease gamma subunit (EC 3.5.1.5) |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Urease subunits | Urease accessory protein UreG |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Urease subunits | Urease accessory protein UreD |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Arginine Deiminase Pathway | Arginine pathway regulatory protein ArgR, repressor of arg regulon |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Arginine Deiminase Pathway | Arginine/ornithine antiporter ArcD |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Arginine Deiminase Pathway | Ornithine carbamoyltransferase (EC 2.1.3.3) |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Urea decomposition | Urease gamma subunit (EC 3.5.1.5) |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Urea decomposition | Urease accessory protein UreG |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Urea decomposition | Urea carboxylase-related amino acid permease |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Urea decomposition | Urease accessory protein UreE |

| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Urea decomposition | Urease accessory protein UreF |
|--------------------------------|----------------------------------|------------------------------------|--|
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Urea decomposition | Urease beta subunit (EC 3.5.1.5) |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Urea decomposition | Urease alpha subunit (EC 3.5.1.5) |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Urea decomposition | Urease accessory protein UreD |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Arginine and Ornithine Degradation | Delta-1-pyrroline-5-carboxylate dehydrogenase (EC 1.2.1.88) |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Arginine and Ornithine Degradation | NADP-specific glutamate dehydrogenase (EC 1.4.1.4) |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Arginine and Ornithine Degradation | Ornithine cyclodeaminase (EC 4.3.1.12) |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Arginine and Ornithine Degradation | Arginine pathway regulatory protein ArgR, repressor of arg regulon |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Arginine and Ornithine Degradation | Arginine/ornithine antiporter ArcD |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Arginine and Ornithine Degradation | Ornithine carbamoyltransferase (EC 2.1.3.3) |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Polyamine Metabolism | Spermidine synthase (EC 2.5.1.16) |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Polyamine Metabolism | Arginine/ornithine antiporter ArcD |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Polyamine Metabolism | 4-aminobutyraldehyde dehydrogenase (EC 1.2.1.19) |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Putrescine utilization pathways | 4-aminobutyraldehyde dehydrogenase (EC 1.2.1.19) |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Putrescine utilization pathways | Gamma-aminobutyrate:alpha-ketoglutarate aminotransferase (EC 2.6.1.19) |
| Amino Acids and Derivatives | Branched-chain amino acids | Valine degradation | 3-hydroxyisobutyrate dehydrogenase (EC 1.1.1.31) |
| Amino Acids and Derivatives | Branched-chain amino acids | Valine degradation | Branched-chain alpha-keto acid dehydrogenase, E1 component, beta subunit (EC 1.2.4.4) |
| Amino Acids and Derivatives | Branched-chain amino acids | Valine degradation | Enoyl-CoA hydratase (EC 4.2.1.17) |
| Amino Acids and Derivatives | Branched-chain amino acids | Valine degradation | Branched-chain alpha-keto acid dehydrogenase, E1 component, alpha subunit (EC 1.2.4.4) |
| Amino Acids and Derivatives | Branched-chain amino acids | Valine degradation | Methylmalonate-semialdehyde dehydrogenase (EC 1.2.1.27) |
| Amino Acids and Derivatives | Branched-chain amino acids | Valine degradation | Branched-chain amino acid aminotransferase (EC 2.6.1.42) |

| Amino Acids and Derivatives | Branched-chain amino acids | Valine degradation | Dihydrolipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex (EC 2.3.1.168) |
|--------------------------------|----------------------------|--|--|
| Amino Acids and Derivatives | Branched-chain amino acids | Valine degradation | 3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35) |
| Amino Acids and Derivatives | Branched-chain amino acids | Valine degradation | 3-hydroxyisobutyryl-CoA hydrolase (EC 3.1.2.4) |
| Amino Acids and Derivatives | Branched-chain amino acids | Branched-Chain Amino Acid Biosynthesis | Acetolactate synthase small subunit (EC 2.2.1.6) |
| Amino Acids and Derivatives | Branched-chain amino acids | Branched-Chain Amino Acid Biosynthesis | 3-isopropylmalate dehydrogenase (EC 1.1.1.85) |
| Amino Acids and Derivatives | Branched-chain amino acids | Branched-Chain Amino Acid Biosynthesis | 3-isopropylmalate dehydratase large subunit (EC 4.2.1.33) |
| Amino Acids and Derivatives | Branched-chain amino acids | Branched-Chain Amino Acid Biosynthesis | 3-isopropylmalate dehydratase small subunit (EC 4.2.1.33) |
| Amino Acids and Derivatives | Branched-chain amino acids | Branched-Chain Amino Acid Biosynthesis | Dihydroxy-acid dehydratase (EC 4.2.1.9) |
| Amino Acids and Derivatives | Branched-chain amino acids | Branched-Chain Amino Acid Biosynthesis | Branched-chain amino acid aminotransferase (EC 2.6.1.42) |
| Amino Acids and Derivatives | Branched-chain amino acids | Branched-Chain Amino Acid Biosynthesis | Leucine-responsive regulatory protein, regulator for leucine (or lrp) regulon and high-affinity branched-chain amino acid transport system |
| Amino Acids and Derivatives | Branched-chain amino acids | Branched-Chain Amino Acid Biosynthesis | Acetolactate synthase large subunit (EC 2.2.1.6) |
| Amino Acids and Derivatives | Branched-chain amino acids | Branched-Chain Amino Acid Biosynthesis | Threonine dehydratase, catabolic (EC 4.3.1.19) |
| Amino Acids and Derivatives | Branched-chain amino acids | Branched-Chain Amino Acid Biosynthesis | 2-isopropylmalate synthase (EC 2.3.3.13) |
| Amino Acids and Derivatives | Branched-chain amino acids | Leucine Biosynthesis | 3-isopropylmalate dehydratase large subunit (EC 4.2.1.33) |
| Amino Acids and Derivatives | Branched-chain amino acids | Leucine Biosynthesis | 2-isopropylmalate synthase (EC 2.3.3.13) |
| Amino Acids and Derivatives | Branched-chain amino acids | Leucine Biosynthesis | Branched-chain amino acid aminotransferase (EC 2.6.1.42) |
| Amino Acids and Derivatives | Branched-chain amino acids | Leucine Biosynthesis | 3-isopropylmalate dehydratase small subunit (EC 4.2.1.33) |
| Amino Acids and Derivatives | Branched-chain amino acids | Leucine Biosynthesis | 3-isopropylmalate dehydrogenase (EC 1.1.1.85) |
| Amino Acids and Derivatives | Branched-chain amino acids | Isoleucine degradation | Enoyl-CoA hydratase (EC 4.2.1.17) |
| Amino Acids and Derivatives | Branched-chain amino acids | Isoleucine degradation | Branched-chain alpha-keto acid dehydrogenase, E1 component, beta subunit (EC 1.2.4.4) |
| Amino Acids and Derivatives | Branched-chain amino acids | Isoleucine degradation | Branched-chain alpha-keto acid dehydrogenase, E1 component, alpha subunit (EC 1.2.4.4) |
| | | | |

| Amino Acids and | | | |
|-----------------------------|---|-------------------------------------|--|
| Derivatives | Branched-chain amino acids | Isoleucine degradation | Branched-chain amino acid aminotransferase (EC 2.6.1.42) |
| Amino Acids and | D 111: : :1 | T. I | 21 - 10 4411 (7022110) |
| Derivatives | Branched-chain amino acids | Isoleucine degradation | 3-ketoacyl-CoA thiolase (EC 2.3.1.16) |
| Amino Acids and | Duomahad ahain amina aaida | Tanlaysina daguadatian | Dihydrolipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase |
| Derivatives | Branched-chain amino acids | Isoleucine degradation | complex (EC 2.3.1.168) |
| Amino Acids and | Branched-chain amino acids | Isoleucine degradation | 3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35) |
| Derivatives | Branched-chain amino acids | Isoleucine degradation | 5-nydroxyacyi-CoA denydrogenase (EC 1.1.1.55) |
| Amino Acids and | Amino Acids and Derivatives - no | Creatine and Creatinine Degradation | Creatinase (EC 3.5.3.3) |
| Derivatives | subcategory | Creatine and Creatinine Degradation | Creatinase (EC 3.3.3.3) |
| Amino Acids and | Amino Acids and Derivatives - no | Creatine and Creatinine Degradation | Creatinine amidohydrolase (EC 3.5.2.10) |
| Derivatives | subcategory | Creatine and Creatinine Degradation | Creatinine aimaonyarolase (EC 3.3.2.10) |
| Amino Acids and | Amino Acids and Derivatives - no | Creatine and Creatinine Degradation | Cytosine deaminase (EC 3.5.4.1) |
| Derivatives | subcategory | Creatine and Creatinine Degradation | Cycosine dealiminase (EC 5.5.1.1) |
| Amino Acids and | Lysine, threonine, methionine, and | Methionine Biosynthesis | 5,10-methylenetetrahydrofolate reductase (EC 1.5.1.20) |
| Derivatives | cysteine | Wednomie Biosynthesis | 5,10 monty encountry diolonic reduction (EC 1.5.1.20) |
| Amino Acids and | Lysine, threonine, methionine, and | Methionine Biosynthesis | Cystathionine beta-synthase (EC 4.2.1.22) |
| Derivatives | cysteine | | -y(: ··) |
| Amino Acids and | Lysine, threonine, methionine, and | Methionine Biosynthesis | Homoserine dehydrogenase (EC 1.1.1.3) |
| Derivatives | cysteine | , | |
| Amino Acids and | Lysine, threonine, methionine, and | Methionine Biosynthesis | Adenosylhomocysteinase (EC 3.3.1.1) |
| Derivatives | cysteine | • | |
| Amino Acids and | Lysine, threonine, methionine, and | Methionine Biosynthesis | Cystathionine gamma-lyase (EC 4.4.1.1) |
| Derivatives | cysteine | · | |
| Amino Acids and | Lysine, threonine, methionine, and | Methionine Biosynthesis | Cystathionine gamma-synthase (EC 2.5.1.48) |
| Derivatives | cysteine | | |
| Amino Acids and | Lysine, threonine, methionine, and | Methionine Biosynthesis | O-acetylhomoserine sulfhydrylase (EC 2.5.1.49) |
| Derivatives | cysteine | | |
| Amino Acids and | Lysine, threonine, methionine, and | Methionine Biosynthesis | S-adenosylmethionine synthetase (EC 2.5.1.6) |
| Derivatives Amino Acids and | cysteine Lysine, threonine, methionine, and | | |
| Derivatives | cysteine | Methionine Biosynthesis | Serine acetyltransferase (EC 2.3.1.30) |
| Amino Acids and | Lysine, threonine, methionine, and | | |
| Derivatives | cysteine | Methionine Biosynthesis | Methionine ABC transporter substrate-binding protein |
| Amino Acids and | Lysine, threonine, methionine, and | | |
| Derivatives | cysteine | Methionine Biosynthesis | Methionine ABC transporter ATP-binding protein |
| Amino Acids and | Lysine, threonine, methionine, and | | |
| Derivatives | cysteine | Methionine Biosynthesis | Homoserine O-acetyltransferase (EC 2.3.1.31) |
| Amino Acids and | Lysine, threonine, methionine, and | | |
| Derivatives | cysteine | Methionine Biosynthesis | 5-methyltetrahydrofolatehomocysteine methyltransferase (EC 2.1.1.13) |
| Amino Acids and | Lysine, threonine, methionine, and | | T |
| Derivatives | cysteine | Methionine Biosynthesis | Homoserine kinase (EC 2.7.1.39) |
| | J | | |

| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Methionine Biosynthesis | O-succinylhomoserine sulfhydrylase (EC 2.5.1.48) |
|--------------------------------|---|--|---|
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Methionine Biosynthesis | Methionine ABC transporter permease protein |
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Methionine Biosynthesis | 5-methyltetrahydropteroyltriglutamatehomocysteine methyltransferase (EC 2.1.1.14) |
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Methionine Biosynthesis | Cysteine synthase (EC 2.5.1.47) |
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Lysine Biosynthesis DAP Pathway, GJO scratch | Diaminopimelate epimerase (EC 5.1.1.7) |
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Lysine Biosynthesis DAP Pathway, GJO scratch | Diaminopimelate decarboxylase (EC 4.1.1.20) |
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Lysine Biosynthesis DAP Pathway, GJO scratch | 4-hydroxy-tetrahydrodipicolinate reductase (EC 1.17.1.8) |
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Lysine Biosynthesis DAP Pathway, GJO scratch | Aspartokinase (EC 2.7.2.4) |
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Lysine Biosynthesis DAP Pathway, GJO scratch | 2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-succinyltransferase (EC 2.3.1.117) |
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Lysine Biosynthesis DAP Pathway, GJO scratch | Aspartate-semialdehyde dehydrogenase (EC 1.2.1.11) |
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Lysine Biosynthesis DAP Pathway, GJO scratch | 4-hydroxy-tetrahydrodipicolinate synthase (EC 4.3.3.7) |
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Lysine Biosynthesis DAP Pathway, GJO scratch | N-succinyl-L,L-diaminopimelate desuccinylase (EC 3.5.1.18) |
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Threonine degradation | Threonine dehydrogenase and related Zn-dependent dehydrogenases |
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Threonine degradation | L-threonine 3-dehydrogenase (EC 1.1.1.103) |
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Threonine degradation | Threonine dehydratase, catabolic (EC 4.3.1.19) |
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Cysteine Biosynthesis | Serine acetyltransferase (EC 2.3.1.30) |
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Cysteine Biosynthesis | Cysteine synthase (EC 2.5.1.47) |
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Cysteine Biosynthesis | Sulfate adenylyltransferase subunit 1 (EC 2.7.7.4) |
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Cysteine Biosynthesis | Phosphoadenylyl-sulfate reductase [thioredoxin] (EC 1.8.4.8) |
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Cysteine Biosynthesis | Sulfate adenylyltransferase subunit 2 (EC 2.7.7.4) |
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Cysteine Biosynthesis | Cystathionine beta-synthase (EC 4.2.1.22) |

| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Cysteine Biosynthesis | Cystathionine gamma-lyase (EC 4.4.1.1) |
|--------------------------------|---|--|---|
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Cysteine Biosynthesis | Sulfate permease |
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Threonine and Homoserine Biosynthesis | Homoserine dehydrogenase (EC 1.1.1.3) |
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Threonine and Homoserine Biosynthesis | Aspartate aminotransferase (EC 2.6.1.1) |
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Threonine and Homoserine Biosynthesis | Threonine synthase (EC 4.2.3.1) |
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Threonine and Homoserine Biosynthesis | Aspartokinase (EC 2.7.2.4) |
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Threonine and Homoserine Biosynthesis | Homoserine kinase (EC 2.7.1.39) |
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Threonine and Homoserine Biosynthesis | Aspartate-semialdehyde dehydrogenase (EC 1.2.1.11) |
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Lysine Biosynthesis DAP Pathway | Aspartokinase (EC 2.7.2.4) |
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Lysine Biosynthesis DAP Pathway | 4-hydroxy-tetrahydrodipicolinate reductase (EC 1.17.1.8) |
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Lysine Biosynthesis DAP Pathway | Diaminopimelate decarboxylase (EC 4.1.1.20) |
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Lysine Biosynthesis DAP Pathway | Diaminopimelate epimerase (EC 5.1.1.7) |
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Lysine Biosynthesis DAP Pathway | N-succinyl-L,L-diaminopimelate desuccinylase (EC 3.5.1.18) |
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Lysine Biosynthesis DAP Pathway | 4-hydroxy-tetrahydrodipicolinate synthase (EC 4.3.3.7) |
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Lysine Biosynthesis DAP Pathway | Aspartate-semialdehyde dehydrogenase (EC 1.2.1.11) |
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Lysine Biosynthesis DAP Pathway | 2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-succinyltransferase (EC 2.3.1.117) |
| Amino Acids and Derivatives | Glutamine, glutamate, aspartate, asparagine; ammonia assimilation | Glutamine, Glutamate, Aspartate and Asparagine Biosynthesis | Aspartate aminotransferase (EC 2.6.1.1) |
| Amino Acids and Derivatives | Glutamine, glutamate, aspartate, asparagine; ammonia assimilation | Glutamine, Glutamate, Aspartate and Asparagine Biosynthesis | NAD-specific glutamate dehydrogenase (EC 1.4.1.2), large form |
| Amino Acids and Derivatives | Glutamine, glutamate, aspartate, asparagine; ammonia assimilation | Glutamine, Glutamate, Aspartate and Asparagine Biosynthesis | Glutamate synthase [NADPH] small chain (EC 1.4.1.13) |
| Amino Acids and Derivatives | Glutamine, glutamate, aspartate, asparagine; ammonia assimilation | Glutamine, Glutamate, Aspartate and Asparagine Biosynthesis | Glutamate racemase (EC 5.1.1.3) |
| Amino Acids and Derivatives | Glutamine, glutamate, aspartate, asparagine; ammonia assimilation | Glutamine, Glutamate, Aspartate and Asparagine Biosynthesis | NADP-specific glutamate dehydrogenase (EC 1.4.1.4) |

| Amino Acids and Derivatives | Glutamine, glutamate, aspartate, asparagine; ammonia assimilation | Glutamine, Glutamate, Aspartate and Asparagine Biosynthesis | Glutamine synthetase type I (EC 6.3.1.2) |
|---|---|--|--|
| Amino Acids and Derivatives | Glutamine, glutamate, aspartate, asparagine; ammonia assimilation | Glutamine, Glutamate, Aspartate and Asparagine Biosynthesis | Leucine-responsive regulatory protein, regulator for leucine (or lrp) regulon and high-affinity branched-chain amino acid transport system |
| Amino Acids and Derivatives | Glutamine, glutamate, aspartate, asparagine; ammonia assimilation | Glutamine, Glutamate, Aspartate and Asparagine Biosynthesis | Aspartate ammonia-lyase (EC 4.3.1.1) |
| Amino Acids and Derivatives | Glutamine, glutamate, aspartate, asparagine; ammonia assimilation | Glutamine, Glutamate, Aspartate and Asparagine Biosynthesis | Glutamate synthase [NADPH] large chain (EC 1.4.1.13) |
| Amino Acids and Derivatives | Glutamine, glutamate, aspartate, asparagine; ammonia assimilation | Glutamate dehydrogenases | NAD-specific glutamate dehydrogenase (EC 1.4.1.2), large form |
| Amino Acids and Derivatives | Glutamine, glutamate, aspartate, asparagine; ammonia assimilation | Glutamate dehydrogenases | NADP-specific glutamate dehydrogenase (EC 1.4.1.4) |
| Amino Acids and Derivatives Amino Acids and | Glutamine, glutamate, aspartate, asparagine; ammonia assimilation | Glutamine synthetases | Glutamine synthetase type I (EC 6.3.1.2) |
| Derivatives Amino Acids and | Histidine Metabolism | Histidine Degradation | Urocanate hydratase (EC 4.2.1.49) |
| Derivatives Amino Acids and | Histidine Metabolism | Histidine Degradation | Imidazolonepropionase (EC 3.5.2.7) |
| Derivatives Amino Acids and | Histidine Metabolism | Histidine Degradation | Histidine transport protein (permease) |
| Derivatives Amino Acids and | Histidine Metabolism Histidine Metabolism | Histidine Degradation Histidine Degradation | Histidine ammonia-lyase (EC 4.3.1.3) Formiminoglutamase (EC 3.5.3.8) |
| Derivatives Amino Acids and | Histidine Metabolism | Histidine Biosynthesis | Imidazoleglycerol-phosphate dehydratase (EC 4.2.1.19) |
| Derivatives Amino Acids and | Histidine Metabolism | Histidine Biosynthesis | Histidinol-phosphatase (EC 3.1.3.15) |
| Derivatives Amino Acids and Derivatives | Histidine Metabolism | Histidine Biosynthesis | Phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase (EC 5.3.1.16) |
| Amino Acids and Derivatives | Histidine Metabolism | Histidine Biosynthesis | Histidinol dehydrogenase (EC 1.1.1.23) |
| Amino Acids and Derivatives | Histidine Metabolism | Histidine Biosynthesis | Phosphoribosyl-AMP cyclohydrolase (EC 3.5.4.19) |
| Amino Acids and Derivatives | Histidine Metabolism | Histidine Biosynthesis | Phosphoribosyl-ATP pyrophosphatase (EC 3.6.1.31) |
| Amino Acids and Derivatives | Histidine Metabolism | Histidine Biosynthesis | Histidinol-phosphatase [alternative form] (EC 3.1.3.15) |
| Amino Acids and Derivatives | Histidine Metabolism | Histidine Biosynthesis | Histidinol-phosphate aminotransferase (EC 2.6.1.9) |
| Amino Acids and Derivatives | Aromatic amino acids and derivatives | Phenylalanine and Tyrosine Branches from Chorismate | Biosynthetic Aromatic amino acid aminotransferase beta (EC 2.6.1.57) |

| Amino Acids and | Aromatic amino acids and | Phenylalanine and Tyrosine Branches from Chorismate | Chorismate mutase I (EC 5.4.99.5) |
|--------------------------------|--------------------------------------|---|---|
| Derivatives Amino Acids and | derivatives Aromatic amino acids and | | |
| Derivatives | derivatives | Phenylalanine and Tyrosine Branches from Chorismate | Prephenate dehydratase (EC 4.2.1.51) |
| Amino Acids and | Aromatic amino acids and | Discontinuo di Transia Danaha fara Chaireata | A |
| Derivatives | derivatives | Phenylalanine and Tyrosine Branches from Chorismate | Arogenate dehydrogenase (EC 1.3.1.43) |
| Amino Acids and | Aromatic amino acids and | Aromatic amino acid degradation | 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase (EC 5.3.3) |
| Derivatives | derivatives | Aromatic animo acid degradation | 2-ilydroxylicpur-2,4-diche-1,7-diodic isoliicrase (EC 5.5.5) |
| Amino Acids and | Aromatic amino acids and | Aromatic amino acid degradation | 5-carboxymethyl-2-hydroxymuconate semialdehyde dehydrogenase (EC 1.2.1.60) |
| Derivatives | derivatives | | |
| Amino Acids and | Aromatic amino acids and | Aromatic amino acid degradation | 5-carboxymethyl-2-oxo-hex-3- ene-1,7-dioate decarboxylase (EC 4.1.1.68) |
| Derivatives | derivatives | <u> </u> | |
| Amino Acids and | Aromatic amino acids and | Aromatic amino acid degradation | Tryptophan 2,3-dioxygenase (EC 1.13.11.11) |
| Derivatives Amino Acids and | derivatives Aromatic amino acids and | | |
| Derivatives | derivatives | Aromatic amino acid degradation | Aromatic-L-amino-acid decarboxylase (EC 4.1.1.28) |
| Amino Acids and | Aromatic amino acids and | | |
| Derivatives | derivatives | Aromatic amino acid degradation | 5-carboxymethyl-2-hydroxymuconate delta-isomerase (EC 5.3.3.10) |
| Amino Acids and | Aromatic amino acids and | Aromatic amino acid degradation 2 | |
| Derivatives | derivatives | | 2-oxo-hepta-3-ene-1,7-dioic acid hydratase (EC 4.2) |
| Amino Acids and | Aromatic amino acids and | A | 4 lead |
| Derivatives | derivatives | Aromatic amino acid degradation | 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27) |
| Amino Acids and | Aromatic amino acids and | Common Pathway For Synthesis of Aromatic Compounds | Shikimate 5-dehydrogenase I alpha (EC 1.1.1.25) |
| Derivatives | derivatives | (DAHP synthase to chorismate) | |
| Amino Acids and | Aromatic amino acids and | Common Pathway For Synthesis of Aromatic Compounds | 3-dehydroquinate dehydratase II (EC 4.2.1.10) |
| Derivatives | derivatives | (DAHP synthase to chorismate) | |
| Amino Acids and | Aromatic amino acids and | Common Pathway For Synthesis of Aromatic Compounds | 2-keto-3-deoxy-D-arabino-heptulosonate-7-phosphate synthase I alpha (EC 2.5.1.54) |
| Derivatives | derivatives | (DAHP synthase to chorismate) | |
| Amino Acids and | Aromatic amino acids and | Common Pathway For Synthesis of Aromatic Compounds | Shikimate kinase I (EC 2.7.1.71) |
| Derivatives Amino Acids and | derivatives Aromatic amino acids and | (DAHP synthase to chorismate) | |
| Derivatives | derivatives | Common Pathway For Synthesis of Aromatic Compounds (DAHP synthase to chorismate) | 2-keto-3-deoxy-D-arabino-heptulosonate-7-phosphate synthase II (EC 2.5.1.54) |
| Amino Acids and | Aromatic amino acids and | Common Pathway For Synthesis of Aromatic Compounds | |
| Derivatives | derivatives | (DAHP synthase to chorismate) | Quinate/shikimate 5-dehydrogenase I delta (EC 1.1.1.25) |
| Amino Acids and | Aromatic amino acids and | Common Pathway For Synthesis of Aromatic Compounds | |
| Derivatives | derivatives | (DAHP synthase to chorismate) | Chorismate synthase (EC 4.2.3.5) |
| Amino Acids and | Aromatic amino acids and | Common Pathway For Synthesis of Aromatic Compounds | |
| Derivatives | derivatives | (DAHP synthase to chorismate) | Shikimate 5-dehydrogenase I gamma (EC 1.1.1.25) |
| Amino Acids and | Aromatic amino acids and | Common Pathway For Synthesis of Aromatic Compounds | 3-dehydroquinate synthase (EC 4.2.3.4) |
| Derivatives | derivatives | (DAHP synthase to chorismate) | 5-denydroquinate synthase (EC 4.2.5.4) |
| Amino Acids and | Aromatic amino acids and | Tryptophan synthesis | Aminodeoxychorismate lyase (EC 4.1.3.38) |
| Derivatives | derivatives | ттургориян зунинсыз | Timinodeoxyenorismate tyase (EC 7.1.5.50) |

| Amino Acids and Derivatives | Aromatic amino acids and derivatives | Tryptophan synthesis | Anthranilate synthase, aminase component (EC 4.1.3.27) |
|--------------------------------|---|---|---|
| Amino Acids and | Aromatic amino acids and | Tryptophan synthesis | Para-aminobenzoate synthase, amidotransferase component (EC 2.6.1.85) |
| Derivatives Amino Acids and | derivatives Aromatic amino acids and | Tryptophan synthesis | Anthranilate phosphoribosyltransferase (EC 2.4.2.18) |
| Derivatives Amino Acids and | derivatives Aromatic amino acids and | 31 1 3 | |
| Derivatives | derivatives | Tryptophan synthesis | Indole-3-glycerol phosphate synthase (EC 4.1.1.48) |
| Amino Acids and Derivatives | Aromatic amino acids and derivatives | Tryptophan synthesis | Tryptophan synthase alpha chain (EC 4.2.1.20) |
| Amino Acids and Derivatives | Aromatic amino acids and derivatives | Tryptophan synthesis | Anthranilate synthase, amidotransferase component (EC 4.1.3.27) |
| Amino Acids and Derivatives | Aromatic amino acids and derivatives | Tryptophan synthesis | Phosphoribosylanthranilate isomerase (EC 5.3.1.24) |
| Amino Acids and Derivatives | Aromatic amino acids and derivatives | Tryptophan synthesis | Tryptophan-associated membrane protein |
| Amino Acids and Derivatives | Aromatic amino acids and derivatives | Tryptophan synthesis | Para-aminobenzoate synthase, aminase component (EC 2.6.1.85) |
| Amino Acids and Derivatives | Aromatic amino acids and derivatives | Tryptophan synthesis | Tryptophan synthase beta chain (EC 4.2.1.20) |
| Amino Acids and Derivatives | Aromatic amino acids and derivatives | Tryptophan synthesis | Acting phosphoribosylanthranilate isomerase (EC 5.3.1.24) |
| Amino Acids and Derivatives | Aromatic amino acids and derivatives | Chorismate: Intermediate for synthesis of Tryptophan, PAPA antibiotics, PABA, 3-hydroxyanthranilate and more. | Anthranilate synthase, aminase component (EC 4.1.3.27) |
| Amino Acids and Derivatives | Aromatic amino acids and derivatives | Chorismate: Intermediate for synthesis of Tryptophan, PAPA antibiotics, PABA, 3-hydroxyanthranilate and | Aminodeoxychorismate lyase (EC 4.1.3.38) |
| Amino Acids and Derivatives | Aromatic amino acids and derivatives | more. Chorismate: Intermediate for synthesis of Tryptophan, PAPA antibiotics, PABA, 3-hydroxyanthranilate and more. | Phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase (EC 5.3.1.16) |
| Amino Acids and Derivatives | Aromatic amino acids and derivatives | Chorismate: Intermediate for synthesis of Tryptophan, PAPA antibiotics, PABA, 3-hydroxyanthranilate and | Para-aminobenzoate synthase, amidotransferase component (EC 2.6.1.85) |
| Amino Acids and Derivatives | Aromatic amino acids and derivatives | more. Chorismate: Intermediate for synthesis of Tryptophan, PAPA antibiotics, PABA, 3-hydroxyanthranilate and more. | Anthranilate phosphoribosyltransferase (EC 2.4.2.18) |
| Amino Acids and Derivatives | Aromatic amino acids and derivatives | Chorismate: Intermediate for synthesis of Tryptophan, PAPA antibiotics, PABA, 3-hydroxyanthranilate and more. | Phosphoribosylanthranilate isomerase (EC 5.3.1.24) |
| Amino Acids and Derivatives | Aromatic amino acids and derivatives | Chorismate: Intermediate for synthesis of Tryptophan, PAPA antibiotics, PABA, 3-hydroxyanthranilate and more. | Anthranilate synthase, amidotransferase component (EC 4.1.3.27) |
| | | | |

| Amino Acids and Derivatives | Aromatic amino acids and derivatives | Chorismate: Intermediate for synthesis of Tryptophan, PAPA antibiotics, PABA, 3-hydroxyanthranilate and | Tryptophan synthase alpha chain (EC 4.2.1.20) |
|-------------------------------------|--|---|--|
| Amino Acids and Derivatives | Aromatic amino acids and derivatives | more. Chorismate: Intermediate for synthesis of Tryptophan, PAPA antibiotics, PABA, 3-hydroxyanthranilate and | Indole-3-glycerol phosphate synthase (EC 4.1.1.48) |
| Amino Acids and Derivatives | Aromatic amino acids and derivatives | more. Chorismate: Intermediate for synthesis of Tryptophan, PAPA antibiotics, PABA, 3-hydroxyanthranilate and more. | Isochorismate synthase (EC 5.4.4.2) |
| Amino Acids and Derivatives | Aromatic amino acids and derivatives | Chorismate: Intermediate for synthesis of Tryptophan, PAPA antibiotics, PABA, 3-hydroxyanthranilate and more. | Tryptophan synthase beta chain (EC 4.2.1.20) |
| Amino Acids and Derivatives | Aromatic amino acids and derivatives | Chorismate: Intermediate for synthesis of Tryptophan, PAPA antibiotics, PABA, 3-hydroxyanthranilate and more. | Para-aminobenzoate synthase, aminase component (EC 2.6.1.85) |
| Amino Acids and Derivatives | Proline and 4-hydroxyproline | Proline Synthesis | NADP-specific glutamate dehydrogenase (EC 1.4.1.4) |
| Amino Acids and Derivatives | Proline and 4-hydroxyproline | Proline Synthesis | Glutamate 5-kinase (EC 2.7.2.11) |
| Amino Acids and Derivatives | Proline and 4-hydroxyproline | Proline Synthesis | RNA-binding C-terminal domain PUA |
| Amino Acids and Derivatives | Proline and 4-hydroxyproline | Proline Synthesis | Pyrroline-5-carboxylate reductase (EC 1.5.1.2) |
| Amino Acids and Derivatives | Proline and 4-hydroxyproline | Proline Synthesis | Gamma-glutamyl phosphate reductase (EC 1.2.1.41) |
| Amino Acids and Derivatives | Proline and 4-hydroxyproline | Proline, 4-hydroxyproline uptake and utilization | Proline iminopeptidase (EC 3.4.11.5) |
| Amino Acids and Derivatives | Proline and 4-hydroxyproline | Proline, 4-hydroxyproline uptake and utilization | D-amino-acid oxidase (EC 1.4.3.3) |
| Amino Acids and Derivatives | Proline and 4-hydroxyproline | Proline, 4-hydroxyproline uptake and utilization | 1-pyrroline-4-hydroxy-2-carboxylate deaminase (EC 3.5.4.22) |
| Amino Acids and Derivatives | Proline and 4-hydroxyproline | Proline, 4-hydroxyproline uptake and utilization | Delta-1-pyrroline-5-carboxylate dehydrogenase (EC 1.2.1.88) |
| Amino Acids and Derivatives | Proline and 4-hydroxyproline | Proline, 4-hydroxyproline uptake and utilization | L-Proline/Glycine betaine transporter ProP |
| Amino Acids and Derivatives | Proline and 4-hydroxyproline | Proline, 4-hydroxyproline uptake and utilization | 4-hydroxyproline epimerase (EC 5.1.1.8) |
| Amino Acids and Derivatives | Proline and 4-hydroxyproline | Proline, 4-hydroxyproline uptake and utilization | Putative oxidoreductase in 4-hydroxyproline catabolic gene cluster |
| Metabolism of Aromatic Compounds | Peripheral pathways for catabolism of aromatic compounds | Benzoate degradation | Benzoate 1,2-dioxygenase, ferredoxin reductase component |
| Metabolism of Aromatic Compounds | Peripheral pathways for catabolism of aromatic compounds | Benzoate degradation | Benzoate transport protein |
| | | | |

| Metabolism of Aromatic Compounds | Peripheral pathways for catabolism of aromatic compounds | Benzoate degradation | Benzoate 1,2-dioxygenase beta subunit (EC 1.14.12.10) |
|-------------------------------------|--|--|--|
| Metabolism of Aromatic Compounds | Peripheral pathways for catabolism of aromatic compounds | Benzoate degradation | 1,2-dihydroxycyclohexa-3,5-diene-1-carboxylate dehydrogenase (EC 1.3.1.25) |
| Metabolism of Aromatic Compounds | Peripheral pathways for catabolism of aromatic compounds | Benzoate degradation | benzoate MFS transporter BenK |
| Metabolism of Aromatic Compounds | Peripheral pathways for catabolism of aromatic compounds | Benzoate degradation | Benzoate 1,2-dioxygenase alpha subunit (EC 1.14.12.10) |
| Metabolism of Aromatic Compounds | Peripheral pathways for catabolism of aromatic compounds | p-Hydroxybenzoate degradation | P-hydroxybenzoate hydroxylase (EC 1.14.13.2) |
| Metabolism of Aromatic Compounds | Peripheral pathways for catabolism of aromatic compounds | p-Hydroxybenzoate degradation | 4-hydroxybenzoate transporter |
| Metabolism of Aromatic Compounds | Peripheral pathways for catabolism of aromatic compounds | Quinate degradation | 3-dehydroquinate dehydratase II (EC 4.2.1.10) |
| Metabolism of Aromatic Compounds | Metabolism of central aromatic intermediates | Catechol branch of beta-ketoadipate pathway | Catechol 1,2-dioxygenase (EC 1.13.11.1) |
| Metabolism of Aromatic Compounds | Metabolism of central aromatic intermediates | Catechol branch of beta-ketoadipate pathway | 3-oxoadipate CoA-transferase subunit A (EC 2.8.3.6) |
| Metabolism of Aromatic Compounds | Metabolism of central aromatic intermediates | Catechol branch of beta-ketoadipate pathway | Catechol 1,2-dioxygenase 1 (EC 1.13.11.1) |
| Metabolism of Aromatic Compounds | Metabolism of central aromatic intermediates | Catechol branch of beta-ketoadipate pathway | Muconolactone isomerase (EC 5.3.3.4) |
| Metabolism of Aromatic Compounds | Metabolism of central aromatic intermediates | Catechol branch of beta-ketoadipate pathway | Succinyl-CoA:3-ketoacid-coenzyme A transferase subunit A (EC 2.8.3.5) |
| Metabolism of Aromatic Compounds | Metabolism of central aromatic intermediates | Catechol branch of beta-ketoadipate pathway | 3-oxoadipate CoA-transferase subunit B (EC 2.8.3.6) |
| Metabolism of Aromatic Compounds | Metabolism of central aromatic intermediates | Catechol branch of beta-ketoadipate pathway | Beta-ketoadipate enol-lactone hydrolase (EC 3.1.1.24) |
| Metabolism of Aromatic Compounds | Metabolism of central aromatic intermediates | Catechol branch of beta-ketoadipate pathway | Muconate cycloisomerase (EC 5.5.1.1) |
| Metabolism of Aromatic Compounds | Metabolism of central aromatic intermediates | Catechol branch of beta-ketoadipate pathway | Succinyl-CoA:3-ketoacid-coenzyme A transferase subunit B (EC 2.8.3.5) |
| Metabolism of Aromatic Compounds | Metabolism of central aromatic intermediates | Salicylate and gentisate catabolism | Putative n-hydroxybenzoate hydroxylase |
| Metabolism of Aromatic Compounds | Metabolism of central aromatic intermediates | Salicylate and gentisate catabolism | Fumarylacetoacetate hydrolase family protein |
| Metabolism of Aromatic Compounds | Metabolism of central aromatic intermediates | Salicylate and gentisate catabolism | 4-hydroxybenzoate transporter |
| Metabolism of Aromatic Compounds | Metabolism of central aromatic intermediates | Salicylate and gentisate catabolism | Gentisate 1,2-dioxygenase (EC 1.13.11.4) |
| Metabolism of Aromatic Compounds | Metabolism of central aromatic intermediates | Central meta-cleavage pathway of aromatic compound degradation | Catechol 2,3-dioxygenase (EC 1.13.11.2) |

| Metabolism of Aromatic Compounds | Metabolism of central aromatic intermediates | Central meta-cleavage pathway of aromatic compound degradation | 5-carboxymethyl-2-hydroxymuconate semialdehyde dehydrogenase (EC 1.2.1.60) |
|---|--|--|--|
| Metabolism of Aromatic Compounds | Metabolism of central aromatic intermediates | Central meta-cleavage pathway of aromatic compound degradation | 5-carboxymethyl-2-hydroxymuconate delta-isomerase (EC 5.3.3.10) |
| Metabolism of Aromatic Compounds | Metabolism of central aromatic intermediates | Central meta-cleavage pathway of aromatic compound degradation | Protocatechuate 4,5-dioxygenase beta chain (EC 1.13.11.8) |
| Metabolism of Aromatic Compounds | Metabolism of central aromatic intermediates | Central meta-cleavage pathway of aromatic compound degradation | 2-oxo-hepta-3-ene-1,7-dioic acid hydratase (EC 4.2) |
| Metabolism of Aromatic Compounds | Metabolism of central aromatic intermediates | Protocatechuate branch of beta-ketoadipate pathway | Succinyl-CoA:3-ketoacid-coenzyme A transferase subunit B (EC 2.8.3.5) |
| Metabolism of Aromatic Compounds | Metabolism of central aromatic intermediates | Protocatechuate branch of beta-ketoadipate pathway | 3-carboxy-cis,cis-muconate cycloisomerase (EC 5.5.1.2) |
| Metabolism of Aromatic Compounds | Metabolism of central aromatic intermediates | Protocatechuate branch of beta-ketoadipate pathway | 4-carboxymuconolactone decarboxylase (EC 4.1.1.44) |
| Metabolism of Aromatic Compounds | Metabolism of central aromatic intermediates | Protocatechuate branch of beta-ketoadipate pathway | Succinyl-CoA:3-ketoacid-coenzyme A transferase subunit A (EC 2.8.3.5) |
| Metabolism of Aromatic Compounds | Metabolism of central aromatic intermediates | Protocatechuate branch of beta-ketoadipate pathway | Pca regulon regulatory protein PcaR |
| Metabolism of Aromatic Compounds | Metabolism of central aromatic intermediates | Protocatechuate branch of beta-ketoadipate pathway | Protocatechuate 3,4-dioxygenase alpha chain (EC 1.13.11.3) |
| Metabolism of Aromatic Compounds | Metabolism of central aromatic intermediates | Protocatechuate branch of beta-ketoadipate pathway | Beta-ketoadipate enol-lactone hydrolase (EC 3.1.1.24) |
| Metabolism of Aromatic Compounds | Metabolism of central aromatic intermediates | Protocatechuate branch of beta-ketoadipate pathway | 3-oxoadipate CoA-transferase subunit B (EC 2.8.3.6) |
| Metabolism of Aromatic Compounds | Metabolism of central aromatic intermediates | Protocatechuate branch of beta-ketoadipate pathway | 3-oxoadipate CoA-transferase subunit A (EC 2.8.3.6) |
| Metabolism of Aromatic Compounds | Metabolism of central aromatic intermediates | Protocatechuate branch of beta-ketoadipate pathway | Protocatechuate 3,4-dioxygenase beta chain (EC 1.13.11.3) |
| Metabolism of Aromatic Compounds | Metabolism of Aromatic Compounds - no subcategory | Gentisate degradation | Gentisate 1,2-dioxygenase (EC 1.13.11.4) |
| Metabolism of Aromatic Compounds | Metabolism of Aromatic Compounds - no subcategory | Gentisate degradation | Fumarylacetoacetate hydrolase family protein |
| Metabolism of Aromatic Compounds | Metabolism of Aromatic Compounds - no subcategory | Gentisate degradation | 4-hydroxybenzoate transporter |
| Metabolism of Aromatic Compounds | Metabolism of Aromatic Compounds - no subcategory | Gentisate degradation | Putative n-hydroxybenzoate hydroxylase |
| Resistance to antibiotics and toxic compounds | Resistance to antibiotics | Beta-lactamase | Metal-dependent hydrolases of the beta-lactamase superfamily III |
| Resistance to antibiotics and toxic compounds | Resistance to antibiotics | Resistance to fluoroquinolones | DNA gyrase subunit A (EC 5.99.1.3) |
| Resistance to antibiotics and toxic compounds | Resistance to antibiotics | Resistance to fluoroquinolones | DNA gyrase subunit B (EC 5.99.1.3) |

| Resistance to antibiotics and toxic compounds | Resistance to heavy metals | Copper homeostasis | Copper resistance protein CopD |
|--|----------------------------|--------------------------------|--|
| Resistance to antibiotics and toxic compounds | Resistance to heavy metals | Copper homeostasis | Copper-translocating P-type ATPase (EC 3.6.3.4) |
| Resistance to antibiotics and toxic compounds | Resistance to heavy metals | Copper homeostasis | Copper resistance protein CopC |
| Resistance to antibiotics and toxic compounds | Resistance to heavy metals | Copper homeostasis | Multidrug resistance transporter, Bcr/CflA family |
| Resistance to antibiotics and toxic compounds | Resistance to heavy metals | Cobalt-zinc-cadmium resistance | Transcriptional regulator, MerR family |
| Resistance to antibiotics and toxic compounds | Resistance to heavy metals | Cobalt-zine-cadmium resistance | Cobalt-zinc-cadmium resistance protein CzcD |
| Resistance to antibiotics and toxic compounds | Resistance to heavy metals | Mercuric reductase | PF00070 family, FAD-dependent NAD(P)-disulphide oxidoreductase |

The annotated genes from the genome of strain H3SJ34-1^T involving in metabolization of carbohydrates, amino acids, and aromatic compounds and resistance to antibiotics and heavy metals.

| Category Subcategory Subsystem Annotated genes and its roles Control | |
|---|---|
| Carbohydrates Central carbohydrate metabolism TCA Cycle Fumarate hydratase class I (EC 4.2.1.2) | |
| Carbohydrates Central carbohydrate metabolism TCA Cycle Isocitrate dehydrogenase [NADP] (EC 1.1.1.42) | |
| Carbohydrates Central carbohydrate metabolism TCA Cycle 2-oxoglutarate dehydrogenase E1 component (EC 1.2.4.2) | |
| Carbohydrates Central carbohydrate metabolism TCA Cycle Dihydrolipoamide dehydrogenase of 2-oxoglutarate dehydrogenase (EC 1.8.1.4) | |
| Carbohydrates Central carbohydrate metabolism TCA Cycle Fumarate hydratase class II (EC 4.2.1.2) | |
| Carbohydrates Central carbohydrate metabolism TCA Cycle Aconitate hydratase (EC 4.2.1.3) | |
| Carbohydrates Central carbohydrate metabolism TCA Cycle Dihydrolipoamide succinyltransferase component (E2) of 2-oxoglutarate dehydrogena | ase complex (EC 2.3.1.61) |
| Carbohydrates Central carbohydrate metabolism TCA Cycle Citrate synthase (si) (EC 2.3.3.1) | (== =================================== |
| Carbohydrates Central carbohydrate metabolism TCA Cycle Succinyl-CoA ligase [ADP-forming] beta chain (EC 6.2.1.5) | |
| Carbohydrates Central carbohydrate metabolism TCA Cycle Dihydrolipoamide dehydrogenase of pyruvate dehydrogenase complex (EC 1.8.1.4) | |
| Carbohydrates Central carbohydrate metabolism TCA Cycle hypothetical protein that offen co-occurs with aconitase | |
| Carbohydrates Central carbohydrate metabolism TCA Cycle Succinyl-CoA ligase [ADP-forming] alpha chain (EC 6.2.1.5) | |
| Carbohydrates Central carbohydrate metabolism TCA Cycle Sdeeniyr-CoA ligase [ADA-I-I-IIIIII] aipha chain (EC 0.2.1.3) Malate dehydrogenase (EC 1.1.1.37) | |
| Carbohydrates Central carbohydrate metabolism II: acetyl-CoA, acetogenesis from pyruvate Pyruvate dehydrogenase E1 component alpha subunit (EC 1.2.4.1) | |
| Carbohydrates Central carbohydrate metabolism II: acetyl-CoA, acetogenesis from pyruvate Tytuvate denydrogenase II: component appia subant (IE: 1.2.4.1) Carbohydrates Central carbohydrate metabolism II: acetyl-CoA, acetogenesis from pyruvate Acetate permease ActP (cation/acetate symporter) | |
| Carbohydrates Central carbohydrate metabolism II: acetyl-CoA, acetogenesis from pyruvate Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase complex (| (EC 2 3 1 12) |
| Carbohydrates Central carbohydrate metabolism II: acetyl-CoA, acetogenesis from pyruvate Aldehyde dehydrogenase (EC 1.2.1.3) | (LC 2.3.1.12) |
| Carbohydrates Central carbohydrate metabolism II: acetyl-CoA, acetogenesis from pyruvate Acetate kinase (EC 2.7.2.1) | |
| Carbohydrates Central carbohydrate metabolism II: acetyl-CoA, acetogenesis from pyruvate Pyruvate dehydrogenase E1 component beta subunit (EC 1.2.4.1) | |
| Carbohydrates Central carbohydrate metabolism II: acetyl-CoA, acetogenesis from pyruvate Carbohydrates Central carbohydrate metabolism II: acetyl-CoA, acetogenesis from pyruvate Dihydrolipoamide dehydrogenase of pyruvate dehydrogenase complex (EC 1.8.1.4) | |
| Carbohydrates Central carbohydrate metabolism II: acetyl-CoA, acetogenesis from pyruvate Dhydrothydrate metabolism Pyruvate metabolism II: acetyl-CoA, acetogenesis from pyruvate NAD-dependent protein deacetylase of SIR2 family | |
| Carbohydrates Central carbohydrate metabolism II: acetyl-CoA, acetogenesis from pyruvate Phosphate acetyltransferase (EC 2.3.1.8) | |
| Carbohydrates Central carbohydrate metabolism II: acetyl-CoA, acetogenesis from pyruvate Acetyl-CoA synthetase (ADP-forming) alpha and beta chains, putative | |
| | |
| | |
| Carbohydrates Central carbohydrate metabolism Methylglyoxal Metabolism Hydroxyacylglutathione hydrolase (EC 3.1.2.6) Carbohydrates Central carbohydrate metabolism Methylglyoxal Metabolism Lactoylglutathione lyase (EC 4.4.1.5) | |
| | |
| Carbohydrates Central carbohydrate metabolism Glycolysis and Gluconeogenesis Glucose-6-phosphate isomerase (EC 5.3.1.9) Carbohydrates Central carbohydrate metabolism Glycolysis and Gluconeogenesis Fructose-1,6-bisphosphatase, GlpX type (EC 3.1.3.11) | |
| | |
| Carbohydrates Central carbohydrate metabolism Glycolysis and Gluconeogenesis Fructose-1,6-bisphosphatase, type I (EC 3.1.3.11) Carbohydrates Central carbohydrate metabolism Glycolysis and Gluconeogenesis Fructose-bisphosphate aldolase class II (EC 4.1.2.13) | |
| | |
| | |
| Carbohydrates Central carbohydrate metabolism Glycolysis and Gluconeogenesis Phosphoglycerate kinase (EC 2.7.2.3) | |
| Carbohydrates Central carbohydrate metabolism Glycolysis and Gluconeogenesis Enolase (EC 4.2.1.11) Carbohydrates Central carbohydrate metabolism Glycolysis and Gluconeogenesis Enolase (EC 4.2.1.11) | |
| Carbohydrates Central carbohydrate metabolism Glycolysis and Gluconeogenesis Pyruvate, phosphate dikinase (EC 2.7.9.1) | |
| Carbohydrates Central carbohydrate metabolism Glycolysis and Gluconeogenesis Pyruvate kinase (EC 2.7.1.40) | |
| Carbohydrates Central carbohydrate metabolism Glycolysis and Gluconeogenesis NAD-dependent glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) | |
| Carbohydrates Central carbohydrate metabolism Glycolysis and Gluconeogenesis Triosephosphate isomerase (EC 5.3.1.1) | |
| Carbohydrates Central carbohydrate metabolism Glycolysis and Gluconeogenesis Fructose-bisphosphate aldolase class I (EC 4.1.2.13) | |
| Carbohydrates Central carbohydrate metabolism Glycolysis and Gluconeogenesis Polyphosphate glucokinase (EC 2.7.1.63) | |
| Carbohydrates Central carbohydrate metabolism Glycolate, glyoxylate interconversions D-Lactate dehydrogenase, cytochrome c-dependent (EC 1.1.2.4) | |
| Carbohydrates Central carbohydrate metabolism Glycolate, glyoxylate interconversions Glycolate dehydrogenase (EC 1.1.99.14), subunit GlcD | |
| Carbohydrates Central carbohydrate metabolism Glycolate, glyoxylate interconversions Glyoxylate reductase (EC 1.1.1.79) Carbohydrates Glyoxylate reductase (EC 1.1.0.14) iron cyling cyling interconversions Glyoxylate reductase (EC 1.1.0.14) iron cyling cyling interconversions | |
| Carbohydrates Central carbohydrate metabolism Glycolate, glyoxylate interconversions Glycolate dehydrogenase (EC 1.1.99.14), iron-sulfur subunit GlcF | |
| Carbohydrates Central carbohydrate metabolism Glycolate, glyoxylate interconversions Phosphoglycolate phosphatase (EC 3.1.3.18) Carbohydrates Central carbohydrate metabolism Glycolate, glyoxylate interconversions Phosphoglycolate phosphatase (EC 3.1.3.18) | |
| Carbohydrates Central carbohydrate metabolism Glycolate, glyoxylate interconversions Hydroxypyruvate reductase (EC 1.1.1.81) Carbohydrates Central carbohydrate metabolism Glycolate, glyoxylate interconversions Glyoxylate reductase (EC 1.1.1.26) | |
| | |
| Carbohydrates Central carbohydrate metabolism Glycolate, glyoxylate interconversions Glycolate dehydrogenase (EC 1.1.99.14), FAD-binding subunit GlcE Carbohydrates Central carbohydrate metabolism Dehydrogenase complexes 2-oxoglutarate dehydrogenase E1 component (EC 1.2.4.2) | |
| Carbohydrates Central carbohydrate metabolism Dehydrogenase complexes 2-oxoglutarate dehydrogenase E1 component (EC 1.2.4.2) Carbohydrates Central carbohydrate metabolism Dehydrogenase complexes Leucine-, valine-, threonine-, and alanine-binding protein | |
| Caronyuraics Central caronyuraic netatonism Denyurogenase complexes Leucine-, isoteucine-, vanne-, unreonine-, and aranine-onium protein | |

| Carbohydrates | Central carbohydrate metabolism | Dehydrogenase complexes | Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase complex (EC 2.3.1.12) |
|---------------|---------------------------------|---|---|
| Carbohydrates | Central carbohydrate metabolism | Dehydrogenase complexes | Pyruvate dehydrogenase E1 component alpha subunit (EC 1.2.4.1) |
| Carbohydrates | Central carbohydrate metabolism | Dehydrogenase complexes | Pyruvate dehydrogenase E1 component beta subunit (EC 1.2.4.1) |
| Carbohydrates | Central carbohydrate metabolism | Dehydrogenase complexes | Dihydrolipoamide dehydrogenase of 2-oxoglutarate dehydrogenase (EC 1.8.1.4) |
| Carbohydrates | Central carbohydrate metabolism | Dehydrogenase complexes | Cytosol aminopeptidase PepA (EC 3.4.11.1) |
| Carbohydrates | Central carbohydrate metabolism | Dehydrogenase complexes | Dihydrolipoamide succinyltransferase component (E2) of 2-oxoglutarate dehydrogenase complex (EC 2.3.1.61) |
| Carbohydrates | Central carbohydrate metabolism | Pyruvate Alanine Serine Interconversions | Omega-amino acidpyruvate aminotransferase (EC 2.6.1.18) |
| Carbohydrates | Central carbohydrate metabolism | Pyruvate Alanine Serine Interconversions | Branched-chain amino acid aminotransferase (EC 2.6.1.42) |
| Carbohydrates | Central carbohydrate metabolism | Pyruvate Alanine Serine Interconversions | Alanine dehydrogenase (EC 1.4.1.1) |
| Carbohydrates | Central carbohydrate metabolism | Pyruvate Alanine Serine Interconversions | Valinepyruvate aminotransferase (EC 2.6.1.66) |
| Carbohydrates | Central carbohydrate metabolism | Pyruvate Alanine Serine Interconversions | Alanine racemase (EC 5.1.1.1) |
| Carbohydrates | Central carbohydrate metabolism | Pentose phosphate pathway | Ribulose-phosphate 3-epimerase (EC 5.1.3.1) |
| Carbohydrates | Central carbohydrate metabolism | Pentose phosphate pathway | Transaldolase (EC 2.2.1.2) |
| Carbohydrates | Central carbohydrate metabolism | Pentose phosphate pathway | 6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44) |
| Carbohydrates | Central carbohydrate metabolism | Pentose phosphate pathway | Xylulose-5-phosphate phosphoketolase (EC 4.1.2.9) |
| Carbohydrates | Central carbohydrate metabolism | Pentose phosphate pathway | Ribose-phosphate pyrophosphokinase (EC 2.7.6.1) |
| Carbohydrates | Central carbohydrate metabolism | Pentose phosphate pathway | Fructose-6-phosphate phosphoketolase (EC 4.1.2.22) |
| Carbohydrates | Central carbohydrate metabolism | Pentose phosphate pathway | Transketolase (EC 2.2.1.1) |
| Carbohydrates | Central carbohydrate metabolism | Pentose phosphate pathway | Glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49) |
| Carbohydrates | Central carbohydrate metabolism | Pentose phosphate pathway | 6-phosphogluconolactonase (EC 3.1.1.31), eukaryotic type |
| Carbohydrates | Central carbohydrate metabolism | Glyoxylate bypass | Malate synthase G (EC 2.3.3.9) |
| Carbohydrates | Central carbohydrate metabolism | Glyoxylate bypass | Aconitate hydratase (EC 4.2.1.3) |
| Carbohydrates | Central carbohydrate metabolism | Glyoxylate bypass | Citrate synthase (si) (EC 2.3.3.1) |
| Carbohydrates | Central carbohydrate metabolism | Glyoxylate bypass | Malate dehydrogenase (EC 1.1.1.37) |
| Carbohydrates | Central carbohydrate metabolism | Glyoxylate bypass | Isocitrate lyase (EC 4.1.3.1) |
| Carbohydrates | Central carbohydrate metabolism | Pyruvate metabolism I: anaplerotic reactions, PEP | Pyruvate kinase (EC 2.7.1.40) |
| Carbohydrates | Central carbohydrate metabolism | Pyruvate metabolism I: anaplerotic reactions, PEP | Pyruvate,phosphate dikinase (EC 2.7.9.1) |
| Carbohydrates | Central carbohydrate metabolism | Pyruvate metabolism I: anaplerotic reactions, PEP | Phosphoenolpyruvate carboxykinase [ATP] (EC 4.1.1.49) |
| Carbohydrates | Central carbohydrate metabolism | Pyruvate metabolism I: anaplerotic reactions, PEP | NADP-dependent malic enzyme (EC 1.1.1.40) |
| Carbohydrates | Monosaccharides | Mannose Metabolism | Phosphomannomutase (EC 5.4.2.8) |
| Carbohydrates | Monosaccharides | Mannose Metabolism | Mannose-6-phosphate isomerase (EC 5.3.1.8) |
| Carbohydrates | Monosaccharides | Mannose Metabolism | Beta-mannosidase (EC 3.2.1.25) |
| Carbohydrates | Monosaccharides | D-gluconate and ketogluconates metabolism | Gluconate 2-dehydrogenase (EC 1.1.99.3), membrane-bound, flavoprotein |
| Carbohydrates | Monosaccharides | D-gluconate and ketogluconates metabolism | Gluconate dehydratase (EC 4.2.1.39) |
| Carbohydrates | Monosaccharides | D-gluconate and ketogluconates metabolism | 6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44) |
| Carbohydrates | Monosaccharides | D-gluconate and ketogluconates metabolism | Gluconokinase (EC 2.7.1.12) |
| Carbohydrates | Monosaccharides | D-gluconate and ketogluconates metabolism | Gluconate 2-dehydrogenase (EC 1.1.99.3), membrane-bound, gamma subunit |
| Carbohydrates | Di- and oligosaccharides | Trehalose Uptake and Utilization | Beta-phosphoglucomutase (EC 5.4.2.6) |
| Carbohydrates | Di- and oligosaccharides | Trehalose Uptake and Utilization | Trehalose phosphorylase (EC 2.4.1.64) |
| Carbohydrates | Di- and oligosaccharides | Trehalose Biosynthesis | Malto-oligosyltrehalose trehalohydrolase (EC 3.2.1.141) |
| Carbohydrates | Di- and oligosaccharides | Trehalose Biosynthesis | Trehalose phosphorylase (EC 2.4.1.64) |
| Carbohydrates | Di- and oligosaccharides | Trehalose Biosynthesis | Alpha,alpha-trehalose-phosphate synthase [UDP-forming] (EC 2.4.1.15) |
| Carbohydrates | Di- and oligosaccharides | Trehalose Biosynthesis | Glucoamylase (EC 3.2.1.3) |
| Carbohydrates | Di- and oligosaccharides | Trehalose Biosynthesis | Trehalose synthase (EC 5.4.99.16) |
| Carbohydrates | Di- and oligosaccharides | Trehalose Biosynthesis | Trehalose-6-phosphate phosphatase (EC 3.1.3.12) |
| Carbohydrates | Di- and oligosaccharides | Trehalose Biosynthesis | Malto-oligosyltrehalose synthase (EC 5.4.99.15) |
| Carbohydrates | Di- and oligosaccharides | Trehalose Biosynthesis | Alpha-amylase (EC 3.2.1.1) |
| Carbohydrates | Di- and oligosaccharides | Trehalose Biosynthesis | 1,4-alpha-glucan (glycogen) branching enzyme, GH-13-type (EC 2.4.1.18) |
| Carbohydrates | Di- and oligosaccharides | Maltose and Maltodextrin Utilization | Alpha-amylase (EC 3.2.1.1) |
| Carbohydrates | Di- and oligosaccharides | Maltose and Maltodextrin Utilization | Malto-oligosyltrehalose synthase (EC 5.4.99.15) |
| Carbohydrates | Di- and oligosaccharides | Maltose and Maltodextrin Utilization | Maltose O-acetyltransferase (EC 2.3.1.79) |
| Carbohydrates | Di- and oligosaccharides | Maltose and Maltodextrin Utilization | Maltose phosphorylase (EC 2.4.1.8) |
| | | | |

| Carbohydrates | Di- and oligosaccharides | Maltose and Maltodextrin Utilization | Beta-phosphoglucomutase (EC 5.4.2.6) |
|-----------------|---|--|---|
| Carbohydrates | Di- and oligosaccharides Di- and oligosaccharides | Maltose and Maltodextrin Utilization | Glucoamylase (EC 3.2.1.3) |
| • | 2 | Maltose and Maltodextrin Utilization | · · · |
| Carbohydrates | Di- and oligosaccharides | | 4-alpha-glucanotransferase (amylomaltase) (EC 2.4.1.25) |
| Carbohydrates | Di- and oligosaccharides | Maltose and Maltodextrin Utilization | Maltodextrin glucosidase (EC 3.2.1.20) |
| Carbohydrates | Di- and oligosaccharides | Maltose and Maltodextrin Utilization | Glycogen phosphorylase (EC 2.4.1.1) |
| Carbohydrates | Polysaccharides | Glycogen metabolism | 1,4-alpha-glucan (glycogen) branching enzyme, GH-13-type (EC 2.4.1.18) |
| Carbohydrates | Polysaccharides | Glycogen metabolism | Glycogen synthase, ADP-glucose transglucosylase (EC 2.4.1.21) |
| Carbohydrates | Polysaccharides | Glycogen metabolism | Glycogen phosphorylase (EC 2.4.1.1) |
| Carbohydrates | Polysaccharides | Glycogen metabolism | 4-alpha-glucanotransferase (amylomaltase) (EC 2.4.1.25) |
| Carbohydrates | Organic acids | Methylcitrate cycle | 2-methylcitrate synthase (EC 2.3.3.5) |
| Carbohydrates | Organic acids | Methylcitrate cycle | Methylisocitrate lyase (EC 4.1.3.30) |
| Carbohydrates | Organic acids | Methylcitrate cycle | 2-methylcitrate dehydratase (EC 4.2.1.79) |
| Carbohydrates | Organic acids | Lactate utilization | L-lactate dehydrogenase (EC 1.1.2.3) |
| Carbohydrates | Organic acids | Lactate utilization | Predicted L-lactate dehydrogenase, hypothetical protein subunit YkgG |
| Carbohydrates | Organic acids | Lactate utilization | Predicted L-lactate dehydrogenase, Iron-sulfur cluster-binding subunit YkgF |
| Carbohydrates | Organic acids | Lactate utilization | Predicted L-lactate dehydrogenase, Fe-S oxidoreductase subunit YkgE |
| Amino Acids and | Lysine, threonine, methionine, and | Lysine Biosynthesis DAP Pathway, GJO scratch | 4-hydroxy-tetrahydrodipicolinate reductase (EC 1.17.1.8) |
| Derivatives | cysteine | Lysine Biosynthesis DAF Fathway, GJO scratch | 4-nydroxy-tetranydrodipiconnate reductase (EC 1.17.1.8) |
| Amino Acids and | Lysine, threonine, methionine, and | Lysine Biosynthesis DAP Pathway, GJO scratch | N contrib I. I. diaminanimalata decentrilese (EC 2.5.1.47) |
| Derivatives | cysteine | Lysine Biosynthesis DAP Pathway, GJO scratch | N-acetyl-L,L-diaminopimelate deacetylase (EC 3.5.1.47) |
| Amino Acids and | Lysine, threonine, methionine, and | I CIO CIO | A |
| Derivatives | cysteine | Lysine Biosynthesis DAP Pathway, GJO scratch | Aspartokinase (EC 2.7.2.4) |
| Amino Acids and | Lysine, threonine, methionine, and | I ' D' 4 ' DADD 4 CIO 41 | D' ' ' 14 ' (F0.5.11.7) |
| Derivatives | cysteine | Lysine Biosynthesis DAP Pathway, GJO scratch | Diaminopimelate epimerase (EC 5.1.1.7) |
| Amino Acids and | Lysine, threonine, methionine, and | T I DI A I DIDDA GIO | P' ' ' (EQ 41120) |
| Derivatives | cysteine | Lysine Biosynthesis DAP Pathway, GJO scratch | Diaminopimelate decarboxylase (EC 4.1.1.20) |
| Amino Acids and | Lysine, threonine, methionine, and | | |
| Derivatives | cysteine | Lysine Biosynthesis DAP Pathway, GJO scratch | 4-hydroxy-tetrahydrodipicolinate synthase (EC 4.3.3.7) |
| Amino Acids and | Lysine, threonine, methionine, and | | |
| Derivatives | cysteine | Lysine Biosynthesis DAP Pathway, GJO scratch | N-succinyl-L,L-diaminopimelate desuccinylase (EC 3.5.1.18) |
| Amino Acids and | Lysine, threonine, methionine, and | | |
| Derivatives | cysteine | Lysine Biosynthesis DAP Pathway, GJO scratch | 2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-succinyltransferase (EC 2.3.1.117) |
| Amino Acids and | Lysine, threonine, methionine, and | | |
| Derivatives | cysteine | Lysine Biosynthesis DAP Pathway, GJO scratch | Aspartate-semialdehyde dehydrogenase (EC 1.2.1.11) |
| Amino Acids and | Lysine, threonine, methionine, and | | |
| Derivatives | cysteine | Methionine Biosynthesis | S-adenosylmethionine synthetase (EC 2.5.1.6) |
| Amino Acids and | Lysine, threonine, methionine, and | | |
| Derivatives | cysteine | Methionine Biosynthesis | Transcriptional activator MetR |
| Amino Acids and | Lysine, threonine, methionine, and | | |
| Derivatives | cysteine | Methionine Biosynthesis | Serine acetyltransferase (EC 2.3.1.30) |
| | 3 | | |
| Amino Acids and | Lysine, threonine, methionine, and | Methionine Biosynthesis | Cysteine synthase (EC 2.5.1.47) |
| Derivatives | cysteine | | |
| Amino Acids and | Lysine, threonine, methionine, and | Methionine Biosynthesis | Cystathionine beta-lyase (EC 4.4.1.8) |
| Derivatives | cysteine | | |
| Amino Acids and | Lysine, threonine, methionine, and | Methionine Biosynthesis | 5-methyltetrahydropteroyltriglutamatehomocysteine methyltransferase (EC 2.1.1.14) |
| Derivatives | cysteine | • | |
| Amino Acids and | Lysine, threonine, methionine, and | Methionine Biosynthesis | Homoserine kinase (EC 2.7.1.39) |
| Derivatives | cysteine | ř | |
| Amino Acids and | Lysine, threonine, methionine, and | Methionine Biosynthesis | O-succinylhomoserine sulfhydrylase (EC 2.5.1.48) |
| Derivatives | cysteine | • | • • • • • • • |
| | | | |

| Amino Acids and | Lysine, threonine, methionine, and | Methionine Biosynthesis | Cystathionine gamma-lyase (EC 4.4.1.1) | |
|-----------------|------------------------------------|--|--|--|
| Derivatives | cysteine | Media Biosymmetri | eysmanomic gamma iyase (20 iiiiii) | |
| Amino Acids and | Lysine, threonine, methionine, and | Methionine Biosynthesis | O-acetylhomoserine sulfhydrylase (EC 2.5.1.49) | |
| Derivatives | cysteine | • | | |
| Amino Acids and | Lysine, threonine, methionine, and | Methionine Biosynthesis | 5,10-methylenetetrahydrofolate reductase (EC 1.5.1.20) | |
| Derivatives | cysteine | • | | |
| Amino Acids and | Lysine, threonine, methionine, and | Methionine Biosynthesis | Cystathionine beta-synthase (EC 4.2.1.22) | |
| Derivatives | cysteine | · | | |
| Amino Acids and | Lysine, threonine, methionine, and | Methionine Biosynthesis | Homoserine dehydrogenase (EC 1.1.1.3) | |
| Derivatives | cysteine | · | | |
| Amino Acids and | Lysine, threonine, methionine, and | Methionine Biosynthesis | Homoserine O-acetyltransferase (EC 2.3.1.31) | |
| Derivatives | cysteine | • | • | |
| Amino Acids and | Lysine, threonine, methionine, and | Methionine Biosynthesis | 5-methyltetrahydrofolatehomocysteine methyltransferase (EC 2.1.1.13) | |
| Derivatives | cysteine | , | | |
| Amino Acids and | Lysine, threonine, methionine, and | Methionine Biosynthesis | Adenosylhomocysteinase (EC 3.3.1.1) | |
| Derivatives | cysteine | , and the second | | |
| Amino Acids and | Lysine, threonine, methionine, and | Threonine degradation | Threonine dehydrogenase and related Zn-dependent dehydrogenases | |
| Derivatives | cysteine | | ,, | |
| Amino Acids and | Lysine, threonine, methionine, and | Threonine degradation | FIG003492: Threonine dehydrogenase and related Zn-dependent dehydrogenases | |
| Derivatives | cysteine | Theomic degladation | 110005 1/21 Throumie deny drogenase and related 211 dependent deny drogenases | |
| Amino Acids and | Lysine, threonine, methionine, and | Lysine Biosynthesis DAP Pathway | Diaminopimelate decarboxylase (EC 4.1.1.20) | |
| Derivatives | cysteine | Eysine Biosyndiesis Brit Tudiway | Diaminophileate decarooxylase (EC 1.1.1.20) | |
| Amino Acids and | Lysine, threonine, methionine, and | Lysine Biosynthesis DAP Pathway | Diaminopimelate epimerase (EC 5.1.1.7) | |
| Derivatives | cysteine | Eysine Biosyndiesis Brit Tudiway | Diaminophileate epinierase (De 3.1.1.7) | |
| Amino Acids and | Lysine, threonine, methionine, and | Lysine Biosynthesis DAP Pathway | Aspartokinase (EC 2.7.2.4) | |
| Derivatives | cysteine | Lysine Biosyndiesis D/H Taunway | Aspartokiliase (EC 2.7.2.4) | |
| Amino Acids and | Lysine, threonine, methionine, and | Lysine Biosynthesis DAP Pathway | N-acetyl-L,L-diaminopimelate deacetylase (EC 3.5.1.47) | |
| Derivatives | cysteine | Lyslic Biosylidicsis DAI Taulway | N-acctyr-L,L-diaminophinelate deacctylase (EC 5.5.1.47) | |
| Amino Acids and | Lysine, threonine, methionine, and | Lysine Biosynthesis DAP Pathway | 4-hydroxy-tetrahydrodipicolinate reductase (EC 1.17.1.8) | |
| Derivatives | cysteine | Lyslic Biosylidicsis DAI Taulway | 4-nydroxy-terranydrodipiconnate reductase (EC 1.17.1.6) | |
| Amino Acids and | Lysine, threonine, methionine, and | Lysine Biosynthesis DAP Pathway | Aspartate-semialdehyde dehydrogenase (EC 1.2.1.11) | |
| Derivatives | cysteine | Lyslic Biosylidicsis DAI Taulway | Aspartate-schilateriyae denyarogenase (EC 1.2.1.11) | |
| Amino Acids and | Lysine, threonine, methionine, and | Lysine Biosynthesis DAP Pathway | 2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-succinyltransferase (EC 2.3.1.117) | |
| Derivatives | cysteine | Lysine Biosyndiesis D/H Taunway | 2,5,4,5-terranydropyridine-2,0-drearboxyrate 14-succinyitransierase (EC 2.5.1.117) | |
| Amino Acids and | Lysine, threonine, methionine, and | Lysine Biosynthesis DAP Pathway | 4-hydroxy-tetrahydrodipicolinate synthase (EC 4.3.3.7) | |
| Derivatives | cysteine | Lyslic Biosylidicsis DAI Taulway | 4-nydroxy-tetranydrodipiconnate synthase (EC 4.5.5.7) | |
| Amino Acids and | Lysine, threonine, methionine, and | Lysine Biosynthesis DAP Pathway | N-succinyl-L,L-diaminopimelate desuccinylase (EC 3.5.1.18) | |
| Derivatives | cysteine | Lysine Biosynthesis DAF Fathway | N-succinyi-L,L-diaminopiniciate desuccinyiase (EC 3.3.1.16) | |
| Amino Acids and | Lysine, threonine, methionine, and | Threonine and Homoserine Biosynthesis | Aspartokinase (EC 2.7.2.4) | |
| Derivatives | cysteine | Threofine and Homosetine Biosynthesis | Aspartokinase (EC 2.7.2.4) | |
| Amino Acids and | Lysine, threonine, methionine, and | Threonine and Homoserine Biosynthesis | Threonine synthase (EC 4.2.3.1) | |
| Derivatives | cysteine | Threofine and Homosetine Biosynthesis | Threothile Synthase (EC 4.2.3.1) | |
| Amino Acids and | Lysine, threonine, methionine, and | Threonine and Homoserine Biosynthesis | Aspartate aminotransferase (EC 2.6.1.1) | |
| Derivatives | cysteine | Threofine and Homosetine Biosynthesis | Aspartate animotransferase (EC 2.0.1.1) | |
| Amino Acids and | Lysine, threonine, methionine, and | Threonine and Homoserine Biosynthesis | Homoserine dehydrogenase (EC 1.1.1.3) | |
| Derivatives | cysteine | Threofine and Homosetine Biosynthesis | Homosetine denydrogenase (EC 1.1.1.3) | |
| Amino Acids and | Lysine, threonine, methionine, and | Threonine and Homoserine Biosynthesis | Aspartate-semialdehyde dehydrogenase (EC 1.2.1.11) | |
| Derivatives | cysteine | Theornic and Homoscille Diosynthesis | risparance-seminardenyute denyurogenase (EC 1.2.1.11) | |
| Amino Acids and | Lysine, threonine, methionine, and | Threonine and Homoserine Biosynthesis | Homoserine kinase (EC 2.7.1.39) | |
| Derivatives | cysteine | Theornic and Homoscille Diosynthesis | Homoseine kindse (EC 2.7.1.37) | |
| | | | | |

| Amino Acids and Derivatives | Lysine, threonine, methionine, and | Cysteine Biosynthesis | Sulfate adenylyltransferase subunit 1 (EC 2.7.7.4) |
|--------------------------------|--|--|---|
| Amino Acids and Derivatives | cysteine Lysine, threonine, methionine, and cysteine | Cysteine Biosynthesis | Serine acetyltransferase (EC 2.3.1.30) |
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Cysteine Biosynthesis | Sulfate and thiosulfate import ATP-binding protein CysA (EC 3.6.3.25) |
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Cysteine Biosynthesis | Cystathionine gamma-lyase (EC 4.4.1.1) |
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Cysteine Biosynthesis | Cystathionine beta-synthase (EC 4.2.1.22) |
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Cysteine Biosynthesis | Sulfate transport system permease protein CysW |
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Cysteine Biosynthesis | Sulfite reductase [NADPH] hemoprotein beta-component (EC 1.8.1.2) |
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Cysteine Biosynthesis | Sulfate adenylyltransferase subunit 2 (EC 2.7.7.4) |
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Cysteine Biosynthesis | Cysteine synthase (EC 2.5.1.47) |
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Cysteine Biosynthesis | Sulfate permease |
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Cysteine Biosynthesis | Adenylylsulfate kinase (EC 2.7.1.25) |
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Cysteine Biosynthesis | Sulfate transport system permease protein CysT |
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Cysteine Biosynthesis | Sulfate and thiosulfate binding protein CysP |
| Amino Acids and Derivatives | Branched-chain amino acids | Leucine Biosynthesis | 3-isopropylmalate dehydratase small subunit (EC 4.2.1.33) |
| Amino Acids and Derivatives | Branched-chain amino acids | Leucine Biosynthesis | Branched-chain amino acid aminotransferase (EC 2.6.1.42) |
| Amino Acids and Derivatives | Branched-chain amino acids | Leucine Biosynthesis | 3-isopropylmalate dehydrogenase (EC 1.1.1.85) |
| Amino Acids and Derivatives | Branched-chain amino acids | Leucine Biosynthesis | 3-isopropylmalate dehydratase large subunit (EC 4.2.1.33) |
| Amino Acids and Derivatives | Branched-chain amino acids | Leucine Biosynthesis | 2-isopropylmalate synthase (EC 2.3.3.13) |
| Amino Acids and Derivatives | Branched-chain amino acids | Branched-Chain Amino Acid Biosynthesis | (R)-citramalate synthase (EC 2.3.1.182) |
| Amino Acids and Derivatives | Branched-chain amino acids | Branched-Chain Amino Acid Biosynthesis | Threonine dehydratase biosynthetic (EC 4.3.1.19) |
| Amino Acids and Derivatives | Branched-chain amino acids | Branched-Chain Amino Acid Biosynthesis | Valinepyruvate aminotransferase (EC 2.6.1.66) |
| Amino Acids and Derivatives | Branched-chain amino acids | Branched-Chain Amino Acid Biosynthesis | 2-isopropylmalate synthase (EC 2.3.3.13) |
| Amino Acids and Derivatives | Branched-chain amino acids | Branched-Chain Amino Acid Biosynthesis | Branched-chain amino acid aminotransferase (EC 2.6.1.42) |
| Amino Acids and Derivatives | Branched-chain amino acids | Branched-Chain Amino Acid Biosynthesis | Dihydroxy-acid dehydratase (EC 4.2.1.9) |
| Amino Acids and Derivatives | Branched-chain amino acids | Branched-Chain Amino Acid Biosynthesis | 3-isopropylmalate dehydratase small subunit (EC 4.2.1.33) |

| Amino Acids and Derivatives | Branched-chain amino acids | Branched-Chain Amino Acid Biosynthesis | Acetolactate synthase large subunit (EC 2.2.1.6) |
|---|----------------------------|--|--|
| Amino Acids and Derivatives | Branched-chain amino acids | Branched-Chain Amino Acid Biosynthesis | 3-isopropylmalate dehydratase large subunit (EC 4.2.1.33) |
| Amino Acids and Derivatives | Branched-chain amino acids | Branched-Chain Amino Acid Biosynthesis | Acetolactate synthase small subunit (EC 2.2.1.6) |
| Amino Acids and Derivatives | Branched-chain amino acids | Branched-Chain Amino Acid Biosynthesis | 3-isopropylmalate dehydrogenase (EC 1.1.1.85) |
| Amino Acids and Derivatives | Branched-chain amino acids | Leucine Degradation and HMG-CoA Metabolism | Methylcrotonyl-CoA carboxylase carboxyl transferase subunit (EC 6.4.1.4) |
| Amino Acids and Derivatives | Branched-chain amino acids | Leucine Degradation and HMG-CoA Metabolism | Isovaleryl-CoA dehydrogenase (EC 1.3.8.4) |
| Amino Acids and Derivatives | Branched-chain amino acids | Leucine Degradation and HMG-CoA Metabolism | Hydroxymethylglutaryl-CoA lyase (EC 4.1.3.4) |
| Amino Acids and Derivatives | Branched-chain amino acids | Leucine Degradation and HMG-CoA Metabolism | Branched-chain amino acid aminotransferase (EC 2.6.1.42) |
| Amino Acids and Derivatives | Branched-chain amino acids | Leucine Degradation and HMG-CoA Metabolism | Methylcrotonyl-CoA carboxylase biotin-containing subunit (EC 6.4.1.4) |
| Amino Acids and Derivatives | Branched-chain amino acids | Leucine Degradation and HMG-CoA Metabolism | Succinyl-CoA:3-ketoacid-coenzyme A transferase subunit A (EC 2.8.3.5) |
| Amino Acids and Derivatives | Branched-chain amino acids | Leucine Degradation and HMG-CoA Metabolism | Succinyl-CoA:3-ketoacid-coenzyme A transferase subunit B (EC 2.8.3.5) |
| Amino Acids and Derivatives | Branched-chain amino acids | Leucine Degradation and HMG-CoA Metabolism | Methylglutaconyl-CoA hydratase (EC 4.2.1.18) |
| Amino Acids and Derivatives | Branched-chain amino acids | Leucine Degradation and HMG-CoA Metabolism | Branched-chain acyl-CoA dehydrogenase (EC 1.3.99.12) |
| Amino Acids and Derivatives | Branched-chain amino acids | Valine degradation | Branched-chain amino acid aminotransferase (EC 2.6.1.42) |
| Amino Acids and Derivatives Amino Acids and | Branched-chain amino acids | Valine degradation | Methylmalonate-semialdehyde dehydrogenase (EC 1.2.1.27) |
| Derivatives Amino Acids and | Branched-chain amino acids | Valine degradation | 3-hydroxyisobutyryl-CoA hydrolase (EC 3.1.2.4) |
| Derivatives Amino Acids and | Branched-chain amino acids | Valine degradation | 3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35) |
| Derivatives Amino Acids and | Branched-chain amino acids | Valine degradation | 3-hydroxyisobutyrate dehydrogenase (EC 1.1.1.31) |
| Derivatives Amino Acids and | Branched-chain amino acids | Valine degradation | Branched-chain acyl-CoA dehydrogenase (EC 1.3.99.12) |
| Derivatives Amino Acids and | Branched-chain amino acids | Valine degradation | Enoyl-CoA hydratase (EC 4.2.1.17) |
| Derivatives Amino Acids and | Branched-chain amino acids | HMG CoA Synthesis | Methylcrotonyl-CoA carboxylase carboxyl transferase subunit (EC 6.4.1.4) |
| Derivatives Amino Acids and | Branched-chain amino acids | HMG CoA Synthesis | Isovaleryl-CoA dehydrogenase (EC 1.3.8.4) |
| Derivatives Amino Acids and | Branched-chain amino acids | HMG CoA Synthesis | Methylcrotonyl-CoA carboxylase biotin-containing subunit (EC 6.4.1.4) |
| Derivatives Amino Acids and | Branched-chain amino acids | HMG CoA Synthesis | Methylglutaconyl-CoA hydratase (EC 4.2.1.18) |
| Derivatives | Branched-chain amino acids | HMG CoA Synthesis | Hydroxymethylglutaryl-CoA lyase (EC 4.1.3.4) |

| Amino Acids and Derivatives | Amino Acids and Derivatives - no subcategory | Creatine and Creatinine Degradation | N-carbamoylsarcosine amidase (EC 3.5.1.59) |
|---|--|--|---|
| Amino Acids and Derivatives | Amino Acids and Derivatives - no subcategory | Creatine and Creatinine Degradation | N-methylhydantoinase B (EC 3.5.2.14) |
| Amino Acids and Derivatives | Amino Acids and Derivatives - no subcategory | Creatine and Creatinine Degradation | N-methylhydantoinase A (EC 3.5.2.14) |
| Amino Acids and Derivatives | Amino Acids and Derivatives - no subcategory | Creatine and Creatinine Degradation | Creatinine amidohydrolase (EC 3.5.2.10) |
| Amino Acids and Derivatives | Amino Acids and Derivatives - no subcategory | Creatine and Creatinine Degradation | Cytosine deaminase (EC 3.5.4.1) |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Urease subunits | Urease accessory protein UreD |
| Amino Acids and Derivatives Amino Acids and | Arginine; urea cycle, polyamines | Urease subunits | Urease accessory protein UreF |
| Derivatives Amino Acids and | Arginine; urea cycle, polyamines | Urease subunits | Urease accessory protein UreE |
| Derivatives Amino Acids and | Arginine; urea cycle, polyamines | Urease subunits | Urease beta subunit (EC 3.5.1.5) |
| Derivatives Amino Acids and | Arginine; urea cycle, polyamines | Urease subunits | Urease alpha subunit (EC 3.5.1.5) |
| Derivatives Amino Acids and | Arginine; urea cycle, polyamines | Urease subunits | Urease gamma subunit (EC 3.5.1.5) |
| Derivatives Amino Acids and | Arginine; urea cycle, polyamines | Urease subunits | Urease accessory protein UreG |
| Derivatives Amino Acids and | Arginine; urea cycle, polyamines Arginine; urea cycle, polyamines | Urea carboxylase and Allophanate hydrolase cluster Urea carboxylase and Allophanate hydrolase cluster | Allophanate hydrolase (EC 3.5.1.54) Biotin carboxylase (EC 6.3.4.14) |
| Derivatives Amino Acids and | Arginine; urea cycle, polyamines | Urea carboxylase and Allophanate hydrolase cluster | Biotin carboxylase (EC 0.3.4.14) Biotin carboxyl carrier protein |
| Derivatives Amino Acids and | Arginine; urea cycle, polyamines | Urea carboxylase and Allophanate hydrolase cluster | Urea carboxylase (EC 6.3.4.6) |
| Derivatives Amino Acids and | Arginine; urea cycle, polyamines | Urea decomposition | Urea ABC transporter, ATPase protein UrtD |
| Derivatives Amino Acids and | Arginine; urea cycle, polyamines | Urea decomposition | Allophanate hydrolase (EC 3.5.1.54) |
| Derivatives Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Urea decomposition | Urease gamma subunit (EC 3.5.1.5) |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Urea decomposition | Urease accessory protein UreG |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Urea decomposition | Urea ABC transporter, permease protein UrtC |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Urea decomposition | Urease beta subunit (EC 3.5.1.5) |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Urea decomposition | Urea ABC transporter, ATPase protein UrtE |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Urea decomposition | Urease accessory protein UreD |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Urea decomposition | Urea carboxylase-related ABC transporter, permease protein |
| | | | |

| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Urea decomposition | Urea carboxylase (EC 6.3.4.6) |
|--------------------------------|----------------------------------|------------------------------------|---|
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Urea decomposition | Urea ABC transporter, permease protein UrtB |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Urea decomposition | Urease accessory protein UreE |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Urea decomposition | Urease accessory protein UreF |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Urea decomposition | Urease alpha subunit (EC 3.5.1.5) |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Polyamine Metabolism | ABC transporter, periplasmic spermidine putrescine-binding protein PotD (TC 3.A.1.11.1) |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Polyamine Metabolism | Putrescine transport system permease protein PotH (TC 3.A.1.11.2) |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Polyamine Metabolism | Spermidine synthase (EC 2.5.1.16) |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Polyamine Metabolism | Putrescine transport ATP-binding protein PotG (TC 3.A.1.11.2) |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Polyamine Metabolism | Putrescine transport ATP-binding protein PotA (TC 3.A.1.11.1) |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Polyamine Metabolism | Putrescine transport system permease protein Potl (TC 3.A.1.11.2) |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Polyamine Metabolism | Putrescine ABC transporter putrescine-binding protein PotF (TC 3.A.1.11.2) |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Polyamine Metabolism | Ornithine decarboxylase (EC 4.1.1.17) |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Arginine and Ornithine Degradation | Ornithine carbamoyltransferase (EC 2.1.3.3) |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Arginine and Ornithine Degradation | Arginase (EC 3.5.3.1) |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Arginine and Ornithine Degradation | Delta-1-pyrroline-5-carboxylate dehydrogenase (EC 1.2.1.88) |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Arginine and Ornithine Degradation | Ornithine decarboxylase (EC 4.1.1.17) |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Arginine and Ornithine Degradation | NADP-specific glutamate dehydrogenase (EC 1.4.1.4) |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Arginine and Ornithine Degradation | Ornithine cyclodeaminase (EC 4.3.1.12) |
| Amino Acids and Derivatives | Alanine, serine, and glycine | Glycine and Serine Utilization | Glycine dehydrogenase [decarboxylating] (glycine cleavage system P2 protein) (EC 1.4.4.2) |
| Amino Acids and Derivatives | Alanine, serine, and glycine | Glycine and Serine Utilization | D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95) |
| Amino Acids and Derivatives | Alanine, serine, and glycine | Glycine and Serine Utilization | Cystathionine gamma-lyase (EC 4.4.1.1) |
| Amino Acids and Derivatives | Alanine, serine, and glycine | Glycine and Serine Utilization | Aminomethyltransferase (glycine cleavage system T protein) (EC 2.1.2.10) |
| Amino Acids and Derivatives | Alanine, serine, and glycine | Glycine and Serine Utilization | Phosphoserine aminotransferase (EC 2.6.1.52) |
| Amino Acids and Derivatives | Alanine, serine, and glycine | Glycine and Serine Utilization | Glycine cleavage system H protein |

| Amino Acids and Derivatives | Alanine, serine, and glycine | Glycine and Serine Utilization | Seryl-tRNA synthetase (EC 6.1.1.11) |
|---|--|--|---|
| Amino Acids and Derivatives | Alanine, serine, and glycine | Glycine and Serine Utilization | Cystathionine beta-synthase (EC 4.2.1.22) |
| Amino Acids and Derivatives | Alanine, serine, and glycine | Glycine and Serine Utilization | Glycine dehydrogenase [decarboxylating] (glycine cleavage system P1 protein) (EC 1.4.4.2) |
| Amino Acids and Derivatives | Alanine, serine, and glycine | Glycine and Serine Utilization | Serine hydroxymethyltransferase (EC 2.1.2.1) |
| Amino Acids and Derivatives | Alanine, serine, and glycine | Glycine and Serine Utilization | Phosphoserine phosphatase (EC 3.1.3.3) |
| Amino Acids and Derivatives | Alanine, serine, and glycine | Glycine Biosynthesis | Serine hydroxymethyltransferase (EC 2.1.2.1) |
| Amino Acids and Derivatives | Alanine, serine, and glycine | Serine Biosynthesis | Phosphoserine phosphatase (EC 3.1.3.3) |
| Amino Acids and Derivatives | Alanine, serine, and glycine | Serine Biosynthesis | D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95) |
| Amino Acids and Derivatives | Alanine, serine, and glycine | Serine Biosynthesis | Serine hydroxymethyltransferase (EC 2.1.2.1) |
| Amino Acids and Derivatives | Alanine, serine, and glycine | Serine Biosynthesis | Phosphoserine aminotransferase (EC 2.6.1.52) |
| Amino Acids and Derivatives Amino Acids and | Alanine, serine, and glycine | Glycine cleavage system | Glycine cleavage system H protein |
| Derivatives Amino Acids and | Alanine, serine, and glycine | Glycine cleavage system | Aminomethyltransferase (glycine cleavage system T protein) (EC 2.1.2.10) |
| Derivatives Amino Acids and | Alanine, serine, and glycine | Glycine cleavage system | Glycine dehydrogenase [decarboxylating] (glycine cleavage system P2 protein) (EC 1.4.4.2) |
| Derivatives Amino Acids and | Alanine, serine, and glycine | Glycine cleavage system | Glycine dehydrogenase [decarboxylating] (glycine cleavage system P1 protein) (EC 1.4.4.2) |
| Derivatives Amino Acids and | Alanine, serine, and glycine | Alanine biosynthesis | Cysteine desulfurase (EC 2.8.1.7) |
| Derivatives Amino Acids and | Alanine, serine, and glycine | Alanine biosynthesis | Ferredoxin, 2Fe-2S |
| Derivatives Amino Acids and | Alanine, serine, and glycine | Alanine biosynthesis | Valinepyruvate aminotransferase (EC 2.6.1.66) |
| Derivatives Amino Acids and | Alanine, serine, and glycine | Alanine biosynthesis | Alanine racemase (EC 5.1.1.1) |
| Derivatives Amino Acids and | Alanine, serine, and glycine | Alanine biosynthesis | Branched-chain amino acid aminotransferase (EC 2.6.1.42) |
| Derivatives Amino Acids and | Proline and 4-hydroxyproline | Proline Synthesis | Gamma-glutamyl phosphate reductase (EC 1.2.1.41) |
| Derivatives Amino Acids and | Proline and 4-hydroxyproline | Proline Synthesis | Pyrroline-5-carboxylate reductase (EC 1.5.1.2) |
| Derivatives Amino Acids and | Proline and 4-hydroxyproline | Proline Synthesis | RNA-binding C-terminal domain PUA |
| Derivatives Amino Acids and | Proline and 4-hydroxyproline Proline and 4-hydroxyproline | Proline Synthesis Proline Synthesis | NADP-specific glutamate dehydrogenase (EC 1.4.1.4) Glutamate 5-kinase (EC 2.7.2.11) |
| Derivatives Amino Acids and Derivatives | Proline and 4-hydroxyproline | Proline, 4-hydroxyproline uptake and utilization | Delta-1-pyrroline-5-carboxylate dehydrogenase (EC 1.2.1.88) |
| Delivatives | | | |

| Amino Acids and Derivatives | Proline and 4-hydroxyproline | Proline, 4-hydroxyproline uptake and utilization | Proline iminopeptidase (EC 3.4.11.5) |
|---|--------------------------------------|---|---|
| Amino Acids and Derivatives | Histidine Metabolism | Histidine Biosynthesis | Phosphoribosyl-ATP pyrophosphatase (EC 3.6.1.31) |
| Amino Acids and Derivatives | Histidine Metabolism | Histidine Biosynthesis | Imidazoleglycerol-phosphate dehydratase (EC 4.2.1.19) |
| Amino Acids and Derivatives | Histidine Metabolism | Histidine Biosynthesis | Phosphoribosyl-AMP cyclohydrolase (EC 3.5.4.19) |
| Amino Acids and Derivatives | Histidine Metabolism | Histidine Biosynthesis | Histidinol dehydrogenase (EC 1.1.1.23) |
| Amino Acids and Derivatives | Histidine Metabolism | Histidine Biosynthesis | Phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase (EC 5.3.1.16) |
| Amino Acids and Derivatives | Histidine Metabolism | Histidine Biosynthesis | Histidinol-phosphatase [alternative form] (EC 3.1.3.15) |
| Amino Acids and Derivatives | Aromatic amino acids and derivatives | Common Pathway For Synthesis of Aromatic Compounds (DAHP synthase to chorismate) | Chorismate synthase (EC 4.2.3.5) |
| Amino Acids and Derivatives | Aromatic amino acids and derivatives | Common Pathway For Synthesis of Aromatic Compounds (DAHP synthase to chorismate) | 3-dehydroquinate synthase (EC 4.2.3.4) |
| Amino Acids and Derivatives | Aromatic amino acids and derivatives | Common Pathway For Synthesis of Aromatic Compounds (DAHP synthase to chorismate) | $\hbox{2-keto-3-deoxy-D-arabino-heptulosonate-7-phosphate synthase II (EC 2.5.1.54)}$ |
| Amino Acids and Derivatives | Aromatic amino acids and derivatives | Common Pathway For Synthesis of Aromatic Compounds (DAHP synthase to chorismate) | Shikimate 5-dehydrogenase I alpha (EC 1.1.1.25) |
| Amino Acids and Derivatives | Aromatic amino acids and derivatives | Common Pathway For Synthesis of Aromatic Compounds (DAHP synthase to chorismate) | 3-dehydroquinate dehydratase II (EC 4.2.1.10) |
| Amino Acids and Derivatives | Aromatic amino acids and derivatives | Chorismate: Intermediate for synthesis of Tryptophan, PAPA antibiotics, PABA, 3-hydroxyanthranilate and more. | Tryptophan synthase beta chain (EC 4.2.1.20) |
| Amino Acids and Derivatives | Aromatic amino acids and derivatives | Chorismate: Intermediate for synthesis of Tryptophan, PAPA antibiotics, PABA, 3-hydroxyanthranilate and more. | Para-aminobenzoate synthase, aminase component (EC 2.6.1.85) |
| Amino Acids and Derivatives | Aromatic amino acids and derivatives | Chorismate: Intermediate for synthesis of Tryptophan, PAPA antibiotics, PABA, 3-hydroxyanthranilate and more. | Indole-3-glycerol phosphate synthase (EC 4.1.1.48) |
| Amino Acids and Derivatives | Aromatic amino acids and derivatives | Chorismate: Intermediate for synthesis of Tryptophan, PAPA antibiotics, PABA, 3-hydroxyanthranilate and more. | Anthranilate synthase, amidotransferase component (EC 4.1.3.27) |
| Amino Acids and Derivatives | Aromatic amino acids and derivatives | Chorismate: Intermediate for synthesis of Tryptophan, PAPA antibiotics, PABA, 3-hydroxyanthranilate and more. | Tryptophan synthase alpha chain (EC 4.2.1.20) |
| Amino Acids and Derivatives | Aromatic amino acids and derivatives | Chorismate: Intermediate for synthesis of Tryptophan, PAPA antibiotics, PABA, 3-hydroxyanthranilate and more. | Phosphoribosylanthranilate isomerase (EC 5.3.1.24) |
| Amino Acids and Derivatives | Aromatic amino acids and derivatives | Chorismate: Intermediate for synthesis of Tryptophan, PAPA antibiotics, PABA, 3-hydroxyanthranilate and more. | Anthranilate phosphoribosyltransferase (EC 2.4.2.18) |
| Amino Acids and Derivatives | Aromatic amino acids and derivatives | Chorismate: Intermediate for synthesis of Tryptophan, PAPA antibiotics, PABA, 3-hydroxyanthranilate and more. | Para-aminobenzoate synthase, amidotransferase component (EC 2.6.1.85) |
| Amino Acids and Derivatives Amino Acids and | Aromatic amino acids and derivatives | Chorismate: Intermediate for synthesis of Tryptophan, PAPA antibiotics, PABA, 3-hydroxyanthranilate and more. | Phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase (EC 5.3.1.16) |
| Derivatives Amino Acids and | Aromatic amino acids and derivatives | Chorismate: Intermediate for synthesis of Tryptophan, PAPA antibiotics, PABA, 3-hydroxyanthranilate and more. Chorismate: Intermediate for synthesis of Tryptophan, PAPA | Aminodeoxychorismate lyase (EC 4.1.3.38) |
| Derivatives Amino Acids and | Aromatic amino acids and derivatives | antibiotics, PABA, 3-hydroxyanthranilate and more. Chorismate: Intermediate for synthesis of Tryptophan, PAPA | Anthranilate synthase, aminase component (EC 4.1.3.27) |
| Derivatives Amino Acids and | Aromatic amino acids and derivatives | antibiotics, PABA, 3-hydroxyanthranilate and more. | Isochorismatase (EC 3.3.2.1) |
| Derivatives | Aromatic amino acids and derivatives | Tryptophan synthesis | Aminodeoxychorismate lyase (EC 4.1.3.38) |

| Amino Acids and Derivatives | Aromatic amino acids and derivatives | Tryptophan synthesis | Indole-3-glycerol phosphate synthase (EC 4.1.1.48) |
|--------------------------------|--------------------------------------|--|--|
| Amino Acids and Derivatives | Aromatic amino acids and derivatives | Tryptophan synthesis | Tryptophan synthase alpha chain (EC 4.2.1.20) |
| Amino Acids and Derivatives | Aromatic amino acids and derivatives | Tryptophan synthesis | Anthranilate synthase, amidotransferase component (EC 4.1.3.27) |
| Amino Acids and Derivatives | Aromatic amino acids and derivatives | Tryptophan synthesis | Phosphoribosylanthranilate isomerase (EC 5.3.1.24) |
| Amino Acids and Derivatives | Aromatic amino acids and derivatives | Tryptophan synthesis | Anthranilate synthase, aminase component (EC 4.1.3.27) |
| Amino Acids and Derivatives | Aromatic amino acids and derivatives | Tryptophan synthesis | Anthranilate phosphoribosyltransferase (EC 2.4.2.18) |
| Amino Acids and Derivatives | Aromatic amino acids and derivatives | Tryptophan synthesis | Tryptophan synthase beta chain (EC 4.2.1.20) |
| Amino Acids and Derivatives | Aromatic amino acids and derivatives | Tryptophan synthesis | Para-aminobenzoate synthase, aminase component (EC 2.6.1.85) |
| Amino Acids and Derivatives | Aromatic amino acids and derivatives | Tryptophan synthesis | Para-aminobenzoate synthase, amidotransferase component (EC 2.6.1.85) |
| Amino Acids and Derivatives | Aromatic amino acids and derivatives | Aromatic amino acid degradation | 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase (EC 5.3.3) |
| Amino Acids and Derivatives | Aromatic amino acids and derivatives | Aromatic amino acid degradation | 3,4-dihydroxyphenylacetate 2,3-dioxygenase (EC 1.13.11.15) |
| Amino Acids and Derivatives | Aromatic amino acids and derivatives | Aromatic amino acid degradation | Predicted 2-keto-4-pentenoate hydratase/2-oxohepta-3-ene-1,7-dioic acid hydratase |
| Amino Acids and Derivatives | Aromatic amino acids and derivatives | Aromatic amino acid degradation | 5-carboxymethyl-2-oxo-hex-3- ene-1,7-dioate decarboxylase (EC 4.1.1.68) |
| Amino Acids and Derivatives | Aromatic amino acids and derivatives | Aromatic amino acid degradation | Kynurenine formamidase, bacterial (EC 3.5.1.9) |
| Amino Acids and Derivatives | Aromatic amino acids and derivatives | Aromatic amino acid degradation | Phenylalanine-4-hydroxylase (EC 1.14.16.1) |
| Amino Acids and Derivatives | Aromatic amino acids and derivatives | Aromatic amino acid degradation | Putative fumarylacetoacetate (FAA) hydrolase |
| Amino Acids and Derivatives | Aromatic amino acids and derivatives | Aromatic amino acid degradation | 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27) |
| Amino Acids and Derivatives | Aromatic amino acids and derivatives | Aromatic amino acid degradation | 2-oxo-hepta-3-ene-1,7-dioic acid hydratase (EC 4.2) |
| Amino Acids and Derivatives | Aromatic amino acids and derivatives | Phenylalanine and Tyrosine Branches from Chorismate | Prephenate and/or arogenate dehydrogenase (unknown specificity) (EC 1.3.1.12)(EC 1.3.1.43) |
| Amino Acids and Derivatives | Aromatic amino acids and derivatives | Phenylalanine and Tyrosine Branches from Chorismate | Biosynthetic Aromatic amino acid aminotransferase beta (EC 2.6.1.57) |
| Amino Acids and Derivatives | Aromatic amino acids and derivatives | Phenylalanine and Tyrosine Branches from Chorismate | Chorismate mutase I (EC 5.4.99.5) |
| Amino Acids and Derivatives | Aromatic amino acids and derivatives | Phenylalanine and Tyrosine Branches from Chorismate | Prephenate dehydratase (EC 4.2.1.51) |
| Amino Acids and Derivatives | Aromatic amino acids and derivatives | Indole-pyruvate oxidoreductase complex | Indolepyruvate oxidoreductase subunit IorB II (EC 1.2.7.8) |
| Amino Acids and Derivatives | Aromatic amino acids and derivatives | Indole-pyruvate oxidoreductase complex | Indolepyruvate oxidoreductase subunit IorA (EC 1.2.7.8) |
| Amino Acids and Derivatives | Aromatic amino acids and derivatives | Aromatic amino acid interconversions with aryl acids | Indolepyruvate ferredoxin oxidoreductase, alpha and beta subunits |

| Amino Acids and Derivatives | Aromatic amino acids and derivatives | Aromatic amino acid interconversions with aryl acids | Indolepyruvate oxidoreductase subunit IorA (EC 1.2.7.8) |
|---------------------------------------|--|---|---|
| Amino Acids and Derivatives | Aromatic amino acids and derivatives | Aromatic amino acid interconversions with aryl acids | Indolepyruvate oxidoreductase subunit IorB II (EC 1.2.7.8) |
| Amino Acids and Derivatives | Glutamine, glutamate, aspartate, asparagine; ammonia assimilation | Glutamate dehydrogenases | NADP-specific glutamate dehydrogenase (EC 1.4.1.4) |
| Amino Acids and Derivatives | Glutamine, glutamate, aspartate, asparagine; ammonia assimilation | Glutamine synthetases | Glutamine synthetase type I (EC 6.3.1.2) |
| Amino Acids and Derivatives | Glutamine, glutamate, aspartate, asparagine; ammonia assimilation | Glutamine synthetases | Glutamine synthetase type II, eukaryotic (EC 6.3.1.2) |
| Amino Acids and Derivatives | Glutamine, glutamate, aspartate, asparagine; ammonia assimilation | Glutamine, Glutamate, Aspartate and Asparagine Biosynthesis | NADP-specific glutamate dehydrogenase (EC 1.4.1.4) |
| Amino Acids and | Glutamine, glutamate, aspartate, | Glutamine, Glutamate, Aspartate and Asparagine Biosynthesis | Glutamine synthetase type I (EC 6.3.1.2) |
| Derivatives Amino Acids and | asparagine; ammonia assimilation Glutamine, glutamate, aspartate, | Glutamine, Glutamate, Aspartate and Asparagine Biosynthesis | Glutamine synthetase type II, eukaryotic (EC 6.3.1.2) |
| Derivatives Amino Acids and | asparagine; ammonia assimilation Glutamine, glutamate, aspartate, | Glutamine, Glutamate, Aspartate and Asparagine Biosynthesis | Aspartate ammonia-lyase (EC 4.3.1.1) |
| Derivatives Amino Acids and | asparagine; ammonia assimilation Glutamine, glutamate, aspartate, | Glutamine, Glutamate, Aspartate and Asparagine Biosynthesis | Ferredoxin-dependent glutamate synthase (EC 1.4.7.1) |
| Derivatives Amino Acids and | asparagine; ammonia assimilation Glutamine, glutamate, aspartate, | Glutamine, Glutamate, Aspartate and Asparagine Biosynthesis | Glutamate synthase [NADPH] large chain (EC 1.4.1.13) |
| Derivatives Amino Acids and | asparagine; ammonia assimilation Glutamine, glutamate, aspartate, | Glutamine, Glutamate, Aspartate and Asparagine Biosynthesis | Aspartate aminotransferase (EC 2.6.1.1) |
| Derivatives Amino Acids and | asparagine; ammonia assimilation Glutamine, glutamate, aspartate, | Glutamine, Glutamate, Aspartate and Asparagine Biosynthesis | Glutaminase (EC 3.5.1.2) |
| Derivatives Amino Acids and | asparagine; ammonia assimilation Glutamine, glutamate, aspartate, | Glutamine, Glutamate, Aspartate and Asparagine Biosynthesis | Glutamate synthase [NADPH] small chain (EC 1.4.1.13) |
| Derivatives Amino Acids and | asparagine; ammonia assimilation Glutamine, glutamate, aspartate, | Glutamine, Glutamate, Aspartate and Asparagine Biosynthesis | Asparagine synthetase [glutamine-hydrolyzing] (EC 6.3.5.4) |
| Derivatives Metabolism of Aromatic | asparagine; ammonia assimilation Metabolism of Aromatic Compounds - | Aromatic Amin Catabolism | 3,4-dihydroxyphenylacetate 2,3-dioxygenase (EC 1.13.11.15) |
| Compounds Metabolism of Aromatic | no subcategory Metabolism of Aromatic Compounds - | Aromatic Amin Catabolism | Nitrilotriacetate monoxygenase component B (EC 1.14.13) |
| Compounds Metabolism of Aromatic | no subcategory Metabolism of Aromatic Compounds - | Gentisate degradation | Putative n-hydroxybenzoate hydroxylase |
| Compounds Metabolism of Aromatic | no subcategory Metabolism of Aromatic Compounds - | Gentisate degradation | Maleylacetoacetate isomerase (EC 5.2.1.2) |
| Compounds Metabolism of Aromatic | no subcategory Metabolism of Aromatic Compounds - | Gentisate degradation | • |
| Compounds Metabolism of Aromatic | no subcategory Metabolism of Aromatic Compounds - | | 4-hydroxybenzoate transporter |
| Compounds Metabolism of Aromatic | no subcategory Metabolism of Aromatic Compounds - | Gentisate degradation | Fumarylacetoacetate hydrolase family protein |
| Compounds Metabolism of Aromatic | no subcategory Metabolism of Aromatic Compounds - | Gentisate degradation | Gentisate 1,2-dioxygenase (EC 1.13.11.4) |
| Compounds Metabolism of Aromatic | no subcategory Metabolism of central aromatic | Gentisate degradation | putative 4-hydroxybenzoyl-CoA thioesterase |
| Compounds Metabolism of Aromatic | intermediates Metabolism of central aromatic | Catechol branch of beta-ketoadipate pathway | Succinyl-CoA:3-ketoacid-coenzyme A transferase subunit B (EC 2.8.3.5) |
| Compounds | intermediates | Catechol branch of beta-ketoadipate pathway | Succinyl-CoA:3-ketoacid-coenzyme A transferase subunit A (EC 2.8.3.5) |

| Metabolism of Aromatic Compounds | Metabolism of central aromatic intermediates | Catechol branch of beta-ketoadipate pathway | Catechol 1,2-dioxygenase (EC 1.13.11.1) |
|-------------------------------------|--|--|--|
| Metabolism of Aromatic Compounds | Metabolism of central aromatic intermediates | Catechol branch of beta-ketoadipate pathway | Catechol 1,2-dioxygenase 1 (EC 1.13.11.1) |
| Metabolism of Aromatic Compounds | Metabolism of central aromatic intermediates | Catechol branch of beta-ketoadipate pathway | Beta-ketoadipate enol-lactone hydrolase (EC 3.1.1.24) |
| Metabolism of Aromatic Compounds | Metabolism of central aromatic intermediates | Catechol branch of beta-ketoadipate pathway | 3-oxoadipate CoA-transferase subunit B (EC 2.8.3.6) |
| Metabolism of Aromatic Compounds | Metabolism of central aromatic intermediates | Homogentisate pathway of aromatic compound degradation | Transcriptional regulator, IclR family |
| Metabolism of Aromatic Compounds | Metabolism of central aromatic intermediates | Homogentisate pathway of aromatic compound degradation | Homogentisate 1,2-dioxygenase (EC 1.13.11.5) |
| Metabolism of Aromatic Compounds | Metabolism of central aromatic intermediates | Homogentisate pathway of aromatic compound degradation | Fumarylacetoacetase (EC 3.7.1.2) |
| Metabolism of Aromatic Compounds | Metabolism of central aromatic intermediates | Homogentisate pathway of aromatic compound degradation | Maleylacetoacetate isomerase (EC 5.2.1.2) |
| Metabolism of Aromatic Compounds | Metabolism of central aromatic intermediates | Homogentisate pathway of aromatic compound degradation | 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27) |
| Metabolism of Aromatic Compounds | Metabolism of central aromatic intermediates | Salicylate and gentisate catabolism | Putative n-hydroxybenzoate hydroxylase |
| Metabolism of Aromatic Compounds | Metabolism of central aromatic intermediates | Salicylate and gentisate catabolism | Fumarylacetoacetase (EC 3.7.1.2) |
| Metabolism of Aromatic Compounds | Metabolism of central aromatic intermediates | Salicylate and gentisate catabolism | Maleylacetoacetate isomerase (EC 5.2.1.2) |
| Metabolism of Aromatic Compounds | Metabolism of central aromatic intermediates | Salicylate and gentisate catabolism | salicylate esterase |
| Metabolism of Aromatic Compounds | Metabolism of central aromatic intermediates | Salicylate and gentisate catabolism | Gentisate 1,2-dioxygenase (EC 1.13.11.4) |
| Metabolism of Aromatic Compounds | Metabolism of central aromatic intermediates | Salicylate and gentisate catabolism | Salicylate hydroxylase (EC 1.14.13.1) |
| Metabolism of Aromatic Compounds | Metabolism of central aromatic intermediates | Salicylate and gentisate catabolism | 4-hydroxybenzoate transporter |
| Metabolism of Aromatic Compounds | Metabolism of central aromatic intermediates | Salicylate and gentisate catabolism | Fumarylacetoacetate hydrolase family protein |
| Metabolism of Aromatic Compounds | Peripheral pathways for catabolism of aromatic compounds | Salicylate ester degradation | Salicylate hydroxylase (EC 1.14.13.1) |
| Metabolism of Aromatic Compounds | Peripheral pathways for catabolism of aromatic compounds | Salicylate ester degradation | salicylate esterase |
| Metabolism of Aromatic Compounds | Peripheral pathways for catabolism of aromatic compounds | Quinate degradation | 3-dehydroquinate dehydratase II (EC 4.2.1.10) |
| Metabolism of Aromatic Compounds | Peripheral pathways for catabolism of aromatic compounds | p-Hydroxybenzoate degradation | P-hydroxybenzoate hydroxylase (EC 1.14.13.2) |
| Metabolism of Aromatic Compounds | Peripheral pathways for catabolism of aromatic compounds | p-Hydroxybenzoate degradation | 4-hydroxybenzoate transporter |
| Metabolism of Aromatic Compounds | Peripheral pathways for catabolism of aromatic compounds | Benzoate degradation | Benzoate 1,2-dioxygenase alpha subunit (EC 1.14.12.10) |
| Metabolism of Aromatic Compounds | Peripheral pathways for catabolism of aromatic compounds | Benzoate degradation | Benzoylformate decarboxylase (EC 4.1.1.7) |
| Metabolism of Aromatic Compounds | Peripheral pathways for catabolism of aromatic compounds | Benzoate degradation | Ortho-halobenzoate 1,2-dioxygenase beta-ISP protein OhbA |

| Metabolism of Aromatic Compounds | Peripheral pathways for catabolism of aromatic compounds | Benzoate degradation | Ortho-halobenzoate 1,2-dioxygenase alpha-ISP protein OhbB |
|---|--|--------------------------------------|--|
| Resistance to antibiotics and toxic compounds | Resistance to antibiotics | Beta-lactamase | Metal-dependent hydrolases of the beta-lactamase superfamily I |
| Resistance to antibiotics and toxic compounds | Resistance to antibiotics | Resistance to fluoroquinolones | DNA gyrase subunit A (EC 5.99.1.3) |
| Resistance to antibiotics and toxic compounds | Resistance to antibiotics | Resistance to fluoroquinolones | Efflux pump Lde |
| Resistance to antibiotics and toxic compounds | Resistance to antibiotics | Resistance to fluoroquinolones | DNA gyrase subunit B (EC 5.99.1.3) |
| Resistance to antibiotics and toxic compounds | Resistance to antibiotics | Tolerance to colicin E2 | Conserved uncharacterized protein CreA |
| Resistance to antibiotics and toxic compounds | Resistance to heavy metals | Copper homeostasis | Copper tolerance protein |
| Resistance to antibiotics and toxic compounds | Resistance to heavy metals | Copper homeostasis | Cytochrome c heme lyase subunit CcmF |
| Resistance to antibiotics and toxic compounds | Resistance to neavy metals | Copper homeostasis | Multidrug resistance transporter, Bcr/CflA family |
| Resistance to antibiotics and toxic compounds | Resistance to heavy metals | Copper homeostasis | Multicopper oxidase |
| Resistance to antibiotics and toxic compounds | Resistance to heavy metals | Copper homeostasis | Copper-translocating P-type ATPase (EC 3.6.3.4) |
| Resistance to antibiotics and toxic compounds | Resistance to heavy metals | Copper homeostasis | Cytochrome c heme lyase subunit CcmH |
| Resistance to antibiotics and toxic compounds | Resistance to neavy metals | Copper homeostasis | CopG protein |
| Resistance to antibiotics and toxic compounds | Resistance to heavy metals | Copper homeostasis: copper tolerance | Copper homeostasis protein CutE |
| Resistance to antibiotics and toxic compounds | Resistance to neavy metals | Arsenic resistance | Arsenical-resistance protein ACR3 |
| Resistance to antibiotics and toxic compounds | Resistance to heavy metals | Arsenic resistance | Arsenic resistance protein ArsH |
| Resistance to antibiotics and toxic compounds | Resistance to neavy metals | Arsenic resistance | Arsenical resistance operon repressor |
| Resistance to antibiotics and toxic compounds | Resistance to neavy metals | Arsenic resistance | Arsenate reductase (EC 1.20.4.1) |
| Resistance to antibiotics and toxic compounds | Resistance to heavy metals | Mercuric reductase | PF00070 family, FAD-dependent NAD(P)-disulphide oxidoreductase |
| Resistance to antibiotics and toxic compounds | Resistance to heavy metals | Mercuric reductase | Mercuric ion reductase (EC 1.16.1.1) |
| Resistance to antibiotics and toxic compounds | Resistance to neavy metals | Resistance to chromium compounds | Chromate transport protein ChrA |
| Resistance to antibiotics and toxic compounds | Resistance to neavy metals | Mercury resistance operon | Mercuric transport protein, MerT |
| Resistance to antibiotics and toxic compounds | Resistance to heavy metals | Mercury resistance operon | Mercuric ion reductase (EC 1.16.1.1) |
| Resistance to antibiotics and toxic compounds | Resistance to neavy metals | Cobalt-zinc-cadmium resistance | Transcriptional regulator, MerR family |
| Resistance to antibiotics and toxic compounds | Resistance to heavy metals | Cobalt-zinc-cadmium resistance | Cobalt-zinc-cadmium resistance protein |

Resistance to antibiotics and toxic compounds
Resistance to antibiotics and Resistance to heavy metals
Resistance to heavy metals toxic compounds

Cobalt-zinc-cadmium resistance

Cobalt-zinc-cadmium resistance

Probable Co/Zn/Cd efflux system membrane fusion protein

Hypothetical protein involved in heavy metal export

The annotated genes from the genome of strain H3M7-6^T involving in metabolizaton of carbohydrates, amino acids, and aromatic compounds and resistance to antibiotics and heavy metals.

| Category | Subcategory | Subsystem | Annotated genes and its roles |
|--------------------------------|--|--|---|
| Carbohydrates | Central carbohydrate metabolism | Glyoxylate bypass | Citrate synthase (si) (EC 2.3.3.1) |
| Carbohydrates | Central carbohydrate metabolism | Glyoxylate bypass | Malate dehydrogenase (EC 1.1.1.37) |
| Carbohydrates | Central carbohydrate metabolism | Glyoxylate bypass | Isocitrate lyase (EC 4.1.3.1) |
| Carbohydrates | Central carbohydrate metabolism | Glyoxylate bypass | Aconitate hydratase 2 (EC 4.2.1.3) |
| Carbohydrates | Central carbohydrate metabolism | Glyoxylate bypass | Malate synthase G (EC 2.3.3.9) |
| Carbohydrates | Central carbohydrate metabolism | Glyoxylate bypass | Aconitate hydratase (EC 4.2.1.3) |
| Carbohydrates | Central carbohydrate metabolism | Glyoxylate bypass | Isocitrate dehydrogenase phosphatase (EC 2.7.11.5)/kinase (EC 3.1.3) |
| Carbohydrates | Central carbohydrate metabolism | Pyruvate metabolism I: anaplerotic reactions, PEP | Pyruvate, phosphate dikinase (EC 2.7.9.1) |
| Carbohydrates | Central carbohydrate metabolism | Pyruvate metabolism I: anaplerotic reactions, PEP | Pyruvate kinase (EC 2.7.1.40) |
| Carbohydrates | Central carbohydrate metabolism | Pyruvate metabolism I: anaplerotic reactions, PEP | Phosphoenolpyruvate carboxylase (EC 4.1.1.31) |
| Carbohydrates | Central carbohydrate metabolism | Pyruvate metabolism I: anaplerotic reactions, PEP | NADP-dependent malic enzyme (EC 1.1.1.40) |
| Carbohydrates | Central carbohydrate metabolism | Pyruvate metabolism I: anaplerotic reactions, PEP | Phosphoenolpyruvate synthase (EC 2.7.9.2) |
| Carbohydrates | Central carbohydrate metabolism | Pyruvate metabolism I: anaplerotic reactions, PEP | Phosphoenolpyruvate carboxykinase [GTP] (EC 4.1.1.32) |
| Carbohydrates | Central carbohydrate metabolism | Pyruvate Alanine Serine Interconversions | Valinepyruvate aminotransferase (EC 2.6.1.66) |
| Carbohydrates | Central carbohydrate metabolism | Pyruvate Alanine Serine Interconversions | Alanine racemase (EC 5.1.1.1) |
| Carbohydrates | Central carbohydrate metabolism | Pyruvate Alanine Serine Interconversions | Branched-chain amino acid aminotransferase (EC 2.6.1.42) |
| Carbohydrates | Central carbohydrate metabolism | Pyruvate Alanine Serine Interconversions | Omega-amino acidpyruvate aminotransferase (EC 2.6.1.18) |
| Carbohydrates | Central carbohydrate metabolism | TCA Cycle | Succinyl-CoA ligase [ADP-forming] alpha chain (EC 6.2.1.5) |
| Carbohydrates | Central carbohydrate metabolism | TCA Cycle | Malate dehydrogenase (EC 1.1.1.37) |
| Carbohydrates | Central carbohydrate metabolism | TCA Cycle | Succinyl-CoA ligase [ADP-forming] beta chain (EC 6.2.1.5) |
| Carbohydrates | Central carbohydrate metabolism | TCA Cycle | Fumarate hydratase class I, aerobic (EC 4.2.1.2) |
| Carbohydrates | Central carbohydrate metabolism | TCA Cycle | Dihydrolipoamide dehydrogenase of pyruvate dehydrogenase complex (EC 1.8.1.4) |
| Carbohydrates | Central carbohydrate metabolism | TCA Cycle | Dihydrolipoamide dehydrogenase of 2-oxoglutarate dehydrogenase (EC 1.8.1.4) |
| Carbohydrates | Central carbohydrate metabolism | TCA Cycle | Dihydrolipoamide succinyltransferase component (E2) of 2-oxoglutarate dehydrogenase complex (EC 2.3.1.61) |
| Carbohydrates | Central carbohydrate metabolism | TCA Cycle | Aconitate hydratase (EC 4.2.1.3) |
| Carbohydrates | Central carbohydrate metabolism | TCA Cycle | Citrate synthase (si) (EC 2.3.3.1) |
| Carbohydrates | Central carbohydrate metabolism | TCA Cycle | Isocitrate dehydrogenase [NADP] (EC 1.1.1.42) |
| Carbohydrates | Central carbohydrate metabolism | TCA Cycle | Aconitate hydratase 2 (EC 4.2.1.3) |
| Carbohydrates | Central carbohydrate metabolism | TCA Cycle | 2-oxoglutarate dehydrogenase E1 component (EC 1.2.4.2) |
| Carbohydrates | Central carbohydrate metabolism | Pyruvate metabolism II: acetyl-CoA, acetogenesis from pyruvate | Phosphate acetyltransferase (EC 2.3.1.8) |
| Carbohydrates | Central carbohydrate metabolism | Pyruvate metabolism II: acetyl-CoA, acetogenesis from pyruvate | Acetyl-CoA synthetase (ADP-forming) alpha and beta chains, putative |
| Carbohydrates | Central carbohydrate metabolism | Pyruvate metabolism II: acetyl-CoA, acetogenesis from pyruvate | NAD-dependent protein deacetylase of SIR2 family |
| Carbohydrates | Central carbohydrate metabolism | Pyruvate metabolism II: acetyl-CoA, acetogenesis from pyruvate | Dihydrolipoamide dehydrogenase of pyruvate dehydrogenase complex (EC 1.8.1.4) |
| Carbohydrates | Central carbohydrate metabolism | Pyruvate metabolism II: acetyl-CoA, acetogenesis from pyruvate | Pyruvate dehydrogenase E1 component (EC 1.2.4.1) |
| Carbohydrates | Central carbohydrate metabolism | Pyruvate metabolism II: acetyl-CoA, acetogenesis from pyruvate | Acetate kinase (EC 2.7.2.1) |
| Carbohydrates | Central carbohydrate metabolism | Pyruvate metabolism II: acetyl-CoA, acetogenesis from pyruvate | Aldehyde dehydrogenase (EC 1.2.1.3) |
| Carbohydrates | Central carbohydrate metabolism | Pyruvate metabolism II: acetyl-CoA, acetogenesis from pyruvate | Acetate permease ActP (cation/acetate symporter) |
| Carbohydrates | Central carbohydrate metabolism | Pyruvate metabolism II: acetyl-CoA, acetogenesis from pyruvate | Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase complex (EC 2.3.1.12) |
| Carbohydrates Carbohydrates | Central carbohydrate metabolism Central carbohydrate metabolism | Glycolysis and Gluconeogenesis Glycolysis and Gluconeogenesis | Pyruvate,phosphate dikinase (EC 2.7.9.1) Pyruvate kinase (EC 2.7.1.40) |

| Carbohydrates | Central carbohydrate metabolism | Glycolysis and Gluconeogenesis | Phosphoglycerate kinase (EC 2.7.2.3) |
|-----------------|------------------------------------|--|--|
| Carbohydrates | Central carbohydrate metabolism | Glycolysis and Gluconeogenesis | Enolase (EC 4.2.1.11) |
| Carbohydrates | Central carbohydrate metabolism | Glycolysis and Gluconeogenesis | Glucokinase (EC 2.7.1.2) |
| Carbohydrates | Central carbohydrate metabolism | Glycolysis and Gluconeogenesis | Fructose-1,6-bisphosphatase, type I (EC 3.1.3.11) |
| Carbohydrates | Central carbohydrate metabolism | Glycolysis and Gluconeogenesis | Fructose-bisphosphate aldolase class II (EC 4.1.2.13) |
| Carbohydrates | Central carbohydrate metabolism | Glycolysis and Gluconeogenesis | Phosphoenolpyruvate synthase (EC 2.7.9.2) |
| Carbohydrates | Central carbohydrate metabolism | Glycolysis and Gluconeogenesis | Triosephosphate isomerase (EC 5.3.1.1) |
| Carbohydrates | Central carbohydrate metabolism | Glycolysis and Gluconeogenesis | NAD-dependent glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) |
| Carbohydrates | Central carbohydrate metabolism | Glycolysis and Gluconeogenesis | Glucose-6-phosphate isomerase (EC 5.3.1.9) |
| Carbohydrates | Central carbohydrate metabolism | Methylglyoxal Metabolism | Aldehyde dehydrogenase (EC 1.2.1.3) |
| Carbohydrates | Central carbohydrate metabolism | Methylglyoxal Metabolism | Hydroxyacylglutathione hydrolase (EC 3.1.2.6) |
| Carbohydrates | Central carbohydrate metabolism | Methylglyoxal Metabolism | Lactoylglutathione lyase (EC 4.4.1.5) |
| Carbohydrates | Central carbohydrate metabolism | Glycolate, glyoxylate interconversions | D-Lactate dehydrogenase, cytochrome c-dependent (EC 1.1.2.4) |
| Carbohydrates | Central carbohydrate metabolism | Glycolate, glyoxylate interconversions | Glycolate dehydrogenase (EC 1.1.99.14), subunit GlcD |
| Carbohydrates | Central carbohydrate metabolism | Glycolate, glyoxylate interconversions | Glyoxylate reductase (EC 1.1.1.79) |
| Carbohydrates | Central carbohydrate metabolism | Glycolate, glyoxylate interconversions | Glycolate dehydrogenase (EC 1.1.99.14), iron-sulfur subunit GlcF |
| Carbohydrates | Central carbohydrate metabolism | Glycolate, glyoxylate interconversions | Phosphoglycolate phosphatase (EC 3.1.3.18) |
| Carbohydrates | Central carbohydrate metabolism | Glycolate, glyoxylate interconversions | Hydroxypyruvate reductase (EC 1.1.1.81) |
| Carbohydrates | Central carbohydrate metabolism | Glycolate, glyoxylate interconversions | Glycolate dehydrogenase (EC 1.1.99.14), FAD-binding subunit GlcE |
| Carbohydrates | Central carbohydrate metabolism | Glycolate, glyoxylate interconversions | Glyoxylate reductase (EC 1.1.1.26) |
| Carbohydrates | Central carbohydrate metabolism | Dehydrogenase complexes | 2-oxoglutarate dehydrogenase E1 component (EC 1.2.4.2) |
| Carbohydrates | Central carbohydrate metabolism | Dehydrogenase complexes | Cytosol aminopeptidase PepA (EC 3.4.11.1) |
| Carbohydrates | Central carbohydrate metabolism | Dehydrogenase complexes | Dihydrolipoamide dehydrogenase of 2-oxoglutarate dehydrogenase (EC 1.8.1.4) |
| Carbohydrates | Central carbohydrate metabolism | Dehydrogenase complexes | Dihydrolipoamide succinyltransferase component (E2) of 2-oxoglutarate dehydrogenase complex (EC 2.3.1.61) |
| Carbohydrates | Central carbohydrate metabolism | Dehydrogenase complexes | Pyruvate dehydrogenase E1 component (EC 1.2.4.1) |
| Carbohydrates | Central carbohydrate metabolism | Dehydrogenase complexes | Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase complex (EC 2.3.1.12) |
| Carbohydrates | Central carbohydrate metabolism | Dehydrogenase complexes | Leucine-, isoleucine-, valine-, threonine-, and alanine-binding protein |
| Carbohydrates | Monosaccharides | Mannose Metabolism | Phosphomannomutase (EC 5.4.2.8) |
| Carbohydrates | Monosaccharides | Mannose Metabolism | Mannose-6-phosphate isomerase (EC 5.3.1.8) |
| Carbohydrates | Di- and oligosaccharides | Maltose and Maltodextrin Utilization | 4-alpha-glucanotransferase (amylomaltase) (EC 2.4.1.25) |
| Carbohydrates | Di- and oligosaccharides | Maltose and Maltodextrin Utilization | Glycogen phosphorylase (EC 2.4.1.1) |
| Carbohydrates | Polysaccharides | Glycogen metabolism | Glycogen synthase, ADP-glucose transglucosylase (EC 2.4.1.21) |
| Carbohydrates | Polysaccharides | Glycogen metabolism | Glycogen phosphorylase (EC 2.4.1.1) |
| Carbohydrates | Polysaccharides | Glycogen metabolism | 4-alpha-glucanotransferase (amylomaltase) (EC 2.4.1.25) |
| Carbohydrates | Polysaccharides | Glycogen metabolism | 1,4-alpha-glucan (glycogen) branching enzyme, GH-13-type (EC 2.4.1.18) |
| Carbohydrates | Polysaccharides | Glycogen metabolism | Glucose-1-phosphate adenylyltransferase (EC 2.7.7.27) |
| Carbohydrates | Organic acids | Propionyl-CoA to Succinyl-CoA Module | Propionyl-CoA carboxylase biotin-containing subunit (EC 6.4.1.3) |
| Carbohydrates | Organic acids | Propionyl-CoA to Succinyl-CoA Module | Methylmalonyl-CoA epimerase (EC 5.1.99.1) |
| Carbohydrates | Organic acids | Propionyl-CoA to Succinyl-CoA Module | B12 binding domain of Methylmalonyl-CoA mutase (EC 5.4.99.2) |
| Carbohydrates | Organic acids | Propionyl-CoA to Succinyl-CoA Module | Methylmalonyl-CoA mutase (EC 5.4.99.2) |
| Carbohydrates | Organic acids | Propionyl-CoA to Succinyl-CoA Module | Propionyl-CoA carboxylase carboxyl transferase subunit (EC 6.4.1.3) |
| Carbohydrates | Organic acids | Glycerate metabolism | Hydroxypyruvate reductase (EC 1.1.1.81) |
| Carbohydrates | Organic acids | Glycerate metabolism | 2-hydroxy-3-oxopropionate reductase (EC 1.1.1.60) |
| Carbohydrates | Organic acids | Glycerate metabolism | Hydroxypyruvate isomerase (EC 5.3.1.22) |
| Carbohydrates | Organic acids | Glycerate metabolism | Pyruvate kinase (EC 2.7.1.40) |
| Carbohydrates | Organic acids | Glycerate metabolism | Glycerate kinase (EC 2.7.1.31) |
| Amino Acids and | Lysine, threonine, methionine, and | Methionine Degradation | Pyruvate dehydrogenase E1 component (EC 1.2.4.1) |
| Derivatives | cysteine | Meditorine Degradation | 1 yiuvate denyalogenase E1 component (EC 1.2.4.1) |
| Amino Acids and | Lysine, threonine, methionine, and | Methionine Degradation | S-adenosylmethionine synthetase (EC 2.5.1.6) |
| Derivatives | cysteine | Memorine Degradation | 5 decress meaning symbols (Ee 2.5.1.0) |
| Amino Acids and | Lysine, threonine, methionine, and | Methionine Degradation | Adenosylhomocysteinase (EC 3.3.1.1) |
| Derivatives | cysteine | Memorine Degradation | Additional formation of the state of the sta |
| | | | |

| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Methionine Degradation | S-adenosylhomocysteine nucleosidase (EC 3.2.2.9) |
|---|--|--|--|
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Lysine degradation | Lysine decarboxylase (EC 4.1.1.18) |
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Lysine degradation | L-lysine permease |
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Cysteine Biosynthesis | Sulfate adenylyltransferase subunit 2 (EC 2.7.7.4) |
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Cysteine Biosynthesis | Sulfite reductase [NADPH] hemoprotein beta-component (EC 1.8.1.2) |
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Cysteine Biosynthesis | Cys regulon transcriptional activator CysB |
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Cysteine Biosynthesis | Serine acetyltransferase (EC 2.3.1.30) |
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Cysteine Biosynthesis | Cysteine synthase (EC 2.5.1.47) |
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Cysteine Biosynthesis | Sulfate adenylyltransferase subunit 1 (EC 2.7.7.4) |
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Cysteine Biosynthesis | Sulfate and thiosulfate import ATP-binding protein CysA (EC 3.6.3.25) |
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Cysteine Biosynthesis | Sulfate transport system permease protein CysT |
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Cysteine Biosynthesis | Sulfate transport system permease protein CysW |
| Amino Acids and Derivatives Amino Acids and | Lysine, threonine, methionine, and cysteine Lysine, threonine, methionine, and | Cysteine Biosynthesis | Cysteine synthase B (EC 2.5.1.47) |
| Derivatives Amino Acids and | cysteine Lysine, threonine, methionine, and | Cysteine Biosynthesis | Sulfate and thiosulfate binding protein CysP |
| Derivatives Amino Acids and | cysteine Lysine, threonine, methionine, and | Lysine Biosynthesis DAP Pathway, GJO scratch | Aspartokinase (EC 2.7.2.4) |
| Derivatives Amino Acids and | cysteine Lysine, threonine, methionine, and | Lysine Biosynthesis DAP Pathway, GJO scratch | 4-hydroxy-tetrahydrodipicolinate reductase (EC 1.17.1.8) |
| Derivatives Amino Acids and | cysteine Lysine, threonine, methionine, and | Lysine Biosynthesis DAP Pathway, GJO scratch | Diaminopimelate decarboxylase (EC 4.1.1.20) |
| Derivatives Amino Acids and | cysteine Lysine, threonine, methionine, and | Lysine Biosynthesis DAP Pathway, GJO scratch | Diaminopimelate epimerase (EC 5.1.1.7) |
| Derivatives Amino Acids and | cysteine Lysine, threonine, methionine, and | Lysine Biosynthesis DAP Pathway, GJO scratch | 4-hydroxy-tetrahydrodipicolinate synthase (EC 4.3.3.7) |
| Derivatives Amino Acids and | cysteine Lysine, threonine, methionine, and | Lysine Biosynthesis DAP Pathway, GJO scratch Lysine Biosynthesis DAP Pathway, GJO scratch | N-succinyl-L,L-diaminopimelate desuccinylase (EC 3.5.1.18) Aspartate-semialdehyde dehydrogenase (EC 1.2.1.11) |
| Derivatives Amino Acids and | cysteine Lysine, threonine, methionine, and | Lysine Biosynthesis DAP Pathway, GJO scratch | 2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-succinyltransferase (EC 2.3.1.117) |
| Derivatives Amino Acids and | cysteine Lysine, threonine, methionine, and | Methionine Biosynthesis | Homoserine dehydrogenase (EC 1.1.1.3) |
| Derivatives Amino Acids and | cysteine Lysine, threonine, methionine, and | Methionine Biosynthesis | Adenosylhomocysteinase (EC 3.3.1.1) |
| Derivatives Amino Acids and Derivatives | cysteine Lysine, threonine, methionine, and cysteine | Methionine Biosynthesis | S-adenosylhomocysteine nucleosidase (EC 3.2.2.9) |
| | | | |

| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Methionine Biosynthesis | 5,10-methylenetetrahydrofolate reductase (EC 1.5.1.20) |
|---|--|--|---|
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Methionine Biosynthesis | O-acetylhomoserine sulfhydrylase (EC 2.5.1.49) |
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Methionine Biosynthesis | Serine acetyltransferase (EC 2.3.1.30) |
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Methionine Biosynthesis | S-adenosylmethionine synthetase (EC 2.5.1.6) |
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Methionine Biosynthesis | 5-methyltetrahydrofolatehomocysteine methyltransferase (EC 2.1.1.13) |
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Methionine Biosynthesis | Homoserine O-acetyltransferase (EC 2.3.1.31) |
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Methionine Biosynthesis | Homoserine kinase (EC 2.7.1.39) |
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Methionine Biosynthesis | O-succinylhomoserine sulfhydrylase (EC 2.5.1.48) |
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Methionine Biosynthesis | Cysteine synthase (EC 2.5.1.47) |
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Methionine Biosynthesis | Cystathionine beta-lyase (EC 4.4.1.8) |
| Amino Acids and Derivatives Amino Acids and | Lysine, threonine, methionine, and cysteine | Lysine Biosynthesis DAP Pathway | 4-hydroxy-tetrahydrodipicolinate synthase (EC 4.3.3.7) |
| Derivatives Amino Acids and | Lysine, threonine, methionine, and cysteine Lysine, threonine, methionine, and | Lysine Biosynthesis DAP Pathway | N-succinyl-L,L-diaminopimelate desuccinylase (EC 3.5.1.18) |
| Derivatives Amino Acids and | cysteine Lysine, threonine, methionine, and | Lysine Biosynthesis DAP Pathway | Aspartate-semialdehyde dehydrogenase (EC 1.2.1.11) |
| Derivatives Amino Acids and | cysteine Lysine, threonine, methionine, and | Lysine Biosynthesis DAP Pathway | 2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-succinyltransferase (EC 2.3.1.117) |
| Derivatives Amino Acids and | cysteine Lysine, threonine, methionine, and | Lysine Biosynthesis DAP Pathway | Aspartokinase (EC 2.7.2.4) |
| Derivatives Amino Acids and | cysteine Lysine, threonine, methionine, and | Lysine Biosynthesis DAP Pathway | 4-hydroxy-tetrahydrodipicolinate reductase (EC 1.17.1.8) |
| Derivatives Amino Acids and | cysteine Lysine, threonine, methionine, and | Lysine Biosynthesis DAP Pathway | Diaminopimelate decarboxylase (EC 4.1.1.20) |
| Derivatives Amino Acids and | cysteine Lysine, threonine, methionine, and | Lysine Biosynthesis DAP Pathway Threonine and Homoserine Biosynthesis | Diaminopimelate epimerase (EC 5.1.1.7) |
| Derivatives Amino Acids and | cysteine Lysine, threonine, methionine, and | Threonine and Homoserine Biosynthesis | Homoserine kinase (EC 2.7.1.39) Aspartate-semialdehyde dehydrogenase (EC 1.2.1.11) |
| Derivatives Amino Acids and | cysteine Lysine, threonine, methionine, and | Threonine and Homoserine Biosynthesis | Threonine synthase (EC 4.2.3.1) |
| Derivatives Amino Acids and | cysteine Lysine, threonine, methionine, and | Threonine and Homoserine Biosynthesis | Aspartate aminotransferase (EC 2.6.1.1) |
| Derivatives Amino Acids and | cysteine Lysine, threonine, methionine, and | Threonine and Homoserine Biosynthesis | Homoserine dehydrogenase (EC 1.1.1.3) |
| Derivatives Amino Acids and | cysteine Lysine, threonine, methionine, and | Threonine and Homoserine Biosynthesis | Aspartokinase (EC 2.7.2.4) |
| Derivatives Amino Acids and Derivatives | cysteine Amino Acids and Derivatives - no subcategory | Creatine and Creatinine Degradation | Creatinine amidohydrolase (EC 3.5.2.10) |
| Derivatives | Succeeding | | |

| Amino Acids and Derivatives | Amino Acids and Derivatives - no subcategory | Creatine and Creatinine Degradation | Cytosine deaminase (EC 3.5.4.1) |
|--------------------------------|--|--|--|
| Amino Acids and Derivatives | Branched-chain amino acids | HMG CoA Synthesis | Acetoacetyl-CoA synthetase [leucine] (EC 6.2.1.16) |
| Amino Acids and Derivatives | Branched-chain amino acids | HMG CoA Synthesis | Methylcrotonyl-CoA carboxylase carboxyl transferase subunit (EC 6.4.1.4) |
| Amino Acids and Derivatives | Branched-chain amino acids | HMG CoA Synthesis | Isovaleryl-CoA dehydrogenase (EC 1.3.8.4) |
| Amino Acids and Derivatives | Branched-chain amino acids | HMG CoA Synthesis | Hydroxymethylglutaryl-CoA lyase (EC 4.1.3.4) |
| Amino Acids and Derivatives | Branched-chain amino acids | HMG CoA Synthesis | Methylcrotonyl-CoA carboxylase biotin-containing subunit (EC 6.4.1.4) |
| Amino Acids and Derivatives | Branched-chain amino acids | HMG CoA Synthesis | Acetoacetyl-CoA synthetase (EC 6.2.1.16) |
| Amino Acids and Derivatives | Branched-chain amino acids | HMG CoA Synthesis | Methylglutaconyl-CoA hydratase (EC 4.2.1.18) |
| Amino Acids and Derivatives | Branched-chain amino acids | Leucine Degradation and HMG-CoA Metabolism | Acetoacetyl-CoA synthetase [leucine] (EC 6.2.1.16) |
| Amino Acids and Derivatives | Branched-chain amino acids | Leucine Degradation and HMG-CoA Metabolism | Succinyl-CoA:3-ketoacid-coenzyme A transferase subunit A (EC 2.8.3.5) |
| Amino Acids and Derivatives | Branched-chain amino acids | Leucine Degradation and HMG-CoA Metabolism | Methylcrotonyl-CoA carboxylase carboxyl transferase subunit (EC 6.4.1.4) |
| Amino Acids and Derivatives | Branched-chain amino acids | Leucine Degradation and HMG-CoA Metabolism | Isovaleryl-CoA dehydrogenase (EC 1.3.8.4) |
| Amino Acids and Derivatives | Branched-chain amino acids | Leucine Degradation and HMG-CoA Metabolism | Branched-chain amino acid aminotransferase (EC 2.6.1.42) |
| Amino Acids and Derivatives | Branched-chain amino acids | Leucine Degradation and HMG-CoA Metabolism | Hydroxymethylglutaryl-CoA lyase (EC 4.1.3.4) |
| Amino Acids and Derivatives | Branched-chain amino acids | Leucine Degradation and HMG-CoA Metabolism | Methylcrotonyl-CoA carboxylase biotin-containing subunit (EC 6.4.1.4) |
| Amino Acids and Derivatives | Branched-chain amino acids | Leucine Degradation and HMG-CoA Metabolism | Succinyl-CoA:3-ketoacid-coenzyme A transferase subunit B (EC 2.8.3.5) |
| Amino Acids and Derivatives | Branched-chain amino acids | Leucine Degradation and HMG-CoA Metabolism | Methylglutaconyl-CoA hydratase (EC 4.2.1.18) |
| Amino Acids and Derivatives | Branched-chain amino acids | Leucine Degradation and HMG-CoA Metabolism | Branched-chain acyl-CoA dehydrogenase (EC 1.3.99.12) |
| Amino Acids and Derivatives | Branched-chain amino acids | Leucine Degradation and HMG-CoA Metabolism | Acetoacetyl-CoA synthetase (EC 6.2.1.16) |
| Amino Acids and Derivatives | Branched-chain amino acids | Branched-Chain Amino Acid Biosynthesis | Acetolactate synthase small subunit (EC 2.2.1.6) |
| Amino Acids and Derivatives | Branched-chain amino acids | Branched-Chain Amino Acid Biosynthesis | 3-isopropylmalate dehydrogenase (EC 1.1.1.85) |
| Amino Acids and Derivatives | Branched-chain amino acids | Branched-Chain Amino Acid Biosynthesis | 3-isopropylmalate dehydratase large subunit (EC 4.2.1.33) |
| Amino Acids and Derivatives | Branched-chain amino acids | Branched-Chain Amino Acid Biosynthesis | 3-isopropylmalate dehydratase small subunit (EC 4.2.1.33) |
| Amino Acids and Derivatives | Branched-chain amino acids | Branched-Chain Amino Acid Biosynthesis | Dihydroxy-acid dehydratase (EC 4.2.1.9) |
| Amino Acids and Derivatives | Branched-chain amino acids | Branched-Chain Amino Acid Biosynthesis | Branched-chain amino acid aminotransferase (EC 2.6.1.42) |

| Amino Acids and | 5 | D. I. I. G. C. A. C. D. C. A. C. | 1.1 |
|--------------------------------|------------------------------------|--|---|
| Derivatives | Branched-chain amino acids | Branched-Chain Amino Acid Biosynthesis | Acetolactate synthase large subunit (EC 2.2.1.6) |
| Amino Acids and | Branched-chain amino acids | Branched-Chain Amino Acid Biosynthesis | Leucine-responsive regulatory protein, regulator for leucine (or lrp) regulon and high-affinity branched-chain amino acid |
| Derivatives | Dianonea chain annie actus | Stationed Chain i minio i iola Biosymilosis | transport system |
| Amino Acids and | Branched-chain amino acids | Branched-Chain Amino Acid Biosynthesis | Valinepyruvate aminotransferase (EC 2.6.1.66) |
| Derivatives Amino Acids and | | | |
| Derivatives | Branched-chain amino acids | Branched-Chain Amino Acid Biosynthesis | Threonine dehydratase biosynthetic (EC 4.3.1.19) |
| Amino Acids and | | P. I. I. G. L. | A |
| Derivatives | Branched-chain amino acids | Branched-Chain Amino Acid Biosynthesis | 2-isopropylmalate synthase (EC 2.3.3.13) |
| Amino Acids and | Branched-chain amino acids | Leucine Biosynthesis | 2-isopropylmalate synthase (EC 2.3.3.13) |
| Derivatives | Branched-chain animo acids | Ecucine Biosynthesis | 2-isopropymatate syntasse (EC 2.3.3.13) |
| Amino Acids and | Branched-chain amino acids | Leucine Biosynthesis | 3-isopropylmalate dehydratase large subunit (EC 4.2.1.33) |
| Derivatives Amino Acids and | | · | |
| Derivatives | Branched-chain amino acids | Leucine Biosynthesis | Branched-chain amino acid aminotransferase (EC 2.6.1.42) |
| Amino Acids and | | | |
| Derivatives | Branched-chain amino acids | Leucine Biosynthesis | 3-isopropylmalate dehydratase small subunit (EC 4.2.1.33) |
| Amino Acids and | Branched-chain amino acids | Leucine Biosynthesis | 3-isopropylmalate dehydrogenase (EC 1.1.1.85) |
| Derivatives | Branched-Chain animo acids | Leucille Biosynthesis | 5-isopropymalate denydrogenase (EC 1.1.1.65) |
| Amino Acids and | Arginine; urea cycle, polyamines | Putrescine utilization pathways | Uncharacterized protein in putrescine utilization cluster |
| Derivatives | <i>y y y y y y y y y y</i> | 1 5 | |
| Amino Acids and | Arginine; urea cycle, polyamines | Putrescine utilization pathways | Gamma-glutamyl-putrescine synthetase (EC 6.3.1.11) |
| Derivatives Amino Acids and | | | |
| Derivatives | Arginine; urea cycle, polyamines | Putrescine utilization pathways | Gamma-glutamyl-GABA hydrolase (EC 3.5.1.94) |
| Amino Acids and | A salada a sana sanala salamata sa | Determine additional and advances | Common determination of the (FCLA2) |
| Derivatives | Arginine; urea cycle, polyamines | Putrescine utilization pathways | Gamma-glutamyl-putrescine oxidase (EC1.4.3) |
| Amino Acids and | Arginine; urea cycle, polyamines | Putrescine utilization pathways | Gamma-aminobutyrate:alpha-ketoglutarate aminotransferase (EC 2.6.1.19) |
| Derivatives | ragamie, area eyere, perjamines | Tuneseme unization paulinaje | cultural annicously two displacements annicously (20 201117) |
| Amino Acids and | Arginine; urea cycle, polyamines | Arginine and Ornithine Degradation | Delta-1-pyrroline-5-carboxylate dehydrogenase (EC 1.2.1.88) |
| Derivatives Amino Acids and | | | |
| Derivatives | Arginine; urea cycle, polyamines | Arginine and Ornithine Degradation | Arginine decarboxylase (EC 4.1.1.19) |
| Amino Acids and | | 10.31. 7. 13 | Name of the Additional Control |
| Derivatives | Arginine; urea cycle, polyamines | Arginine and Ornithine Degradation | NADP-specific glutamate dehydrogenase (EC 1.4.1.4) |
| Amino Acids and | Arginine; urea cycle, polyamines | Arginine and Ornithine Degradation | Ornithine decarboxylase (EC 4.1.1.17) |
| Derivatives | riigiimie, area cycle, poryammes | riginine and ornamic Degradation | ormanic accarbonymoc (20 mmm) |
| Amino Acids and | Arginine; urea cycle, polyamines | Arginine and Ornithine Degradation | Agmatinase (EC 3.5.3.11) |
| Derivatives Amino Acids and | | - | |
| Derivatives | Arginine; urea cycle, polyamines | Arginine and Ornithine Degradation | Ornithine carbamoyltransferase (EC 2.1.3.3) |
| Amino Acids and | | | |
| Derivatives | Arginine; urea cycle, polyamines | Polyamine Metabolism | Putrescine ABC transporter putrescine-binding protein PotF (TC 3.A.1.11.2) |
| Amino Acids and | Arginine; urea cycle, polyamines | Polyamine Metabolism | Probable two-component sensor, near polyamine transporter |
| Derivatives | ragamie, area cycle, poryamines | 1 organime metabolism | 1100000 two component sensor, near poryamine dansporter |
| Amino Acids and | Arginine; urea cycle, polyamines | Polyamine Metabolism | Ornithine decarboxylase (EC 4.1.1.17) |
| Derivatives Amino Acids and | - · · · · · · | | |
| Derivatives | Arginine; urea cycle, polyamines | Polyamine Metabolism | 5'-methylthioadenosine nucleosidase (EC 3.2.2.16) |
| Delivatives | | | |

| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Polyamine Metabolism | S-adenosylmethionine decarboxylase proenzyme (EC 4.1.1.50), prokaryotic class 1B |
|--------------------------------|----------------------------------|--|--|
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Polyamine Metabolism | Agmatinase (EC 3.5.3.11) |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Polyamine Metabolism | Putrescine transport ATP-binding protein PotG (TC 3.A.1.11.2) |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Polyamine Metabolism | Putrescine transport system permease protein PotI (TC 3.A.1.11.2) |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Polyamine Metabolism | Spermidine synthase (EC 2.5.1.16) |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Polyamine Metabolism | Arginine decarboxylase (EC 4.1.1.19) |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Polyamine Metabolism | Putrescine transport system permease protein PotH (TC 3.A.1.11.2) |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Urea decomposition | Allophanate hydrolase (EC 3.5.1.54) |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Urea decomposition | Urea ABC transporter, ATPase protein UrtD |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Urea decomposition | Urease beta subunit (EC 3.5.1.5) |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Urea decomposition | Urea ABC transporter, permease protein UrtC |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Urea decomposition | Urease gamma subunit (EC 3.5.1.5) |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Urea decomposition | Urease accessory protein UreG |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Urea decomposition | Urease accessory protein UreD |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Urea decomposition | Urea ABC transporter, ATPase protein UrtE |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Urea decomposition | Urease accessory protein UreF |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Urea decomposition | Urease accessory protein UreE |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Urea decomposition | Urea ABC transporter, permease protein UrtB |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Urea decomposition | Urease alpha subunit (EC 3.5.1.5) |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Cyanophycin Metabolism | Cyanophycin synthase (EC 6.3.2.29)(EC 6.3.2.30) |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Cyanophycin Metabolism | Asparagine synthetase [glutamine-hydrolyzing] (EC 6.3.5.4) |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Urea carboxylase and Allophanate hydrolase cluster | Allophanate hydrolase (EC 3.5.1.54) |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Urease subunits | Urease accessory protein UreD |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Urease subunits | Urease gamma subunit (EC 3.5.1.5) |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Urease subunits | Urease accessory protein UreG |

| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Urease subunits | Urease accessory protein UreE |
|---|--|---|---|
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Urease subunits | Urease accessory protein UreF |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Urease subunits | Urease alpha subunit (EC 3.5.1.5) |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Urease subunits | Urease beta subunit (EC 3.5.1.5) |
| Amino Acids and Derivatives | Alanine, serine, and glycine | Glycine and Serine Utilization | Glycine cleavage system H protein |
| Amino Acids and Derivatives | Alanine, serine, and glycine | Glycine and Serine Utilization | Seryl-tRNA synthetase (EC 6.1.1.11) |
| Amino Acids and Derivatives | Alanine, serine, and glycine | Glycine and Serine Utilization | Aminomethyltransferase (glycine cleavage system T protein) (EC 2.1.2.10) |
| Amino Acids and Derivatives Amino Acids and | Alanine, serine, and glycine | Glycine and Serine Utilization | Glycerate kinase (EC 2.7.1.31) |
| Derivatives Amino Acids and | Alanine, serine, and glycine | Glycine and Serine Utilization | Phosphoserine aminotransferase (EC 2.6.1.52) |
| Derivatives Amino Acids and | Alanine, serine, and glycine | Glycine and Serine Utilization | D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95) |
| Derivatives Amino Acids and | Alanine, serine, and glycine | Glycine and Serine Utilization | Glycine dehydrogenase [decarboxylating] (glycine cleavage system P protein) (EC 1.4.4.2) |
| Derivatives Amino Acids and | Alanine, serine, and glycine | Glycine and Serine Utilization | Serine hydroxymethyltransferase (EC 2.1.2.1) |
| Derivatives Amino Acids and | Alanine, serine, and glycine | Glycine and Serine Utilization | Phosphoserine phosphatase (EC 3.1.3.3) |
| Derivatives Amino Acids and | Alanine, serine, and glycine | Glycine Biosynthesis | Serine hydroxymethyltransferase (EC 2.1.2.1) |
| Derivatives Amino Acids and | Alanine, serine, and glycine | Glycine cleavage system | Aminomethyltransferase (glycine cleavage system T protein) (EC 2.1.2.10) |
| Derivatives Amino Acids and | Alanine, serine, and glycine Alanine, serine, and glycine | Glycine cleavage system Glycine cleavage system | Glycine cleavage system H protein Glycine dehydrogenase [decarboxylating] (glycine cleavage system P protein) (EC 1.4.4.2) |
| Derivatives Amino Acids and | Alanine, serine, and glycine | Serine Biosynthesis | D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95) |
| Derivatives Amino Acids and | Alanine, serine, and glycine | Serine Biosynthesis | Phosphoserine phosphatase (EC 3.1.3.3) |
| Derivatives Amino Acids and | Alanine, serine, and glycine | Serine Biosynthesis | Serine hydroxymethyltransferase (EC 2.1.2.1) |
| Derivatives Amino Acids and | Alanine, serine, and glycine | Serine Biosynthesis | Phosphoserine aminotransferase (EC 2.6.1.52) |
| Derivatives Amino Acids and | Alanine, serine, and glycine | Alanine biosynthesis | Valinepyruvate aminotransferase (EC 2.6.1.66) |
| Derivatives Amino Acids and | Alanine, serine, and glycine | Alanine biosynthesis | Ferredoxin, 2Fe-2S |
| Derivatives Amino Acids and | Alanine, serine, and glycine | Alanine biosynthesis | Iron-sulfur cluster assembly scaffold protein IscU |
| Derivatives Amino Acids and Derivatives | Alanine, serine, and glycine | Alanine biosynthesis | Alanine racemase (EC 5.1.1.1) |

| Amino Acids and Derivatives | Alanine, serine, and glycine | Alanine biosynthesis | Cysteine desulfurase (EC 2.8.1.7) |
|---|--------------------------------------|--|---|
| Amino Acids and Derivatives | Alanine, serine, and glycine | Alanine biosynthesis | Chaperone protein HscA |
| Amino Acids and Derivatives | Alanine, serine, and glycine | Alanine biosynthesis | Branched-chain amino acid aminotransferase (EC 2.6.1.42) |
| Amino Acids and Derivatives | Alanine, serine, and glycine | Alanine biosynthesis | Iron-sulfur cluster regulator IscR |
| Amino Acids and Derivatives | Proline and 4-hydroxyproline | Proline, 4-hydroxyproline uptake and utilization | Proline iminopeptidase (EC 3.4.11.5) |
| Amino Acids and Derivatives | Proline and 4-hydroxyproline | Proline, 4-hydroxyproline uptake and utilization | Similar to eukaryotic Peptidyl prolyl 4-hydroxylase, alpha subunit (EC 1.14.11.2) |
| Amino Acids and Derivatives | Proline and 4-hydroxyproline | Proline, 4-hydroxyproline uptake and utilization | ProQ: influences osmotic activation of compatible solute ProP |
| Amino Acids and Derivatives | Proline and 4-hydroxyproline | Proline, 4-hydroxyproline uptake and utilization | Delta-1-pyrroline-5-carboxylate dehydrogenase (EC 1.2.1.88) |
| Amino Acids and Derivatives | Proline and 4-hydroxyproline | Proline Synthesis | Glutamate 5-kinase (EC 2.7.2.11) |
| Amino Acids and Derivatives | Proline and 4-hydroxyproline | Proline Synthesis | NADP-specific glutamate dehydrogenase (EC 1.4.1.4) |
| Amino Acids and Derivatives Amino Acids and | Proline and 4-hydroxyproline | Proline Synthesis | RNA-binding C-terminal domain PUA |
| Derivatives Amino Acids and | Proline and 4-hydroxyproline | Proline Synthesis | Gamma-glutamyl phosphate reductase (EC 1.2.1.41) |
| Derivatives Amino Acids and | Proline and 4-hydroxyproline | Proline Synthesis | Pyrroline-5-carboxylate reductase (EC 1.5.1.2) |
| Derivatives Amino Acids and | Histidine Metabolism | Histidine Biosynthesis | Phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase (EC 5.3.1.16) |
| Derivatives Amino Acids and | Histidine Metabolism | Histidine Biosynthesis | Histidinol-phosphatase (EC 3.1.3.15) |
| Derivatives Amino Acids and | Histidine Metabolism | Histidine Biosynthesis | Imidazoleglycerol-phosphate dehydratase (EC 4.2.1.19) |
| Derivatives Amino Acids and | Histidine Metabolism | Histidine Biosynthesis | ATP phosphoribosyltransferase regulatory subunit (EC 2.4.2.17) |
| Derivatives Amino Acids and | Histidine Metabolism | Histidine Biosynthesis | Histidinol-phosphate aminotransferase (EC 2.6.1.9) |
| Derivatives Amino Acids and | Histidine Metabolism | Histidine Biosynthesis | Histidinol dehydrogenase (EC 1.1.1.23) |
| Derivatives Amino Acids and | Histidine Metabolism | Histidine Biosynthesis | Phosphoribosyl-AMP cyclohydrolase (EC 3.5.4.19) |
| Derivatives Amino Acids and | Histidine Metabolism | Histidine Biosynthesis | Phosphoribosyl-ATP pyrophosphatase (EC 3.6.1.31) |
| Derivatives Amino Acids and | Aromatic amino acids and derivatives | Aromatic amino acid interconversions with aryl acids Chorismate: Intermediate for synthesis of Tryptophan, PAPA | Indolepyruvate ferredoxin oxidoreductase, alpha and beta subunits |
| Derivatives Amino Acids and | Aromatic amino acids and derivatives | antibiotics, PABA, 3-hydroxyanthranilate and more. Chorismate: Intermediate for synthesis of Tryptophan, PAPA | Isochorismatase (EC 3.3.2.1) |
| Derivatives Amino Acids and | Aromatic amino acids and derivatives | antibiotics, PABA, 3-hydroxyanthranilate and more. Chorismate: Intermediate for synthesis of Tryptophan, PAPA | Anthranilate synthase, aminase component (EC 4.1.3.27) |
| Derivatives | Aromatic amino acids and derivatives | antibiotics, PABA, 3-hydroxyanthranilate and more. | Aminodeoxychorismate lyase (EC 4.1.3.38) |

| Amino Acids and | Aromatic amino acids and derivatives | Chorismate: Intermediate for synthesis of Tryptophan, PAPA | Phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase (EC 5.3.1.16) |
|-----------------|---------------------------------------|--|---|
| Derivatives | | antibiotics, PABA, 3-hydroxyanthranilate and more. | |
| Amino Acids and | Aromatic amino acids and derivatives | Chorismate: Intermediate for synthesis of Tryptophan, PAPA | Para-aminobenzoate synthase, amidotransferase component (EC 2.6.1.85) |
| Derivatives | | antibiotics, PABA, 3-hydroxyanthranilate and more. | |
| Amino Acids and | Aromatic amino acids and derivatives | Chorismate: Intermediate for synthesis of Tryptophan, PAPA | Anthranilate phosphoribosyltransferase (EC 2.4.2.18) |
| Derivatives | | antibiotics, PABA, 3-hydroxyanthranilate and more. | |
| Amino Acids and | Aromatic amino acids and derivatives | Chorismate: Intermediate for synthesis of Tryptophan, PAPA | Phosphoribosylanthranilate isomerase (EC 5.3.1.24) |
| Derivatives | | antibiotics, PABA, 3-hydroxyanthranilate and more. | |
| Amino Acids and | Aromatic amino acids and derivatives | Chorismate: Intermediate for synthesis of Tryptophan, PAPA | Tryptophan synthase alpha chain (EC 4.2.1.20) |
| Derivatives | | antibiotics, PABA, 3-hydroxyanthranilate and more. | |
| Amino Acids and | Aromatic amino acids and derivatives | Chorismate: Intermediate for synthesis of Tryptophan, PAPA | Anthranilate synthase, amidotransferase component (EC 4.1.3.27) |
| Derivatives | | antibiotics, PABA, 3-hydroxyanthranilate and more. | |
| Amino Acids and | Aromatic amino acids and derivatives | Chorismate: Intermediate for synthesis of Tryptophan, PAPA | Indole-3-glycerol phosphate synthase (EC 4.1.1.48) |
| Derivatives | | antibiotics, PABA, 3-hydroxyanthranilate and more. | |
| Amino Acids and | Aromatic amino acids and derivatives | Chorismate: Intermediate for synthesis of Tryptophan, PAPA | Tryptophan synthase beta chain (EC 4.2.1.20) |
| Derivatives | Thomasic uninic uctus und derivutives | antibiotics, PABA, 3-hydroxyanthranilate and more. | Trypropriate Systems (DC 11211125) |
| Amino Acids and | Aromatic amino acids and derivatives | Chorismate: Intermediate for synthesis of Tryptophan, PAPA | Para-aminobenzoate synthase, aminase component (EC 2.6.1.85) |
| Derivatives | | antibiotics, PABA, 3-hydroxyanthranilate and more. | (—) |
| Amino Acids and | Aromatic amino acids and derivatives | Common Pathway For Synthesis of Aromatic Compounds | Shikimate kinase I (EC 2.7.1.71) |
| Derivatives | | (DAHP synthase to chorismate) | |
| Amino Acids and | Aromatic amino acids and derivatives | Common Pathway For Synthesis of Aromatic Compounds | Chorismate synthase (EC 4.2.3.5) |
| Derivatives | Thomasic uninic uctus und derivutives | (DAHP synthase to chorismate) | enormano symmot (20 m2.50) |
| Amino Acids and | Aromatic amino acids and derivatives | Common Pathway For Synthesis of Aromatic Compounds | 3-dehydroquinate synthase (EC 4.2.3.4) |
| Derivatives | Thomasic uninic uctus und derivutives | (DAHP synthase to chorismate) | 5 denyaroquilate synthesis (20 1121511) |
| Amino Acids and | Aromatic amino acids and derivatives | Common Pathway For Synthesis of Aromatic Compounds | Shikimate 5-dehydrogenase I alpha (EC 1.1.1.25) |
| Derivatives | Thomasic uninic uctus und derivutives | (DAHP synthase to chorismate) | Similare C denjuregenate Lupia (20 1111125) |
| Amino Acids and | Aromatic amino acids and derivatives | Common Pathway For Synthesis of Aromatic Compounds | 3-dehydroquinate dehydratase II (EC 4.2.1.10) |
| Derivatives | | (DAHP synthase to chorismate) | ·yy (· ··/ |
| Amino Acids and | Aromatic amino acids and derivatives | Common Pathway For Synthesis of Aromatic Compounds | 2-keto-3-deoxy-D-arabino-heptulosonate-7-phosphate synthase I alpha (EC 2.5.1.54) |
| Derivatives | Thomasic uninic uctus und derivutives | (DAHP synthase to chorismate) | 2 note 3 deerly B distance neptutesender / prospilate synamos ruspiu (20 2001101) |
| Amino Acids and | Aromatic amino acids and derivatives | Tryptophan synthesis | Para-aminobenzoate synthase, aminase component (EC 2.6.1.85) |
| Derivatives | | >[| (—) |
| Amino Acids and | Aromatic amino acids and derivatives | Tryptophan synthesis | Tryptophan synthase beta chain (EC 4.2.1.20) |
| Derivatives | | >[| |
| Amino Acids and | Aromatic amino acids and derivatives | Tryptophan synthesis | Para-aminobenzoate synthase, amidotransferase component (EC 2.6.1.85) |
| Derivatives | | >[| () |
| Amino Acids and | Aromatic amino acids and derivatives | Tryptophan synthesis | Anthranilate phosphoribosyltransferase (EC 2.4.2.18) |
| Derivatives | | 31 1 3 | |
| Amino Acids and | Aromatic amino acids and derivatives | Tryptophan synthesis | Anthranilate synthase, amidotransferase component (EC 4.1.3.27) |
| Derivatives | | >[| |
| Amino Acids and | Aromatic amino acids and derivatives | Tryptophan synthesis | Tryptophan synthase alpha chain (EC 4.2.1.20) |
| Derivatives | | >[| |
| Amino Acids and | Aromatic amino acids and derivatives | Tryptophan synthesis | Aminodeoxychorismate lyase (EC 4.1.3.38) |
| Derivatives | Thomasic uninic uctus und derivutives | 11)ptopium synthesis | Timilouvoriyenorisimile lyuse (De 1115/50) |
| Amino Acids and | Aromatic amino acids and derivatives | Tryptophan synthesis | Indole-3-glycerol phosphate synthase (EC 4.1.1.48) |
| Derivatives | Thomasic uninic uctus und derivutives | 11)ptopium synthesis | made 5 glyberer phosphino symmetry |
| Amino Acids and | Aromatic amino acids and derivatives | Tryptophan synthesis | Anthranilate synthase, aminase component (EC 4.1.3.27) |
| Derivatives | | 71 1 J | , |
| Amino Acids and | Aromatic amino acids and derivatives | Tryptophan synthesis | Phosphoribosylanthranilate isomerase (EC 5.3.1.24) |
| Derivatives | | ×1 1 7 | |
| | | | |

Amino Acids and Aromatic amino acids and derivatives Phenylalanine and Tyrosine Branches from Chorismate Prephenate dehydratase (EC 4.2.1.51) Derivatives Amino Acids and Chorismate mutase I (EC 5.4.99.5) Aromatic amino acids and derivatives Phenylalanine and Tyrosine Branches from Chorismate Derivatives Amino Acids and Aromatic amino acids and derivatives Phenylalanine and Tyrosine Branches from Chorismate Biosynthetic Aromatic amino acid aminotransferase alpha (EC 2.6.1.57) Derivatives Amino Acids and Aromatic amino acids and derivatives Phenylalanine and Tyrosine Branches from Chorismate Cyclohexadienyl dehydrogenase (EC 1.3.1.12)(EC 1.3.1.43) Derivatives Amino Acids and Glutamine, glutamate, aspartate, Glutamine, Glutamate, Aspartate and Asparagine Biosynthesis Glutamate synthase [NADPH] small chain (EC 1.4.1.13) Derivatives asparagine; ammonia assimilation Amino Acids and Glutamine, glutamate, aspartate, Glutamate racemase (EC 5.1.1.3) Glutamine, Glutamate, Aspartate and Asparagine Biosynthesis asparagine; ammonia assimilation Derivatives Amino Acids and Glutamine, glutamate, aspartate, Glutamine, Glutamate, Aspartate and Asparagine Biosynthesis Asparagine synthetase [glutamine-hydrolyzing] (EC 6.3.5.4) Derivatives asparagine; ammonia assimilation Glutamine, glutamate, aspartate, Amino Acids and Glutamine, Glutamate, Aspartate and Asparagine Biosynthesis L-asparaginase (EC 3.5.1.1) Derivatives asparagine; ammonia assimilation Amino Acids and Glutamine, glutamate, aspartate, Glutamine, Glutamate, Aspartate and Asparagine Biosynthesis Aspartate aminotransferase (EC 2.6.1.1) Derivatives asparagine; ammonia assimilation Amino Acids and Glutamine, glutamate, aspartate, Glutamine, Glutamate, Aspartate and Asparagine Biosynthesis Glutamate synthase [NADPH] large chain (EC 1.4.1.13) Derivatives asparagine; ammonia assimilation Amino Acids and Glutamine, glutamate, aspartate, Glutamine, Glutamate, Aspartate and Asparagine Biosynthesis Ferredoxin-dependent glutamate synthase (EC 1.4.7.1) Derivatives asparagine; ammonia assimilation Amino Acids and Glutamine, glutamate, aspartate, Leucine-responsive regulatory protein, regulator for leucine (or lrp) regulon and high-affinity branched-chain amino acid Glutamine, Glutamate, Aspartate and Asparagine Biosynthesis Derivatives asparagine; ammonia assimilation transport system Amino Acids and Glutamine, glutamate, aspartate, Glutamine, Glutamate, Aspartate and Asparagine Biosynthesis Glutamine synthetase type I (EC 6.3.1.2) asparagine; ammonia assimilation Derivatives Amino Acids and Glutamine, glutamate, aspartate, Glutamine, Glutamate, Aspartate and Asparagine Biosynthesis NADP-specific glutamate dehydrogenase (EC 1.4.1.4) Derivatives asparagine; ammonia assimilation Amino Acids and Glutamine, glutamate, aspartate, Glutamine synthetases Glutamine synthetase type I (EC 6.3.1.2) Derivatives asparagine; ammonia assimilation Amino Acids and Glutamine, glutamate, aspartate, Glutamate dehydrogenases NADP-specific glutamate dehydrogenase (EC 1.4.1.4) Derivatives asparagine; ammonia assimilation Metabolism of Aromatic Peripheral pathways for catabolism of Benzoate degradation Benzoate 1,2-dioxygenase alpha subunit (EC 1.14.12.10) Compounds aromatic compounds Metabolism of Aromatic Peripheral pathways for catabolism of Benzoate degradation Benzoate transport protein Compounds aromatic compounds Metabolism of Aromatic Peripheral pathways for catabolism of Benzoate degradation Benzoate 1,2-dioxygenase beta subunit (EC 1.14.12.10) Compounds aromatic compounds Metabolism of Aromatic Peripheral pathways for catabolism of Benzoate degradation Ortho-halobenzoate 1,2-dioxygenase alpha-ISP protein OhbB Compounds aromatic compounds Metabolism of Aromatic Peripheral pathways for catabolism of Benzoate degradation Ortho-halobenzoate 1,2-dioxygenase beta-ISP protein OhbA Compounds aromatic compounds Metabolism of Aromatic Peripheral pathways for catabolism of Quinate degradation 3-dehydroquinate dehydratase II (EC 4.2.1.10) Compounds aromatic compounds Metabolism of Aromatic Peripheral pathways for catabolism of Biphenyl Degradation 4-hydroxy-2-oxovalerate aldolase (EC 4.1.3.39) Compounds aromatic compounds Metabolism of Aromatic Peripheral pathways for catabolism of Biphenyl Degradation Large subunit naph/bph dioxygenase Compounds aromatic compounds Metabolism of Aromatic Peripheral pathways for catabolism of Biphenyl Degradation Biphenyl dioxygenase system ferredoxin component Compounds aromatic compounds

| Metabolism of Aromatic Compounds Peripheral pathways for catabolism of aromatic compounds Biphenyl Degradation Biphenyl dioxygenase beta subunit (EC 1.14.12.18) | |
|--|--|
| Metabolism of Aromatic Peripheral pathways for catabolism of Compounds Peripheral pathways for catabolism of aromatic compounds Biphenyl Degradation 2-keto-4-pentenoate hydratase (EC 4.2.1.80) | |
| Metabolism of Aromatic Compounds Peripheral pathways for catabolism of aromatic compounds Peripheral pathways for catabolism of aromatic compounds Biphenyl Degradation 2,3-dihydroxybiphenyl 1,2-dioxygenase (EC 1.13.11.39) | |
| Metabolism of Aromatic Compounds Peripheral pathways for catabolism of aromatic compounds Biphenyl Degradation Acetaldehyde dehydrogenase, acetylating, (EC 1.2.1.10) in gene cluster for degradation Acetaldehyde dehydrogenase, acetylating, (EC 1.2.1.10) in gene cluster for degradation | radation of phenols, cresols, catechol |
| Metabolism of Aromatic Peripheral pathways for catabolism of Compounds Peripheral pathways for catabolism of Compounds Peripheral pathways for catabolism of Sphenyl Degradation 2-hydroxy-6-oxo-6-phenylhexa-2,4-dienoate hydrolase (EC 3.7.1) | |
| Metabolism of Aromatic Peripheral pathways for catabolism of Compounds Biphenyl Degradation Biphenyl Degradation Biphenyl dioxygenase alpha subunit (EC 1.14.12.18) | |
| Metabolism of Aromatic Peripheral pathways for catabolism of Compounds Peripheral pathways for catabolism of Compounds Dihydrodiol dehydrogenase (EC 1.3.1.56) | |
| Metabolism of Aromatic Compounds Salicylate ester degradation Peripheral pathways for catabolism of Compounds Salicylate ester degradation putative facilitator of salicylate uptake | |
| Metabolism of Aromatic Compounds - no Compounds - subcategory Metabolism of Aromatic Metabolism of | |
| Metabolism of Aromatic Compounds Metabolism of Aromatic Compounds Metabolism of Aromatic Me | |
| Compounds subcategory Metabolism of Arometic Compounds ro | |
| Compounds subcategory putative 4-nydroxybenzoyi-CoA tinoesterase Metabolism of Aromatic Metabolism of central aromatic | |
| Compounds intermediates Salicylate and gentisate catabolism Gentisate 1,2-dioxygenase (EC 1.13.11.4) Metabolism of Aromatic Metabolism of central aromatic | |
| Compounds intermediates Salicylate and gentisate catabolism Fumarylacetoacetate hydrolase family protein Metabolism of Aromatic Metabolism of central grounds | |
| Compounds intermediates Salicylate and gentisate catabolism putative facilitator of salicylate uptake Metabolism of Aromatic Metabolism of central aromatic | |
| Compounds intermediates Salicylate and gentisate catabolism Metabolism of Aromatic Metabolism of central aromatic Metabolism of Aromatic Metabolism of central aromatic Metabolism of Aromatic Metabolism of central aromatic Metabolism of Salicylate and gentisate catabolism Salicylate and gentisate catabolism Putative n-hydroxybenzoate hydroxylase Salicylate and gentisate catabolism Salicylate and gentisate ca | |
| Compounds intermediates Metabolism of Aromatic Metabolism of central aromatic Metabolism of Aromatic Metabolism of Control by the first part of the last of last and the second part of the last of the last of last and the second part of the last of last and the second part of the last of last of the last of last and the second part of the last of last la | |
| Compounds intermediates Resistance to antibiotics Tolerance to colicin E2 Catechol branch of beta-ketoadipate pathway Succinyl-CoA:3-ketoacid-coenzyme A transferase subunit B (EC 2.8.3.5) Conserved uncharacterized protein CreA | |
| and toxic compounds Resistance to antibiotics Resistance to antibiotics Resistance to antibiotics Resistance to antibiotics Resistance to fluoroquinolones DNA gyrase subunit B (EC 5.99.1.3) | |
| and toxic compounds Resistance to antibiotics Resistance to fluoroquinolones DNA gyrase subunit A (EC 5.99.1.3) | |
| and toxic compounds Resistance to antibiotics Resistance to heavy metals Cobalt-zinc-cadmium resistance Heavy metal sensor histidine kinase | |
| and toxic compounds Resistance to antibiotics Resistance to heavy metals Cobalt-zinc-cadmium resistance Cobalt-zinc-cadmium resistance Cobalt-zinc-cadmium resistance Cobalt-zinc-cadmium resistance | |
| and toxic compounds Resistance to antibiotics Resistance to heavy metals Cobalt-zinc-cadmium resistance Transcriptional regulator, MerR family | |
| and toxic compounds Resistance to antibiotics and toxic compounds Resistance to heavy metals Cobalt-zinc-cadmium resistance Copper-sensing two-component system response regulator CusR | |

| Resistance to antibiotics and toxic compounds | Resistance |
|---|------------|
| Resistance to antibiotics and toxic compounds | Resistance |
| Resistance to antibiotics and toxic compounds | Resistance |
| Resistance to antibiotics and toxic compounds | Resistance |
| Resistance to antibiotics and toxic compounds | Resistance |
| Resistance to antibiotics and toxic compounds | Resistance |
| Resistance to antibiotics and toxic compounds | Resistance |
| Resistance to antibiotics and toxic compounds | Resistance |
| Resistance to antibiotics | Resistance |
| and toxic compounds Resistance to antibiotics | Resistance |
| and toxic compounds Resistance to antibiotics | Resistance |
| and toxic compounds Resistance to antibiotics | Resistance |
| and toxic compounds | |

| S | Resistance to heavy metals | Resistance to chromium compounds | Chromate transport protein ChrA |
|---|----------------------------|--------------------------------------|---|
| S | Resistance to heavy metals | Copper homeostasis | Copper tolerance protein |
| s | Resistance to heavy metals | Copper homeostasis | Multidrug resistance transporter, Bcr/CflA family |
| s | Resistance to heavy metals | Copper homeostasis | Multicopper oxidase |
| S | Resistance to heavy metals | Copper homeostasis | Copper resistance protein B |
| s | Resistance to heavy metals | Copper homeostasis | Copper chaperone |
| S | Resistance to heavy metals | Copper homeostasis | Copper-translocating P-type ATPase (EC 3.6.3.4) |
| s | Resistance to heavy metals | Copper homeostasis | Copper resistance protein D |
| S | Resistance to heavy metals | Copper homeostasis | CopG protein |
| s | Resistance to heavy metals | Copper homeostasis | Copper-sensing two-component system response regulator CusR |
| s | Resistance to heavy metals | Copper homeostasis: copper tolerance | Magnesium and cobalt efflux protein CorC |
| s | Resistance to heavy metals | Copper homeostasis: copper tolerance | Copper homeostasis protein CutE |

The annotated genes from the genome of strain H39-3-26^T involving in metabolizaton of carbohydrates, amino acids, and aromatic compounds and resistance to antibiotics and heavy metals.

| Category | Subcategory | Subsystem | Annotated genes and its roles |
|---------------|---------------------------------|--|---|
| Carbohydrates | Central carbohydrate metabolism | TCA Cycle | Malate dehydrogenase (EC 1.1.1.37) |
| Carbohydrates | Central carbohydrate metabolism | TCA Cycle | Succinyl-CoA ligase [ADP-forming] alpha chain (EC 6.2.1.5) |
| Carbohydrates | Central carbohydrate metabolism | TCA Cycle | Dihydrolipoamide dehydrogenase of pyruvate dehydrogenase complex (EC 1.8.1.4) |
| Carbohydrates | Central carbohydrate metabolism | TCA Cycle | Succinyl-CoA ligase [ADP-forming] beta chain (EC 6.2.1.5) |
| Carbohydrates | Central carbohydrate metabolism | TCA Cycle | Fumarate hydratase class I, aerobic (EC 4.2.1.2) |
| Carbohydrates | Central carbohydrate metabolism | TCA Cycle | Citrate synthase (si) (EC 2.3.3.1) |
| Carbohydrates | Central carbohydrate metabolism | TCA Cycle | Aconitate hydratase (EC 4.2.1.3) |
| Carbohydrates | Central carbohydrate metabolism | TCA Cycle | Dihydrolipoamide succinyltransferase component (E2) of 2-oxoglutarate dehydrogenase complex (EC 2.3.1.61) |
| Carbohydrates | Central carbohydrate metabolism | TCA Cycle | Dihydrolipoamide dehydrogenase of 2-oxoglutarate dehydrogenase (EC 1.8.1.4) |
| Carbohydrates | Central carbohydrate metabolism | TCA Cycle | Fumarate hydratase class II (EC 4.2.1.2) |
| Carbohydrates | Central carbohydrate metabolism | TCA Cycle | Aconitate hydratase 2 (EC 4.2.1.3) |
| Carbohydrates | Central carbohydrate metabolism | TCA Cycle | 2-oxoglutarate dehydrogenase E1 component (EC 1.2.4.2) |
| Carbohydrates | Central carbohydrate metabolism | TCA Cycle | Isocitrate dehydrogenase [NADP] (EC 1.1.1.42) |
| Carbohydrates | Central carbohydrate metabolism | Pyruvate metabolism II: acetyl-CoA, acetogenesis from pyruvate | NAD-dependent protein deacetylase of SIR2 family |
| Carbohydrates | Central carbohydrate metabolism | Pyruvate metabolism II: acetyl-CoA, acetogenesis from pyruvate | Phosphate acetyltransferase (EC 2.3.1.8) |
| Carbohydrates | Central carbohydrate metabolism | Pyruvate metabolism II: acetyl-CoA, acetogenesis from pyruvate | Dihydrolipoamide dehydrogenase of pyruvate dehydrogenase complex (EC 1.8.1.4) |
| Carbohydrates | Central carbohydrate metabolism | Pyruvate metabolism II: acetyl-CoA, acetogenesis from pyruvate | Pyruvate dehydrogenase E1 component (EC 1.2.4.1) |
| Carbohydrates | Central carbohydrate metabolism | Pyruvate metabolism II: acetyl-CoA, acetogenesis from pyruvate | Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase complex (EC 2.3.1.12) |
| Carbohydrates | Central carbohydrate metabolism | Pyruvate metabolism II: acetyl-CoA, acetogenesis from pyruvate | Acetate permease ActP (cation/acetate symporter) |
| Carbohydrates | Central carbohydrate metabolism | Pyruvate metabolism II: acetyl-CoA, acetogenesis from pyruvate | Acetate kinase (EC 2.7.2.1) |
| Carbohydrates | Central carbohydrate metabolism | Pyruvate metabolism II: acetyl-CoA, acetogenesis from pyruvate | Aldehyde dehydrogenase (EC 1.2.1.3) |
| Carbohydrates | Central carbohydrate metabolism | Glycolysis and Gluconeogenesis | Phosphoenolpyruvate synthase (EC 2.7.9.2) |
| Carbohydrates | Central carbohydrate metabolism | Glycolysis and Gluconeogenesis | Fructose-bisphosphate aldolase class II (EC 4.1.2.13) |
| Carbohydrates | Central carbohydrate metabolism | Glycolysis and Gluconeogenesis | Fructose-1,6-bisphosphatase, type I (EC 3.1.3.11) |
| Carbohydrates | Central carbohydrate metabolism | Glycolysis and Gluconeogenesis | Enolase (EC 4.2.1.11) |
| Carbohydrates | Central carbohydrate metabolism | Glycolysis and Gluconeogenesis | Phosphoglycerate kinase (EC 2.7.2.3) |
| Carbohydrates | Central carbohydrate metabolism | Glycolysis and Gluconeogenesis | Pyruvate kinase (EC 2.7.1.40) |
| Carbohydrates | Central carbohydrate metabolism | Glycolysis and Gluconeogenesis | Pyruvate,phosphate dikinase (EC 2.7.9.1) |

| Carbohydrates | Central carbohydrate metabolism | Glycolysis and Gluconeogenesis | Glucose-6-phosphate isomerase (EC 5.3.1.9) |
|---------------|---------------------------------|---|---|
| Carbohydrates | Central carbohydrate metabolism | Glycolysis and Gluconeogenesis | NAD-dependent glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) |
| Carbohydrates | Central carbohydrate metabolism | Glycolysis and Gluconeogenesis | Triosephosphate isomerase (EC 5.3.1.1) |
| Carbohydrates | Central carbohydrate metabolism | Methylglyoxal Metabolism | Aldehyde dehydrogenase (EC 1.2.1.3) |
| Carbohydrates | Central carbohydrate metabolism | Methylglyoxal Metabolism | Hydroxyacylglutathione hydrolase (EC 3.1.2.6) |
| Carbohydrates | Central carbohydrate metabolism | Methylglyoxal Metabolism | Lactoylglutathione lyase (EC 4.4.1.5) |
| Carbohydrates | Central carbohydrate metabolism | Glycolate, glyoxylate interconversions | D-Lactate dehydrogenase, cytochrome c-dependent (EC 1.1.2.4) |
| Carbohydrates | Central carbohydrate metabolism | Glycolate, glyoxylate interconversions | Glycolate dehydrogenase (EC 1.1.99.14), subunit GlcD |
| Carbohydrates | Central carbohydrate metabolism | Glycolate, glyoxylate interconversions | Glyoxylate reductase (EC 1.1.1.79) |
| Carbohydrates | Central carbohydrate metabolism | Glycolate, glyoxylate interconversions | Glycolate dehydrogenase (EC 1.1.99.14), iron-sulfur subunit GlcF |
| Carbohydrates | Central carbohydrate metabolism | Glycolate, glyoxylate interconversions | Phosphoglycolate phosphatase (EC 3.1.3.18) |
| Carbohydrates | Central carbohydrate metabolism | Glycolate, glyoxylate interconversions | Hydroxypyruvate reductase (EC 1.1.1.81) |
| Carbohydrates | Central carbohydrate metabolism | Glycolate, glyoxylate interconversions | Glyoxylate reductase (EC 1.1.1.26) |
| Carbohydrates | Central carbohydrate metabolism | Glycolate, glyoxylate interconversions | Glycolate dehydrogenase (EC 1.1.99.14), FAD-binding subunit GlcE |
| Carbohydrates | Central carbohydrate metabolism | Dehydrogenase complexes | 2-oxoglutarate dehydrogenase E1 component (EC 1.2.4.2) |
| Carbohydrates | Central carbohydrate metabolism | Dehydrogenase complexes | Dihydrolipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex (EC 2.3.1.168) |
| Carbohydrates | Central carbohydrate metabolism | Dehydrogenase complexes | Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase complex (EC 2.3.1.12) |
| Carbohydrates | Central carbohydrate metabolism | Dehydrogenase complexes | Pyruvate dehydrogenase E1 component (EC 1.2.4.1) |
| Carbohydrates | Central carbohydrate metabolism | Dehydrogenase complexes | Dihydrolipoamide dehydrogenase of 2-oxoglutarate dehydrogenase (EC 1.8.1.4) |
| Carbohydrates | Central carbohydrate metabolism | Dehydrogenase complexes | Cytosol aminopeptidase PepA (EC 3.4.11.1) |
| Carbohydrates | Central carbohydrate metabolism | Dehydrogenase complexes | Dihydrolipoamide succinyltransferase component (E2) of 2-oxoglutarate dehydrogenase complex (EC 2.3.1.61) |
| Carbohydrates | Central carbohydrate metabolism | Pyruvate metabolism I: anaplerotic reactions, PEP | Phosphoenolpyruvate carboxykinase [GTP] (EC 4.1.1.32) |
| Carbohydrates | Central carbohydrate metabolism | Pyruvate metabolism I: anaplerotic reactions, PEP | Phosphoenolpyruvate synthase (EC 2.7.9.2) |
| Carbohydrates | Central carbohydrate metabolism | Pyruvate metabolism I: anaplerotic reactions, PEP | NADP-dependent malic enzyme (EC 1.1.1.40) |
| Carbohydrates | Central carbohydrate metabolism | Pyruvate metabolism I: anaplerotic reactions, PEP | Pyruvate,phosphate dikinase (EC 2.7.9.1) |
| Carbohydrates | Central carbohydrate metabolism | Pyruvate metabolism I: anaplerotic reactions, PEP | Pyruvate kinase (EC 2.7.1.40) |
| Carbohydrates | Central carbohydrate metabolism | Glyoxylate bypass | Malate synthase G (EC 2.3.3.9) |
| Carbohydrates | Central carbohydrate metabolism | Glyoxylate bypass | Isocitrate dehydrogenase phosphatase (EC 2.7.11.5)/kinase (EC 3.1.3) |
| Carbohydrates | Central carbohydrate metabolism | Glyoxylate bypass | Aconitate hydratase (EC 4.2.1.3) |
| Carbohydrates | Central carbohydrate metabolism | Glyoxylate bypass | Malate dehydrogenase (EC 1.1.1.37) |
| | | | |

| Carbohydrates | Central carbohydrate metabolism | Glyoxylate bypass | Citrate synthase (si) (EC 2.3.3.1) |
|--------------------------------|---|---|--|
| Carbohydrates | Central carbohydrate metabolism | Glyoxylate bypass | Isocitrate lyase (EC 4.1.3.1) |
| Carbohydrates | Central carbohydrate metabolism | Glyoxylate bypass | Aconitate hydratase 2 (EC 4.2.1.3) |
| Carbohydrates | Central carbohydrate metabolism | Pyruvate Alanine Serine Interconversions | Alanine racemase (EC 5.1.1.1) |
| Carbohydrates | Central carbohydrate metabolism | Pyruvate Alanine Serine Interconversions | Valinepyruvate aminotransferase (EC 2.6.1.66) |
| Carbohydrates | Central carbohydrate metabolism | Pyruvate Alanine Serine Interconversions | Branched-chain amino acid aminotransferase (EC 2.6.1.42) |
| Carbohydrates | Central carbohydrate metabolism | Pyruvate Alanine Serine Interconversions | D-alanine aminotransferase (EC 2.6.1.21) |
| Carbohydrates | Central carbohydrate metabolism | Pyruvate Alanine Serine Interconversions | Omega-amino acidpyruvate aminotransferase (EC 2.6.1.18) |
| Carbohydrates | Monosaccharides | Mannose Metabolism | Mannose-6-phosphate isomerase (EC 5.3.1.8) |
| Carbohydrates | Monosaccharides | Mannose Metabolism | Phosphomannomutase (EC 5.4.2.8) |
| Carbohydrates | Di- and oligosaccharides | Trehalose Biosynthesis | Alpha,alpha-trehalose-phosphate synthase [UDP-forming] (EC 2.4.1.15) |
| Carbohydrates | Di- and oligosaccharides | Trehalose Biosynthesis | Trehalose-6-phosphate phosphatase (EC 3.1.3.12) |
| Carbohydrates | Di- and oligosaccharides | Trehalose Biosynthesis | Glucoamylase (EC 3.2.1.3) |
| Carbohydrates | Organic acids | Propionyl-CoA to Succinyl-CoA Module | Propionyl-CoA carboxylase carboxyl transferase subunit (EC 6.4.1.3) |
| Carbohydrates | Organic acids | Propionyl-CoA to Succinyl-CoA Module | Methylmalonyl-CoA epimerase (EC 5.1.99.1) |
| Carbohydrates | Organic acids | Propionyl-CoA to Succinyl-CoA Module | Propionyl-CoA carboxylase biotin-containing subunit (EC 6.4.1.3) |
| Carbohydrates | Organic acids | Propionyl-CoA to Succinyl-CoA Module | B12 binding domain of Methylmalonyl-CoA mutase (EC 5.4.99.2) |
| Carbohydrates | Organic acids | Propionyl-CoA to Succinyl-CoA Module | Methylmalonyl-CoA mutase (EC 5.4.99.2) |
| Amino Acids and Derivatives | Glutamine, glutamate, aspartate, asparagine; ammonia assimilation | Glutamine, Glutamate, Aspartate and Asparagine Biosynthesis | L-asparaginase (EC 3.5.1.1) |
| Amino Acids and Derivatives | Glutamine, glutamate, aspartate, asparagine; ammonia assimilation | Glutamine, Glutamate, Aspartate and Asparagine Biosynthesis | Glutaminase (EC 3.5.1.2) |
| Amino Acids and Derivatives | Glutamine, glutamate, aspartate, asparagine; ammonia assimilation | Glutamine, Glutamate, Aspartate and Asparagine Biosynthesis | Glutamate synthase [NADPH] small chain (EC 1.4.1.13) |
| Amino Acids and Derivatives | Glutamine, glutamate, aspartate, asparagine; ammonia assimilation | Glutamine, Glutamate, Aspartate and Asparagine Biosynthesis | Glutamate racemase (EC 5.1.1.3) |
| Amino Acids and Derivatives | Glutamine, glutamate, aspartate, asparagine; ammonia assimilation | Glutamine, Glutamate, Aspartate and Asparagine Biosynthesis | Aspartate aminotransferase (EC 2.6.1.1) |
| Amino Acids and Derivatives | Glutamine, glutamate, aspartate, asparagine; ammonia assimilation | Glutamine, Glutamate, Aspartate and Asparagine Biosynthesis | NAD-specific glutamate dehydrogenase (EC 1.4.1.2) |
| Amino Acids and Derivatives | Glutamine, glutamate, aspartate, asparagine; ammonia assimilation | Glutamine, Glutamate, Aspartate and Asparagine Biosynthesis | Glutamine synthetase type I (EC 6.3.1.2) |
| Amino Acids and Derivatives | Glutamine, glutamate, aspartate, asparagine; ammonia assimilation | Glutamine, Glutamate, Aspartate and Asparagine Biosynthesis | Leucine-responsive regulatory protein, regulator for leucine (or lrp) regulon and high-affinity branched-chain amino acid transport system |
| Amino Acids and Derivatives | Glutamine, glutamate, aspartate, asparagine; ammonia assimilation | Glutamine, Glutamate, Aspartate and Asparagine Biosynthesis | Ferredoxin-dependent glutamate synthase (EC 1.4.7.1) |
| Amino Acids and Derivatives | Glutamine, glutamate, aspartate, asparagine; ammonia assimilation | Glutamine, Glutamate, Aspartate and Asparagine Biosynthesis | Glutamate synthase [NADPH] large chain (EC 1.4.1.13) |
| | | | |

| Amino Acids and Derivatives | Glutamine, glutamate, aspartate, asparagine; ammonia assimilation | Glutamine, Glutamate, Aspartate and Asparagine Biosynthesis | NADP-specific glutamate dehydrogenase (EC 1.4.1.4) |
|---|---|---|---|
| Amino Acids and Derivatives | Glutamine, glutamate, aspartate, asparagine; ammonia assimilation | Glutamine synthetases | Glutamine synthetase type I (EC 6.3.1.2) |
| Amino Acids and Derivatives | Glutamine, glutamate, aspartate, asparagine; ammonia assimilation | Glutamate dehydrogenases | NAD-specific glutamate dehydrogenase (EC 1.4.1.2) |
| Amino Acids and Derivatives | Glutamine, glutamate, aspartate, asparagine; ammonia assimilation | Glutamate dehydrogenases | NADP-specific glutamate dehydrogenase (EC 1.4.1.4) |
| Amino Acids and Derivatives | Aromatic amino acids and derivatives | Chorismate: Intermediate for synthesis of Tryptophan, PAPA antibiotics, PABA, 3-hydroxyanthranilate and more. | Tryptophan synthase beta chain (EC 4.2.1.20) |
| Amino Acids and Derivatives | Aromatic amino acids and derivatives | Chorismate: Intermediate for synthesis of Tryptophan, PAPA antibiotics, PABA, 3-hydroxyanthranilate and more. | Para-aminobenzoate synthase, amidotransferase component (EC 2.6.1.85) |
| Amino Acids and Derivatives | Aromatic amino acids and derivatives | Chorismate: Intermediate for synthesis of Tryptophan, PAPA antibiotics, PABA, 3-hydroxyanthranilate and more. | Phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase (EC 5.3.1.16) |
| Amino Acids and Derivatives | Aromatic amino acids and derivatives | Chorismate: Intermediate for synthesis of Tryptophan, PAPA antibiotics, PABA, 3-hydroxyanthranilate and more. | Indole-3-glycerol phosphate synthase (EC 4.1.1.48) |
| Amino Acids and Derivatives | Aromatic amino acids and derivatives | Chorismate: Intermediate for synthesis of Tryptophan, PAPA antibiotics, PABA, 3-hydroxyanthranilate and more. | Anthranilate synthase, amidotransferase component (EC 4.1.3.27) |
| Amino Acids and Derivatives | Aromatic amino acids and derivatives | Chorismate: Intermediate for synthesis of Tryptophan, PAPA antibiotics, PABA, 3-hydroxyanthranilate and more. | Tryptophan synthase alpha chain (EC 4.2.1.20) |
| Amino Acids and Derivatives | Aromatic amino acids and derivatives | Chorismate: Intermediate for synthesis of Tryptophan, PAPA antibiotics, PABA, 3-hydroxyanthranilate and more. | Phosphoribosylanthranilate isomerase (EC 5.3.1.24) |
| Amino Acids and Derivatives | Aromatic amino acids and derivatives | Chorismate: Intermediate for synthesis of Tryptophan, PAPA antibiotics, PABA, 3-hydroxyanthranilate and more. | Anthranilate synthase, aminase component (EC 4.1.3.27) |
| Amino Acids and Derivatives | Aromatic amino acids and derivatives | Chorismate: Intermediate for synthesis of Tryptophan, PAPA antibiotics, PABA, 3-hydroxyanthranilate and more. | Anthranilate phosphoribosyltransferase (EC 2.4.2.18) |
| Amino Acids and Derivatives | Aromatic amino acids and derivatives | Chorismate: Intermediate for synthesis of Tryptophan, PAPA antibiotics, PABA, 3-hydroxyanthranilate and more. | Isochorismatase (EC 3.3.2.1) |
| Amino Acids and Derivatives | Aromatic amino acids and derivatives | Aromatic amino acid interconversions with aryl acids | Indolepyruvate ferredoxin oxidoreductase, alpha and beta subunits |
| Amino Acids and Derivatives | Aromatic amino acids and derivatives | Tryptophan synthesis | Anthranilate synthase, aminase component (EC 4.1.3.27) |
| Amino Acids and Derivatives | Aromatic amino acids and derivatives | Tryptophan synthesis | Phosphoribosylanthranilate isomerase (EC 5.3.1.24) |
| Amino Acids and Derivatives | Aromatic amino acids and derivatives | Tryptophan synthesis | Anthranilate synthase, amidotransferase component (EC 4.1.3.27) |
| Amino Acids and Derivatives | Aromatic amino acids and derivatives | Tryptophan synthesis | Tryptophan synthase alpha chain (EC 4.2.1.20) |
| Amino Acids and Derivatives | Aromatic amino acids and derivatives | Tryptophan synthesis | Indole-3-glycerol phosphate synthase (EC 4.1.1.48) |
| Amino Acids and Derivatives Amino Acids and | Aromatic amino acids and derivatives | Tryptophan synthesis | Anthranilate phosphoribosyltransferase (EC 2.4.2.18) |
| Derivatives Amino Acids and | Aromatic amino acids and derivatives | Tryptophan synthesis | Para-aminobenzoate synthase, amidotransferase component (EC 2.6.1.85) |
| Derivatives Amino Acids and | Aromatic amino acids and derivatives | Tryptophan synthesis Common Pathway For Synthesis of Aromatic Compounds (DAHP | Tryptophan synthase beta chain (EC 4.2.1.20) |
| Derivatives Amino Acids and | Aromatic amino acids and derivatives | synthase to chorismate) Common Pathway For Synthesis of Aromatic Compounds (DAHP Common Pathway For Synthesis of Aromatic Compounds (DAHP | Shikimate 5-dehydrogenase I alpha (EC 1.1.1.25) |
| Derivatives | Aromatic amino acids and derivatives | synthase to chorismate) | 3-dehydroquinate dehydratase II (EC 4.2.1.10) |

| Amino Acids and | | Common Pathway For Synthesis of Aromatic Compounds (DAHP | |
|-----------------------------|---------------------------------------|--|---|
| Derivatives | Aromatic amino acids and derivatives | synthase to chorismate) | 2-keto-3-deoxy-D-arabino-heptulosonate-7-phosphate synthase I alpha (EC 2.5.1.54) |
| Amino Acids and | | Common Pathway For Synthesis of Aromatic Compounds (DAHP | ALTI- 11 - X (TO A T 1 T 1) |
| Derivatives | Aromatic amino acids and derivatives | synthase to chorismate) | Shikimate kinase I (EC 2.7.1.71) |
| Amino Acids and | | Common Pathway For Synthesis of Aromatic Compounds (DAHP | |
| Derivatives | Aromatic amino acids and derivatives | synthase to chorismate) | Chorismate synthase (EC 4.2.3.5) |
| Amino Acids and | | Common Pathway For Synthesis of Aromatic Compounds (DAHP | |
| Derivatives | Aromatic amino acids and derivatives | synthase to chorismate) | 3-dehydroquinate synthase (EC 4.2.3.4) |
| Amino Acids and | | • | D. J. (11.1 ((FG.42171) |
| Derivatives | Aromatic amino acids and derivatives | Phenylalanine and Tyrosine Branches from Chorismate | Prephenate dehydratase (EC 4.2.1.51) |
| Amino Acids and | | N 11: IT : D 1 C CI : . | Cl. ' I (FG 5 4 00 5) |
| Derivatives | Aromatic amino acids and derivatives | Phenylalanine and Tyrosine Branches from Chorismate | Chorismate mutase I (EC 5.4.99.5) |
| Amino Acids and | Aromatic amino acids and derivatives | Phenylalanine and Tyrosine Branches from Chorismate | Biosynthetic Aromatic amino acid aminotransferase alpha (EC 2.6.1.57) |
| Derivatives | Aromatic amino acids and derivatives | Phenylalanine and Tyrosine Branches from Chorismate | Biosynthetic Aromatic amino acid aminotransferase alpha (EC 2.6.1.57) |
| Amino Acids and | Aromatic amino acids and derivatives | Dhanylalanina and Tymasina Duanahaa from Chaniamata | Cycloboxyddianyl dabydaganaga (EC 1.2.1.12)/EC 1.2.1.42) |
| Derivatives | Aromatic amino acids and derivatives | Phenylalanine and Tyrosine Branches from Chorismate | Cyclohexadienyl dehydrogenase (EC 1.3.1.12)(EC 1.3.1.43) |
| Amino Acids and | Aromatic amino acids and derivatives | Aramatia amina agid dagradatian | 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase (EC 5.3.3) |
| Derivatives | Aromatic amino acids and derivatives | Aromatic amino acid degradation | 2-nydroxynepia-2,4-diene-1,/-dioate isomerase (EC 3.3.3) |
| Amino Acids and | Aromatic amino acids and derivatives | Aromatic amino acid degradation | Phenylalanine-4-hydroxylase (EC 1.14.16.1) |
| Derivatives | Aromatic amino acids and derivatives | Afoniatic amino acid degradation | Filenyiaiaiiiiie-4-nydroxyiase (EC 1.14.10.1) |
| Amino Acids and | Aromatic amino acids and derivatives | Aromatic amino acid degradation | 4-hydroxyphenylpyruvate dioxygenase (EC 1.13.11.27) |
| Derivatives | Aromatic amino acids and derivatives | Aromatic amino acid degradation | 4-nydroxyphenyipytuvate dioxygenase (EC 1.13.11.27) |
| Amino Acids and | Aromatic amino acids and derivatives | Aromatic amino acid degradation | 5-carboxymethyl-2-oxo-hex-3- ene-1,7-dioate decarboxylase (EC 4.1.1.68) |
| Derivatives | Atomatic animo acids and derivatives | Atomatic animo acid degradation | 5-carboxymeuryr-2-oxo-nex-5- ene-1,7-diodic decarboxydase (Ee 4.1.1.00) |
| Amino Acids and | Aromatic amino acids and derivatives | Aromatic amino acid degradation | Predicted 2-keto-4-pentenoate hydratase/2-oxohepta-3-ene-1,7-dioic acid hydratase |
| Derivatives | Thomatic ariano acras and acrivatives | Atomatic annio dela degradation | 1 redicted 2 keto 1 pentenoute nyaratass 2 okonepia 3 ene 1,7 distre acid nyaratass |
| Amino Acids and | Histidine Metabolism | Histidine Biosynthesis | Histidinol-phosphate aminotransferase (EC 2.6.1.9) |
| Derivatives | | | (—/ |
| Amino Acids and | Histidine Metabolism | Histidine Biosynthesis | Histidinol dehydrogenase (EC 1.1.1.23) |
| Derivatives | | | |
| Amino Acids and | Histidine Metabolism | Histidine Biosynthesis | Phosphoribosyl-AMP cyclohydrolase (EC 3.5.4.19) |
| Derivatives | | , | |
| Amino Acids and | Histidine Metabolism | Histidine Biosynthesis | Phosphoribosyl-ATP pyrophosphatase (EC 3.6.1.31) |
| Derivatives | | • | |
| Amino Acids and | Histidine Metabolism | Histidine Biosynthesis | Phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase (EC 5.3.1.16) |
| Derivatives | | • | • • |
| Amino Acids and | Histidine Metabolism | Histidine Biosynthesis | Histidinol-phosphatase (EC 3.1.3.15) |
| Derivatives | | | |
| Amino Acids and | Histidine Metabolism | Histidine Biosynthesis | Imidazoleglycerol-phosphate dehydratase (EC 4.2.1.19) |
| Derivatives | | | |
| Amino Acids and | Histidine Metabolism | Histidine Biosynthesis | ATP phosphoribosyltransferase regulatory subunit (EC 2.4.2.17) |
| Derivatives Amino Acids and | | | |
| Derivatives | Histidine Metabolism | Histidine Degradation | Urocanate hydratase (EC 4.2.1.49) |
| Amino Acids and | | | |
| Derivatives | Histidine Metabolism | Histidine Degradation | Formiminoglutamic iminohydrolase (EC 3.5.3.13) |
| Amino Acids and | | | |
| Derivatives | Histidine Metabolism | Histidine Degradation | Imidazolonepropionase (EC 3.5.2.7) |
| Amino Acids and | | | |
| Derivatives | Histidine Metabolism | Histidine Degradation | Histidine utilization repressor |
| | | | |

| Amino Acids and Derivatives | Histidine Metabolism | Histidine Degradation | N-formylglutamate deformylase (EC 3.5.1.68) |
|--------------------------------|------------------------------|--|---|
| Amino Acids and Derivatives | Histidine Metabolism | Histidine Degradation | Histidine ammonia-lyase (EC 4.3.1.3) |
| Amino Acids and Derivatives | Proline and 4-hydroxyproline | Proline Synthesis | RNA-binding C-terminal domain PUA |
| Amino Acids and Derivatives | Proline and 4-hydroxyproline | Proline Synthesis | Pyrroline-5-carboxylate reductase (EC 1.5.1.2) |
| Amino Acids and Derivatives | Proline and 4-hydroxyproline | Proline Synthesis | Gamma-glutamyl phosphate reductase (EC 1.2.1.41) |
| Amino Acids and Derivatives | Proline and 4-hydroxyproline | Proline Synthesis | Glutamate 5-kinase (EC 2.7.2.11) |
| Amino Acids and Derivatives | Proline and 4-hydroxyproline | Proline Synthesis | NADP-specific glutamate dehydrogenase (EC 1.4.1.4) |
| Amino Acids and Derivatives | Proline and 4-hydroxyproline | Proline, 4-hydroxyproline uptake and utilization | Delta-1-pyrroline-5-carboxylate dehydrogenase (EC 1.2.1.88) |
| Amino Acids and Derivatives | Alanine, serine, and glycine | Alanine biosynthesis | Cysteine desulfurase (EC 2.8.1.7) |
| Amino Acids and Derivatives | Alanine, serine, and glycine | Alanine biosynthesis | Valinepyruvate aminotransferase (EC 2.6.1.66) |
| Amino Acids and Derivatives | Alanine, serine, and glycine | Alanine biosynthesis | Iron-sulfur cluster assembly scaffold protein IscU |
| Amino Acids and Derivatives | Alanine, serine, and glycine | Alanine biosynthesis | Alanine racemase (EC 5.1.1.1) |
| Amino Acids and Derivatives | Alanine, serine, and glycine | Alanine biosynthesis | Ferredoxin, 2Fe-2S |
| Amino Acids and Derivatives | Alanine, serine, and glycine | Alanine biosynthesis | Branched-chain amino acid aminotransferase (EC 2.6.1.42) |
| Amino Acids and Derivatives | Alanine, serine, and glycine | Alanine biosynthesis | Iron-sulfur cluster regulator IscR |
| Amino Acids and Derivatives | Alanine, serine, and glycine | Alanine biosynthesis | Chaperone protein HscA |
| Amino Acids and Derivatives | Alanine, serine, and glycine | Glycine and Serine Utilization | Phosphoserine aminotransferase (EC 2.6.1.52) |
| Amino Acids and Derivatives | Alanine, serine, and glycine | Glycine and Serine Utilization | Glycine cleavage system H protein |
| Amino Acids and Derivatives | Alanine, serine, and glycine | Glycine and Serine Utilization | Seryl-tRNA synthetase (EC 6.1.1.11) |
| Amino Acids and Derivatives | Alanine, serine, and glycine | Glycine and Serine Utilization | L-serine dehydratase, (PLP)-dependent (EC 4.3.1.17) |
| Amino Acids and Derivatives | Alanine, serine, and glycine | Glycine and Serine Utilization | D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95) |
| Amino Acids and Derivatives | Alanine, serine, and glycine | Glycine and Serine Utilization | Threonine dehydratase, catabolic (EC 4.3.1.19) |
| Amino Acids and Derivatives | Alanine, serine, and glycine | Glycine and Serine Utilization | Serine hydroxymethyltransferase (EC 2.1.2.1) |
| Amino Acids and Derivatives | Alanine, serine, and glycine | Glycine and Serine Utilization | Phosphoserine phosphatase (EC 3.1.3.3) |
| Amino Acids and Derivatives | Alanine, serine, and glycine | Glycine Biosynthesis | Serine hydroxymethyltransferase (EC 2.1.2.1) |

| Amino Acids and Derivatives | Alanine, serine, and glycine | Serine Biosynthesis | D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95) |
|--------------------------------|----------------------------------|------------------------------------|--|
| Amino Acids and Derivatives | Alanine, serine, and glycine | Serine Biosynthesis | Phosphoserine phosphatase (EC 3.1.3.3) |
| Amino Acids and Derivatives | Alanine, serine, and glycine | Serine Biosynthesis | Phosphoserine aminotransferase (EC 2.6.1.52) |
| Amino Acids and Derivatives | Alanine, serine, and glycine | Serine Biosynthesis | Serine hydroxymethyltransferase (EC 2.1.2.1) |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Arginine and Ornithine Degradation | Ornithine cyclodeaminase (EC 4.3.1.12) |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Arginine and Ornithine Degradation | NADP-specific glutamate dehydrogenase (EC 1.4.1.4) |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Arginine and Ornithine Degradation | Arginase (EC 3.5.3.1) |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Arginine and Ornithine Degradation | Delta-1-pyrroline-5-carboxylate dehydrogenase (EC 1.2.1.88) |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Arginine and Ornithine Degradation | Arginine decarboxylase (EC 4.1.1.19) |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Arginine and Ornithine Degradation | Ornithine decarboxylase (EC 4.1.1.17) |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Arginine and Ornithine Degradation | Ornithine carbamoyltransferase (EC 2.1.3.3) |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Polyamine Metabolism | Arginine decarboxylase (EC 4.1.1.19) |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Polyamine Metabolism | Putrescine transport system permease protein PotH (TC 3.A.1.11.2) |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Polyamine Metabolism | Spermidine synthase (EC 2.5.1.16) |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Polyamine Metabolism | Putrescine ABC transporter putrescine-binding protein PotF (TC 3.A.1.11.2) |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Polyamine Metabolism | Probable two-component sensor, near polyamine transporter |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Polyamine Metabolism | Ornithine decarboxylase (EC 4.1.1.17) |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Polyamine Metabolism | 5'-methylthioadenosine nucleosidase (EC 3.2.2.16) |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Polyamine Metabolism | Putrescine transport ATP-binding protein PotG (TC 3.A.1.11.2) |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Polyamine Metabolism | S-adenosylmethionine decarboxylase proenzyme (EC 4.1.1.50), prokaryotic class 1B |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Polyamine Metabolism | Putrescine transport system permease protein PotI (TC 3.A.1.11.2) |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Urease subunits | Urease accessory protein UreD |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Urease subunits | Nickel-binding accessory protein UreJ-HupE |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Urease subunits | Urease accessory protein UreG |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Urease subunits | Urease gamma subunit (EC 3.5.1.5) |

| Amino Acids and | Arginine; urea cycle, polyamines | Urease subunits | Urease alpha subunit (EC 3.5.1.5) |
|--------------------------------|----------------------------------|--|--|
| Derivatives | Arginine, urea cycle, poryanimes | Orease Subumits | Orease alpha subuliit (EC 3.3.1.3) |
| Amino Acids and | Arginine; urea cycle, polyamines | Urease subunits | Urease beta subunit (EC 3.5.1.5) |
| Derivatives Amino Acids and | | | |
| Derivatives | Arginine; urea cycle, polyamines | Urease subunits | Urease accessory protein UreF |
| Amino Acids and | Aii | Harry advanta | H |
| Derivatives | Arginine; urea cycle, polyamines | Urease subunits | Urease accessory protein UreE |
| Amino Acids and | Arginine; urea cycle, polyamines | Urea carboxylase and Allophanate hydrolase cluster | Allophanate hydrolase (EC 3.5.1.54) |
| Derivatives | 3 /1 3 | 1 3 | 1 7 (11 7) |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Urea decomposition | Urea ABC transporter, ATPase protein UrtE |
| Amino Acids and | | | |
| Derivatives | Arginine; urea cycle, polyamines | Urea decomposition | Urease accessory protein UreD |
| Amino Acids and | Arginine; urea cycle, polyamines | Urea decomposition | Urea ABC transporter, permease protein UrtB |
| Derivatives | Arginine, urea cycle, poryanimes | Orea decomposition | Orea ABC transporter, permease protein Orth |
| Amino Acids and | Arginine; urea cycle, polyamines | Urea decomposition | Urease accessory protein UreE |
| Derivatives | | 1 | 7.1 |
| Amino Acids and Derivatives | Arginine; urea cycle, polyamines | Urea decomposition | Urease accessory protein UreF |
| Amino Acids and | | | |
| Derivatives | Arginine; urea cycle, polyamines | Urea decomposition | Urease alpha subunit (EC 3.5.1.5) |
| Amino Acids and | Arginine; urea cycle, polyamines | Urea decomposition | Urea ABC transporter, ATPase protein UrtD |
| Derivatives | Arginine, urea cycle, poryanimes | Orea decomposition | orea ABC transporter, ATT asc protein orth |
| Amino Acids and | Arginine; urea cycle, polyamines | Urea decomposition | Allophanate hydrolase (EC 3.5.1.54) |
| Derivatives Amino Acids and | | • | |
| Derivatives | Arginine; urea cycle, polyamines | Urea decomposition | Urease gamma subunit (EC 3.5.1.5) |
| Amino Acids and | | | |
| Derivatives | Arginine; urea cycle, polyamines | Urea decomposition | Urease accessory protein UreG |
| Amino Acids and | Arginine; urea cycle, polyamines | Urea decomposition | Urea ABC transporter, permease protein UrtC |
| Derivatives | Augmine, area cycle, polyamines | Orea decomposition | orea ABC transporter, permease protein orte |
| Amino Acids and | Arginine; urea cycle, polyamines | Urea decomposition | Urease beta subunit (EC 3.5.1.5) |
| Derivatives Amino Acids and | Amino Acids and Derivatives - no | | |
| Derivatives | subcategory | Creatine and Creatinine Degradation | Creatinine amidohydrolase (EC 3.5.2.10) |
| Amino Acids and | Amino Acids and Derivatives - no | 0 4 10 41 0 14 | 0.1.1.1.1.0000000 |
| Derivatives | subcategory | Creatine and Creatinine Degradation | Cytosine deaminase (EC 3.5.4.1) |
| Amino Acids and | Branched-chain amino acids | Branched-Chain Amino Acid Biosynthesis | 3-isopropylmalate dehydrogenase (EC 1.1.1.85) |
| Derivatives | Branched chain animo acido | Branched Chain Annino Acta Biosynthesis | 5 isopropymianae denydrogenase (EC 1.1.1.65) |
| Amino Acids and | Branched-chain amino acids | Branched-Chain Amino Acid Biosynthesis | Threonine dehydratase biosynthetic (EC 4.3.1.19) |
| Derivatives Amino Acids and | | | |
| Derivatives | Branched-chain amino acids | Branched-Chain Amino Acid Biosynthesis | Threonine dehydratase, catabolic (EC 4.3.1.19) |
| Amino Acids and | D 111: : :1 | B 1 161 'A ' A 'IB' 4 ' | W.F |
| Derivatives | Branched-chain amino acids | Branched-Chain Amino Acid Biosynthesis | Valinepyruvate aminotransferase (EC 2.6.1.66) |
| Amino Acids and | Branched-chain amino acids | Branched-Chain Amino Acid Biosynthesis | 2-isopropylmalate synthase (EC 2.3.3.13) |
| Derivatives | | | 1 |
| Amino Acids and | Branched-chain amino acids | Branched-Chain Amino Acid Biosynthesis | Dihydroxy-acid dehydratase (EC 4.2.1.9) |
| Derivatives | | | |

| Amino Acids and | | | |
|--------------------------------|-----------------------------|--|--|
| Derivatives | Branched-chain amino acids | Branched-Chain Amino Acid Biosynthesis | Acetolactate synthase large subunit (EC 2.2.1.6) |
| Amino Acids and | Branched-chain amino acids | Branched-Chain Amino Acid Biosynthesis | Leucine-responsive regulatory protein, regulator for leucine (or lrp) regulon and high-affinity branched-chain amino |
| Derivatives | | | acid transport system |
| Amino Acids and | Branched-chain amino acids | Branched-Chain Amino Acid Biosynthesis | 3-isopropylmalate dehydratase large subunit (EC 4.2.1.33) |
| Derivatives Amino Acids and | | | |
| Derivatives | Branched-chain amino acids | Branched-Chain Amino Acid Biosynthesis | Acetolactate synthase small subunit (EC 2.2.1.6) |
| Amino Acids and | Branched-chain amino acids | Door do d Chair Amira Anid Diagondaria | Developed their coning and developed (FC 2 C 1 42) |
| Derivatives | Branched-chain amino acids | Branched-Chain Amino Acid Biosynthesis | Branched-chain amino acid aminotransferase (EC 2.6.1.42) |
| Amino Acids and | Branched-chain amino acids | Branched-Chain Amino Acid Biosynthesis | 3-isopropylmalate dehydratase small subunit (EC 4.2.1.33) |
| Derivatives | | | |
| Amino Acids and | Branched-chain amino acids | Leucine Biosynthesis | 3-isopropylmalate dehydrogenase (EC 1.1.1.85) |
| Derivatives Amino Acids and | | | |
| Derivatives | Branched-chain amino acids | Leucine Biosynthesis | Branched-chain amino acid aminotransferase (EC 2.6.1.42) |
| Amino Acids and | | r i pi di i | 2 |
| Derivatives | Branched-chain amino acids | Leucine Biosynthesis | 3-isopropylmalate dehydratase small subunit (EC 4.2.1.33) |
| Amino Acids and | Branched-chain amino acids | Leucine Biosynthesis | 3-isopropylmalate dehydratase large subunit (EC 4.2.1.33) |
| Derivatives | Branched Chain annio delas | Leacine Biosynthesis | 5 Ropropy manage deny dramatic marge submin (De 1.2.1.35) |
| Amino Acids and | Branched-chain amino acids | Leucine Biosynthesis | 2-isopropylmalate synthase (EC 2.3.3.13) |
| Derivatives Amino Acids and | | • | |
| Derivatives | Branched-chain amino acids | HMG CoA Synthesis | Hydroxymethylglutaryl-CoA lyase (EC 4.1.3.4) |
| Amino Acids and | | TR. C. | William Tarakana Tarakana |
| Derivatives | Branched-chain amino acids | HMG CoA Synthesis | Methylglutaconyl-CoA hydratase (EC 4.2.1.18) |
| Amino Acids and | Branched-chain amino acids | HMG CoA Synthesis | Acetoacetyl-CoA synthetase [leucine] (EC 6.2.1.16) |
| Derivatives | Dianched-chain animo acids | Third CoA Synthesis | Activately Feor synthetise [reteine] (EC 0.2.1.10) |
| Amino Acids and | Branched-chain amino acids | HMG CoA Synthesis | Isovaleryl-CoA dehydrogenase (EC 1.3.8.4) |
| Derivatives | | , | |
| Amino Acids and Derivatives | Branched-chain amino acids | HMG CoA Synthesis | Methylcrotonyl-CoA carboxylase carboxyl transferase subunit (EC 6.4.1.4) |
| Amino Acids and | | | |
| Derivatives | Branched-chain amino acids | HMG CoA Synthesis | Methylcrotonyl-CoA carboxylase biotin-containing subunit (EC 6.4.1.4) |
| Amino Acids and | Branched-chain amino acids | Lavaina Dagradation and HMG Co A Matabalian | Agotogostyl Co Agynthotogo Floyging (FC 6.2.1.16) |
| Derivatives | Branched-chain annino acids | Leucine Degradation and HMG-CoA Metabolism | Acetoacetyl-CoA synthetase [leucine] (EC 6.2.1.16) |
| Amino Acids and | Branched-chain amino acids | Leucine Degradation and HMG-CoA Metabolism | Succinyl-CoA:3-ketoacid-coenzyme A transferase subunit A (EC 2.8.3.5) |
| Derivatives | | č | |
| Amino Acids and Derivatives | Branched-chain amino acids | Leucine Degradation and HMG-CoA Metabolism | Methylcrotonyl-CoA carboxylase carboxyl transferase subunit (EC 6.4.1.4) |
| Amino Acids and | | | |
| Derivatives | Branched-chain amino acids | Leucine Degradation and HMG-CoA Metabolism | Isovaleryl-CoA dehydrogenase (EC 1.3.8.4) |
| Amino Acids and | Branched-chain amino acids | Leucine Degradation and HMG-CoA Metabolism | Dihydrolipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex (EC |
| Derivatives | Branched-chain annino acids | Leucine Degradation and Tivio-Coa Metabolism | 2.3.1.168) |
| Amino Acids and | Branched-chain amino acids | Leucine Degradation and HMG-CoA Metabolism | Branched-chain amino acid aminotransferase (EC 2.6.1.42) |
| Derivatives | | | |
| Amino Acids and Derivatives | Branched-chain amino acids | Leucine Degradation and HMG-CoA Metabolism | Hydroxymethylglutaryl-CoA lyase (EC 4.1.3.4) |
| Amino Acids and | | | |
| Derivatives | Branched-chain amino acids | Leucine Degradation and HMG-CoA Metabolism | Methylcrotonyl-CoA carboxylase biotin-containing subunit (EC 6.4.1.4) |
| | | | |

| Amino Acids and Derivatives | Branched-chain amino acids | Leucine Degradation and HMG-CoA Metabolism | Branched-chain acyl-CoA dehydrogenase (EC 1.3.99.12) |
|--------------------------------|---|--|---|
| Amino Acids and Derivatives | Branched-chain amino acids | Leucine Degradation and HMG-CoA Metabolism | Succinyl-CoA:3-ketoacid-coenzyme A transferase subunit B (EC 2.8.3.5) |
| Amino Acids and Derivatives | Branched-chain amino acids | Leucine Degradation and HMG-CoA Metabolism | Methylglutaconyl-CoA hydratase (EC 4.2.1.18) |
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Lysine Biosynthesis DAP Pathway | Aspartate-semialdehyde dehydrogenase (EC 1.2.1.11) |
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Lysine Biosynthesis DAP Pathway | 2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-succinyltransferase (EC 2.3.1.117) |
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Lysine Biosynthesis DAP Pathway | N-succinyl-L,L-diaminopimelate desuccinylase (EC 3.5.1.18) |
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Lysine Biosynthesis DAP Pathway | 4-hydroxy-tetrahydrodipicolinate synthase (EC 4.3.3.7) |
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Lysine Biosynthesis DAP Pathway | Diaminopimelate decarboxylase (EC 4.1.1.20) |
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Lysine Biosynthesis DAP Pathway | Diaminopimelate epimerase (EC 5.1.1.7) |
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Lysine Biosynthesis DAP Pathway | Aspartokinase (EC 2.7.2.4) |
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Lysine Biosynthesis DAP Pathway | 4-hydroxy-tetrahydrodipicolinate reductase (EC 1.17.1.8) |
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Threonine and Homoserine Biosynthesis | Aspartate aminotransferase (EC 2.6.1.1) |
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Threonine and Homoserine Biosynthesis | Homoserine dehydrogenase (EC 1.1.1.3) |
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Threonine and Homoserine Biosynthesis | Threonine synthase (EC 4.2.3.1) |
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Threonine and Homoserine Biosynthesis | Aspartokinase (EC 2.7.2.4) |
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Threonine and Homoserine Biosynthesis | Aspartate-semialdehyde dehydrogenase (EC 1.2.1.11) |
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Threonine and Homoserine Biosynthesis | Homoserine kinase (EC 2.7.1.39) |
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Methionine Biosynthesis | O-succinylhomoserine sulfhydrylase (EC 2.5.1.48) |
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Methionine Biosynthesis | Homoserine kinase (EC 2.7.1.39) |
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Methionine Biosynthesis | O-acetylhomoserine sulfhydrylase (EC 2.5.1.49) |
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Methionine Biosynthesis | 5,10-methylenetetrahydrofolate reductase (EC 1.5.1.20) |
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Methionine Biosynthesis | Adenosylhomocysteinase (EC 3.3.1.1) |
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Methionine Biosynthesis | Homoserine O-acetyltransferase (EC 2.3.1.31) |
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Methionine Biosynthesis | S-adenosylhomocysteine nucleosidase (EC 3.2.2.9) |
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Methionine Biosynthesis | Homoserine dehydrogenase (EC 1.1.1.3) |
| | | | |

| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine Methionine Biosynthesis | S-adenosylmethionine synthetase (EC 2.5.1.6) |
|---|--|---|
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine Methionine Biosynthesis | Cysteine synthase (EC 2.5.1.47) |
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine Methionine Biosynthesis | Cystathionine beta-lyase (EC 4.4.1.8) |
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine Methionine Biosynthesis | Serine acetyltransferase (EC 2.3.1.30) |
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine Lysine Biosynthesis DAP Pathway, GJO scratch | 2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-succinyltransferase (EC 2.3.1.117) |
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine Lysine Biosynthesis DAP Pathway, GJO scratch | Aspartate-semialdehyde dehydrogenase (EC 1.2.1.11) |
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine Lysine Biosynthesis DAP Pathway, GJO scratch | 4-hydroxy-tetrahydrodipicolinate synthase (EC 4.3.3.7) |
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine Lysine Biosynthesis DAP Pathway, GJO scratch | N-succinyl-L,L-diaminopimelate desuccinylase (EC 3.5.1.18) |
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine Lysine Biosynthesis DAP Pathway, GJO scratch | Diaminopimelate epimerase (EC 5.1.1.7) |
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine Lysine Biosynthesis DAP Pathway, GJO scratch | Diaminopimelate decarboxylase (EC 4.1.1.20) |
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine Lysine Biosynthesis DAP Pathway, GJO scratch | 4-hydroxy-tetrahydrodipicolinate reductase (EC 1.17.1.8) |
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine Lysine Biosynthesis DAP Pathway, GJO scratch | Aspartokinase (EC 2.7.2.4) |
| Amino Acids and Derivatives Amino Acids and | Lysine, threonine, methionine, and cysteine Methionine Degradation | S-adenosylhomocysteine nucleosidase (EC 3.2.2.9) |
| Derivatives Amino Acids and | Lysine, threonine, methionine, and cysteine Methionine Degradation | Adenosylhomocysteinase (EC 3.3.1.1) |
| Derivatives Amino Acids and | Lysine, threonine, methionine, and cysteine Methionine Degradation | S-adenosylmethionine synthetase (EC 2.5.1.6) |
| Derivatives Amino Acids and | Lysine, threonine, methionine, and cysteine Methionine Degradation | 2-Oxobutyrate oxidase, putative |
| Derivatives Amino Acids and | Lysine, threonine, methionine, and cysteine Methionine Degradation | Pyruvate dehydrogenase E1 component (EC 1.2.4.1) |
| Derivatives Amino Acids and | Lysine, threonine, methionine, and cysteine Cysteine Biosynthesis | Sulfite reductase [NADPH] hemoprotein beta-component (EC 1.8.1.2) |
| Derivatives Amino Acids and | Lysine, threonine, methionine, and cysteine Cysteine Biosynthesis | Sulfate adenylyltransferase subunit 2 (EC 2.7.7.4) |
| Derivatives Amino Acids and | Lysine, threonine, methionine, and cysteine Cysteine Biosynthesis | Sulfate adenylyltransferase subunit 1 (EC 2.7.7.4) |
| Derivatives Amino Acids and | Lysine, threonine, methionine, and cysteine Cysteine Biosynthesis | Cysteine synthase (EC 2.5.1.47) |
| Derivatives Amino Acids and | Lysine, threonine, methionine, and cysteine Cysteine Biosynthesis | Serine acetyltransferase (EC 2.3.1.30) |
| Derivatives Amino Acids and | Lysine, threonine, methionine, and cysteine Cysteine Biosynthesis | Cys regulon transcriptional activator CysB |
| Derivatives Amino Acids and | Lysine, threonine, methionine, and cysteine Cysteine Biosynthesis | Sulfate transport system permease protein CysT |
| Derivatives | Lysine, threonine, methionine, and cysteine Cysteine Biosynthesis | Sulfate and thiosulfate import ATP-binding protein CysA (EC 3.6.3.25) |

| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Cysteine Biosynthesis | Sulfate and thiosulfate binding protein CysP |
|--|---|---|---|
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Cysteine Biosynthesis | Cysteine synthase B (EC 2.5.1.47) |
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Cysteine Biosynthesis | Sulfate transport system permease protein CysW |
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Lysine degradation | Lysine decarboxylase (EC 4.1.1.18) |
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Threonine degradation | Threonine dehydratase, catabolic (EC 4.3.1.19) |
| Amino Acids and Derivatives | Lysine, threonine, methionine, and cysteine | Threonine degradation | low-specificity D-threonine aldolase |
| Metabolism of Aromatic Compounds | Peripheral pathways for catabolism of aromatic compounds | Quinate degradation | 3-dehydroquinate dehydratase II (EC 4.2.1.10) |
| Metabolism of Aromatic Compounds | Peripheral pathways for catabolism of aromatic compounds | Benzoate degradation | Ortho-halobenzoate 1,2-dioxygenase alpha-ISP protein OhbB |
| Metabolism of Aromatic Compounds | Peripheral pathways for catabolism of aromatic compounds | Benzoate degradation | Ortho-halobenzoate 1,2-dioxygenase beta-ISP protein OhbA |
| Metabolism of Aromatic Compounds | Metabolism of central aromatic intermediates | Catechol branch of beta-ketoadipate pathway | Succinyl-CoA:3-ketoacid-coenzyme A transferase subunit B (EC 2.8.3.5) |
| Metabolism of Aromatic Compounds | Metabolism of central aromatic intermediates | Catechol branch of beta-ketoadipate pathway | 3-oxoadipate CoA-transferase subunit B (EC 2.8.3.6) |
| Metabolism of Aromatic Compounds | Metabolism of central aromatic intermediates | Catechol branch of beta-ketoadipate pathway | Succinyl-CoA:3-ketoacid-coenzyme A transferase subunit A (EC 2.8.3.5) |
| Metabolism of Aromatic Compounds | Metabolism of central aromatic intermediates | Catechol branch of beta-ketoadipate pathway | 3-oxoadipate CoA-transferase subunit A (EC 2.8.3.6) |
| Metabolism of Aromatic Compounds | Metabolism of central aromatic intermediates | Salicylate and gentisate catabolism | Fumarylacetoacetate hydrolase family protein |
| Metabolism of Aromatic Compounds | Metabolism of central aromatic intermediates | Salicylate and gentisate catabolism | Gentisate 1,2-dioxygenase (EC 1.13.11.4) |
| Metabolism of Aromatic Compounds | Metabolism of central aromatic intermediates | Salicylate and gentisate catabolism | Putative n-hydroxybenzoate hydroxylase |
| Metabolism of Aromatic | Metabolism of central aromatic intermediates | Salicylate and gentisate catabolism | Maleylacetoacetate isomerase (EC 5.2.1.2) |
| Compounds Metabolism of Aromatic Compounds | Metabolism of Aromatic Compounds - no subcategory | Gentisate degradation | Maleylacetoacetate isomerase (EC 5.2.1.2) |
| Metabolism of Aromatic Compounds | Metabolism of Aromatic Compounds - no subcategory | Gentisate degradation | Putative n-hydroxybenzoate hydroxylase |
| Metabolism of Aromatic Compounds | Metabolism of Aromatic Compounds - no subcategory | Gentisate degradation | putative 4-hydroxybenzoyl-CoA thioesterase |
| Metabolism of Aromatic | Metabolism of Aromatic Compounds - no | Gentisate degradation | Gentisate 1,2-dioxygenase (EC 1.13.11.4) |
| Compounds Metabolism of Aromatic Compounds | subcategory Metabolism of Aromatic Compounds - no subcategory | Gentisate degradation | Fumarylacetoacetate hydrolase family protein |
| Resistance to antibiotics and toxic compounds | Resistance to antibiotics | Beta-lactamase | Metal-dependent hydrolases of the beta-lactamase superfamily I |
| Resistance to antibiotics and toxic compounds | Resistance to antibiotics | Resistance to fluoroquinolones | DNA gyrase subunit A (EC 5.99.1.3) |
| Resistance to antibiotics and toxic compounds | Resistance to antibiotics | Resistance to fluoroquinolones | DNA gyrase subunit B (EC 5.99.1.3) |

Resistance to antibiotics and toxic compounds Resistance to antibiotics and toxic compounds

| es | Resistance to heavy metals | Copper homeostasis | Copper-sensing two-component system response regulator CusR |
|----|----------------------------|--------------------------------------|---|
| es | Resistance to heavy metals | Copper homeostasis | Copper-translocating P-type ATPase (EC 3.6.3.4) |
| es | Resistance to heavy metals | Copper homeostasis | Copper chaperone |
| es | Resistance to heavy metals | Copper homeostasis | Copper resistance protein B |
| es | Resistance to heavy metals | Copper homeostasis | Multidrug resistance transporter, Bcr/CflA family |
| es | Resistance to heavy metals | Copper homeostasis | Copper sensory histidine kinase CusS |
| es | Resistance to heavy metals | Copper homeostasis | Multicopper oxidase |
| es | Resistance to heavy metals | Copper homeostasis | Cu(I)-responsive transcriptional regulator |
| es | Resistance to heavy metals | Copper homeostasis | Copper tolerance protein |
| es | Resistance to heavy metals | Copper homeostasis: copper tolerance | Magnesium and cobalt efflux protein CorC |
| es | Resistance to heavy metals | Copper homeostasis: copper tolerance | Copper homeostasis protein CutE |
| es | Resistance to heavy metals | Cobalt-zinc-cadmium resistance | DNA-binding heavy metal response regulator |
| es | Resistance to heavy metals | Cobalt-zinc-cadmium resistance | Copper sensory histidine kinase CusS |
| es | Resistance to heavy metals | Cobalt-zinc-cadmium resistance | Transcriptional regulator, MerR family |
| es | Resistance to heavy metals | Cobalt-zinc-cadmium resistance | Cobalt-zinc-cadmium resistance protein |
| es | Resistance to heavy metals | Cobalt-zinc-cadmium resistance | Copper-sensing two-component system response regulator CusR |
| es | Resistance to heavy metals | Resistance to chromium compounds | Chromate transport protein ChrA |

The predicted prophage-related proteins from the genome of strain H39-3-26^T by PHAEST program.

| Number | Category | CDS Position | BLAST Hit |
|--------|----------------------|----------------|---|
| 1 | Head protein | 18494381849728 | PP_01780;putative head-tail adaptor;phage;-;PHAGE_Geobac_E2_NC_009552 |
| 2 | Head protein | 18497521850030 | PP_01781;head-tail connector family protein;phage;-;PHAGE_Pseudo_phi2_NC_030931 |
| 3 | Head protein | 18540681854490 | PP_01786;putative prohead protease;phage;-;PHAGE_Clostr_phi3626_NC_003524 |
| 4 | Head protein | 18546151855841 | PP_01787;major capsid protein;phage;-;PHAGE_Synech_S_CBS3_NC_015465 |
| 5 | Head protein | 32698293270722 | PP_03157;Mu-like prophage major head subunit gpT;phage;-;PHAGE_Pseudo_JBD25_NC_027992 |
| 6 | Hypothetical protein | 18522971852854 | PP_01784;hypothetical protein;phage;-;PHAGE_Paraco_Shpa_NC_041868 |
| 7 | Hypothetical protein | 18578121858015 | PP_01789;hypothetical protein;phage;-;PHAGE_Burkho_BcepIL02_NC_012743 |
| 8 | Hypothetical protein | 32676613268077 | PP_03154;hypothetical protein;phage;-;PHAGE_Bacill_BalMu_1_NC_030945 |
| 9 | Hypothetical protein | 32693903269800 | PP_03156;hypothetical protein;phage;-;PHAGE_Pseudo_JBD25_NC_027992 |
| 10 | Hypothetical protein | 32724223273339 | PP_03162;hypothetical protein;phage;-;PHAGE_Rhodob_RcapMu_NC_016165 |
| 11 | Integrase | 18594321860469 | PP_01792;putative integrase;phage;-;PHAGE_Pseudo_H66_NC_042342 |
| 12 | Phage-like protein | 18569351857768 | PP_01788;putative DNA topoisomerase;phage;-;PHAGE_Pseudo_PaMx25_NC_041953 |
| 13 | Phage-like protein | 32672133267659 | PP_03153;gp02;phage;-;PHAGE_Burkho_BcepMu_NC_005882 |
| 14 | Phage-like protein | 32707523271048 | PP_03158;Mu phage uncharacterized protein;phage;-;PHAGE_Ralsto_RS138_NC_029107 |
| 15 | Phage-like protein | 32711923271728 | PP_03159;PF07030 family protein;phage;-;PHAGE_Pseudo_JBD25_NC_027992 |
| 16 | Portal protein | 18502341851733 | PP_01782;portal protein;phage;-;PHAGE_Escher_ECP1_NC_049926 |
| 17 | Portal protein | 18528631854035 | PP_01785;portal-like protein;phage;-;PHAGE_Paraco_Shpa_NC_041868 |
| 18 | Protease | 32681983269364 | PP_03155;protease (I) and scaffold (Z) protein;phage;-;PHAGE_Pseudo_JBD93_NC_030918 |
| 19 | Tail protein | 32743013279232 | PP_03166;putative tail component protein;phage;-;PHAGE_Pseudo_MP48_NC_024782 |
| 20 | Terminase | 18518871852219 | PP_01783;terminase small subunit;phage;-;PHAGE_Entero_mEp390_NC_019721 |
| | | | |

The predicted prophage-related proteins from the genome of strain H3SJ34-1^T by PHAEST program.

| Number | Category | CDS Position | BLAST Hit |
|--------|----------------------|----------------|---|
| 1 | Fiber protein | 22948942297308 | PP_02294;tail hyaluronidase/tail fiber;phage;-;PHAGE_Bacter_crAss001_NC_049977 |
| 2 | Head protein | 22788752280014 | PP_01781;head-tail connector family protein;phage;-;PHAGE_Pseudo_phi2_NC_030931 |
| 3 | Head protein | 22800162280639 | PP_02272;head decoration protein D;phage;-;PHAGE_Aurant_AmM_1_NC_027334 |
| 4 | Head protein | 22807552281780 | PP_02273;major capsid;phage;-;PHAGE_Aurant_AmM_1_NC_027334 |
| 5 | Hypothetical protein | 32698293270722 | PP_02284;hypothetical protein;phage;-;PHAGE_Rhizob_RHEph04_NC_041908 |
| 6 | Hypothetical protein | 22888812289129 | PP_02285;hypothetical protein;phage;-;PHAGE_Rhizob_RHEph04_NC_041908 |
| 7 | Hypothetical protein | 22891462290030 | PP_02286;hypothetical protein;phage;-;PHAGE_Rhizob_RHEph04_NC_041908 |
| 8 | Hypothetical protein | 22921442292962 | PP_02290;hypothetical protein;phage;-;PHAGE_Rhizob_RHEph04_NC_041908 |
| 9 | Hypothetical protein | 22992362300276 | PP_02299;hypothetical protein;phage;-;PHAGE_Bacill_BM5_NC_029069 |
| 10 | Phage-like protein | 22819352282339 | PP_02274; putative structural protein; phage; -; PHAGE_Rhizob_RHEph04_NC_041908 |
| 11 | Phage-like protein | 22847782285206 | PP_02278; putative structural protein; phage; -; PHAGE_Rhizob_RHEph04_NC_041908 |
| 12 | Phage-like protein | 22974372298036 | PP_02295;putative endolysin;phage;-;PHAGE_Acinet_phiAC_1_NC_028995 |
| 13 | Plate protein | 22900872290662 | PP_02287; putative baseplate assembly protein; phage; -; PHAGE_Rhizob_RHEph04_NC_041908 |
| 14 | Plate protein | 22908512291213 | PP_02288; putative baseplate component; phage; -; PHAGE_Pantoe_vB_PagM_AAM37_NC_048766 |
| 15 | Plate protein | 22912322292140 | PP_02289; putative baseplate assembly protein; phage; -; PHAGE_Rhizob_RHEph04_NC_041908 |
| 16 | Tail protein | 22833232284753 | PP_02277;tail collar domain;phage;-;PHAGE_Sinorh_phiLM21_NC_029046 |
| 17 | Tail protein | 22929852293770 | PP_02291; putative tail collar domain-containing protein; phage; -; PHAGE_Pseudo_PPpW_3_NC_023006 |

The predicted prophage-related proteins from the genome of strain H3M7-6^T by PHAEST program.

| Number | Category | CDS Position | BLAST Hit |
|--------|----------------------|----------------|--|
| 1 | Head protein | 25800962581073 | PP_02402;major capsid protein;phage;-;PHAGE_Rheinh_vB_RspM_Barba18A_NC_048189 |
| 2 | Head protein | 25811332581501 | PP_01781;head-tail connector family protein;phage;-;PHAGE_Pseudo_phi2_NC_030931 |
| 3 | Head protein | 25815292582767 | PP_02404; putative capsid assembly protein/protease; phage; -; PHAGE_Burkho_phiE125_NC_003309 |
| 4 | Head protein | 25849012585392 | PP_02408;capsid-related protein;phage;-;PHAGE_Sinorh_phiM7_NC_041929 |
| 5 | Head protein | 32698293270722 | PP_02418;RuvC-like resolvase;phage;-;PHAGE_Rhodoc_Sleepyhead_NC_048782 |
| 6 | Hypothetical protein | 25637822564072 | PP_02386;hypothetical protein;phage;-;PHAGE_Rhizob_vB_RleS_L338C_NC_023502 |
| 7 | Hypothetical protein | 25641492564307 | PP_02387;hypothetical protein;phage;-;PHAGE_Ralsto_RS138_NC_029107 |
| 8 | Hypothetical protein | 25667772567862 | PP_02390;hypothetical protein;phage;-;PHAGE_Ralsto_RS138_NC_029107 |
| 9 | Hypothetical protein | 25727202573061 | PP_02393;hypothetical protein;phage;-;PHAGE_Ralsto_RS138_NC_029107 |
| 10 | Hypothetical protein | 25793462579792 | PP_02400;hypothetical protein;phage;-;PHAGE_Synech_S_CBS3_NC_015465 |
| 11 | Hypothetical protein | 25845092584874 | PP_02407;hypothetical protein;phage;-;PHAGE_Rhizob_vB_RleM_PPF1_NC_025427 |
| 12 | Hypothetical protein | 25880342588231 | PP_02411;hypothetical protein;phage;-;PHAGE_Agroba_Atu_ph07_NC_042013 |
| 13 | Hypothetical protein | 25939002596086 | PP_02419;hypothetical protein;phage;-;PHAGE_Bacill_phi105_NC_004167 |
| 14 | Hypothetical protein | 25982102599064 | PP_02423;hypothetical protein;phage;-;PHAGE_Pseudo_YMC11/02/R656_NC_028657 |
| 15 | Hypothetical protein | 26010622601373 | PP_02427;hypothetical protein;phage;-;PHAGE_Pseudo_PPpW_3_NC_023006 |
| 16 | Hypothetical protein | 26041222604676 | PP_02432;hypothetical protein;phage;-;PHAGE_Mycoba_Adler_NC_023591 |
| 17 | Hypothetical protein | 26047272604960 | PP_02433;hypothetical protein;phage;-;PHAGE_Entero_mEp390_NC_019721 |
| 18 | Integrase | 26020052603252 | PP_02430;site-specific integrase;phage;-;PHAGE_Entero_EFC_1_NC_025453 |
| 19 | Phage-like protein | 25628452563303 | PP_02384;p15;phage;-;PHAGE_Bacill_Nf_NC_049976 |
| 20 | Phage-like protein | 25896722590847 | PP_02414;DNA modification methylase;phage;-;PHAGE_Bacill_vB_BtS_B83_NC_048762 |
| 21 | Phage-like protein | 25909402592445 | PP_02415;DNA methylase;phage;-;PHAGE_Psychr_pOW20_A_NC_020841 |
| 22 | Phage-like protein | 25961842596780 | PP_02420;RNA polymerase sigma factor;phage;-;PHAGE_Klebsi_ST13_OXA48phi12.1_NC_049453 |
| 23 | Phage-like protein | 25969822597653 | PP_02421;putative nuclease;phage;-;PHAGE_Entero_CAjan_NC_028776 |
| 24 | Phage-like protein | 25997232600553 | PP_02425;ATPase;phage;-;PHAGE_Escher_Seurat_NC_027378 |
| 25 | Portal protein | 25827772584201 | PP_02405;portal protein;phage;-;PHAGE_Vibrio_vB_VpaM_MAR_NC_019722 |
| 26 | Regulatory protein | 25607352561421 | PP_02382;hybrid sensor histidine kinase - response regulator;phage;-;PHAGE_Altero_vB_AmeM_PT11_V22_NC_048847 |
| 27 | Tail protein | 25643632566381 | PP_02388;putative tail protein c;phage;-;PHAGE_Stenot_S1_NC_011589 |
| 28 | Tail protein | 25678662569131 | PP_02391;tail assembly protein;phage;-;PHAGE_Stenot_vB_SmaS_DLP_5_NC_042082 |
| 29 | Tail protein | 25691552572718 | PP_02392;putative tail protein b;phage;-;PHAGE_Stenot_S1_NC_011589 |
| 30 | Tail protein | 25730722577115 | PP_02394;phage tail tape measure protein;phage;-;PHAGE_Cronob_ENT39118_NC_019934 |
| 31 | Tail protein | 25783972579077 | PP_02398;putative tail sheath protein;phage;-;PHAGE_Pseudo_vB_PaeS_PM105_NC_028667 |
| 32 | Terminase | 25854102587269 | PP_02409;large terminase subunit;phage;-;PHAGE_Synech_S_CBS3_NC_015465 |
| | | | |

The predicted plasimid sequences from the genome of strain ${\rm H39\text{-}3\text{-}26^{T.}}$

| Sample name | Contig name | Probability (%) | Contig length (bp) | GC content | Acc num | Acc plasmid name | Identity (%) |
|------------------------|----------------------|-----------------|-----------------------|------------|---------------|------------------|--------------|
| H39_3_26_GCF_029211125 | NZ_JARGEN010000088.1 | - 1 | 642 | 56.23 | - | - | - |
| H39_3_26_GCF_029211125 | NZ_JARGEN010000092.1 | 75.52 | 7528 | 63.67 | - | - | - |
| H39_3_26_GCF_029211125 | NZ_JARGEN010000004.1 | 81.79 | 3661 | 59.85 | - | - | - |
| H39_3_26_GCF_029211125 | NZ_JARGEN010000060.1 | 81.31 | 14768 | 61.79 | NZ_LR594670.1 | 5 | 99.746 |
| H39_3_26_GCF_029211125 | NZ_JARGEN010000090.1 | - | 564 | 61.17 | NZ_CP045303.1 | unnamed1 | 80.226 |
| H39_3_26_GCF_029211125 | NZ_JARGEN010000020.1 | - | 4412 | 57.77 | - | - | - |
| H39_3_26_GCF_029211125 | NZ_JARGEN010000099.1 | - | 801 | 47.44 | - | - | - |
| H39_3_26_GCF_029211125 | NZ_JARGEN010000072.1 | 97.42 | 1192 | 56.96 | NZ_CP027671.1 | unnamed2 | 89.567 |
| H39_3_26_GCF_029211125 | NZ_JARGEN010000066.1 | 75.7 | 3351 | 60.73 | - | - | - |
| H39 3 26 GCF 029211125 | NZ JARGEN010000078.1 | 98.44 | 12536 | 57.68 | NZ KR106190.1 | pHS87a | 85.106 |
| H39 3 26 GCF 029211125 | NZ JARGEN010000044.1 | 96.63 | 1494 | 62.38 | NC 007974.2 | | 78.906 |
| H39 3 26 GCF 029211125 | NZ JARGEN010000041.1 | - | 3933 | 56.34 | - | - | - |
| H39 3 26 GCF 029211125 | NZ JARGEN010000098.1 | 89.04 | 753 | 58.83 | NZ CP019241.1 | unnamed1 | 85.557 |
| H39 3 26 GCF 029211125 | NZ JARGEN010000086.1 | 71.81 | 13968 | 63.6 | - | _ | - |
| H39 3 26 GCF 029211125 | NZ_JARGEN010000081.1 | _ | 1440 | 56.11 | _ | _ | _ |

The predicted plasimid sequences from the genome of strain $H3SJ34-1^{T.}$

| | | Probability | Contig length | GC content | | | |
|------------------------|------------------------|-------------|---------------|------------|---------------|------------------|--------------|
| Sample name | Contig name | (%) | (bp) | (%) | Acc num | Acc plasmid name | Identity (%) |
| H3SJ34_1_GCA_029222685 | JARHVB010000068.1 | 98.33 | 4918 | 62.91 | NZ_CP023451.1 | p2 | 75.385 |
| H3SJ34_1_GCA_029222685 | JARHVB010000078.1 | 72.13 | 883 | 62.4 | NZ_CP034088.1 | pGW6_2 | 77.477 |
| H3SJ34_1_GCA_029222685 | JARHVB010000051.1 | 90.16 | 16505 | 59.93 | NZ_CP034088.1 | pGW6_2 | 76.566 |
| H3SJ34_1_GCA_029222685 | JARHVB010000079.1 | 77.93 | 43284 | 60.25 | NZ_CP044544.1 | pBbPL7HG1 | 84.925 |
| H3SJ34_1_GCA_029222685 | JARHVB010000080.1 | 98.4 | 551 | 67.7 | NC_011987.1 | pAtK84c | 77.315 |
| H3SJ34_1_GCA_029222685 | JARHVB010000066.1 | 99.74 | 1624 | 63.49 | NZ_AP014687.1 | pNK6c | 95.135 |
| H3SJ34_1_GCA_029222685 | JARHVB010000052.1 | 94.25 | 23059 | 62.88 | NZ_CP032695.1 | pRCCGE525c | 75.897 |
| H3SJ34_1_GCA_029222685 | JARHVB010000053.1 | 79.98 | 30371 | 57.98 | NZ_CP047896.1 | pC33 | 79.757 |
| H3SJ34_1_GCA_029222685 | JARHVB010000056.1 | 87.24 | 1418 | 64.32 | NZ_CP049700.1 | pB323S2a | 90.909 |
| H3SJ34_1_GCA_029222685 | JARHVB010000016.1 | 92.54 | 42156 | 57.45 | NZ_CP044330.1 | unnamed2 | 79.615 |
| H3SJ34_1_GCA_029222685 | JARHVB010000073.1 | 96.63 | 625 | 58.88 | - | - | - |
| H3SJ34_1_GCA_029222685 | JARHVB010000077.1 | 96.79 | 79861 | 61.01 | NZ_CP025114.1 | unnamed | 89.647 |
| H3SJ34_1_GCA_029222685 | JARHVB010000047.1 | 98.74 | 20137 | 62.09 | NZ_CP015743.1 | pShin-07 | 75.68 |
| H3SJ34_1_GCA_029222685 | JARHVB010000007.1 | 97.17 | 54405 | 60.52 | NC_009621.1 | pSMED02 | 77.262 |
| H3SJ34_1_GCA_029222685 | JARHVB010000074.1 | 98.73 | 1255 | 60.16 | - | - | - |
| H3SJ34_1_GCA_029222685 | JARHVB010000075.1 | 73.86 | 506 | 63.24 | - | - | - |
| H3SJ34_1_GCA_029222685 | JARHVB010000009.1 | 87.61 | 29083 | 58.54 | NZ_AP014659.1 | pNK6a | 92.875 |
| H3SJ34_1_GCA_029222685 | JARHVB010000027.1 | 95.62 | 168407 | 62.81 | NZ_CP033508.1 | pMJ700743a | 82.484 |
| H3SJ34_1_GCA_029222685 | JARHVB010000029.1 | 70.26 | 124507 | 58.19 | NC_008242.1 | 1 | 79.049 |
| H3SJ34_1_GCA_029222685 | JARHVB010000026.1 | 95.27 | 25733 | 62.56 | NZ_CP044544.1 | pBbPL7HG1 | 87.473 |
| H3SJ34_1_GCA_029222685 | JARHVB010000070.1 | 97.4 | 6191 | 61.09 | NZ_LR134450.1 | 8 | 80.189 |
| H3SJ34_1_GCA_029222685 | JARHVB010000041.1 | 76.95 | 74830 | 63.32 | NC_014007.1 | pCHQ1 | 81.501 |
| H3SJ34_1_GCA_029222685 | JARHVB010000069.1 | 98.77 | 7358 | 60.7 | NZ_CP032827.1 | unnamed2 | 81.026 |
| H3SJ34_1_GCA_029222685 | JARHVB010000045.1 | 96.41 | 20561 | 60.99 | NZ_AP014705.1 | pMaq22A_1p | 82.713 |
| H3SJ34_1_GCA_029222685 | JARHVB010000034.1 | 79.49 | 544 | 58.09 | NZ_CP006990.1 | pRetIE4771d | 72.753 |
| H3SJ34_1_GCA_029222685 | JARHVB010000064.1 | 85.01 | 7271 | 55.93 | NZ_CP049700.1 | pB323S2a | 99.01 |
| H3SJ34_1_GCA_029222685 | JARHVB010000022.1 | 71.42 | 17852 | 62.47 | NZ_AP014705.1 | pMaq22A_1p | 77.9 |
| H3SJ34_1_GCA_029222685 | JARHVB010000048.1 | 95.98 | 16530 | 60.16 | NC_017966.1 | pTM2 | 72.572 |
| H3SJ34_1_GCA_029222685 | JARHVB010000015.1 | 91.27 | 59225 | 62.18 | NZ AP014579.1 | pl DNA | 76.081 |
| H3SJ34 1 GCA 029222685 | 37 HC11 v B010000013.1 | | | | | | |
| H38J34_1_GCA_029222083 | JARHVB010000013.1 | 96.41 | 142045 | 63.41 | NC_017536.1 | pHCG3B | 79.981 |

The predicted plasimid sequences from the genome of strain ${\rm H3M7-6}^{\rm T}$.

| Sample name | Contig name | Probability (%) | Contig length (bp) | GC content (%) | Acc num | Acc plasmid name | Identity (%) |
|----------------------|----------------------|-----------------|-----------------------|----------------|---------------|------------------|--------------|
| ****** | | . , | | | 377 | | |
| H3M7_6_GCF_029211265 | NZ_JARGEL010000040.1 | 92.89 | 924 | 70.02 | NZ_CP011839.1 | pSg1-NDM | 97.817 |
| H3M7_6_GCF_029211265 | NZ_JARGEL010000045.1 | 91.26 | 2919 | 61.22 | CP045288.2 | pCff1 | 81.139 |
| H3M7_6_GCF_029211265 | NZ_JARGEL010000017.1 | 71.24 | 139989 | 59.73 | NC_006823.1 | 1 | 97.397 |
| H3M7_6_GCF_029211265 | NZ_JARGEL010000035.1 | 84.28 | 566 | 61.66 | - | - | - |
| H3M7_6_GCF_029211265 | NZ_JARGEL010000049.1 | 89.6 | 9271 | 56.59 | NZ_CP040718.1 | pHX3 | 79.641 |
| H3M7_6_GCF_029211265 | NZ_JARGEL010000009.1 | 80.9 | 61432 | 65.41 | NZ_CP039632.3 | unnamed | 96.571 |
| | | | | | | | |

The predicted plasimid sequences from the genome of strain $H3Y2-7^T$.

| Sample name | Contig name | Probability (%) | Contig length (bp) | GC content (%) | Acc num | Acc plasmid name | Identity (%) |
|----------------------|-------------------|-----------------|--------------------|----------------|---------------|------------------|--------------|
| H3Y2 7 GCA 029076445 | JARESG010000086.1 | 79.38 | 570 | 68.77 | - | - | - |
| H3Y2 7 GCA 029076445 | JARESG010000069.1 | 93.65 | 1855 | 64.31 | NC 015147.1 | pASPHE302 | 85.314 |
| H3Y2 7 GCA 029076445 | JARESG010000034.1 | 94.9 | 23121 | 62.75 | NZ CP047900.1 | unnamed2 | 90.44 |
| H3Y2_7_GCA_029076445 | JARESG010000089.1 | - | 523 | 60.8 | NZ_CP029643.1 | pDCT5 | 97.08 |
| H3Y2_7_GCA_029076445 | JARESG010000084.1 | 73.77 | 659 | 63.88 | NZ_CP005191.1 | pMI2 | 99.697 |
| H3Y2_7_GCA_029076445 | JARESG010000085.1 | 79.52 | 630 | 61.9 | - | - | - |
| H3Y2_7_GCA_029076445 | JARESG010000016.1 | 86.49 | 104249 | 63 | NZ_KJ410765.1 | p2MP | 94.817 |
| H3Y2_7_GCA_029076445 | JARESG010000049.1 | - | 6416 | 61.07 | NZ_CP017422.1 | pZXY21 | 88.673 |
| H3Y2_7_GCA_029076445 | JARESG010000050.1 | 82.82 | 6231 | 63.97 | NZ_KJ410765.1 | p2MP | 89.917 |
| H3Y2_7_GCA_029076445 | JARESG010000056.1 | 83.25 | 4959 | 64.73 | NC_019339.1 | pJ349-116 | 95.691 |
| H3Y2_7_GCA_029076445 | JARESG010000087.1 | 82.29 | 564 | 70.57 | - | - | - |
| H3Y2_7_GCA_029076445 | JARESG010000080.1 | - | 900 | 64.22 | NZ_CP046569.1 | pII | 76.496 |
| H3Y2_7_GCA_029076445 | JARESG010000037.1 | - | 20565 | 59.73 | NZ_KJ410765.1 | p2MP | 91.742 |
| H3Y2_7_GCA_029076445 | JARESG010000026.1 | 88.49 | 41126 | 61.91 | NC_019339.1 | pJ349-116 | 91.548 |
| H3Y2_7_GCA_029076445 | JARESG010000090.1 | 79.32 | 512 | 70.7 | - | - | - |
| H3Y2_7_GCA_029076445 | JARESG010000076.1 | - | 1415 | 62.83 | - | - | - |
| H3Y2_7_GCA_029076445 | JARESG010000048.1 | 97.79 | 7232 | 60.25 | NZ_CP017426.1 | pZXY25 | 80.66 |
| H3Y2_7_GCA_029076445 | JARESG010000054.1 | - | 5053 | 58.26 | - | - | - |
| H3Y2_7_GCA_029076445 | JARESG010000045.1 | - | 10326 | 61.89 | NZ_CP029643.1 | pDCT5 | 89.593 |
| H3Y2_7_GCA_029076445 | JARESG010000067.1 | - | 1964 | 65.22 | NZ_CP029643.1 | pDCT5 | 97.659 |
| H3Y2_7_GCA_029076445 | JARESG010000057.1 | 89.53 | 4780 | 64.23 | NC_015146.1 | pASPHE301 | 78.956 |
| H3Y2_7_GCA_029076445 | JARESG010000070.1 | - | 1823 | 66.43 | NZ_KJ410765.1 | p2MP | 86.207 |
| H3Y2_7_GCA_029076445 | JARESG010000032.1 | 96.53 | 26862 | 61.44 | NC_011881.1 | pACHL02 | 85.167 |
| H3Y2_7_GCA_029076445 | JARESG010000042.1 | 77.79 | 12178 | 62.89 | NC_019332.1 | pJ353-116 | 94.223 |
| H3Y2_7_GCA_029076445 | JARESG010000043.1 | 74.55 | 12087 | 62.89 | NC_008712.1 | pTC1 | 86.764 |
| H3Y2_7_GCA_029076445 | JARESG010000060.1 | - | 3080 | 59.42 | NZ_LR134469.1 | 27 | 76.78 |