

The structure of the catalog of orthologs.

| Enzyme name                               | Number of orthologs | Bacterial origin (genus)                                                                                                                                                | Function                                                   |
|-------------------------------------------|---------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------|
| 2-oxoisovalerate dehydrogenase alpha      | 5                   | <i>Enterococcus, Lactobacillus, Listeria, Pseudomonas, Streptococcus</i>                                                                                                | Isovaleric acid synthesis (KADH pathway)                   |
| 2-oxoisovalerate dehydrogenase beta       | 5                   | <i>Enterococcus, Lactobacillus, Listeria, Pseudomonas, Streptococcus</i>                                                                                                | Isovaleric acid synthesis (KADH pathway)                   |
| Aldehyde dehydrogenase                    | 10                  | <i>Bacteroides, Clostridium, Coprococcus, Corynebacterium, Eggerthella, Escherichia, Eubacterium, Listeria, Pseudomonas, Streptococcus</i>                              | Isovaleric acid synthesis (KADH pathway)                   |
| Pyruvate decarboxylase                    | 1                   | <i>Escherichia</i>                                                                                                                                                      | Isovaleric acid synthesis (KADC pathway)                   |
| 4-aminobutyrate aminotransferase gabT     | 12                  | <i>Anaerostipes, Bifidobacterium, Blautia, Citrobacter, Clostridium, Coprococcus, Enterobacter, Escherichia, Eubacterium, Klebsiella, Roseburia, Streptococcus</i>      | GABA degradation                                           |
| 4-aminobutyrate aminotransferase PuuE     | 4                   | <i>Citrobacter, Enterobacter, Escherichia, Klebsiella</i>                                                                                                               | GABA degradation                                           |
| 4-cresol dehydrogenase                    | 1                   | <i>Pseudomonas</i>                                                                                                                                                      | p-Cresol degradation                                       |
| Protocatechuate 3,4-dioxygenase pcaG      | 7                   | <i>Citrobacter, Enterobacter, Escherichia, Klebsiella, Proteus, Pseudomonas, Streptococcus</i>                                                                          | p-Cresol degradation                                       |
| Protocatechuate 3,4-dioxygenase pcaH      | 7                   | <i>Citrobacter, Enterobacter, Escherichia, Klebsiella, Proteus, Pseudomonas, Streptococcus</i>                                                                          | p-Cresol degradation                                       |
| 4-hydroxyphenylacetate decarboxylase hpdB | 8                   | <i>Alistipes, Bacteroides, Bacteroides, Clostridioides, Escherichia, Lactobacillus, Roseburia, Ruminococcus</i>                                                         | p-Cresol synthesis                                         |
| 4-hydroxybutyrate dehydrogenase           | 13                  | <i>Alistipes, Anaerostipes, Bifidobacterium, Blautia, Citrobacter, Clostridium, Dorea, Enterobacter, Escherichia, Eubacterium, Megasphaera, Roseburia, Ruminococcus</i> | $\gamma$ -hydroxybutyric acid degradation                  |
| 4-hydroxyphenylacetate 3-monooxygenase    | 7                   | <i>Citrobacter, Enterobacter, Escherichia, Klebsiella, Proteus, Providencia, Streptococcus</i>                                                                          | Degradation of aromatic compounds (4-hydroxyphenylacetate) |

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| Acetylserotonin O-methyltransferase | 8  | <i>Bacillus, Bacteroides, Chromobacterium, Clostridium, Desulfovibrio, Enterobacter, Pseudomonas</i>                                                                                                                                                                                                                                                  | Melatonin synthesis                         |
| Alanine racemase alr                | 6  | <i>Citrobacter, Enterobacter, Escherichia, Klebsiella, Proteus, Providencia</i>                                                                                                                                                                                                                                                                       | D-Alanine synthesis                         |
| Alanine racemase dadx               | 6  | <i>Citrobacter, Enterobacter, Escherichia, Klebsiella, Proteus, Providencia</i>                                                                                                                                                                                                                                                                       | D-Alanine synthesis                         |
| Argininosuccinate lyase             | 27 | <i>Alistipes, Anaerostipes, Bacteroides, Blautia, Butyrivibrio, Citrobacter, Clostridium, Coprococcus, Desulfovibrio, Dialister, Dorea, Enterobacter, Enterococcus, Escherichia, Eubacterium, Faecalibacterium, Klebsiella, Lactobacillus, Odoribacter, Parabacteroides, Prevotella, Proteus, Providencia, Roseburia, Ruminococcus, Streptococcus</i> | Arginine synthesis                          |
| Aromatic amino acid hydroxylases    | 7  | <i>Chromobacterium, Enterobacter, Ferrimonas, Pseudomonas, Streptococcus, Vibrio, Vibrio</i>                                                                                                                                                                                                                                                          | Catecholamines' synthesis                   |
| Asparagine synthetase asnA          | 16 | <i>Alistipes, Alistipes, Bacteroides, Bifidobacterium, Clostridium, Enterobacter, Enterococcus, Escherichia, Eubacterium, Faecalibacterium, Klebsiella, Lactobacillus, Prevotella, Proteus, Roseburia, Streptococcus</i>                                                                                                                              | Biosynthesis of asparagine                  |
| Asparagine synthetase asnB          | 7  | <i>Alistipes, Bacteroides, Enterobacter, Enterococcus, Escherichia, Klebsiella, Prevotella</i>                                                                                                                                                                                                                                                        | Biosynthesis of asparagine                  |
| Aspartate aminotransferase          | 7  | <i>Citrobacter, Enterobacter, Escherichia, Helicobacter, Klebsiella, Proteus, Providencia</i>                                                                                                                                                                                                                                                         | Kynurenine acid formation out of kynurenine |
| Butyrate kinase                     | 28 | <i>Acidaminococcus, Alistipes, Anaerotruncus, Bacteroides, Blautia, Butyrivibrio, Clostridium, Desulfovibrio, Enterococcus, Eubacterium, Faecalibacterium, Klebsiella, Lactobacillus, Listeria, Prevotella, Roseburia, Streptococcus</i>                                                                                                              | Butyrate synthesis                          |

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| Butyryl-CoA dehydrogenase | 32 | <i>Actinomyces, Alistipes, Anaerostipes, Blautia, Butyrivibrio, Citrobacter, Clostridium, Dialister, Dorea, Eggerthella, Enterobacter, Enterococcus, Escherichia, Eubacterium, Faecalibacterium, Fusobacterium, Gordonibacter, Helicobacter, Lactobacillus, Listeria, Megasphaera, Odoribacter, Peptoclostridium, Prevotella, Proteus, Providencia, Roseburia, Ruminococcus, Streptococcus</i> | Butyric acid synthesis            |
| Carboxylesterase          | 6  | <i>Citrobacter, Enterobacter, Escherichia, Klebsiella, Proteus, Streptococcus</i>                                                                                                                                                                                                                                                                                                              | Benzoic acid synthesis            |
| Carnitine dehydrogenase   | 2  | <i>Enterobacter, Pseudomonas</i>                                                                                                                                                                                                                                                                                                                                                               | Utilization of L- and D-carnitine |
| Catalase                  | 11 | <i>Anaerococcus, Clostridium, Dorea, Enterococcus, Escherichia, Faecalibacterium, Helicobacter, Lactobacillus, Listeria, Proteus, Streptococcus</i>                                                                                                                                                                                                                                            | Antioxidant                       |
| Glutathione peroxidase    | 24 | <i>Actinomyces, Alistipes, Bacteroides, Bifidobacterium, Butyrivibrio, Citrobacter, Clostridium, Dialister, Dorea, Enterobacter, Enterococcus, Escherichia, Eubacterium, Klebsiella, Lactobacillus, Lactococcus, Listeria, Megasphaera, Prevotella, Proteus, Providencia, Roseburia, Ruminococcus, Streptococcus</i>                                                                           | Antioxidant                       |
| Superoxide dismutase SodA | 15 | <i>Alistipes, Bacteroides, Citrobacter, Clostridium, Desulfovibrio, Enterobacter, Enterococcus, Escherichia, Eubacterium, Klebsiella, Oxalobacter, Prevotella, Proteus, Providencia, Streptococcus</i>                                                                                                                                                                                         | Antioxidant                       |
| Superoxide dismutase SodB | 12 | <i>Alistipes, Bacteroides, Citrobacter, Enterobacter, Escherichia, Helicobacter, Klebsiella, Oxalobacter, Prevotella, Proteus, Providencia, Streptococcus</i>                                                                                                                                                                                                                                  | Antioxidant                       |

|                                        |    |                                                                                                                                                                                 |                                                                             |
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| Superoxide dismutase<br>SodC           | 11 | <i>Citrobacter, Clostridium, Desulfovibrio, Enterobacter, Escherichia, Eubacterium, Helicobacter, Klebsiella, Proteus, Providencia, Streptococcus</i>                           | Antioxidant                                                                 |
| Cell wall hydrolase P40                | 1  | <i>Lactocaseibacillus</i>                                                                                                                                                       | Bacterial cell wall defense                                                 |
| Cell wall hydrolase P75                | 1  | <i>Lactobacillaceae</i>                                                                                                                                                         | Bacterial cell wall defense                                                 |
| Chorismate mutase                      | 8  | <i>Actinomyces, Citrobacter, Clostridium, Enterobacter, Escherichia, Proteus, Providencia, Streptococcus</i>                                                                    | Prephenate formation, part of phenylalanine and tyrosine synthesis pathways |
| Creatinine amidohydrolase              | 5  | <i>Anaerostipes, Anaerotruncus, Clostridium, Clostridium, Pseudomonas</i>                                                                                                       | Creatinine synthesis                                                        |
| Diacylglycerol kinase                  | 8  | <i>Citrobacter, Desulfovibrio, Enterobacter, Escherichia, Helicobacter, Proteus, Providencia, Streptococcus</i>                                                                 | Phosphatidic acid and diacylglycerol synthesis                              |
| Dihydrolipoyl dehydrogenase            | 14 | <i>Bacteroides, Bifidobacterium, Clostridium, Coprococcus, Dorea, Enterococcus, Escherichia, Eubacterium, Lactobacillus, Listeria, Pseudomonas, Ruminococcus, Streptococcus</i> | Regulatory protein (host-bacterium)                                         |
| Dihydroxyacetone phosphatase           | 5  | <i>Bacteroides, Bifidobacterium, Blautia, Clostridium, Corynebacterium</i>                                                                                                      | Produce 1,3-dihydroxyacetone                                                |
| D-lactate dehydrogenase                | 13 | <i>Citrobacter, Clostridium, Desulfovibrio, Enterobacter, Enterococcus, Escherichia, Lactobacillus, Proteus, Providencia, Streptococcus</i>                                     | D-lactic acid formation                                                     |
| Dopa decarboxylase                     | 10 | <i>Bacillus, Bacteroides, Desulfovibrio, Desulfovibrio, Pseudomonas, Pseudonocardia, Rubrobacter, Streptococcus, Yersinia</i>                                                   | Serotonin, dopamine and norepinephrine synthesis                            |
| D-serine/D-alanine/glycine transporter | 6  | <i>Citrobacter, Enterobacter, Escherichia, Klebsiella, Proteus, Providencia</i>                                                                                                 | Transportation of D-serine, D- alanine and glycine                          |

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| Estradiol 17-beta-dehydrogenase | 29 | <i>Acidaminococcus, Actinomyces, Alistipes, Anaerofustis, Anaerostipes, Bacteroides, Blautia, Butyrivibrio, Citrobacter, Clostridium, Coprococcus, Dialister, Dorea, Enterobacter, Enterococcus, Escherichia, Eubacterium, Faecalibacterium, Klebsiella, Lactobacillus, Megamonas, Megasphaera, Oxalobacter, Prevotella, Proteus, Providencia, Roseburia, Ruminococcus, Streptococcus</i> | 17-beta-Estradiol degradation |
| Ethanolamine ammonia-lyase eutB | 10 | <i>Citrobacter, Clostridium, Desulfovibrio, Enterobacter, Enterococcus, Escherichia, Klebsiella, Listeria, Proteus, Providencia</i>                                                                                                                                                                                                                                                       | Ethanolamine catabolism       |
| Ethanolamine ammonia-lyase eutC | 9  | <i>Citrobacter, Clostridium, Enterobacter, Enterococcus, Escherichia, Klebsiella, Listeria, Proteus, Providencia</i>                                                                                                                                                                                                                                                                      | Ethanolamine catabolism       |
| Gamma-aminobutyrate antiporter  | 20 | <i>Alistipes, Alistipes, Bacteroides, Bifidobacterium, Clostridium, Desulfovibrio, Enterobacter, Enterococcus, Escherichia, Eubacterium, Lactobacillus, Listeria, Megasphaera, Odoribacter, Parabacteroides, Prevotella</i>                                                                                                                                                               | GABA transportation           |
| Gamma-glutamyltranspeptidase    | 12 | <i>Acidaminococcus, Bacillus, Bacteroides, Citrobacter, Clostridium, Enterobacter, Escherichia, Helicobacter, Klebsiella, Proteus, Providencia, Streptococcus</i>                                                                                                                                                                                                                         | Glutathione degradation       |
| Glutamate decarboxylase         | 28 | <i>Alistipes, Bacteroides, Bifidobacterium, Bifidobacterium, Clostridium, Clostridium, Desulfovibrio, Eggerthella, Enterococcus, Escherichia, Eubacterium, Gordonibacter, Helicobacter, Lactobacillus, Lactococcus, Listeria, Odoribacter, Parabacteroides, Parvimonas, Prevotella, Proteus, Streptococcus</i>                                                                            | GABA synthesis                |
| Glutamate mutase glmE           | 8  | <i>Bacteroides, Blautia, Citrobacter, Clostridium, Enterobacter, Escherichia, Prevotella, Proteus</i>                                                                                                                                                                                                                                                                                     | Glutamate II degradation      |

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| Glutamate mutase glmS         | 8  | <i>Bacteroides, Blautia, Citrobacter, Clostridium, Enterobacter, Escherichia, Prevotella, Proteus</i>                                                                                                                                       | Glutamate II degradation |
| Methylaspartate ammonia-lyase | 8  | <i>Bacteroides, Blautia, Citrobacter, Clostridium, Enterobacter, Escherichia, Prevotella, Proteus</i>                                                                                                                                       | Glutamate II degradation |
| Glutamate synthase gltB       | 11 | <i>Anaerostipes, Bacillus, Bifidobacterium, Blautia, Clostridium, Escherichia, Lactobacillus, Listeria, Roseburia, Ruminococcus, Streptococcus</i>                                                                                          | Glutamate II synthesis   |
| Glutamate synthase gltD       | 11 | <i>Anaerostipes, Bacillus, Bifidobacterium, Blautia, Clostridium, Escherichia, Lactobacillus, Listeria, Roseburia, Ruminococcus, Streptococcus</i>                                                                                          | Glutamate II synthesis   |
| Glutamine synthetase          | 17 | <i>Bacteroides, Bifidobacterium, Citrobacter, Clostridium, Coprococcus, Enterobacter, Enterococcus, Escherichia, Eubacterium, Faecalibacterium, Klebsiella, Lactobacillus, Proteus, Providencia, Roseburia, Ruminococcus, Streptococcus</i> | L-glutamine formation    |
| Glutathione reductase         | 13 | <i>Bifidobacterium, Citrobacter, Clostridium, Enterobacter, Enterococcus, Escherichia, Faecalibacterium, Klebsiella, Lactobacillus, Listeria, Proteus, Providencia, Streptococcus</i>                                                       | Glutathione degradation  |
| Glutathione S-transferase     | 10 | <i>Citrobacter, Enterobacter, Enterococcus, Escherichia, Klebsiella, Lactobacillus, Oxalobacter, Proteus, Providencia, Streptococcus</i>                                                                                                    | Glutathione degradation  |
| Glutathione synthetase        | 12 | <i>Citrobacter, Clostridium, Enterobacter, Enterococcus, Escherichia, Klebsiella, Lactobacillus, Listeria, Pediococcus, Proteus, Providencia, Streptococcus</i>                                                                             | Glutathione synthesis    |
| Glycine amidinotransferase    | 1  | <i>Streptomyces</i>                                                                                                                                                                                                                         | GABA degradation         |

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| Histidine ammonia-lyase         | 20 | <i>Acidaminococcus, Actinomyces, Alistipes, Bacteroides, Bifidobacterium, Blautia, Citrobacter, Clostridium, Enterobacter, Enterococcus, Escherichia, Eubacterium, Klebsiella, Lactobacillus, Odoribacter, Prevotella, Providencia, Roseburia, Streptococcus</i>               | Histamine degradation                          |
| Histidine decarboxylase         | 13 | <i>Bifidobacterium, Citrobacter, Clostridium, Eggerthella, Enterobacter, Gordonibacter, Klebsiella, Lactobacillus, Morganella, Staphylococcus, Streptococcus</i>                                                                                                               | Histamine synthesis                            |
| Kynurenine formamidase<br>KynB  | 1  | <i>Klebsiella</i>                                                                                                                                                                                                                                                              | Degradation of tryptophan to kynurenine        |
| Lactocepin                      | 2  | <i>Lactobacillus, Lactococcus</i>                                                                                                                                                                                                                                              | Degradation of proinflammatory chemokine IP-10 |
| Lactoyl-CoA dehydratase         | 3  | <i>Clostridium, Coprococcus, Megasphaera</i>                                                                                                                                                                                                                                   | Propionic acid synthesis                       |
| Methylmalonyl-CoA decarboxylase | 29 | <i>Actinomyces, Alistipes, Bacteroides, Bifidobacterium, Blautia, Butyrivibrio, Clostridium, Dialister, Dorea, Eubacterium, Holdemania, Lactobacillus, Megasphaera, Odoribacter, Parabacteroides, Phascolarctobacterium, Prevotella, Roseburia, Streptococcus, Veillonella</i> | Propionic acid synthesis                       |
| Propionaldehyde dehydrogenase   | 15 | <i>Blautia, Citrobacter, Clostridium, Dorea, Enterobacter, Enterococcus, Eubacterium, Lactobacillus, Listeria, Roseburia, Ruminococcus, Streptococcus</i>                                                                                                                      | Propionic acid synthesis                       |
| L-aspartate oxidase             | 10 | <i>Citrobacter, Clostridium, Enterobacter, Escherichia, Faecalibacterium, Klebsiella, Oxalobacter, Proteus, Providencia, Streptococcus</i>                                                                                                                                     | N-acetyl aspartate degradation                 |
| Linoleic acid isomerase         | 23 | <i>Actinomyces, Alistipes, Anaerostipes, Bacteroides, Bifidobacterium, Blautia, Butyrivibrio, Carnobacterium, Clostridium, Eggerthella, Enterococcus, Eubacterium, Gordonibacter, Helicobacter, Holdemania, Lactobacillus, Lactococcus, Listeria, Roseburia, Ruminococcus</i>  | Linoleic acid conjugation                      |

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| Microbial anti-inflammatory molecule | 1  | <i>Faecalibacterium</i>                                                                                                                                               | Inhibition of transcription factor (NF)-kB and immune response of t-lymphocytes Th-1 and Th-2 |
| Monoamine oxidase                    | 5  | <i>Enterobacter, Escherichia, Klebsiella, Proteus, Pseudomonas</i>                                                                                                    | Serotonin, dopamine and norepinephrine degradation                                            |
| Myo-inositol 2-dehydrogenase         | 13 | <i>Anaerostipes, Bacteroides, Bifidobacterium, Blautia, Clostridium, Enterobacter, Enterococcus, Klebsiella, Lactobacillus, Listeria, Ruminococcus, Streptococcus</i> | Inositol degradation                                                                          |
| Myo-inositol-1(or 4)-monophosphatase | 10 | <i>Acinetobacter, Bacteroides, Bifidobacterium, Enterobacter, Enterococcus, Escherichia, Lactobacillus, Listeria, Streptococcus</i>                                   | Inositol synthesis                                                                            |
| Myo-inositol-1-phosphate synthase    | 1  | <i>Streptomyces</i>                                                                                                                                                   | Inositol                                                                                      |
| Nitric oxide dioxygenase             | 10 | <i>Bacillus, Citrobacter, Clostridiales, Enterobacter, Escherichia, Klebsiella, Listeria, Proteus, Providencia, Streptococcus</i>                                     | Nitric oxide degradation                                                                      |
| Nitric oxide reductase NorB          | 2  | <i>Enterobacter, Pseudomonas</i>                                                                                                                                      | Nitric oxide degradation                                                                      |
| Nitric oxide reductase NorC          | 2  | <i>Enterobacter, Pseudomonas</i>                                                                                                                                      | Nitric oxide degradation                                                                      |
| Nitric oxide synthase                | 6  | <i>Bacillus, Geobacillus, Listeria, Staphylococcus, Streptococcus, Streptomyces</i>                                                                                   | Nitric oxide synthesis                                                                        |
| Ornithine carbamoyltransferase       | 5  | <i>Escherichia, Megamonas, Mitsuokella, Moritella, Veillonella</i>                                                                                                    | Arginine synthesis pathway in prokaryotes                                                     |
| Phenylalanine aminotransferase       | 3  | <i>Actinomyces, Bifidobacterium, Streptococcus</i>                                                                                                                    | Phenylalanine synthesis                                                                       |
| Phenylalanine-specific permease      | 6  | <i>Citrobacter, Enterobacter, Escherichia, Klebsiella, Proteus, Providencia</i>                                                                                       | Phenylalanine transportation                                                                  |
| Phenyllactate dehydratase            | 9  | <i>Bacteroides, Blautia, Butyrivibrio, Clostridium, Coprococcus, Dorea, Eubacterium, Lactobacillus, Roseburia</i>                                                     | Indole-3-propionic acid formation                                                             |



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| Phenyllactate dehydrogenase | 7  | <i>Bifidobacterium, Clostridium, Enterococcus, Eubacterium, Roseburia, Ruminococcus</i>                                                                                                                                                                                                                                                                                                                        | Formation of 4-hydroxyphenyl pyruvate from prephenate, part of phenylalanine and tyrosine synthesis metabolic pathway |
| Phosphotransacetylase       | 43 | <i>Actinomyces, Alistipes, Anaerostipes, Bacillus, Bacteroides, Bifidobacterium, Blautia, Butyrivibrio, Citrobacter, Clostridium, Corynebacterium, Desulfovibrio, Dorea, Eggerthella, Enterobacter, Enterococcus, Escherichia, Eubacterium, Gordonibacter, Helicobacter, Lactobacillus, Listeria, Megasphaera, Odoribacter, Parabacteroides, Prevotella, Proteus, Providencia, Ruminococcus, Streptococcus</i> | Acetic acid synthesis                                                                                                 |
| Phosphotransbutyrylase      | 3  | <i>Blautia, Clostridium, Streptococcus</i>                                                                                                                                                                                                                                                                                                                                                                     | Formation of outer cell d-(-)-3-hydroxybutyric acid                                                                   |
| Prephenate dehydrogenase    | 10 | <i>Citrobacter, Enterobacter, Enterococcus, Escherichia, Lactobacillus, Lactococcus, Listeria, Proteus, Providencia, Streptococcus</i>                                                                                                                                                                                                                                                                         | Tyrosine synthesis form prephenate                                                                                    |
| Pyruvate dehydrogenase aceE | 8  | <i>Citrobacter, Enterobacter, Escherichia, Helicobacter, Klebsiella, Oxalobacter, Proteus, Providencia</i>                                                                                                                                                                                                                                                                                                     | Pyruvic acid synthesis out of glucose                                                                                 |
| Pyruvate dehydrogenase aceF | 6  | <i>Citrobacter, Enterobacter, Escherichia, Klebsiella, Proteus, Providencia</i>                                                                                                                                                                                                                                                                                                                                | Pyruvic acid synthesis out of glucose                                                                                 |
| Pyruvate kinase pykA        | 6  | <i>Citrobacter, Enterobacter, Escherichia, Klebsiella, Proteus, Providencia</i>                                                                                                                                                                                                                                                                                                                                | Pyruvic acid synthesis out of glucose                                                                                 |
| Pyruvate kinase pykF        | 13 | <i>Bacteroides, Bifidobacterium, Citrobacter, Clostridium, Enterobacter, Escherichia, Eubacterium, Klebsiella, Lactobacillus, Proteus, Providencia, Roseburia, Ruminococcus</i>                                                                                                                                                                                                                                | Pyruvic acid synthesis out of glucose                                                                                 |
| Quinolinate synthase        | 10 | <i>Citrobacter, Clostridium, Enterobacter, Escherichia, Faecalibacterium, Klebsiella, Oxalobacter, Proteus, Providencia, Streptococcus</i>                                                                                                                                                                                                                                                                     | Participation in degradation of quinolinic acid to nicotinamide adenine dinucleotide (NAD)                            |

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| Serine hydroxymethyltransferase       | 24 | <i>Alistipes, Anaerostipes, Bacteroides, Bifidobacterium, Blautia, Citrobacter, Clostridium, Desulfovibrio, Dorea, Enterobacter, Enterococcus, Escherichia, Eubacterium, Faecalibacterium, Helicobacter, Klebsiella, Lactobacillus, Listeria, Oxalobacter, Proteus, Providencia, Roseburia, Ruminococcus, Streptococcus</i> | Glycine formation from serine                                         |
| Serine racemase                       | 3  | <i>Enterococcus, Listeria, Streptococcus</i>                                                                                                                                                                                                                                                                                | Formation of D-serine from L-serine                                   |
| Serotonin N-acetyltransferase         | 24 | <i>Anaerostipes, Blautia, Butyrivibrio, Butyrivibrio, Clostridium, Desulfovibrio, Dialister, Dorea, Enterococcus, Eubacterium, Lactobacillus, Megasphaera, Roseburia, Ruminococcus, Streptococcus</i>                                                                                                                       | Serotonin degradation for melatonin formation                         |
| Serpin                                | 2  | <i>Bifidobacterium</i>                                                                                                                                                                                                                                                                                                      | Inhibitor of pancreatic and neutrophilic elastase during inflammation |
| Spermidine synthase                   | 26 | <i>Bacteroides, Blautia, Butyrivibrio, Citrobacter, Clostridium, Enterobacter, Enterococcus, Escherichia, Eubacterium, Megasphaera, Peptoclostridium, Roseburia, Ruminococcus, Streptococcus</i>                                                                                                                            | Spermidine synthesis                                                  |
| Tryptophan 2,3-dioxygenase            | 3  | <i>Enterobacteriales, Klebsiella, Streptococcus</i>                                                                                                                                                                                                                                                                         | Degradation of tryptophan to kynurenine                               |
| Tryptophan permease                   | 3  | <i>Citrobacter, Enterobacter, Escherichia</i>                                                                                                                                                                                                                                                                               | Tryptophan transportation                                             |
| Tryptophan-specific transport protein | 4  | <i>Citrobacter, Enterobacter, Escherichia, Klebsiella</i>                                                                                                                                                                                                                                                                   | Tryptophan transportation                                             |
| Tryptophan synthase alpha             | 13 | <i>Anaerostipes, Bacteroides, Bifidobacterium, Blautia, Citrobacter, Clostridium, Enterobacter, Enterococcus, Escherichia, Eubacterium, Lactobacillus, Proteus, Roseburia</i>                                                                                                                                               | Tryptophan synthesis                                                  |
| Tryptophan synthase beta              | 13 | <i>Anaerostipes, Bacteroides, Bifidobacterium, Blautia, Citrobacter, Clostridium, Enterobacter, Enterococcus, Escherichia, Eubacterium, Lactobacillus, Proteus, Roseburia</i>                                                                                                                                               | Tryptophan synthesis                                                  |

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| Tryptophanase                       | 7  | <i>Alistipes, Bacteroides, Citrobacter, Clostridium, Enterobacter, Escherichia, Proteus</i>                                            | Synthesis of indole from tryptophan |
| Tyrosine aminotransferase           | 6  | <i>Citrobacter, Enterobacter, Escherichia, Klebsiella, Proteus, Providencia</i>                                                        | Tyrosine synthesis                  |
| Tyrosine decarboxylase              | 12 | <i>Bifidobacterium, Clostridium, Dialister, Enterococcus, Escherichia, Eubacterium, Lactobacillus, Peptoclostridium, Streptococcus</i> | Synthesis of tyramine and dopamine  |
| Tyrosine-specific transport protein | 6  | <i>Citrobacter, Enterobacter, Escherichia, Klebsiella, Proteus, Providencia</i>                                                        | Tyrosine transportation             |
| Vinylphenol reductase               | 7  | <i>Bacteroides, Blautia, Butyrivibrio, Clostridium, Collinsella, Eubacterium, Lactobacillus</i>                                        | 4-Ethyl phenol formation            |