| action name | | Enzumo | E.C. | enome-scale metabolic model of F Locus(reh) Gene(reh) | reaction with marvin charges (pH6) | reaction with marvin charges (pH7) | reaction with marvin charges (pH8) |
|-------------|--|--|-----------|--|---|---|--|
| | 1- and 2- | 1-methylnaphthalene | number | | mnapth + o2 + nadh + h -> hmnapth + nad + | mnapth + o2 + nadh + h -> hmnapth + nad | |
| NAPTH | degradation | hydroxylase | 1.14.13 | H16_B1480/H16_B2135 unknown/unknown | h2o | + h2o | h2o |
| Dn | 1- and 2- Methylnaphthalene degradation | alcohol dehydrogenase | 11.1.1 | H16_B0517/H16_B1433/ wn/adhP/unknown/ H16_B1699/H16_B1745/ nknown/unknown/u H16_B1834/H16_B2470 nknown | U hmnapth + nad -> napthah + nadh + h | hmnapth + nad -> napthah + nadh + h | hmnapth + nad -> napthah + nadh + h |
| CBZP | 1- and 2- Methylnaphthalene degradation | 2-hydroxy-3- carboxy- benzalpyruvate hydratase-aldolase | 4.2.1 | H16_A1069/H16_A1070/ unknown/unknown/ H16_A1289/H16_A2151/ unknown/unknown/ H16_A3307/H16_B0359/ unknown/unknown/ H16_B0706 unknown/ | 2h2chamar i h2o a feolog i mar | 2h3cbzpyr + h2o -> fsalac + pyr | 2h3cbzpyr + h2o -> fsalac + pyr |
| MBZP | | 2-hydroxy-3- methylbenzalpyruvat e hydratase-aldolase | 4.2.1 | H16_A1069/H16_A1070/ unknown/unknown/ H16_A1289/H16_A2151/ unknown/unknown/ H16_A3307/H16_B0359/ unknown/unknown/ | | 2h3mbzpyr + h2o -> msalcah + pyr | 2h3mbzpyr + h2o -> msalcah + pyr |
| СНЗ | 1- and 2- Methylnaphthalene | salicylate hydroxylase | 1.14.13.1 | H16_B0706 unknown/ H16_A0578/H16_A0922/ unknown/unknown/ H16_A1785/H16_B0750/ unknown/unknown/ | | msalc + o2 + nadh + 2 h -> dhtolen + nad + co2 + h2o | msalc + o2 + nadh + 2 h -> dhtolen + nad + co2 + h2o |
| SOPD | Methylnaphthalene | 2- hydroxyisophthalate decarboxylase | 4.1.1 | H16_B0876 unknown H16_B2447 unknown | hxsp + h -> salcyl + co2 | hxsp + h -> salcyl + co2 | hxsp + h -> salcyl + co2 |
| :H4 | 1- and 2- | | 1.14.13.1 | H16_A0578/H16_A0922/ unknown/unknown/ H16_A1785/H16_B0750/ unknown/unknown/ H16_B0876 unknown | | msalc4 + o2 + nadh + 2 h -> 4mctch + nad + h2o + co2 | msalc4 + o2 + nadh + 2 h -> 4mctch + nad + h2o + co2 |
| IAPTH | | nydroxyiase | 1.14.13 | H16_A1145/H16_B0495/ unknown/unknown/ H16_B1480/H16_B2135 unknown/unknown | 2mnapth + o2 + nadh + h -> 2napthm + nad + h2o | 2mnapth + o2 + nadh + h -> 2napthm + nad + h2o | $2mnapth + o2 + nadh + 2 h \rightarrow 2napthm + nad + h2o$ |
| NAPS | 1- and 2- Methylnaphthalene degradation | methyl-succinyl-CoA | 2.8.3 | H16_B0355/H16_B0367/ unknown/unknown/ H16_B0488/H16_B0655/ unknown/unknown/ H16_B0656/H16_B0847/ unknown/unknown/ H16_B0914 unknown/ | | napth2ms + succoa -> napmsccoa + succ | napth2ms + succoa -> napmsccoa + succ |
| PMSCD | 1- and 2- Methylnaphthalene degradation | transferase naphthyl-2-methyl- succinyl-CoA dehydrogenase | 1.3.99 | H16_A2143/H16_A2149/ unknown/unknown/ H16_A2808/H16_B0675/ unknown/unknown/ H16_B0699 unknown/ | | napmsccoa -> nap2msuccoa + h2 | napmsccoa -> nap2msuccoa + h2 |
| ORTS | 1- and 2- Methylnaphthalene degradation | | 4.2.1 | H16_A1069/H16_A1070/ unknown/unknown/ H16_A1289/H16_A2151/ unknown/unknown/ H16_A3307/H16_B0359/ unknown/unknown/ H16_B0706 unknown/ | | nap2msuccoa + h2o -> naphmsuccoa | nap2msuccoa + h2o -> naphmsuccoa |
| OLS | 1- and 2- Methylnaphthalene degradation | thiolase | 2.3.1 | H16, A0039/H16, A0240/ unknown/unknown/ H16, A0269/H16, A0609/ unknown/unknown/ H16, A1315/H16, A1564/ unknown/unknown/ H16, A1583/H16, A3017/ unknown/unknown/ H16, A3759/H16, A3017/ unknown/unknown/ H16, A3293/H16, A3212/ unknown/unknown/ H16, A3253/H16, A3221/ unknown/unknown/ H16, B3032/H16, B0212/ wn/unknown/unknown/ H16, B3123/H16, B0213/ unknown/unknown/ H16, B3123/H16, B3123/ phn/Unknown/unkn H16, B3143/H16, B3123/ phn/Unknown/unkn H16, B1407/H16, B1663/ own/unknown/unkn H16, B1407/H16, B1663/ own/unknown/unkn | napomsuccoa + coa -> 2naptcoa + succoa | napomsuccoa + coa -> 2naptcoa + succoa | napomsuccoa + coa -> 2naptcoa + succoa |
| APTCT | degradation | 2-naphthoate CoA- transferase | 2.8.3 | H16_B0355/H16_B0367/ unknown/unknown/ H16_B0488/H16_B0655/ unknown/unknown/ H16_B0656/H16_B0847/ unknown/unknown/ H16_B0914 unknown/ H16_A0757/H16_A3330/ adh/unknown/unkn | 2naptcoa + h2o -> 2naptha + coa + h | 2naptcoa + h2o -> 2naptha + coa + h | 2naptcoa + h2o -> 2naptha + coa + h |
| Dnp | degradation | denydrogenase | 1.1.1.1 | H16_B0517/H16_B1433/ wn/adhP/unknown/u H16_B1699/H16_B1745/ nknown/unknown/u H16_B1834/H16_B2470 nknown | ^u 2napthm + nad -> 2napald + nadh + h | 2napthm + nad -> 2napald + nadh + h | 2napthm + nad -> 2napald + nadh + h |
| HMBZP | 1- and 2- Methylnaphthalene degradation | 2-hydroxy-4- hydroxymethylbenzal pyruvate hydratase- aldolase | 4.2.1 | H16_A1069/H16_A1070/ unknown/unknown/ H16_A1289/H16_A2151/ unknown/unknown/ H16_A3307/H16_B0359/ unknown/unknown/ H16_B0706 unknown/ | 2h4hmhnnyr + h2o -> 4hmscald + nyr | 2h4hmbnpyr + h2o -> 4hmscald + pyr | 2h4hmbnpyr + h2o -> 4hmscald + pyr |
| CH5 | 1- and 2- Methylnaphthalene degradation 1,1,1-Trichloro-2,2- | salicylate hydroxylase | 1.14.13.1 | H16_A0578/H16_A0922/ unknown/unknown/ H16_A1785/H16_B0750/ unknown/unknown/ H16_B0876 unknown | | 4hmsalc + o2 + nadh + 2 h -> 4hmcatech + nad + h2o + co2 | 4hmsalc + o2 + nadh + 2 h -> 4hmcatech + nad + $h2o$ + $co2$ |
| DDT1 | Pri 141 | cis-2,3-dihydrodiol DDT dehydrogenase | 1.3.1 | H16_B0731/H16_B0734 unknown/unknown | c23dhddt + nad -> 23doddt + nadh + h | c23dhddt + nad -> 23doddt + nadh + h | c23dhddt + nad -> 23doddt + nadh + h |
| DDTp | Chlorophenyl)Ethan e (DDT) degradation | cis-2,3-dihydrodiol DDT dehydrogenase | 1.3.1 | H16_B0731/H16_B0734 unknown/unknown | c23dhddt + nadp -> 23doddt + nadph + 2 h | c23dhddt + nadp -> 23doddt + nadph + h | c23dhddt + nadp -> 23doddt + nadph + h |
| PD2 | e (DDT) degradation 1,1,1-Trichloro-2,2- | 2-nitropropane dioxygenase | 1.13.11 | H16_A0633/H16_B0223/ pcaH2/unknown/un H16_B0757/H16_B1109/ nown/unknown/unk H16_B1420/H16_B1836 nown/unknown | | 23doddt + o2 -> ohtchod + h | 23doddt + o2 -> ohtchod + h |
| D4BZ | Bis-(4'- Chlorophenyl)Ethan e (DDT) degradation 1,1,1-Trichloro-2,2- | multi-step reaction | | | ohtchod + o.5 h2 -> 2 4chbenz + h | ohtchod + 0.5 h2 -> 2 4chbenz + h | ohtchod + o.5 h2 -> 2 4chbenz + h |
| PD3 | Ric.(4'- | 2-nitropropane dioxygenase | 1.13.11 | H16_A0633/H16_B0223/ pcaH2/unknown/un H16_B0757/H16_B1109/ nown/unknown/unk H16_B1420/H16_B1836 nown/unknown | | dchdchche + o2 -> ohchtcht + h | dchdchche + o2 -> ohchtcht |
| | Bis-(4'- Chlorophenyl)Ethan e (DDT) degradation 1,1,1-Trichloro-2,2- | phenylacrylic acid decarboxylase | 41.1 | H16_B2447 unknown | dda + h -> ddm + co2 | dda + h -> ddm + co2 | dda + h -> ddm + co2 |
| 4CH | Bis-(4'- Chlorophenyl)Ethan e (DDT) degradation | multi-step reaction | | H16 A0232/H16 A0745/ unknown/unknown/ | ddm + 3 co2 + 4 h2 -> 2 4chphac + 2 h2o + 2 h | ddm + 3 co2 + 4 h2 -> 2 4chphac + 2 h2o + 2 h | ddm + 3 co2 + 4 h2 -> 2 4chphac + 2 h2o + 2 h |
| D15 | 1,2-Dichloroethane degradation | aldehyde dehydrogenase (NAD+) | 1.2.1.3 | H16_A1114/H16_A1495/ unknown/unknown/ H16_B0212/H16_B0421/ unknown/unknown/ | chacald + nad + h2o -> chac + nadh + 2 h | chacald + nad + h2o -> chac + nadh + 2 h | chacald + nad + h2o -> chac + nadh + 2 h |
| IR2 | 1,4- Dichlorobenzene degradation | maleylacetate reductase | 1.3.1.32 | H16_A1786/H16_B0970 unknown/pcpE | 2bromoac + nadh -> 2mac + nad + br | 2bromoac + nadh -> 2mac + nad + br | 2bromoac + nadh -> 2mac + nad + br |
| BLD3 | 1,4- Dichlorobenzene degradation 1,4- | carboxymethylenebut enolidase | 3.1.1.45 | H16_A2215/H16_A2739/ unknown/unknown/ H16_A3488 unknown | c2ch4cmo + h2o -> 2chmac + h | c2ch4cmo + h2o -> 2chmac + h | c2ch4cmo + h2o -> 2chmac + h |
| CR3 | Dichlorobenzene degradation 1,4- | reductase | 1.3.1.32 | H16_A1786/H16_B0970 unknown/pcpE | 2chmac + nadh -> 2mac + nad + cl | 2chmac + nadh -> 2mac + nad + cl | 2chmac + nadh -> 2mac + nad + cl |
| 1010 | Dichlorobenzene degradation | chlorophenol 4- monooxygenase | 1.14.13 | H16_A1145/H16_B0495/ unknown/unknown/ H16_B1480/H16_B2135 unknown/unknown | 246tchph + 2 nadh + o2 + 2 h -> 26dchhq + 2 nad + h2o + cl | 246 t chph + 2 nadh + o2 + h -> 26 d chhq + 2 nad + h2o + cl | 246tchph + 2 nadh + o2 + h -> 26dchhq + 2 nad + h2o + cl |

| FBMO11 | 1,4- Dichlorobenzene | chlorophenol 4- monooxygenase | 1.14.13 | H16_A1145/H16_B0495/ H16_B1480/H16_B2135 | | 26dchp + o2 + nadh + h -> 26dchhq + nad + h2o | 26dchp + o2 + nadh + h -> 26dchhq + nad + h2o | 26dchp + o2 + nadh + h -> 26dchhq + nad + h2o |
|------------------|---|--|---------------------|---|--|--|--|--|
| CMBLD4 | degradation 1,4- Dichlorobenzene degradation | carboxymethylenebut enolidase | 3.1.1.45 | H16_A2215/H16_A2739/ | | c4cmbo + h2o -> 2mac + h | c4cmbo + h2o -> 2mac + h | c4cmbo + h2o -> 2mac + h |
| CMBLD5 | 1,4- Dichlorobenzene degradation | carboxymethylenebut enolidase | 3.1.1.45 | H16_A2215/H16_A2739/ H16_A3488 | unknown/unknown/ unknown | protmn + h2o -> cacac + h | protmn + h2o -> cacac + h | protmn + h2o -> cacac + h |
| MCCIS2 | 1,4- Dichlorobenzene degradation | muconate cycloisomerase | 5.5.1.1 | H16_A1966/H16_B0536 | catB3/catB4 | 3chccm + h -> protmn + hcl + co2 | 3chccm + h -> protmn + hcl + co2 | 3chccm + h -> protmn + hcl + co2 |
| CATCHDG4 | 1,4- Dichlorobenzene degradation | catechol 1,2- dioxygenase | 1.13.11.1 | H16_A1964/H16_B0968 | catA/pcpA | 4chcat + o2 -> 3chccm + 2 h | 4chcat + o2 -> 3chccm + 2 h | 4chcat + o2 -> 3chccm + 2 h |
| CATCHD4 | 1,4- Dichlorobenzene degradation | catechol 2,3- dioxygenase | 1.13.11.2 | H16_B0546 | unknown | 4chcat + o2 -> 5ch2hmcs + h | 4chcat + o2 -> 5ch2hmcs + h | 4chcat + o2 -> 5ch2hmcs + h |
| 6CHQD | 1,4- Dichlorobenzene degradation | 6-Chlorobenzene- 1,2,4-triol:oxygen 7S,8S-oxidoreductase | | | | 6chq + o2 -> 2chmac + 2 h | 6chq + o2 -> 2chmac + 2 h | 6chq + o2 -> 2chmac + 2 h |
| 26DICH | 1,4- Dichlorobenzene | 2,6-DiCH chlorohydolase | | | | 26dchhq + h2o -> 6chq + hcl + h | 26dchhq + h2o -> 6chq + hcl | 26dchhq + h2o -> 6chq + hd |
| 4HBZCT | degradation 2,4- Dichlorobenzoate | 4-hydroxybenzoyl- CoA thioesterase | 3.1.2.23 | H16_A1529/H16_A2456 | unknown/unknown | 4hbzcoa + h2o -> 4hb + coa + h | 4hbzcoa + h2o -> 4hb + coa + h | 4hbzcoa + h2o -> 4hb + coa + h |
| NTPPD4 | degradation 2,4- Dichlorobenzoate | 2-nitropropane dioxygenase | 1.13.11 | | nown/unknown/unk | 4sulcat + o2 -> 3sulmc + 2 h | 4sulcat + o2 -> 3sulmc + 2 h | 4sulcat + o2 -> 3sulmc + 2 h |
| ESTLP | 2,4- Dichlorobenzoate | | 3.1.1 | H16_B1420/H16_B1836 H16_A1422/H16_A1554/ H16_A3634/H16_B0287/ H16_B0633/H16_B1090/ H16_B1112/H16_B1249/ | unknown/unknown/ unknown/unknown/ unknown/unknown/ unknown/unknown/ | 4sullac + h2o -> so3 + 2mac + h | 4sullac + h2o -> so3 + 2mac + h | 4sullac + h2o -> so3 + 2mac + h |
| | degradation | | | H16_B1475/H16_B2049/ H16_B2068 H16_A0757/H16_A3330/ | nown | | | |
| ALCDt | 3-Chloroacrylic acid degradation | alcohol dehydrogenase | 1.1.1.1 | H16_B0517/H16_B1433/ H16_B1699/H16_B1745/ H16_B1834/H16_B2470 | nknown/unknown/u nknown | t3chp -> 3chroald + h2 | t3chp -> 3chroald + h2 | t3chp -> 3chroald + h2 |
| ALHD13 | 3-Chloroacrylic acid degradation | aldehyde dehydrogenase (NAD+) | 12.1.3 | H16_A0232/H16_A0745/ H16_A1114/H16_A1495/ H16_B0212/H16_B0421/ H16_B0737/H16_B0833/ H16_B1534/H16_B1735/ H16_B1751/H16_B1835/ H16_B1960/H16_B2444 | unknown/unknown/ unknown/unknown/ unknown/unknown/ unknown/unknown/ unknown/unknown/ | 3chroald + h2o -> t3chc + h + h2 | 3chroald + h2o -> t3chc + h + h2 | 3chroald + h2o -> t3chc + h + h2 |
| ACLDc | 3-Chloroacrylic acid degradation | alcohol dehydrogenase | 11.1.1 | H16_A0757/H16_A3330/ H16_B0517/H16_B1433/ H16_B1699/H16_B1745/ H16_B1834/H16_B2470 | adh/unknown/unkno wn/adhP/unknown/u nknown/unknown/u | | c3chp -> c3chroald + h2 | c3chp -> c3chroald + h2 |
| ALHD14 | 3-Chloroacrylic acid degradation | aldehyde dehydrogenase (NAD+) | 1.2.1.3 | H16_A0232/H16_A0745/ H16_A1114/H16_A1495/ H16_B0212/H16_B0421/ H16_B0737/H16_B0833/ H16_B1534/H16_B1735/ H16_B1751/H16_B1835/ H16_B1960/H16_B2444 | unknown/unknown/ unknown/unknown/ unknown/unknown/ unknown/unknown/ unknown/unknown/ | c3chroald + h2o -> c3chroc + h2 + h | c3chroald + h2o -> c3chroc + h2 + h | c3chroald + h2o -> c3chroc + h2 + h |
| PAAD7 | 3-Chloroacrylic acid degradation | phenylacrylic acid decarboxylase | 4.1.1 | | unknown | 3opp + h -> acal + co2 | 3opp + h -> acal + co2 | 3opp + h -> acal + co2 |
| DADH | Alanine and Aspartate Metabolism | D-Amino acid dehydrogenase | 1.4.99.1 | H16_A0770/H16_A0817/ H16_A1505/H16_B0508/ H16_B1893 | dadA2/dadA1/dadA 5/dadA6/dadA7 | dala + fad + h2o -> fadh2 + nh4 + pyr | dala + fad + h2o + h -> fadh2 + nh4 + pyr | dala + fad + h2o + h -> fadh2 + nh4 + pyr |
| ASPTA | Alanine and Aspartate Metabolism | aspartate transaminase | 2.6.1.1 | H16_A2857 | unknown | akg + asp <-> glu + oaa | akg + asp <-> glu + oaa | akg + asp <-> glu + oaa |
| ASNN | Alanine and Aspartate Metabolism | L-asparaginase | 3.5.1.1 | H16_A2102 | ansB | asn + h2o -> asp + nh4 | asn + h2o -> asp + nh4 | asn + h2o -> asp + nh4 |
| GLNAS | Alanine and Aspartate Metabolism | glutamin-(asparagin-)ase | 3.5.1.38 | H16_A1910 | ansA | asn + h2o -> asp + nh4 | asn + h2o -> asp + nh4 | asn + h2o -> asp + nh4 |
| ALAR | Alanine and Aspartate Metabolism | alanine racemase | 5.1.1.1 | H16_A2113 | dadX | ala <-> dala | ala <-> dala | ala <-> dala |
| ASNS | Alanine and Aspartate Metabolism | asparagine synthase (glutamine- hydrolysing) | 6.3.5.4 | H16_A3223 | unknown | asp + atp + gln + h2o -> amp + asn + glu + ppi | $ \begin{array}{llllllllllllllllllllllllllllllllllll$ | $ asp + atp + gln + h2o \rightarrow amp + asn + glu + ppi \\ + 2 h $ |
| ASP4D | Alanine and Aspartate Metabolism | aspartate 4- decarboxylase | 4.1.1.12 | H16_A3009 | asdA | asp + h -> ala + co2 | asp + h -> ala + co2 | asp + h -> ala + co2 |
| ARGSUCS | Alanine and Aspartate Metabolism | argininosuccinate synthase | 6.3.4.5 | H16_B2531 | argG | asp + atp + citr -> amp + argsucc + ppi | asp + atp + citr -> amp + argsucc + ppi + 2 h | asp + atp + citr -> amp + argsucc + ppi + 2 h |
| 4AMBUAT | Alanine and Aspartate Metabolism | 4-aminobutyrate aminotransferase | 2.6.1.19 | H16_B0981 | gabT | bala + akg <-> 3opp + glu | bala + akg <-> 3opp + glu | bala + akg <-> 3opp + glu |
| BAPYRT | Alanine and Aspartate Metabolism | beta-alanine pyruvate transaminase | 2.6.1.18 | H16_A0272 | aptA | ala + 3opp <-> pyr + bala | ala + 3opp <-> pyr + bala | ala + 3opp <-> pyr + bala |
| ASPR | Alanine and Aspartate Metabolism | aspartate racemase | 5.1.1.13 | H16_B2421 | racX | asp <-> asp-D | asp <-> asp-D | asp <-> asp-D |
| LAAO1 | Alanine and Aspartate Metabolism | L-amino-acid oxidase | 1.4.3.2 | H16_A0845/H16_A0856 | lao1/lao2 | asp + h2o + o2 <-> oaa + nh4 + h2o2 | asp + h2o + o2 <-> oaa + nh4 + h2o2 | asp + h2o + o2 <-> oaa + nh4 + h2o2 |
| ASPOX1 | Alanine and Aspartate Metabolism | L-aspartate oxidase | 1.4.3.16 | H16_A3036 | nadB | asp + h2o + o2 <-> oaa + nh4 + h2o2 | asp + h2o + o2 <-> oaa + nh4 + h2o2 | asp + h2o + o2 <-> oaa + nh4 + h2o2 |
| SUCSD1 | Alanine and Aspartate Metabolism | succinate- semialdehyde dehydrogenase (NADP) | 1.2.1.16 | H16_B0982/H16_B1179/ H16_B1537/H16_B2057 | | h2o + nadp + sucsal <-> 3 h + nadph + succ | h2o + nadp + sucsal <-> 2 h + nadph + succ | h2o + nadp + sucsal <-> 2 h + nadph + succ |
| ASP1DCB | Alanine and Aspartate Metabolism | aspartate 1- decarboxylase | 4.1.1.11 | H16_A3129 | panD | asp + h -> bala + co2 | asp + h -> bala + co2 | asp + h -> bala + co2 |
| GTADT2 | Alanine and aspartate metabolism | aspartyl- tRNA(Asn)/glutamyl- tRNA (Gln) amidotransferase | 6.3.5.6 | H16_A0108&H16_A011 1&H16_A0112&H16_A1 509&H16_A1882 | gatB&gatA1&gatC& gatA3&unknown | $ asptrna + gln + atp + h2o -> asntrna + glu + pi \\ + adp + h $ | asptrna + gln + atp + h2o -> asntrna + glu + pi + adp + 2 h | asptrna + gln + atp + h2o -> asntrna + glu + pi + adp + 2 h |
| METTRFT | Aminoacyl-tRNA Biosynthesis Aminoacyl-tRNA | Methionyl-tRNA formyltransferase tyrosyl-tRNA | 2.1.2.9 | · = ····· | fmt | fthf + mettrna -> fmettrna + h + thf | fthf + mettrna -> fmettrna + h + thf atp + trnatyr + tyr -> amp + ppi + tyrtrna + | fthf + mettrna -> fmettrna + h + thf |
| TYRTRS METTRS | Biosynthesis Aminoacyl-tRNA | synthetase Methionyl-tRNA | 6.1.1.1 6.1.1.10 | _ | tyrS metG | atp + h + met + trnamet -> amp + mettrna + | h atp + met + trnamet -> amp + mettrna + | atp + trnatyr + tyr -> amp + ppi + tyrtma + h atp + met + trnamet -> amp + mettrna + ppi + |
| SERTRS | Biosynthesis Aminoacyl-tRNA Biosynthesis | synthetase Seryl-tRNA synthetase | | H16_A0764/H16_B0015 | | ppi atp + ser + trnaser -> amp + ppi + sertrna | ppi + h atp + ser + trnaser -> amp + ppi + sertrna + 2 h | h atp + ser + trnaser -> amp + ppi + sertma + 2 h |
| ASPTRS | Aminoacyl-tRNA Biosynthesis | Aspartyl-tRNA synthetase | 6.1.1.12 | H16_A0453 | aspS | asp + atp + h + trnaasp -> amp + asptrna + ppi | asp + atp + trnaasp -> amp + asptrna + ppi + h | asp + atp + trnaasp -> amp + asptrna + ppi + h |
| GLYTRS | Aminoacyl-tRNA Biosynthesis | Glycyl-tRNA synthetase | 6.1.1.14 | H16_A0521/H16_A0523 | glyS/glyQ | atp + gly + h + trnagly -> amp + glytrna + ppi | atp + gly + trnagly -> amp + glytrna + ppi + h | atp + gly + tmagly -> amp + glytrna + ppi + h |
| | , · · · · | | | | | | | |

| PROTRS | Aminoacyl-tRNA | Prolyl-tRNA | 6.1.1.15 | H16_A3246 | proS | atp + h + pro + trnapro -> amp + ppi + protma | atp + pro + trnapro -> amp + ppi + protrna | atp + pro + trnapro -> amp + ppi + protrna + h |
|----------------|------------------------------------|---|--------------------|---|-----------------------|---|---|---|
| CYSTRS | Biosynthesis Aminoacyl-tRNA | synthetase Cysteinyl-tRNA | | H16_A1221 | | | + h atp + cys + trnacys -> amp + cystrna + ppi | |
| | Biosynthesis Aminoacyl-tRNA | synthetase Glutaminyl-tRNA | | | cysS | atp + cys + h + trnacys -> amp + cystrna + ppi | + h atp + gln + trnagln -> amp + glntrna + ppi | atp + cys + trnacys -> amp + cystrna + ppi + h |
| GLNTRS | Biosynthesis Aminoacyl-tRNA | synthetase Arginyl-tRNA | 6.1.1.18 | H16_A2784 | glnS | atp + gln + h + trnagln -> amp + glntma + ppi | + h arg + atp + trnaarg -> amp + argtma + ppi | atp + gln + trnagln -> amp + glntrna + ppi + h |
| ARGTRS | Biosynthesis Aminoacyl-tRNA | synthetase Tryptophanyl-tRNA | 6.1.1.19 | H16_A0159 | agrS | arg + atp + h + trnaarg -> amp + argtrna + ppi | + h atp + trnatrp + trp -> amp + ppi + trptrna | arg + atp + trnaarg -> amp + argtrna + ppi + h |
| TRPTRS | Biosynthesis | synthetase | 6.1.1.2 | H16_A0515 | trpS | atp + h + trnatrp + trp -> amp + ppi + trptrna | + h | atp + trnatrp + trp -> amp + ppi + trptrna + h |
| PHETRS | Aminoacyl-tRNA Biosynthesis | Phenylalanyl-tRNA synthetase | 6.1.1.20 | H16_A1343&H16_A134 4 | pheS&pheT | atp + h + phe + trnaphe -> amp + phetrna + ppi | ppi + h | atp + phe + trnaphe -> amp + phetrna + ppi + h |
| HISTRS | Aminoacyl-tRNA Biosynthesis | Histidyl-tRNA synthetase | 6.1.1.21 | H16_A2363 | hisS | atp + his + trnahis -> amp + histrna + ppi | atp + his + trnahis -> amp + histma + ppi + h | atp + his + trnahis -> amp + histrna + ppi + h |
| THRTRS | Aminoacyl-tRNA Biosynthesis | Threonyl-tRNA synthetase | 6.1.1.3 | H16_A1339 | thrS | atp + thr + trnathr -> amp + ppi + thrtrna | atp + thr + trnathr -> amp + ppi + thrtrna + 2 h | atp + thr + trnathr -> amp + ppi + thrtma + 2 h |
| LEUTRS | Aminoacyl-tRNA Biosynthesis | Leucyl-tRNA synthetase | 6.1.1.4 | H16_A3139 | leuS | atp + h + leu + trnaleu -> amp + leutrna + ppi | atp + leu + trnaleu -> amp + leutrna + ppi + h | atp + leu + trnaleu -> amp + leutrna + ppi + h |
| ILETRS | Aminoacyl-tRNA Biosynthesis | Isoleucyl-tRNA synthetase | 6.1.1.5 | H16_A3046 | ileS | atp + h + ile + trnaile -> amp + iletrna + ppi | atp + ile + trnaile -> amp + iletrna + ppi + h | atp + ile + trnaile -> amp + iletrna + ppi + h |
| LYSTRS | Aminoacyl-tRNA Biosynthesis | Lysyl-tRNA synthetase | 6.1.1.6 | H16_A1167 | lysU | atp + h + lys + trnalys -> amp + lystrna + ppi | atp + lys + trnalys -> amp + lystrna + ppi + | atp + lys + trnalys -> amp + lystrna + ppi + h |
| ALATRS | Aminoacyl-tRNA Biosynthesis | Alanyl-tRNA synthetase | 6.1.1.7 | H16_A2769 | alaS | ala + atp + h + trnaala -> alatrna + amp + ppi | ala + atp + trnaala -> alatrna + amp + ppi + h | ala + atp + trnaala -> alatrna + amp + ppi + h |
| VALTRS | Aminoacyl-tRNA Biosynthesis | ValyI-tRNA synthetase | 6.1.1.9 | H16_A2751 | valS | atp + h + trnaval + val -> amp + ppi + valtrna | atp + trnaval + val -> amp + ppi + valtrna + | atp + trnaval + val -> amp + ppi + valtrna + h |
| | | N- | | | | | 11 | |
| ACG6PD | Aminosugars metabolism | acetylglucosamine-6- phosphate deacetylase | 3.5.1.25 | H16_A0314 | nagA | naga6p + h2o -> ac + ga6p | naga6p + h2o -> ac + ga6p | naga6p + h2o -> ac + ga6p |
| GM6PD | Aminosugars metabolism | glucosamine-6- phosphate | 3.5.99.6 | H16_A0315 | nagB | ga6p + h2o -> f6p + nh4 | ga6p + h2o -> f6p + nh4 | ga6p + h2o -> f6p + nh4 |
| | metabolism | deaminase | | | | | | |
| UAEPGR | Aminosugars metabolism | UDP-N- acetylenolpyruvoylgl ucosamine reductase | 1.1.1.158 | H16_A3061 | murB | 2 h + nadph + uaccg -> nadp + udpnam | h + nadph + uaccg -> nadp + udpnam | h + nadph + uaccg -> nadp + udpnam |
| GA1PACT | Aminosugars metabolism | glucosamine-1- phosphate N- | 2.3.1.157 | H16_A0262 | glmU | accoa + galp -> nagalp + coa + h | accoa + galp -> nagalp + coa + h | accoa + galp -> nagalp + coa |
| | metabolism | acetyltransferase | | | | | | |
| UNAGCVT | Aminosugars | UDP-N- acetylglucosamine 1- | 2.5.1.7 | H16_A3418 | murA | pep + udpnag -> pi + uaccg | pep + udpnag -> h + pi + uaccg | pep + udpnag -> h + pi + uaccg |
| | metabolism | carboxyvinyltransfera se | | _ | | | | |
| GF6PT | Aminosugars | glutamine-fructose- 6-phosphate | 2.6.1.16 | H16 A0263 | glmS | f6p + gln -> ga6p + glu | f6p + gln -> ga6p + glu | f6p + gln -> ga6p + glu |
| GI GI I | metabolism | transaminase UDP-N- | 2.0.1.10 | 1110_10203 | giiis | Top + gill + guop + giu | Top - gill - gaop - gia | Top + giii - guop + giu |
| UNAGDP | Aminosugars metabolism | acetylglucosamine diphosphorylase | 2.7.7.23 | H16_A0262 | glmU | nagalp + utp -> ppi + udpnag | nagalp + utp -> ppi + udpnag | naga1p + utp -> ppi + udpnag |
| PGAMT | Aminosugars metabolism | phosphoglucosamine mutase | 5.4.2.10 | H16_A2445 | manB3 | galp <-> ga6p | ga1p <-> ga6p | galp + h <-> ga6p |
| | Aminosugars | predicted acid phosphatase (N- | | H16_A0168/H16_A0520, | / acak /unknown /unkn | | | |
| ACMANAPP | metabolism | Acetyl-D- mannosamine) | 3.1.3 | H16_B0594/H16_B1063 | | nadma + pi <-> nadma6p + h2o | nadma + pi <-> nadma6p + h2o | nadma + pi <-> nadma6p + h2o |
| UDPACG | Aminosugars metabolism | UDP-N- acetylglucosamine 4- | 5.1.3.7 | | | udpnag <-> udpacgal | udpnag <-> udpacgal | udpnag <-> udpacgal |
| ME1 | Anaplerotic | epimerase malic enzyme (NAD) | 11129 | H16_A3153 | maeA | mal + nad -> co2 + nadh + pyr | mal + nad -> co2 + nadh + pyr | mal + nad -> co2 + nadh + pyr |
| ME2 | Reactions Anaplerotic | malic enzyme (WID) | 1.1.1.40 | H16_A1002 | maeB | mal + nadp -> co2 + h + nadph + pyr | mal + nadp -> co2 + nadph + pyr | mal + nadp -> co2 + nadph + pyr |
| PPA1 | Reactions Anaplerotic | (NADP) inorganic | 3.6.1.1 | H16_A0746 | | | h2o + ppi -> 2 pi + h | |
| | Reactions Anaplerotic | diphosphatase inorganic | | H10_A0/40 | ppa | h2o + ppi -> 2 pi | | h2o + ppi -> 2 pi |
| PPA2 | Reactions Anaplerotic | triphosphatase phosphoenolpyruvat | 3.6.1.25 | | | h2o + pppi -> pi + ppi | h2o + pppi -> 2 h + pi + ppi | h2o + pppi -> h + pi + ppi |
| PPC | Reactions Anaplerotic | e carboxylase phosphoenolpyruvat | 4.1.1.31 | H16_A2921 | ppc | co2 + h2o + pep -> h + oaa + pi | h2o + pep + co2 -> 2 h + oaa + pi | co2 + h2o + pep -> 2 h + oaa + pi |
| PPCK | Reactions Anaplerotic | e carboxykinase | 4.1.1.32 | H16_A3711 | pepck | atp + h + oaa -> adp + co2 + pep | atp + h + oaa -> adp + co2 + pep | atp + h + oaa -> adp + co2 + pep |
| ICL | Reactions | Isocitrate lyase | 4.1.3.1 4.1.3.2 | H16_A2211/H16_A2227 | icIA/icIB | icit -> glx + succ | icit -> glx + succ | icit -> glx + succ |
| MALS | Anaplerotic Reactions | malate synthase | (2.3.3.9 in | H16_A2217 | aceB | accoa + glx + h2o -> coa + h + mal | accoa + glx + h2o -> coa + h + mal | accoa + glx + h2o -> coa + h + mal |
| 05.004 | Arginine and | 1-pyrroline-5- | kegg) | | | | | |
| P5CD1 | Proline Metabolisn | denydrogenase | 1.5.1.12 | H16_A3631 | putA | p5c + 2 h2o + nad -> glu + 2 h + nadh | p5c + 2 h2o + nad -> glu + h + nadh | p5c + 2 h2o + nad -> glu + h + nadh |
| P5CR1 | Arginine and Proline Metabolisn | pyrroline-5- carboxylate reductase | 1.5.1.2 | H16_A3106 | proC | pSc + 2 h + nadph -> nadp + pro | p5c + 2 h + nadph -> nadp + pro | p5c + 2 h + nadph -> nadp + pro |
| PROD2 | Arginine and Proline Metabolisn | Proline dehydrogenase | 1.5.99.8 | H16_A3631 | putA | fad + pro -> p5c + fadh2 | fad + pro -> p5c + fadh2 | fad + pro -> p5c + fadh2 |
| ORNCBT | Arginine and | ornithine | 2.1.3.3 | H16 A3063 | argF | cap + orn <-> citr + h + pi | cap + orn <-> citr + h + pi | cap + om <-> citr + h + pi |
| | Proline Metabolisn Arginine and | argininosuccinate | | - | | | | |
| ARGSCL | Proline Metabolisn | n lyase | 4.3.2.1 | H16_A2925 | argH | argsucc <-> arg + fum | argsucc <-> arg + fum | argsucc <-> arg + fum |
| GLU5SDT | Arginine and Proline Metabolisn | L-glutamate 5- semialdehyde n dehydratase | spontaneo us | spontaneous | spontaneous | glugsal -> p5c + h2o | glugsal -> p5c + h + h2o | glugsal -> p5c + h + h2o |
| GLUDH4 | Arginine and | (spontaneous) glutamate | 1412 | H16 A0471 | adh A 1 | alu pad i b2a - alaa i bb4 i badh i b | glu + nad + h2o <-> akg + nh4 + nadh + | qlu + nad + h2o <-> akq + nh4 + nadh + h |
| GLUDH4 | Proline metabolism | 1-pyrroline-5- | 1.4.1.3 | H16_A04/1 | gdhA1 | glu + nad + h2o <-> akg + nh4 + nadh + h | h | giu + nau + nzo <-> akg + nn4 + naun + n |
| P5CD2 | Arginine and Proline metabolisn | carboxylate dehydrogenase | 1.5.1.12 | H16_A3631 | putA | glugsal + nad + h2o <-> glu + nadh + 2 h | glugsal + nad + h2o <-> glu + nadh + 2 h | glugsal + nad + h2o <-> glu + nadh + 2 h |
| ORNC | Arginine and Proline metabolisn | ornithine cyclodeaminase | 4.3.1.12 | H16_A0689/H16_A1394, H16_A3673/H16_B1881 | | orn <-> pro + nh4 | orn <-> pro + nh4 | orn <-> pro + nh4 |
| P4HX | Arginine and Proline metabolism | prolyl 4-hydroxylase | 1.14.11.2 | H16_A3244 | phy | pro + akg + o2 -> 4hpro + succ + co2 | pro + akg + o2 -> 4hpro + succ + co2 | pro + akg + o2 -> 4hpro + succ + co2 |
| P5CD3 | Arginine and Proline metabolism | 1-pyrroline-5- carboxylate | 1.5.1.12 | H16_A3631 | putA | 4hpro + fad -> l1p3h5c + fadh2 + h | 4hpro + fad -> l1p3h5c + fadh2 | 4hpro + fad -> l1p3h5c + fadh2 |
| PROD3 | Arginine and Proline metabolisn | Proline Proline | 1.5.99.8 | H16_A3631 | putA | 4hpro + fad -> l1p3h5c + fadh2 + h | 4hpro + fad -> l1p3h5c + fadh2 | 4hpro + fad -> l1p3h5c + fadh2 |
| P5CR2 | Arginine and | pyrroline-5- | 1.5.1.2 | H16_A3106 | proC | I1p3h5c + nadh + 2 h -> 4hpro + nad | l1p3h5c + nadh + 2 h -> 4hpro + nad | l1p3h5c + nadh + 2 h -> 4hpro + nad |
| P5CD4 | Proline metabolism | reductase 1-pyrroline-5- | | | putA | l1p3h5c + nad + 2 h2o -> e4hglu + nadh + h | l1p3h5c + nad + 2 h2o -> e4hglu + nadh + | |
| 1 30.04 | Arginine and | | | | | Approprie + mau + Z mzu + z ennquu + nagn + h | h | l1p3h5c + nad + 2 h2o -> e4hglu + nadh + h |
| | Proline metabolism | carboxylate dehydrogenase | 1.5.1.12 | H16_A3631 | puin | | | |
| PTO4H | | dehydrogenase | 1.5.1.12 | H16_A3631 | puin | | I1p3h5c + h2o + h <-> 4hglusa | I1p3h5c + h2o + h <>> 4hglusa |
| PTO4H P5CD5 | Proline metabolism Arginine and | 1 dehydrogenase 1-pyrroline-5- | | H16_A3631 | putA | | | Itp3h5c + h2o + h <> 4hglusa e4hglu + nad <-> 4hglusa + nadh + h2o |

| Heave of the control | PROD4 | Arginine and Proline metabolisr | Proline n dehydrogenase | 1.5.99.8 | H16_A3631 | putA | e4hglu + nad <-> 4hglusa + nadh + h2o | e4hglu + nad <-> 4hglusa + nadh + h2o | e4hglu + nad <-> 4hglusa + nadh + h2o |
|--|---------|---|---|------------|--|--|--|---|--|
| March Marc | DATA2 | Arginine and | D-alanine | 2.6.1.21 | H16_A2521 | dat | e4hglu + oaa -> asp-D + hydroxyakg | e4hglu + oaa -> asp-D + hydroxyakg | e4hglu + oaa -> asp-D + hydroxyakg |
| Marie | ASPAM4 | | | 2.6.1.1 | H16_A2857 | unknown | e4hglu + akg -> hydroxyakg + glu | e4hglu + akg -> hydroxyakg + glu | e4hglu + akg -> hydroxyakg + glu |
| Horizon processor of the control of | HOGAD | | | 4.1.2.14 | H16_B1213 | eda | hydroxyakg <-> pyr + glx | hydroxyakg <-> pyr + glx | hydroxyakg <-> pyr + glx |
| March Marc | CREAH | Arginine and | creatinine | | H16_A1736 | unknown | cretn + h2o -> creatine + h | cretn + h2o -> creatine | cretn + h2o -> creatine |
| Marche M | CARSA | Arginine and | N- carbamoylsarcosine | 3.5.1.59 | H16_A0926 | unknown | carbs + h2o + 2 h -> sarcs + co2 + nh4 | carbs + h2o + 2 h -> sarcs + co2 + nh4 | carbs + h2o + 2 h -> sarcs + co2 + nh4 |
| Marie Mari | P5CD1p | | 1-pyrroline-5- carboxylate | 1.5.1.12 | H16_A3631 | putA | p5c + 2 h2o + nadp -> glu + 3 h + nadph | p5c + 2 h2o + nadp -> glu + h + nadph | p5c + 2 h2o + nadp -> glu + h + nadph |
| Marche | P5CR2p | | pyrroline-5- carboxylate | 1.5.1.2 | H16_A3106 | proC | l1p3h5c + nadph + 3 h -> 4hpro + nadp | l1p3h5c + nadph + 2 h -> 4hpro + nadp | l1p3h5c + nadph + 2 h -> 4hpro + nadp |
| Marie Mari | GLTN1 | | | 3.1.1.17 | | gnl1/gnl2/gnl3 | g14l + h2o <-> guln + h | g14l + h2o <-> guln + h | g14l + h2o <-> guln + h |
| Reference of the control of the cont | GLCRDH | Ascorbate and Aldarate | | 4.2.1.40 | | unknown | dgluca -> d4dg + h2o | dgluca -> d4dg + h2o | dgluca -> d4dg + h2o |
| Mariane Mari | GALCTDH | Ascorbate and | galactarate | 42.1.42 | | | dgal -> d4dg + h2o | dgal -> d4dg + h2o | dgal -> d4dg + h2o |
| Ministry | | metabolism Ascorbate and Aldarate | aldehyde dehydrogenase | 12.1.3 | H16_A0232/H16_A0745, H16_A1114/H16_A1495, H16_B0212/H16_B0421, H16_B0737/H16_B0833, H16_B1534/H16_B1735, H16_B1751/H16_B1835, | / unknown/unknown/ / unknown/unknown/ unknown/unknown/ unknown/unknown/ unknown/unknown/ unknown/unknown/ | | | |
| Marche M | GLCRD2 | Aldarate | | 4.2.1.40 | H16_B0127 | unknown | dgluca <-> d3dg + h2o | dgluca <-> d3dg + h2o | dgluca <-> d3dg + h2o |
| Comparison Appendix Appendi | DDGD | Ascorbate and Aldarate | deoxyglucarate | 4.2.1.41 | H16_B0131 | unknown | d4dg <-> 25dop + h2o + co2 | d4dg <-> 25dop + h2o + co2 | d4dg <-> 25dop + h2o + co2 |
| March Marc | CCPPMD | | cyclopropylmelamine | 3.5.4 | H16_B0862 | unknown | cyromz + h2o -> ccpam + nh4 | cyromz + h2o + h -> ccpam + nh4 | cyromz + h2o + h -> ccpam + nh4 |
| Marche M | CCPPAME | | cyclopropylammeline | 3.5.4 | H16_B0862 | unknown | ccpam + h2o + h -> ccpamd + nh4 | ccpam + h2o + h -> ccpamd + nh4 | ccpam + h2o + h -> ccpamd + nh4 |
| Michael Mich | CCPAMA | | cyclopropylammelide | | H16_B0862 | unknown | ccpamd + h2o + h -> cyanr + ccppam | ccpamd + h2o + h -> cyanr + ccppam | ccpamd + h2o + h -> cyanr + ccppam |
| March Separation Separati | HATRAZE | | | 3.5.99.3 | H16_A1363 | unknown | hatraz + h2o + h -> isoppam + ethlam | hatraz + h2o + h -> isoppam + ethlam | hatraz + h2o + h -> isoppam + ethlam |
| March Marc | HATRAZE | 2 degradation | | 3.5.99.3 | H16_A1363 | unknown | 2c4h6at + h2o -> ammld + hcl + h | 2c4h6at + h2o -> ammld + hcl + h | 2c4h6at + h2o -> ammld + hcl + h |
| Miles Mile | 4HBZDC | degradation via | | 4.1.1.61 | H16_B2446 | unknown | phenol + co2 -> 4hb + h | phenol + co2 -> 4hb + h | phenol + co2 -> 4hb + h |
| Manual M | NITLS | degradation via CoA ligation | nitrilase | 3.5.5.1 | H16_A1125 | nit | bzonit + 2 h2o -> benzot + nh4 | bzonit + 2 h2o -> benzot + nh4 | bzonit + 2 h2o -> benzot + nh4 |
| Description | AMDS6 | degradation via CoA ligation | amidase | 3.5.1.4 | | | bzamid + h2o -> benzot + nh4 | bzamid + h2o -> benzot + nh4 | bzamid + h2o -> benzot + nh4 |
| Part | BZOTD1 | degradation via CoA ligation | | 1.14.12.10 | | benC&benB&benA | benzot + nadh + h + o2 -> 16dh24checc + nad | benzot + nadh + h + o2 -> 16dh24checc + nad | benzot + nadh + h + o2 -> 16dh24checc + nad |
| April Comparision Compar | BZOTD1p | degradation via | | 1.14.12.10 | | benC&benB&benA | | • | • |
| APP | 16DCDC1 | degradation via | 2,4-diene-1- carboxylate | 1.3.1.25 | H16_A1960 | benD | 16dh24checc + nad -> catech + nadh + co2 | 16dh24checc + nad -> catech + nadh + co2 | 16dh24checc + nad -> catech + nadh + co2 |
| Benoate Benoate Benoate Benoate Col Igation Co | APPS3 | degradation via CoA ligation | acylphosphatase | 3.6.1.7 | H16_A3325 | acyP | bzop + h2o -> benzot + pi | bzop + h2o -> benzot + pi + h | bzop + h2o -> benzot + pi + h |
| High High High High High High High High | BZOTCOA | degradation via | benzoate-CoA ligase | 6.2.1.25 | | | benzot + atp + coa + h -> amp + ppi + bzocoa | benzot + atp + coa -> amp + ppi + bzocoa + h | benzot + atp + coa -> amp + ppi + bzocoa + h |
| Second Englation via Cock Englation via Englation | ACDH5 | degradation via | acyl dehydratase | 4.2.1 | H16_A1289/H16_A2151 H16_A3307/H16_B0359, | unknown/unknown/ unknown/unknown/ | 6hcecoa + h2o -> 26dhccoa | 6hcecoa + h2o -> 26dhccoa | 6hcecoa + h2o -> 26dhccoa |
| CCHCCOAL degradation via CoA ligation Part CoA ligase 2-CHCCOA (algase 3-CHCCOA (a | 2KCHCCH | degradation via CoA ligation | ketocyclohexanecarb oxyl-CoA hydrolase | | | | 2kchccoa + h2o -> pmcoa | 2kchccoa + h2o -> pmcoa | 2kchccoa + h2o -> pmcoa + h |
| Benzoate degradation via CoA ligation CoA li | CCHCCOA | L degradation via | te-CoA ligase | 6.2.1 | H16_B1693 | unknown | cchc + coa + atp + h -> cchccoa + amp + ppi | cchc + coa + atp -> cchccoa + amp + ppi + h | cchc + coa + atp -> cchccoa + amp + ppi + h |
| Benzoate degradation via CoA ligation CoA li | 2HCHCCC | A degradation via | hydroxycyclohexanec arboxyl-CoA | 1.1.1 | H16_B1696 | unknown | hcchccoa + nad -> 2kchccoa + nadh + h | hcchccoa + nad -> 2kchccoa + nadh + h | hcchccoa + nad -> 2kchccoa + nadh + h |
| ACDH6 degradation via CoA ligation H16, A1289/H16, A2151/unknown/unknown/ H16, A3037/H16, B0359/ unknown/unknown/ H16, A3158/H16, A3158/H16, A3047/ unknown/unknown/ H16, A3158/H16, A315 | PMCOAD | degradation via | pimeloyl-CoA | 1.3.1.62 | H16_B0371&H16_B0372 | pimC&pimD | pmcoa + nad -> 6checoa + nadh + 2 h | pmcoa + nad -> 6checoa + nadh + 2 h | pmcoa + nad -> 6checoa + nadh + h |
| H16_A0039/H16_A0240/ unknown/unknown/ | ACDH6 | degradation via | acyl dehydratase | 4.2.1 | H16_A1289/H16_A2151 H16_A3307/H16_B0359 | unknown/unknown/ unknown/unknown/ | 6checoa + h2o -> hpimcoa | 6checoa + h2o -> hpimcoa | 6checoa + h2o -> hpimcoa |
| GLUCD2 degradation via dehydronenase 1.3.99.7 H16_A2818 gcdH glutcoa + fad -> gl1coa + fadh2 glutcoa + fad + h -> gl1coa + fadh2 glutcoa + fad + h -> gl1coa + fadh2 | ACTF4 | Benzoate degradation via CoA ligation | acetyltransferase | 23.1 | H16, A0039/H16, A0240 H16, A0269/H16, A0699, H16, A1315/H16, A1564, H16, A1683/H16, A1802, H16, A3759/H16, A3071, H16, A3093/H16, A3221, H16, B0018/H16, B0012, H16, B0018/H16, B0012, H16, B178/H16, B1292, H16, B1407/H16, B1292, | unknown/unknown/ unknown/unknown/ unknown/unknown/ unknown/unknown/ unknown/unknown/ unknown/unknown/ unknown/junknown/ unknown/junknown/ unknown/unknown/ unknown/unknown/ unknown/unknown/ own/unknown/unknown/ own/unknown/ | | opimcoa + coa -> glutcoa + accoa | opimcoa + coa -> glutcoa + accoa |
| | GLUCD2 | degradation via | | 1.3.99.7 | H16_A2818 | gcdH | glutcoa + fad -> gl1coa + fadh2 | glutcoa + fad + h -> gl1coa + fadh2 | glutcoa + fad + h -> gl1coa + fadh2 |

| CCPPCCOAL | Benzoate degradation via CoA ligation | cyclopropanecarboxy late:CoA ligase | | H16_A0866/H16_A0871, H16_A1230/H16_A1519, H16_A1700/H16_A1718, H16_A2252/H16_A2794, H16_A0807/H16_A2797, H16_B0174/H16_B06777, H16_B0910/H16_B1148/ H16_B1264/H16_B1335/ H16_B1662/H16_B1309/ | / unknown/unknown/ / unknown/unknown/ / unknown/unknown/ / unknown/unknown/ unknown/unknown/ unknown/unknown/ unknown/unknown/ unknown/unknown/ | ccppc + coa + atp + h -> ccppccoa + adp + pi | ccppc + coa + atp -> ccppccoa + adp + pi | ccppc + coa + atp -> ccppccoa + adp + pi |
|-----------|--|---|------------|--|--|--|--|--|
| 3HBCDH | Benzoate degradation via | 3-hydroxybutyryl- | 1.1.1.157 | H16_B2522 H16_A1102 | unknown/ paaH2 | 3hbcoa + nadp -> aacoa + nadph + 2 h | 3hbcoa + nadp -> aacoa + nadph + h | 3hbcoa + nadp -> aacoa + nadph + h |
| | CoA ligation | CoA dehydrogenase | | H16_A0039/H16_A0240, | | , , | | |
| ACTF5 | Benzoate degradation via CoA ligation | acetyltransferase | 23.1 | H16_A0269/H16_A0699, H16_A1315/H16_A1564, H16_A1683/H16_A1802, H16_A2759/H16_A3071, H16_A3093/H16_A3226, H16_B0018/H16_A3586, H16_B0018/H16_B0021/ H16_B1278/H16_B1292/ H16_B1407/H16_B1292/ H16_B1407/H16_B1899/H16_B2397/ | / unknown/unknown/ / unknown/unknown/ / unknown/unknown/ / unknown/unknown/ / unknown/pat/unkno wn/unknown/wbpD/ unknown/unknown/ phnT/unknown/unknown/unknown/unknown/unknown/unknown/unknown/unknown/unknown/unknown/unkn | 3hSohcoa + coa -> 3hbcoa + accoa | 3h5ohcoa + coa -> 3hbcoa + accoa | 3hSohcoa + coa -> 3hbcoa + accoa |
| BZALDD6 | Benzoate degradation via Hydroxylation | benzaldehyde dehydrogenase (NAD) | 1.2.1.28 | H16_A1772 | unknown | 4hbzald + nad + h2o <-> 4hb + nadh + 2 h | 4hbzald + nad + h2o <-> 4hb + nadh + 2 h | 4hbzald + nad + h2o <-> 4hb + nadh + h |
| PHBZMN | Benzoate degradation via Hydroxylation | p-hydroxybenzoate 3-monooxygenase | 1.14.13.2 | H16_B2286 | pobA | 4hb + o2 + nadph + 2 h -> 34dhb + nadp + h2o | 4hb + o2 + nadph + h -> 34dhb + nadp + h2o | 4hb + o2 + nadph + h -> 34dhb + nadp + h2o |
| PROTCC1 | Benzoate degradation via | protocatechuate 3,4- dioxygenase | 1.13.11.3 | H16_B0795/(H16_B2290 &H16_B2291) | unknown/(pcaG&pca H1) | 34dhb + o2 -> carccm + 2 h | 34dhb + o2 -> carccm + 2 h | 34dhb + o2 -> carccm + 2 h |
| PAAD9 | Hydroxylation Benzoate degradation via | phenylacrylic acid decarboxylase | 4.1.1 | H16_B2447 | unknown | zoe + h2o + h -> hopt + co2 | zoe + h2o + h -> hopt + co2 | zoe + h2o + h -> hopt + co2 |
| OXCTD2 | Hydroxylation Benzoate degradation via | 4-oxalocrotonate decarboxylase | 4.1.1.77 | H16_B0549 | unknown | zoe + h -> op4en + co2 | zoe + h -> op4en + co2 | zoe + h -> op4en + co2 |
| 4OXCTT | Hydroxylation Benzoate degradation via | 4-oxalocrotonate | 5.3.2 | H16_A2763/H16_A3184, | | 2hmuc -> zoe | 2hmuc -> zoe | 2hmuc -> zoe |
| CATCHDG5 | Hydroxylation Benzoate degradation via | tautomerase catechol 1,2- | | H16_B0550 | unknown | catech + o2 -> ccmuc + 2 h | | catech + o2 -> ccmuc + 2 h |
| | Hydroxylation Benzoate | dioxygenase catechol 2,3- | | H16_A1964/H16_B0968 | | | catech + o2 -> ccmuc + 2 h | |
| CATCHD5 | degradation via Hydroxylation Benzoate | dioxygenase | 1.13.11.2 | H16_B0546 | unknown | catech + o2 -> 2hmucsald + h | catech + o2 -> 2hmucsald + h | catech + o2 -> 2hmucsald + h |
| MCCIS3 | degradation via Hydroxylation Benzoate | cycloisomerase | 5.5.1.1 | H16_A1966/H16_B0536 | catB3/catB4 | ccmuc + h <-> mclact | ccmuc + h <-> mclact | ccmuc + h <-> mclact |
| MCLACi | degradation via Hydroxylation Benzoate | muconolactone D- isomerase | 5.3.3.4 | H16_A1967/H16_B1584 | | mclact <-> 2odhfac | mclact <-> 2odhfac | mclact <-> 2odhfac |
| 3OXAPLC | degradation via Hydroxylation | 3-oxoadipate enol- lactonase | 3.1.1.24 | H16_A0147/H16_A1968, H16_B1583 | unknown/catD1/catD 2 | 2odhfac + h2o -> oadip + h | 2odhfac + h2o -> oadip + h | 2odhfac + h2o -> oadip + h |
| 3OXAPT | Benzoate degradation via Hydroxylation | 3-oxoadipate CoA- transferase | 2.8.3.6 | H16_B0198/H16_B0199 | pcaI/pcaJ | succoa + oadip -> succ + ooadpcoa | succoa + oadip -> succ + ooadpcoa | succoa + oadip -> succ + ooadpcoa |
| 3OXADCT | Benzoate degradation via Hydroxylation | 3-oxoadipyl-CoA thiolase | 2.3.1.16 | H16_A0462/H16_A1290, H16_B0200 | unknown/unknown/ pcaF | ooadpcoa + coa -> succoa + accoa | ooadpcoa + coa -> succoa + accoa | ooadpcoa + coa -> succoa + accoa |
| HMSALD3 | Benzoate degradation via Hydroxylation | 2-hydroxymuconic semialdehyde dehydrogenase | 1.2.1.32 | H16_B0547 | unknown | 2hmucsald + nad + h2o -> 2hmuc + nadh + 2 h | 2hmucsald + nad + h2o -> 2hmuc + nadh + 2 h | 2hmucsald + nad + h2o -> 2hmuc + nadh + 2 h |
| CATCHD6 | Benzoate degradation via Hydroxylation | catechol 2,3- dioxygenase | 1.13.11.2 | H16_B0546 | unknown | sulcatech + o2 + h2o -> 2hmuc + so3 + 2 h | sulcatech + o2 + h2o -> 2hmuc + so3 + 2 h | sulcatech + o2 + h2o -> 2hmuc + so3 + 2 h |
| 3CMUCC | Benzoate degradation via Hydroxylation | 3-carboxy-cis,cis- muconate cycloisomerase | 5.5.1.2 | H16_A2422/H16_B2289 | pcaB2/pcaB1 | carccm + h <-> gcarmclc | carccm + h <-> gcarmclc | carccm + h <-> gcarmclc |
| 4CBMCLC | Benzoate degradation via Hydroxylation | 4- carboxymuconolacto ne decarboxylase | 4.1.1.44 | H16_A0535/H16_B2288 | unknown/pcaCD | gcarmclc + h <-> 2odhfac + co2 | gcarmclc + h <-> 2odhfac + co2 | gcarmclc + h <-> 2odhfac + co2 |
| PROTCD | Benzoate degradation via | protocatechuate 3,4- dioxygenase | 1.13.11 | | | 34dhb + o2 + nadh + 2 h -> thbn + co2 + nad + h2o | 34dhb + o2 + nadh + 2 h -> thbn + co2 + nad + h2o | 34dhb + o2 + nadh + 2 h -> thbn + co2 + nad + h2o |
| MACR4 | Hydroxylation Benzoate degradation via | maleylacetate reductase | 1.3.1.32 | H16_B1420/H16_B1836 H16_A1786/H16_B0970 | | 2mac + nadh + h -> oadip + nad | 2mac + nadh + h -> oadip + nad | 2mac + nadh + h -> oadip + nad |
| BZFORCL2 | Hydroxylation Benzoate degradation via | benzoylformate carboxy-lyase | 4.1.1.7 | H16_A1113 | unknown | 4hbzald + co2 -> 4hpheglyx + h | 4hbzald + co2 -> 4hpheglyx + h | 4hbzald + co2 -> 4hpheglyx + h |
| MCCIS4 | Hydroxylation Benzoate degradation via | muconate | 5.5.1.1 | H16_A1966/H16_B0536 | catB3/catB4 | 4c2hmucsah -> 2h2hpd | 4c2hmucsah -> 2h2hpd | 4c2hmucsah -> 2h2hpd |
| PROTCC2 | Hydroxylation Benzoate degradation via | cycloisomerase protocatechuate 3,4- | 1.13.11.3 | H16_B0795/(H16_B2290 | unknown/(pcaG&pca | qallate + o2 -> 2py46dc + h2o + h | gallate + o2 -> 2py46dc + h2o + h | qallate + o2 -> 2py46dc + h2o + h |
| CARHM2 | Hydroxylation Benzoate | dioxygenase 5-carboxymethyl-2- | | &H16_B2291) | H1) | 4c2hhd <-> 4obtc | 4c2hhd <-> 4obtc | 4c2hhd <-> 4obtc |
| CARHIVIZ | degradation via Hydroxylation Benzoate | hydroxymuconate isomerase | 3.3.3.10 | H16_A0624/H16_B1250 H16_A1069/H16_A1070, | unknown/unknown/ | 4CZIIIG C-> 4ODIC | ACZINIO C-> AODIC | 4c21110 <-> 400tc |
| ACDH7 | degradation via Hydroxylation | acyl dehydratase | 42.1 | | unknown/unknown/ unknown/ | 4c2hmucsah + h2o -> 4c4h2oadip | 4c2hmucsah + h2o -> 4c4h2oadip | 4c2hmucsah + h2o -> 4c4h2oadip |
| ACDH8 | Benzoate degradation via Hydroxylation | acyl dehydratase | 4.2.1 | H16_A1069/H16_A1070, H16_A1289/H16_A2151, H16_A3307/H16_B0359, H16_B0706 | unknown/unknown/ | 4c2o4pent + h2o -> ppyr | 4c2o4pent + h2o -> ppyr | 4c2o4pent + h2o -> ppyr |
| 3HBZOR | Benzoate degradation via hydroxylation | 3- hydroxybenzoate,NA DH:oxygen oxidoreductase | 1.14.13.24 | | | 3hbenzot + o2 + nadh + h -> gensa + nad + h2o | 3hbenzot + o2 + nadh + h -> gensa + nad + h2o | 3hbenzot + o2 + nadh + h -> gensa + nad + h2o |
| PROTCDp | Benzoate degradation via Hydroxylation | protocatechuate 3,4- dioxygenase | 1.13.11 | H16_A0633/H16_B0223/ H16_B0757/H16_B1109/ H16_B1420/H16_B1836 | nown/unknown/unk | 34dnb + 02 + nadpn + 3 n -> tnbn + co2 + | 34dhb + o2 + nadph + 2 h -> thbn + co2 + nadp + h2o | 34dhb + o2 + nadph + 2 h -> thbn + co2 + nadp + h2o |
| MACR4p | Benzoate degradation via Hydroxylation | maleylacetate reductase | 1.3.1.32 | H16_A1786/H16_B0970 | unknown/pcpE | 2mac + nadph + 2 h -> oadip + nadp | 2mac + nadph + h -> oadip + nadp | 2mac + nadph + h -> oadip + nadp |
| ANDO | Benzoate degradation via hydroxylation | anthranilate 1,2- dioxygenase | 1.14.12.1 | | | | an + 1.25 o2 + 3 h + nadh -> catech + nh4 + co2 + nad + 0.5 h2o | an + 1.25 o2 + 3 h + nadh -> catech + nh4 + co2 + nad + 0.5 h2o |
| DMRATT | Biosynthesis of steroids Biosynthesis of | geranyltranstransfera se geranyltranstransfera | 2.5.1.10 | H16_A2733 | ispa | dmpp + ipp -> gpp + ppi | dmpp + ipp -> gpp + ppi + h | dmpp + ipp -> gpp + ppi + h |
| GRATT | steroids | se 4-(cytidine 5'- | 2.5.1.10 | H16_A2733 | ispa | gpp + ipp -> frdp + ppi | gpp + ipp -> frdp + ppi + h | gpp + ipp -> frdp + ppi + h |
| CDPMDEK | Biosynthesis of steroids | diphospho)-2-C- methyl-D-erythritol kinase | 2.7.1.148 | H16_A0374 | unknown | cdpmde + atp -> 2pcdpmde + adp | cdpmde + atp -> 2pcdpmde + adp + h | cdpmde + atp -> 2pcdpmde + adp + h |

| HMB4PPR | Biosynthesis of steroids | 1-hydroxy-2-methyl- 2-(E)-butenyl 4- diphosphate | 1.17.1.2 | H16_A3031/H16_B2169 | ispH | h + hmb4pp + nadh -> dmpp + h2o + nad | $h + hmb4pp + nadh \rightarrow dmpp + h2o + nad$ | h + hmb4pp + nadh -> dmpp + h2o + nad |
|----------|---|--|------------------------------------|--|--|--|---|--|
| DOXRTI | Biosynthesis of | reductase (dmpp) 1-deoxy-D-xylulose | 111267 | H16_A2049 | dxp | dx5p + 2 h + nadph -> mde4p + nadp | dx5p + h + nadph -> mde4p + nadp | dx5p + h + nadph -> mde4p + nadp |
| DOXPS | steroids Biosynthesis of | reductoisomerase 1-deoxy-D-xylulose 5-phosphate | 2.2.1.7 | H16_A2732 | dxs | g3p + h + pyr -> co2 + dx5p | g3p + h + pyr -> co2 + dx5p | g3p + h + pyr -> co2 + dx5p |
| DOALS | steroids | synthase 1-hydroxy-2-methyl- | 2.2.1.7 | 1110_12732 | u.s | gsp + 11 + pyr -> coz + axsp | g.sp + 11 + py1 -> co2 + dxsp | gsp + 11 + pyr -> co2 + axsp |
| HMB4DPR | Biosynthesis of steroids | 2-(E)-butenyl 4- diphosphate reductase | 1.17.1.2 | H16_A3031/H16_B2169 | ispH/ispH | $h + hmb4pp + nadh \rightarrow h2o + ipp + nad$ | h + hmb4pp + nadh -> h2o + ipp + nad | h + hmb4pp + nadh -> h2o + ipp + nad |
| MECDPDHT | Biosynthesis of steroids | 2C-methyl-D- erythritol 2,4 cyclodiphosphate dehydratase 2-C-methyl-D- | 1.17.4.3 | H16_A2364 | ispG | mdecpp + h + nadh -> hmb4pp + h2o + nad | mdecpp + h + nadh -> hmb4pp + h2o + nad | mdecpp + nadh -> hmb4pp + h2o + nad |
| MECDPS | Biosynthesis of steroids | erythritol 2,4- cyclodiphosphate synthase 2-C-methyl-D- | 4.6.1.12 | H16_A1457 | unknown | 2pcdpmde -> mdecpp + cmp | 2pcdpmde -> mdecpp + cmp | 2pcdpmde -> mdecpp + cmp |
| ME4PCT | Biosynthesis of steroids | erythritol 4- phosphate cytidylyltransferase | | H16_A1456 | unknown | mde4p + ctp -> cdpmde + ppi | mde4p + ctp -> cdpmde + ppi | mde4p + ctp -> cdpmde + ppi |
| OCTPPS | Biosynthesis of steroids | Octaprenyl pyrophosphate synthase | 2.5.1.29/2. 5.1.33/2.5. 1.30 | multi step reaction | multi step reaction | frdp + 5 ipp -> opp + 5 ppi | frdp + 5 ipp -> opp + 5 ppi + 5 h | frdp + 5 ipp -> opp + 5 ppi + 5 h |
| FDFT1 | Biosynthesis of steroids | farnesyl-diphosphate farnesyltransferase | 2.5.1.21 | H16_B0208 | unknown | 2 frdp -> ppi + pqppi | 2 frdp -> ppi + pqppi + h | 2 frdp -> ppi + pqppi + h |
| FDFT2 | Biosynthesis of steroids | farnesyl-diphosphate farnesyltransferase | 2.5.1.21 | H16_B0208 | unknown | pqppi + nadph + 2 h -> ppi + sql + nadp | pqppi + nadph -> ppi + sql + nadp | pqppi + nadph -> ppi + sql + nadp |
| THPT | Biosynthesis of steroids | trans- hexaprenyltranstransf erase | 2.5.1.30 | H16_A3253 | grcC | hppp + ipp -> heppp + ppi | hppp + ipp -> heppp + ppi + h | hppp + ipp -> heppp + ppi + h |
| AOXNS | Biotin Metabolism | 8-amino-7- oxononanoate synthase adenosylmethionine- | 2.3.1.47 | H16_A0181 | bioF | ala + pmcoa <-> aona + co2 + coa | ala + pmcoa <-> aona + co2 + coa | ala + h + pmcoa <-> aona + co2 + coa |
| AMAOXNT | Biotin Metabolism | 8-amino-7- oxononanoate | 2.6.1.62 | H16_A0180/H16_B2123 | bioA/unknown | aona + sam <-> samob + danna + h | aona + sam <-> samob + danna + h | aona + sam <-> samob + danna + h |
| BIOTS | Biotin Metabolism | transaminase Biotin synthase dethiobiotin | 2.8.1.6 | H16_A0183 | bioB | sam + dtb + s -> bt + da-5 + met + h | sam + dtb + s -> bt + da-5 + met + h | sam + dtb + s -> bt + da-5 + met |
| DTBTS | Biotin Metabolism | synthase 6-carboxyhexanoate- | 6.3.3.3 | H16_A0182 | bioD | atp + co2 + danna -> adp + dtb + 2 h + pi | atp + co2 + danna -> adp + dtb + 3 h + pi | atp + co2 + danna -> adp + dtb + 2 h + pi |
| 6CARHC | Biotin metabolism | -CoA ligase | 6.2.1.14 | H16_B0928/H16_B1438 | unknown/unknown | pimlt + atp + coa + 2 h -> amp + ppi + pmcoa | pimlt + atp + coa -> amp + ppi + pmcoa | pimlt + atp + coa -> amp + ppi + pmcoa + h |
| BTNACL | Biotin metabolism | biotin-[acetyl-CoA- carboxylase] ligase | | H16_A0135/H16_A2946 | bitA/unknown | atp + bt + h -> ppi + b5amp | atp + bt -> ppi + b5amp | atp + bt -> ppi + b5amp |
| BPHEDO1 | Biphenyl degradation | biphenyl-2,3-diol 1,2- dioxygenase | 1.13.11.39 | H16_B0654 | bphC | bp23d + o2 -> hophd + h | bp23d + o2 -> hophd + h | bp23d + o2 -> hophd + h |
| BIPHED1 | Biphenyl degradation | 2,6-Dioxo-6- phenylhexa-3-enoate benzoylhydrolase | | H16_B0600 | bphD | hophd + h2o -> benzot + op4en + h | hophd + h2o -> benzot + op4en + h | hophd + h2o -> benzot + op4en + h |
| BPHEDO2 | Biphenyl degradation | biphenyl-2,3-diol 1,2- dioxygenase | 1.13.11.39 | H16_B0654 | bphC | dhchph + o2 -> hochphhd + h | dhchph + o2 -> hochphhd + h | dhchph + o2 -> hochphhd + h |
| BIPHED2 | Biphenyl degradation | 2,6-Dioxo-6- phenylhexa-3-enoate benzoylhydrolase | 3.7.1.8 | H16_B0600 | bphD | hochphhd + h2o -> 4chbenz + op4en + h | hochphhd + h2o -> 4chbenz + op4en + h | hochphhd + h2o -> 4chbenz + op4en + h |
| ВРНЕНВ | Bisphenol A | bisphenol A | 1.14.13 | | | bisphenol + nadh + h + o2 -> 12bhpp + nad + | bisphenol + nadh + h + o2 -> 12bhpp + | bisphenol + nadh + h + o2 -> 12bhpp + nad + h2o |
| ВРНЕНА | degradation Bisphenol A degradation | hydroxylase B bisphenol A hydroxylase A | 1.14.13 | H16_B1480/H16_B2135 H16_A1145/H16_B0495/ H16_B1480/H16_B2135 | unknown/unknown/ | bisphenol + nadh + h + o2 -> 22bhpp + nad + | nad + h2o bisphenol + nadh + h + o2 -> 22bhpp + nad + h2o | bisphenol + nadh + h + o2 -> 22bhpp + nad + h2o |
| 2ВНРРРН | Bisphenol A degradation | 2,2-bis(4- hydroxyphenyl)-1- propanol hydroxylase | 1.14.13 | H16_A1145/H16_B0495/ H16_B1480/H16_B2135 | | 22bhpp + nadh + h + o2 -> 23bhpp + nad + h2o | 22bhpp + nadh + h + o2 -> 23bhpp + nad + h2o | 22bhpp + nadh + h + o2 -> 23bhpp + nad + h2o |
| 4ETHPMH | Bisphenol A degradation | 4-ethylphenol methylenehydroxylas e | 1.14.13 | H16_A1145/H16_B0495/ H16_B1480/H16_B2135 | | 4ethp + nadph + 2 h + o2 -> 14hpeth + nadp + h2o | 4ethp + nadph + h + o2 -> 14hpeth + nadp + h2o | 4ethp + nadph + h + o2 -> 14hpeth + nadp + h2o |
| 14HPED | Bisphenol A degradation | 1-(4'- hydroxyphenyl)ethan ol dehydrogenase | 111 | H16_A0679/H16_A0893/ H16_A1256/H16_A1828/ H16_A2460/H16_A2586/ H16_B0034/H16_B0572/ H16_B0663/H16_B0831/ H16_B1417/H16_B2561 | / unknown/unknown/ / abmB/unknown/wec C/unknown/unknow n/unknown/unknow | 14hpeth + nad -> 4hactph + nadh + h | 14hpeth + nad -> 4hactph + nadh + h | 14hpeth + nad -> 4hactph + nadh + 2 h |
| MALDO | Butanoate metabolism | malate decarboxylating oxidoreductase | 1.1.1.83 | H16_A0477 | leuB1 | dmal + nad + 2 h -> co2 + nadh + pyr | dmal + nad + 3 h -> co2 + nadh + pyr | dmal + nad + 3 h -> co2 + nadh + pyr |
| ALHD4 | Butanoate metabolism | aldehyde dehydrogenase (butanal, NAD) | 1.1.1 | H16_A0478/H16_A0679/ H16_A0861/H16_A0893/ H16_A1256/H16_A1562/ H16_A1702/H16_A1528/ H16_A2460/H16_A2474/ H16_A2586/H16_B0034/ H16_B0712/H16_B06812/ H16_B0713/H16_B0831/ H16_B0941/H16_B0942/ H16_B1417/H16_B16894/ | own/unknown/unkn own/unknown/unkn own/unknown/abmB /unknown/unknown/ wecC/unknown/unkr own/unknown/unkn own/unknown/unkn | | butanal + h2o + nad -> 1boh + 2 h + nadh | butanal + h2o + nad -> 1boh + 2 h + nadh |
| MALEAI | Butanoate | maleate isomerase | 5.2.1.1 | H16_B2561/ H16_A0923/H16_B0811 | | malta cas fum | malte <-> fum | malte <-> fum |
| | metabolism Butanoate | acetaldehyde | | H16_A1806/H16_A2747/ | | | | |
| ACALDb | metabolism Butanoate | dehydrogenase 4-hydroxybutyrate | 1.2.1.10 | H16_B0551/H16_B0596 | mhpF/unknown | butanal + coa + nad -> c040coa + nadh + h | butanal + coa + nad -> c040coa + nadh + h | |
| 4HBTD | metabolism | dehydrogenase acetyl-CoA: 4- hydroxybutanoate | 1.1.1.61 | H16_A1553 | gbd | 4hbt + nad <-> sucsal + nadh + h | 4hbt + nad <-> sucsal + nadh + h | 4hbt + nad <-> sucsal + nadh + h |
| AC4HB | Butanoate metabolism | CoA transferase (two-step reaction, unclear reaction) | | | | 4hbt + accoa <-> 3btecoa + ac + h2o | 4hbt + accoa <-> 3btecoa + ac + h2o | 4hbt + accoa <-> 3btecoa + ac + h2o |
| 3HBCD | Butanoate metabolism | 3-hydroxybutyryl- CoA dehydratase | 4.2.1.55 | H16_B1843/H16_B2534 | unknown/unknown | r3hbcoa <-> ccoa + h2o | r3hbcoa <-> ccoa + h2o | r3hbcoa <-> ccoa + h2o |
| PHAS | Butanoate metabolism | and the other confidence of the same and | 2.3.1 | H16_A1437/H16_A2003 | phaC1/phaC2 | r3hbcoa <-> pbhb + coa | r3hbcoa <-> pbhb + coa | r3hbcoa <-> pbhb + coa |
| PHBD | Butanoate metabolism | poly(3- hydroxybutyrate) | 3.1.1.75 | | /phaZ5/phaZ6/phaZ | pbhb + h2o <-> r3hbn2 + r3rhbb + h | pbhb + h2o <-> r3hbn2 + r3rhbb + h | pbhb + h2o <-> r3hbn2 + r3rhbb + h |
| HBDH | Butanoate | depolymerase hydroxybutyrate- | 21177 | H16_B2073/H16_B2401 | | r3rhhh + h2o> 2 -2hho - h | r3rhbb + h2o <-> 2 r3hbn + h | r3rhhh + h2o 2 -2hha + h |
| | metabolism Butanoate | dimer hydrolase 3-hydroxybutyrate | | H16_A2251 | phaY1 | r3rhbb + h2o <-> 2 r3hbn + h | | r3rhbb + h2o <-> 2 r3hbn + h |
| 3HBD | metabolism | dehydrogenase | 1.1.1.30 | | | r3hbn + nad <-> acac + nadh + h | r3hbn + nad <-> acac + nadh + h | r3hbn + nad <-> acac + nadh + h |
| ALHDS | Butanoate metabolism | aldehyde dehydrogenase (NAD+) | 12.1.3 | H16_A0232/H16_A0745/ H16_A1114/H16_A1495/ H16_B0212/H16_B0421/ H16_B0737/H16_B0833/ H16_B1534/H16_B1735/ H16_B1751/H16_B1835/ H16_B1960/H16_B2444 | dunknown/unknown/ unknown/unknown/ unknown/unknown/ unknown/unknown/ unknown/unknown/ | 3b1a + nad + h2o -> 3but + nadh + 2 h | 3b1a + nad + h2o -> 3but + nadh + 2 h | 3b1a + nad + h2o -> 3but + nadh + 2 h |
| | | | | | | | | |

| | Butanoate | acetoacetyl-CoA | | H16 A1439/H16 A2002/ | | | | |
|-------------------------------------|--|--|--|---|--|---|--|--|
| AACOAR | metabolism | acetoacetyl-CoA reductase | 1.1.1.36 | H16_A1439/H16_A2002/ H16_A2171 | phaB1/phaB2/phaB3 | r3hbcoa + nadp <-> aacoa + nadph + 2 h | r3hbcoa + nadp <-> aacoa + nadph + h | r3hbcoa + nadp <-> aacoa + nadph + h |
| AACOAS | Butanoate | acetoacetyl-CoA | 6.2.1.16 | H16_A2860 | unknown | atp + acac + coa + h -> amp + ppi + aacoa | atp + acac + coa -> amp + ppi + aacoa + | atp + acac + coa -> amp + ppi + aacoa + h |
| | metabolism Butanoate | synthetase 3-oxoacid CoA- | | | | | h | |
| 3OACT | metabolism | transferase | 2.8.3.5 | | | succoa + acac <-> succ + aacoa | succoa + acac <-> succ + aacoa | succoa + acac <-> succ + aacoa |
| | Butanoate | hydroxymethylglutar | | H16_A0186/H16_A1235/ | unknown/mvaB/unk | 21.2 | 21.0 | 21.2 |
| HXMGL | metabolism | yl-CoA lyase | 4.1.3.4 | H16_A1547/H16_A2385/ H16_B2494 | nown/hmgL1/hmgL2 | 3h3mgcoa -> accoa + acac | 3h3mgcoa -> accoa + acac | 3h3mgcoa -> accoa + acac |
| | | | | H16_A1069/H16_A1070/ | | | | |
| ACDH1 | Butanoate metabolism | acyl dehydratase | 4.2.1 | H16_A1289/H16_A2151/ H16_A3307/H16_B0359/ | | gl1coa + h2o <-> hgcoa | gl1coa + h2o <-> hgcoa | gl1coa + h2o <-> hgcoa |
| | metabolism | | | | unknown/ | | | |
| | Butanoate | butyrate-CoA | | | | | | |
| BTCAL | metabolism | ligase/short-chain acyl-CoA synthetase | 6.2.1.2 | | | butn + atp + coa -> c040coa + amp +ppi | butn + atp + coa -> c040coa + amp +ppi | butn + atp + coa -> c040coa + amp +ppi |
| | C5-Branched | succinyl-CoA | | | | | | |
| SUCCS | Dibasic acid | synthetase | 6.2.1.5 | H16_A0547/H16_A0548 | sucC/sucD | atp + itcn + coa + h <-> adp + pi + itcncoa | atp + itcn + coa <-> adp + pi + itcncoa | atp + itcn + coa <-> adp + pi + itcncoa |
| | metabolism Calvin-Benson- | | | | | 3 co2 + 5 h2o + 9 atp + 6 nadph + 12 h -> 9 | 3 co2 + 5 h2o + 9 atp + 6 nadph -> 9 adp + 8 | 3 co2 + 5 h2o + 9 atp + 6 nadph -> 9 adp + 8 |
| CBBCYC | Bassham cycle | | | | | | pi + g3p + 6 nadp + 3 h | pi + g3p + 6 nadp + 3 h |
| 2AMBZC | Carbazole degradation | 2-aminobenzoate- CoA ligase | 6.2.1.32 | H16_A2457 | abmG | atp + an + coa + h -> amp + ppi + anthcoa | atp + an + coa -> amp + ppi + anthcoa + h | atp + an + coa -> amp + ppi + anthcoa + h |
| A N. T. I I AN I 1 | Carbazole | anthraniloyl-CoA | 1 1 4 1 2 40 | 1116 42461 | -h A | anthcoa + o2 + 2 nadh + 2 h -> 2amoeccoa + | anthcoa + o2 + 2 nadh + 2 h -> 2amoeccoa + | anthcoa + o2 + 2 nadh + 2 h -> 2amoeccoa + |
| ANTHMN1 | degradation | monooxygenase | 1.14.13.40 | H16_A2461 | abmA | | h2o + 2 nad | h2o + 2 nad |
| ANTHMN2 | Carbazole degradation | anthraniloyl-CoA monooxygenase | 1.14.13.40 | H16_A2461 | abmA | anthcoa + o2 + 2 nadph + 4 h -> 2amoeccoa + h2o + 2 nadp | anthcoa + o2 + 2 nadph + 2 h -> 2amoeccoa + h2o + 2 nadp | anthcoa + o2 + 2 nadph + 2 h -> 2amoeccoa + h2o + 2 nadp |
| | 9 | , 5 | | H16_A1465/H16_A1546/ | unknown/unknown/ | | | |
| | | | | H16_A1732/H16_A1734/ | | | | |
| | Carprolactam | | | H16_A2086/H16_A3386/ | | | | |
| FTOLAM | degradation | Hydrolase | 3.5.1 | H16_B0814/H16_B1172/ H16_B1643/H16_B1666/ | | cchfor + h2o -> cchlam + formate | cchfor + h2o -> cchlam + formate | cchfor + h2o -> cchlam + formate |
| | | | | H16_B2013/H16_B2014/ | | | | |
| | | | | H16_B2069/H16_B2126 | unknown/unknown | | | |
| CCHNM1 | Carprolactam | cyclohexanone | 1 14 13 22 | H16_B1746 | unknown | cchexo + o2 + nadph + 2 h \leftarrow 6hnld + nadp + | | |
| | degradation Carprolactam | monooxygenase | | H16_A3012/H16_B0345/ H16_B1441 | | h2o | + h2o | h2o |
| GLTN3 | degradation | gluconolactonase | 3.1.1.17 | H16_B1441 | gnl1/gnl2/gnl3 | 6hnld + h2o -> 6hhn + h | 6hnld + h2o -> 6hhn + h | 6hnld + h2o -> 6hhn + h |
| | _ | | | H16_A0866/H16_A0871/ | | | | |
| | | | | H16_A1230/H16_A1519/ H16_A1700/H16_A1718/ | | | | |
| | | | | H16_A2252/H16_A2794/ | | | | |
| ADIPL | Carprolactam | adipate-CoA ligase | 621. | H16_A2807/H16_A2978/ | unknown/unknown/ | adip + coa + atp + h -> adipcoa + amp + ppi | adip + coa + atp -> adipcoa + amp + ppi + | adip + coa + atp -> adipcoa + amp + ppi + h |
| ADIFL | degradation | adipate-COA ligase | 0.2.1 | H16_B0174/H16_B0677/ | | aup + coa + atp + II -> aupcoa + amp + ppi | h | aup + coa + atp -> aupcoa + amp + ppi + m |
| | | | | H16_B0910/H16_B1148/ H16_B1264/H16_B1335/ | | | | |
| | | | | H16_B1662/H16_B1709/ | unknown/unknown/ | | | |
| | | | | H16_B2522 | unknown/ | | | |
| ACOADG | Carprolactam degradation | acyl-CoA dehydrogenase | 1.3.99 | H16_B2555 | unknown | adipcoa + fad -> carpcoa + fadh2 | adipcoa + fad + h -> carpcoa + fadh2 | adipcoa + fad + h -> carpcoa + fadh2 |
| CCHNM2 | Carprolactam | cyclohexanone | 1141222 | 111C P174C | lea even | nadph + hccho + 2 h + o2 -> nadp + oohoch + | nadph + hccho + h + o2 -> nadp + oohoch | nadph + hccho + h + o2 -> nadp + oohoch + |
| CCHNM2 | degradation | monooxygenase | 1.14.13.22 | H16_B1746 | unknown | h2o | + h2o | h2o |
| MDH1 | Citric Acid Cycle | malate dehydrogenase | 1.1.1.37 | H16_A2634/H16_B0334 | mdh1/mdh2 | mal + nad <-> h + nadh + oaa | mal + nad <-> h + nadh + oaa | mal + nad <-> h + nadh + oaa |
| | | isocitrate | | | | | | |
| ICITD | Citric Acid Cycle | dehydrogenase | 1.1.1.41 | H16_B1016 | icd3 | icit + nad <-> akg + co2 + nadh | icit + nad <-> akg + co2 + nadh | icit + nad <-> akg + co2 + nadh |
| | | (NAD) isocitrate | | | | | | |
| ICITDp | Citric Acid Cycle | dehydrogenase | 1.1.1.42 | H16_A3056/H16_B1931 | icd1/icd2 | icit + nadp <-> akg + co2 + h + nadph | icit + nadp <-> akg + co2 + nadph | icit + nadp <-> akg + co2 + nadph |
| | | (NADP) | | | | | | |
| | | Malate | | | | | | |
| MDH2 | Citric Acid Cycle | dehydrogenase (ubiquinone 8 as | 1.1.99.16 | | | mal + uq -> oaa + uqh2 | mal + uq -> oaa + uqh2 | mal + uq -> oaa + uqh2 |
| | | acceptor) | | | | | | |
| CITL | Citric Acid Cycle | Citrate lyase | 4.1.3.6 | H16_A2635/H16_B0353/ | | cit -> ac + oaa | cit -> ac + oaa | cit -> ac + oaa |
| FUMR | Citric Acid Cycle | fumarase | 4.2.1.2 | H16_B0680/H16_B2113 H16_A2528/H16_B0103 | fumA/fumC | fum + h2o <-> mal | fum + h2o <-> mal | fum + h2o <-> mal |
| ACONT1 | Citric Acid Cycle | aconitase (citrate | 4.2.1.3 | H16_A1907/H16_A2638/ | acnM/acnA/acnB | cit <-> acon-C + h2o | cit <-> acon-C + h2o | cit <-> acon-C + h2o |
| ACOIVII | Citile Acid Cycle | hydro-lyase) | 4.2.1.3 | | | CR <-> acon-c + nzo | acon-c + 1120 | Cit <-> acon-C + nzo |
| ACONT2 | Citric Acid Cycle | aconitase (isocitrate hydro-lyase) | 4.2.1.3 | H16_A1907/H16_A2638/ H16_B0568 | acnM/acnA/acnB | acon-C + h2o <-> icit | acon-C + h2o <-> icit | acon-C + h2o <-> icit |
| | | succinyl-CoA | | H16 A05478;H16 A054 | | | | |
| SUCOAS | Citric Acid Cycle | synthetase (ADP- | 6.2.1.5 | 8 | sucC&sucD | atp + coa + succ + h <-> adp + pi + succoa | atp + coa + succ -> succoa + adp + pi | atp + coa + succ <-> adp + pi + succoa |
| | | forming) | | (H16_A2325)(H16_A137 | | | | |
| AKGDH | Citric Acid Cycle | 2-Oxogluterate | | 7/H16_A2323/H16_A372 | (odhA)(pdhL/odhL/lp | akg + coa + nad -> co2 + nadh + succoa | akg + coa + nad -> co2 + nadh + succoa | akg + coa + nad -> co2 + nadh + succoa |
| ANGUN | Citric Acid Cycle | dehydrogenase | | 4/H10_B1090)(H10_A25 |) | akg + coa + nau -> coz + naun + succoa | akg + coa + nau -> coz + naun + succoa | aky + coa + nau -> coz + naun + succoa |
| | | | | 24) H16_A1229/H16_A2627/ | unknown/cisY/unkno | | | |
| CITS | Citric Acid Cycle | citrate synthase | 2.3.3.1 | | | accoa + h2o + oaa -> cit + coa + h | accoa + h2o + oaa -> cit + coa + h | accoa + h2o + oaa -> cit + coa + h |
| | | | | H16_B2211 | wn | | | |
| SUCCD3 | Citric Acid Cycle | succinate dehydrogenase | 1.3.99.1 | | sdhB&sdhA&sdhD& | succ + fad -> fum + fadh2 | succ + fad + h -> fum + fadh2 | succ + fad + h -> fum + fadh2 |
| 300003 | Citile Acid Cycle | (irreversible) | 1.3.33.1 | 632&H16_B0204 | sdhC&unknown | Succ + lad -> lulii + ladiiz | Succ + lad + II -> lulii + ladii2 | Succ + lad + II -> lulii + lauliz |
| NITL2 | Cyanoamino acid | nitrilase | 3.5.5.1 | | nit | aamppn + 2 h2o -> ala + nh4 | aamppn + 2 h2o + h -> ala + nh4 | aamppn + 2 h2o + h -> ala + nh4 |
| | metabolism | | | H16_A1069/H16_A1070/ | | • | - | |
| ACDH4 | Cyanoamino acid | acyl dehydratase | 4.2.1 | H16_A1289/H16_A2151/ | unknown/unknown/ | hcyst + 2 cn + h2 -> aagcya + hcys + tcynt + h | hcyst + 2 cn + h2 -> aagcya + hcys + tcynt | hcyst + 2 cn + h2 -> aagcya + hcys + tcynt + h |
| ACD/14 | metabolism | ocyr uenydialase | f.2.1." | H16_A3307/H16_B0359/ | | negot . 2 cm + n2 -> aageyd + neys + teynt + n | + h | neys 2 cm + n2 -> dageyd + neys + teynt + n |
| Agree | Cyanoamino acid | -14-11 | 2555 | | unknown/ | 212 | | |
| NITL3 | metabolism | nitrilase | 3.5.5.1 | H16_A1125 | nit | gagcya + 2 h2o -> glu + nh4 | gagcya + 2 h2o + h -> glu + nh4 | gagcya + 2 h2o + h -> glu + nh4 |
| GGMT1 | Cyanoamino acid | gamma- glutamyltranspeptida | 2222 | H16_A0784/H16_A1098/ | | grada + glu + h gahan + h2 2 | grada + glu + h - gaban - taa | cuada + du + 2 h - nobon - kaa |
| GGM11 | metabolism | glutamyltranspeptida se | 2.5.2.2 | H16_A2780/H16_B0984 | | cyaala + glu + h -> ggbap + h2o + co2 | cyaala + glu + h -> ggbap + h2o + co2 | cyaala + glu + 2 h -> ggbap + h2o + co2 |
| | Cyanoamino acid | gamma- | | H16_A0784/H16_A1098/ | aat2a/unknown/aat | | | |
| GGMT2 | Cyanoamino acid metabolism | glutamyltranspeptida | 2.3.2.2 | H16_A0784/H16_A1098/ H16_A2780/H16_B0984 | | cyaala + glu -> ggbcya + h2o | cyaala + glu -> ggbcya + h2o | cyaala + glu + h -> ggbcya + h2o |
| | Cysteine | se serine O- | | | | | | |
| SEROAT | Metabolism | acetyltransferase | 2.3.1.30 | H16_A1216 | cysE | accoa + ser <-> aser + coa | accoa + ser <-> aser + coa | accoa + ser <-> aser + coa |
| CYSSULD | Cysteine | L-cysteine sulfinic | 4.1.1.12 | H16_A3009 | asdA | 3slala + h -> ala + so2 | 3slala + h -> ala + so2 | 3slala + h -> ala + so2 |
| | Metabolism Cysteine | acid desulfurase | | H16 A0807/H16 A1902/ | | | | |
| CYSST1 | Metabolism | · · · | 2.5.1.47 | H16_B2378 | cysK1/cysK2/cysK4 | aser + h2s -> ac + cys + h | aser + h2s -> ac + cys | aser + h2s -> ac + cys |
| CYSTBL2 | Cysteine | cystathionine beta- | 4.4.1.8 | H16_A1447 | metC | cyst + h2o -> pyr + nh4 + tcys | cyst + h2o -> pyr + nh4 + tcys | cyst + h2o -> pyr + nh4 + tcys |
| | metabolism | lyase cystathionine | | | | | | |
| CYTTS6 | Cysteine | | 2.5.1.48 | H16_A2606 | metB | aser + tsul -> sslcys + ac + h | aser + tsul -> sslcys + ac + h | aser + tsul -> sslcys + ac + h |
| | Cysteine metabolism | gamma-synthase | | H16_A0807/H16_A1903/ | cysK1/cysK2/cysK4 | aser + tsul -> sslcys + ac + h | aser + tsul -> sslcys + ac + h | aser + tsul -> sslcys + ac + h |
| CYSST2 | metabolism Cysteine | | 2.5.1.47 | | | | | and the second s |
| | metabolism Cysteine metabolism | cysteine synthase | 2.5.1.47 | H16_B2378 | | ŕ | | |
| CYSST2 SERDHT2 | metabolism Cysteine | | | H16_B2378 | sdaA | ser -> 2aa + h2o | ser -> 2aa + h2o | ser -> 2aa + h2o |
| SERDHT2 | metabolism Cysteine metabolism Cysteine metabolism Cysteine | cysteine synthase L-serine dehydratase O-acetylhomoserine | 4.3.1.17 | H16_B2378 H16_A3622 | sdaA | ser -> 2aa + h2o | aser + tsul + rthio -> cys + so3 + othio + | |
| SERDHT2 OAHSL2 | metabolism Cysteine metabolism Cysteine metabolism Cysteine metabolism | cysteine synthase L-serine dehydratase O-acetylhomoserine (thiol)-lyase | 4.3.1.17 2.5.1.49 | H16_B2378 H16_A3622 H16_A1313/H16_B2229 H16_A0807/H16_A1903/ | sdaA metY1/metY2 | ser -> 2aa + h2o aser + tsul + rthio -> cys + so3 + othio + ac + h | aser + tsul + rthio -> cys + so3 + othio + ac + h | aser + tsul + rthio -> cys + so3 + othio + ac + h |
| SERDHT2 | metabolism Cysteine metabolism Cysteine metabolism Cysteine | cysteine synthase L-serine dehydratase O-acetylhomoserine | 4.3.1.17 | H16_B2378 H16_A3622 H16_A1313/H16_B2229 H16_A0807/H16_A1903/ | sdaA | ser -> 2aa + h2o | aser + tsul + rthio -> cys + so3 + othio + | |
| SERDHT2 OAHSL2 | metabolism Cysteine metabolism Cysteine metabolism Cysteine metabolism Cysteine metabolism Cysteine | cysteine synthase L-serine dehydratase O-acetylhomoserine (thiol)-lyase cysteine synthase aspartate | 43.1.17 2.5.1.49 2.5.1.47 | H16_B2378 H16_A3622 H16_A1313/H16_B2229 H16_A0807/H16_A1903/ H16_B2378 | sdaA metY1/metY2 cysK1/cysK2/cysK4 | ser -> 2aa + h2o aser + tsul + rthio -> cys + so3 + othio + ac + h aser + tsul + rthio -> cys + so3 + othio + ac + h | aser + tsul + rthio -> cys + so3 + othio + ac + h aser + tsul + rthio -> cys + so3 + othio + ac + h | aser + tsul + rthio -> cys + so3 + othio + ac + h aser + tsul + rthio -> cys + so3 + othio + ac + h |
| SERDHT2 OAHSL2 CYSST3 ASPAM1 | metabolism Cysteine metabolism Cysteine metabolism Cysteine metabolism Cysteine metabolism Cysteine metabolism metabolism | cysteine synthase L-serine dehydratase O-acetylhomoserine (thiol)-lyase cysteine synthase aspartate aminotransferase | 4.3.1.17 2.5.1.49 2.5.1.47 2.6.1.1 | H16_B2378 H16_A3622 H16_A1313/H16_B2229 H16_A0807/H16_A1903/ H16_B2378 H16_A2857 | sdaA metY1/metY2 | ser -> 2aa + h2o aser + tsul + rthio -> cys + so3 + othio + ac + h aser + tsul + rthio -> cys + so3 + othio + ac + h mpyr + glu -> cys + akg | aser + tsul + rthio -> cys + so3 + othio + ac + h aser + tsul + rthio -> cys + so3 + othio + | aser + tsul + rthio -> cys + so3 + othio + ac + h |
| SERDHT2 OAHSL2 CYSST3 | metabolism Cysteine metabolism Cysteine metabolism Cysteine metabolism Cysteine metabolism Cysteine | cysteine synthase L-serine dehydratase O-acetylhomoserine (thiol)-lyase cysteine synthase aspartate | 43.1.17 2.5.1.49 2.5.1.47 | H16_B2378 H16_A3622 H16_A1313/H16_B2229 H16_A0807/H16_A1903/ H16_B2378 H16_A2857 | sdaA metY1/metY2 cysK1/cysK2/cysK4 | ser -> 2aa + h2o aser + tsul + rthio -> cys + so3 + othio + ac + h aser + tsul + rthio -> cys + so3 + othio + ac + h | aser + tsul + rthio -> cys + so3 + othio + ac + h aser + tsul + rthio -> cys + so3 + othio + ac + h | aser + tsul + rthio -> cys + so3 + othio + ac + h aser + tsul + rthio -> cys + so3 + othio + ac + h |
| SERDHT2 OAHSL2 CYSST3 ASPAM1 ASPAM2 | metabolism Cysteine metabolism Cysteine metabolism Cysteine metabolism Cysteine metabolism Cysteine metabolism Cysteine metabolism Cysteine cysteine | cysteine synthase L-serine dehydratase O-acetylhomoserine (thiol)-lyase cysteine synthase aspartate aminotransferase aspartate aminotransferase aspartate | 4.3.1.17 2.5.1.49 2.5.1.47 2.6.1.1 | H16_B2378 H16_A3622 H16_A1313/H16_B2229 H16_A0807/H16_A1903/ H16_B2378 H16_A2857 H16_A2857 | sdaA metY1/metY2 cysK1/cysK2/cysK4 unknown | ser -> 2aa + h2o aser + tsul + rthio -> cys + so3 + othio + ac + h aser + tsul + rthio -> cys + so3 + othio + ac + h mpyr + glu -> cys + akg 3slala + akg + h -> 3sfpyr + glu | aser + tsul + rthio -> cys + so3 + othio + ac + h aser + tsul + rthio -> cys + so3 + othio + ac + h mpyr + glu -> cys + akg 3slala + akg + h -> 3sfpyr + glu | aser + tsul + rthio -> cys + so3 + othio + ac + h aser + tsul + rthio -> cys + so3 + othio + ac + h mpyr + glu -> cys + akg 3slala + akg -> 3sfpyr + glu |
| SERDHT2 OAHSL2 CYSST3 ASPAM1 | metabolism Cysteine metabolism Cysteine metabolism Cysteine metabolism Cysteine metabolism Cysteine metabolism Cysteine metabolism Cysteine metabolism Cysteine metabolism | cysteine synthase L-serine dehydratase O-acetylhomoserine (thiol)-lyase cysteine synthase aspartate aminotransferase aspartate aminotransferase aspartate aminotransferase | 4.3.1.17 2.5.1.49 2.5.1.47 2.6.1.1 2.6.1.1 | H16_B2378 H16_A3622 H16_A1313/H16_B2229 H16_A0807/H16_A1903/ H16_B2378 H16_A2857 H16_A2857 | sdaA metY1/metY2 cysK1/cysK2/cysK4 unknown unknown | ser -> 2aa + h2o aser + tsul + rthio -> cys + so3 + othio + ac + h aser + tsul + rthio -> cys + so3 + othio + ac + h mpyr + glu -> cys + akg | aser + tsul + rthio -> cys + so3 + othio + ac + h aser + tsul + rthio -> cys + so3 + othio + ac + h mpyr + glu -> cys + akg | aser + tsul + rthio -> cys + so3 + othio + ac + h aser + tsul + rthio -> cys + so3 + othio + ac + h mpyr + glu -> cys + akg |
| SERDHT2 OAHSL2 CYSST3 ASPAM1 ASPAM2 | metabolism Cysteine metabolism Cysteine metabolism Cysteine metabolism Cysteine metabolism Cysteine metabolism Cysteine metabolism Cysteine cysteine | cysteine synthase L-serine dehydratase O-acetylhomoserine (thiol)-lyase cysteine synthase aspartate aminotransferase aspartate aminotransferase aspartate | 4.3.1.17 2.5.1.49 2.5.1.47 2.6.1.1 2.6.1.1 | H16_B2378 H16_A3622 H16_A1313/H16_B2229 H16_A0807/H16_A1903/ H16_B2378 H16_B2378 H16_A2857 H16_A2857 | sdaA metY1/metY2 cysK1/cysK2/cysK4 unknown unknown | ser -> 2aa + h2o aser + tsul + rthio -> cys + so3 + othio + ac + h aser + tsul + rthio -> cys + so3 + othio + ac + h mpyr + glu -> cys + akg 3slala + akg + h -> 3sfpyr + glu | aser + tsul + rthio -> cys + so3 + othio + ac + h aser + tsul + rthio -> cys + so3 + othio + ac + h mpyr + glu -> cys + akg 3slala + akg + h -> 3sfpyr + glu | aser + tsul + rthio -> cys + so3 + othio + ac + h aser + tsul + rthio -> cys + so3 + othio + ac + h mpyr + glu -> cys + akg 3slala + akg -> 3sfpyr + glu |

| SADT2 | Cysteine Metabolism | Sulfate adenyltransferase | | | | atp + selnt <-> ppi + aselnt | atp + selnt <-> ppi + aselnt + h | atp + selnt <-> ppi + aselnt + h |
|-----------|--------------------------------|--|--|--|--|--|--|---|
| ALAALAL | D-alanine metabolism | D-alanine-D-alanine ligase | 6.3.2.4 | H16_A3271 | ddlB | 2 dala + atp <-> adp + alaala + pi | 2 dala + atp <-> adp + alaala + h + pi | 2 dala + atp <-> adp + alaala + 2 h + pi |
| DATA4 | D-alanine metabolism | D-alanine transaminase | 2.6.1.21 | H16_A2521 | dat | dala + akg <-> pyr + dglu | dala + akg <-> pyr + dglu | dala + akg <-> pyr + dglu |
| GLUN2 | D-glutamine and D-glutamate | glutaminase | 3.5.1.38 | H16_A1910/H16_A2280 | ansA/unknown | dgln + h2o -> dglu + nh4 | dgln + h2o -> dglu + nh4 | dgln + h2o -> dglu + nh4 |
| BZACCOAT1 | metabolism Ethylbenzene | benzoyl acetyl-CoA | 2.3.1.16 | H16_A0462/H16_A1290/ | | bzaccoa + coa -> bzocoa + accoa | bzaccoa + coa -> bzocoa + accoa | bzaccoa + coa -> bzocoa + accoa |
| BZACCUATI | degradation | thiolase | 23.1.16 | | pcaF unknown/unknown/ unknown/unknown/ unknown/unknown/ unknown/unknown/ | pzaccoa + coa -> pzocoa + accoa | DZaccoa + coa -> DZOCoa + accoa | DZRCCOB + COB -> DZRCCOB + BCCOB |
| BZACCOAT2 | Ethylbenzene degradation | benzoyl acetyl-CoA thiolase | 23.1 | H16_A3093/H16_A3221/ H16_A3529/H16_A3586/ H16_B0018/H16_B0021/ H16_B0032/H16_B0219/ H16_B1278/H16_B1292/ H16_B1407/H16_B1663/ H16_B1899/H16_B2397/ | unknown/pat/unkno wn/unknown/wbpD/ unknown/unknown/ phnT/unknown/unknown/unknown/unknown/unknown/unkn | Dzaccoa + coa -> Dzocoa + accoa | bzaccoa + coa -> bzocoa + accoa | bzaccoa + coa -> bzocoa + accoa |
| FABC120 | Fatty acid biosynthesis | Fatty acid biosynthesis (dodecanoic acid; c12:0) | 2.3.1.41 AND 2.3.1.179 AND 2.3.1.180 AND 1.1.1.100 2.3.1.41 | | | acACP + 5 malACP + 10 nadph + 25 h -> 10 nadp + c120ACP + 5 co2 + 5 ACP + 5 h2o | acACP + 5 malACP + 10 nadph + 15 h -> 10 nadp + c120ACP + 5 co2 + 5 ACP + 5 h2o | acACP + 5 malACP + 10 nadph + 15 h -> 10 nadp + c120ACP + 5 co2 + 5 ACP + 5 h2o |
| FABC140 | Fatty acid biosynthesis | Fatty acid biosynthesis (tetradecanoic acid; c14:0) | AND 2.3.1.179 AND 2.3.1.180 AND 1.1.1.100 | | | acACP + 6 malACP + 12 nadph + 30 h -> 12 nadp + c140ACP + 6 co2 + 6 ACP + 6 h2o | acACP + 6 malACP + 12 nadph + 18 h -> 12 nadp + c140ACP + 6 co2 + 6 ACP + 6 h2o | acACP + 6 malACP + 12 nadph + 18 h -> 12 nadp + c140ACP + 6 co2 + 6 ACP + 6 h2o |
| FABC141 | Fatty acid biosynthesis | Fatty acid biosynthesis (tetradecanoic acid; c14:1) | 2.3.1.41 AND 2.3.1.179 AND 2.3.1.180 AND 1.1.1.100 2.3.1.41 | | | acACP + 6 malACP + 11 nadph + 28 h -> 11 nadp + c141ACP + 6 co2 + 6 ACP + 6 h2o | acACP + 6 malACP + 11 nadph + 17 h -> 11 nadp + c141ACP + 6 co2 + 6 ACP + 6 h2o | acACP + 6 malACP + 11 nadph + 17 h -> 11 nadp + c141ACP + 6 co2 + 6 ACP + 6 h2o |
| FABC150 | Fatty acid biosynthesis | Fatty acid biosynthesis (pentadecanoic acid; c15:0) | AND 2.3.1.179 AND 2.3.1.180 AND 1.1.1.100 2.3.1.41 | | | ppacp + 6 malACP + 12 nadph + 30 h -> 12 nadp + c150ACP + 6 co2 + 6 ACP + 6 h2o | ppacp + 6 malACP + 12 nadph + 18 h -> 12 nadp + 6 co2 + 6 ACP + 6 h2o + c150ACP | $\label{eq:ppacp} \mbox{ppacp} + 6 \; \mbox{malACP} + 12 \; \mbox{nadp} + c150 \mbox{ACP} + 6 \; \mbox{co} 2 + 6 \; \mbox{ACP} + 6 \; \mbox{h2o}$ |
| FABC151 | Fatty acid biosynthesis | Fatty acid biosynthesis (pentadecanoic acid; c15:1) | AND 2.3.1.179 AND 2.3.1.180 AND 11.1.100 2.3.1.41 | | | ppacp + 6 malACP + 11 nadph + 28 h -> 11 nadp + c151ACP + 6 co2 + 6 ACP + 6 h2o | ppacp + 6 malACP + 11 nadph + 17 h -> 11 nadp + 6 co2 + 6 ACP + 6 h2o + c151ACP | ppacp + 6 malACP + 11 nadph + 17 h -> 11 nadp + c151ACP + 6 co2 + 6 ACP + 6 h2o |
| FABC160 | Fatty acid biosynthesis | Fatty acid biosynthesis (hexadecanoic acid; c16:0) | AND 2.3.1.179 AND 2.3.1.180 AND 1.1.1.100 | | | acACP + 7 malACP + 14 nadph + 36 h -> 14 nadp + c160ACP + 7 co2 + 7 ACP + 7 h2o | acACP + 7 malACP + 14 nadph + 22 h -> 14 nadp + c160ACP + 7 co2 + 7 ACP + 7 h2o | acACP + 7 malACP + 14 nadph + 22 h -> 14 nadp + c160ACP + 7 co2 + 7 ACP + 7 h2o |
| FABC161 | Fatty acid biosynthesis | Fatty acid biosynthesis (hexadecanoic acid; c16:1) | 2.3.1.41 AND 2.3.1.179 AND 2.3.1.180 AND 1.1.1.100 | | | acACP + 7 malACP + 13 nadph + 34 h -> 13 nadp + c161ACP + 7 co2 + 7 ACP + 7 h2o | acACP + 7 malACP + 13 nadph + 21 h -> 13 nadp + c161ACP + 7 co2 + 7 ACP + 7 h2o | acACP + 7 malACP + 13 nadph + 21 h -> 13 nadp + c161ACP + 7 co2 + 7 ACP + 7 h2o |
| FABC170 | Fatty acid biosynthesis | Fatty acid biosynthesis (heptadecanoic acid; c17:0) | 2.3.1.41 AND 2.3.1.179 AND 2.3.1.180 AND 1.1.1.100 2.3.1.41 | | | ppacp + 7 malACP + 14 nadph + 35 h -> 14 nadp + c170ACP + 7 co2 + 7 ACP + 7 h2o | ppacp + 7 malACP + 14 nadph + 21 h -> 14 nadp + 7 co2 + 7 ACP + 7 h2o + c170ACP | ppacp + 7 malACP + 14 nadph + 21 h -> 14 nadp + c170ACP + 7 co2 + 7 ACP + 7 h2o |
| FABC171 | Fatty acid biosynthesis | Fatty acid biosynthesis (heptadecanoic acid; c17:1) | AND 2.3.1.179 AND 2.3.1.180 AND 11.1.100 2.3.1.41 | | | ppacp + 7 malACP + 13 nadph + 33 h -> 13 nadp + c171ACP + 7 co2 + 7 ACP + 7 h2o | ppacp + 7 malACP + 13 nadph + 20 h -> 13 nadp + 7 co2 + 7 ACP + 7 h2o + c171ACP | ppacp + 7 malACP + 13 nadph + 20 h -> 13 nadp + c171ACP + 7 co2 + 7 ACP + 7 h2o |
| FABC180 | Fatty acid biosynthesis | Fatty acid biosynthesis (octadecanoic acid; c18:0) | AND 2.3.1.179 AND 2.3.1.180 AND 1.1.1.100 2.3.1.41 | | | acACP + 8 malACP + 16 nadph + 41 h -> 16 nadp + c180ACP + 8 co2 + 8 ACP + 8 h2o | acACP + 8 malACP + 16 nadph + 25 h -> 16 nadp + c180ACP + 8 co2 + 8 ACP + 8 h2o | acACP + 8 malACP + 16 nadph + 25 h -> 16 nadp + c180ACP + 8 co2 + 8 ACP + 8 h2o |
| FABC181 | Fatty acid biosynthesis | Fatty acid biosynthesis (octadecanoic acid; c18:1) | AND 2.3.1.179 AND 2.3.1.180 AND 11.1.100 2.3.1.41 | | | acACP + 8 malACP + 15 nadph + 39 h -> 15 nadp + c181ACP + 8 co2 + 8 ACP + 8 h2o | acACP + 8 malACP + 15 nadph + 24 h -> 15 nadp + c181ACP + 8 co2 + 8 ACP + 8 h2o | acACP + 8 malACP + 15 nadph + 24 h -> 15 nadp + c181ACP + 8 co2 + 8 ACP + 8 h2o |
| FABC190 | Fatty acid biosynthesis | Fatty acid biosynthesis (nonadecanoic acid; c19:0) | AND 2.3.1.179 AND 2.3.1.180 AND 1.1.1.100 | | | ppacp + 8 malACP + 16 nadph + 40 h -> 16 nadp + c190ACP + 8 co2 + 8 ACP + 8 h2o | ppacp + 8 malACP + 16 nadph + 24 h -> 16 nadp + 8 co2 + 8 ACP + 8 h2o + c190ACP | ppacp + 8 malACP + 16 nadph + 24 h -> 16 nadp + c190ACP + 8 co2 + 8 ACP + 8 h2o |
| ACCOAT | Fatty acid biosynthesis | Acetyl-CoA ACP transacylase | 2.3.1.179/ 2.3.1.180/ 2.3.1.86/2. 3.1.41 2.3.1.179/ | | | ACP + accoa <-> acACP + coa | ACP + accoa <-> acACP + coa | ACP + accoa <-> acACP + coa |
| PPCOAT | Fatty acid biosynthesis | Propionyl-CoA ACP transacylase | 2.3.1.180/ 2.3.1.86/2. | | | ACP + ppcoa <-> ppacp + coa | ACP + ppcoa <-> coa + ppacp | ACP + ppcoa <-> ppacp + coa |
| MALCOAT | Fatty acid | Malonyl-CoA-ACP | 3.1.41 2.3.1.39/2. | (H16_A2568)/(H16_A197 | (fabD)/(unknown) | ACP + malcoa <-> coa + malACP | ACP + malcoa <-> coa + malACP | ACP + malcoa <-> coa + malACP |
| BKACPS1 | Fatty acid biosynthesis | transacylase beta-ketoacyl-ACP synthase | 3.1.86 2.3.1.41/2. 3.1.179/2. 3.1.86/2.3. | 1) | | acACP + h + malACP -> ACP + actACP + co2 | acACP + h + malACP -> ACP + actACP + co2 | acACP + h + malACP -> ACP + actACP + co2 |
| ACCOAC | Fatty acid | acetyl-CoA | 1.41 | H16_A1223&H16_A261 | assA19: | accept the there are the third | accoa + atp + hco3 -> adp + h + malcoa + | access to the character of the contracter of |
| ACCOACB | biosynthesis | carboxylase | 6.4.1.2 | 1 | occutox9CCD | accoa + atp + hco3 -> adp + h + malcoa + pi | pi | accoa + atp + hco3 -> adp + h + malcoa + pi |

| BITCB | Fatty acid biosynthesis | biotin carboxylase | 6.3.4.14 | H16_A0184/H16_A3172/ accC1/accC2/accC3/ H16_A3290/H16_B1757 unknown | accoa + atp + hco3 -> adp + h + malcoa + pi | accoa + atp + hco3 -> adp + h + malcoa + pi | accoa + atp + hco3 -> adp + h + malcoa + pi |
|----------|----------------------------|--|--|---|--|--|---|
| BKACPS2 | Fatty acid biosynthesis | beta-ketoacyl-ACP synthase | 2.3.1.41/2. 3.1.179/2. 3.1.86/2.3. 1.41 | | accoa + h + malACP -> actACP + co2 + coa | accoa + h + malACP -> actACP + co2 + coa | accoa + h + malACP -> actACP + co2 + coa |
| FAMC120 | Fatty acid metabolism | Fatty acid metabolism (dodecanoic acid; c12:0) | 6.2.1.3 AND 1.3.99.3A ND 4.2.1.17A ND 1.1.1.35A ND 6.2.1.3 | | c120 + 6 coa + 5 fad + 5 nad + atp + 5 h2o -> 6 accoa + 5 fadh2 + 5 nadh + amp + ppi + 4 h | | c120 + 6 coa + 5 fad + 5 nad + atp + 5 h2o -> 6 accoa + 5 fadh2 + 5 nadh + amp + ppi + h |
| FAMC140 | Fatty acid metabolism | Fatty acid metabolism (tetradecanoic acid; c14:0) | AND 13.99.3A ND 42.1.17A ND 11.1.35A ND | | c140 + 7 coa + 6 fad + 6 nad + atp + 6 h2o -> 7 accoa + 6 fadh2 + 6 nadh + amp + ppi + 5 h | | c140 + 7 coa + 6 fad + 6 nad + atp + 6 h2o -> 7 accoa + 6 fadh2 + 6 nadh + amp + ppi + h |
| FAMC141 | Fatty acid metabolism | Fatty acid metabolism (tetradecanoic acid; c14:1) | 62.1.3 AND 13.99.3A ND 42.1.17A ND 11.1.35A ND 62.1.3 | | ttdcea + 7 coa + 6 fad + 6 nad + atp + 6 h2o -> 7 accoa + 6 fadh2 + 6 nadh + amp + ppi + 5 h | | ttdcea + 7 coa + 6 fad + 6 nad + atp + 6 h2o -> 7 accoa + 6 fadh2 + 6 nadh + amp + ppi + h |
| FAMC150 | Fatty acid metabolism | Fatty acid metabolism (pentadecanoic acid; c15:0) | AND 13.99.3A ND 42.1.17A ND 1.1.1.35A ND | | c150 + 7 coa + 6 fad + 6 nad + atp + 6 h2o -> 6 accoa + ppcoa + 6 fadh2 + 6 nadh + amp + ppi + 5 h | + ppcoa + 6 fadh2 + 6 nadh + amp + ppi + | |
| FAMC151 | Fatty acid metabolism | Fatty acid metabolism (pentadecanoic acid; c15:1) | ND 1.1.1.35A ND | | c151 + 7 coa + 6 fad + 6 nad + atp + 6 h2o -> 6 accoa + ppcoa + 6 fadh2 + 6 nadh + amp + ppi + 5 h | + ppcoa + 6 fadh2 + 6 nadh + amp + ppi + | |
| FAMC160 | Fatty acid metabolism | Fatty acid metabolism (hexadecanoic acid; c16:0) | 6.2.1.3 AND 1.3.99.3A ND 4.2.1.17A ND 1.1.1.35A ND | | c160 + 8 coa + 7 fad + 7 nad + atp + 7 h2o -> 8 accoa + 7 fadh2 + 7 nadh + amp + ppi + 6 h | | c160 + 8 coa + 7 fad + 7 nad + atp + 7 h2o -> 8 accoa + 7 fadh2 + 7 nadh + amp + ppi + h |
| FAMC161 | Fatty acid metabolism | Fatty acid metabolism (hexadecanoic acid; c16:1) | 6.2.1.3 AND 1.3.99.3A ND 4.2.1.17A ND 1.1.1.35A ND | | c161 + 8 coa + 7 fad + 7 nad + atp + 7 h2o -> 8 accoa + 7 fadh2 + 7 nadh + amp + ppi + 6 h | | c161 + 8 coa + 7 fad + 7 nad + atp + 7 h2o -> 8 accoa + 7 fadh2 + 7 nadh + amp + ppi + h |
| FAMC170 | Fatty acid metabolism | Fatty acid metabolism (heptadecanoic acid; c17:0) | ND 1.1.1.35A ND | | | c170 + 8 coa + 7 fad + 7 nad + atp -> 7 accoa + ppcoa + 7 fadh2 + 7 nadh + amp + ppi + h | |
| FAMC171 | Fatty acid metabolism | Fatty acid metabolism (heptadecanoic acid; c17:1) | ND 1.1.1.35A ND | | c17I + 8 coa + 7 fad + 7 nad + atp + 7 h2o -> 7 accoa + ppcoa + 7 fadh2 + 7 nadh + amp + ppi + 6 h | + ppcoa + 7 fadh2 + 7 nadh + amp + ppi + | |
| FAMC180 | Fatty acid metabolism | Fatty acid metabolism (octadecanoic acid; c18:0) | ND 1.1.1.35A ND | | c180 + 9 coa + 8 fad + 8 nad + atp + 8 h2o -> 9 accoa + 8 fadh2 + 8 nadh + amp + ppi + 7 h | | c180 + 9 coa + 8 fad + 8 nad + atp + 8 h2o -> 9 accoa + 8 fadh2 + 8 nadh + amp + ppi + h |
| FAMC181 | Fatty acid metabolism | Fatty acid metabolism (octadecanoic acid; c18:1) | 6.2.1.3 AND 1.3.99.3A ND 4.2.1.17A ND 1.1.1.35A ND 6.2.1.3 | | c181 + 9 coa + 8 fad + 8 nad + atp + 8 h2o -> 9 accoa + 8 fadh2 + 8 nadh + amp + ppi + 7 h | | c181 + 9 coa + 8 fad + 8 nad + atp + 8 h2o -> 9 accoa + 8 fadh2 + 8 nadh + amp + ppi + h |
| FAMC190 | Fatty acid metabolism | Fatty acid metabolism (nonadecanoic acid; c19:0) | AND 1.3.99.3A ND | | c190 + 9 coa + 8 fad + 8 nad + atp + 8 h2o -> 8 accoa + ppcoa + 8 fadh2 + 8 nadh + amp + ppi + 7 h | | |
| HACOAD1 | Fatty acid metabolism | 3-hydroxyacyl-CoA dehydrogenase (acetoacetyl-CoA) | 1.1.1.35 | H16_A0282/H16_A0602/ paaH1/unknown/paa H16_A1102/H16_A1888/ H2/unknown/unkno H16_B0388/H16_B0724/ wn/unknown/unkno H16_B1652 wn | 3hbcoa + nad -> aacoa + h + nadh | 3hbcoa + nad -> aacoa + h + nadh | 3hbcoa + nad -> aacoa + h + nadh |
| ACOADH1 | Fatty acid metabolism | acyl-CoA dehydrogenase (butanoyl-CoA) | 1.3.99.2 | H16_A0172/H16_B0485/ unknown/unknown/ H16_B0752/H16_B0850/ unknown/unknown/ H16_B1371 unknown/unknown H16_A0170/H16_A0867/ unknown/unknown/ | c040coa + fad <-> ccoa + fadh2 | c040coa + fad + h <-> ccoa + fadh2 | c040coa + fad + h <-> ccoa + fadh2 |
| ACCOAAT1 | Fatty acid metabolism | acetyl-CoA C- acetyltransferase | 23.1.9 | 116_0889/116_08072 unknown/unknown/ H16_A1297/H16_A1839 unknown/phaA/b184 H16_A1459/H6_A1528/ unknown/unknown/ H16_A123/H16_A1528/ unknown/unknown/ H16_A173/H16_A1720/ unknown/unknown/ H16_A1887/H6_A2148/ unknown/unknown/ H16_B080/H16_B0831 unknown/unknown/ H16_B08664 B08622 unknown/unknown/ H16_B06664 B08622 unknown/unknown/ H16_B06684 B08622 unknown/unknown/ H16_B1869/H16_B1771 unknown/ H16_B1869/H16_B1771 unknown/ | 2 accoa <-> aacoa + coa | 2 accoa <-> aacoa + coa | 2 accoa <-> aacoa + coa |

| EN | NCOAH1 | Fatty acid metabolism | enoyl-CoA hydratase | 421.17 | H16_A0100/H16_A0142/ H16_A0179/H16_A0461/ H16_A0464/H16_A0813/ H16_A01864/H16_A0813/ H16_A1101/H16_A1126/ H16_A119/H16_A1126/ H16_A187/H16_A1186/ H16_A1887/H16_A1889/ H16_A2188/H16_A2186/ H16_A2188/H16_A2186/ H16_A2188/H16_A2186/ H16_A2188/H16_A2186/ H16_A2188/H16_A2186/ H16_B0328/H16_B0389/ H16_B0402/H16_B0418/ H16_B0428/H16_B0418/ H16_B0428/H16_B0418/ H16_B0428/H16_B0418/ H16_B0428/H16_B0418/ H16_B0428/H16_B0418/ H16_B0428/H16_B0418/ H16_B0418/H16_B0418/ H16_B148/H16_B1446/ H16_B144/H16_B1446/ H16_B144/H16_B1446/ H16_B144/H16_B1446/ H16_B144/H16_B1446/ H16_B144/H16_B1446/ H16_B144/H16_B1446/ H16_B144/H16_B1446/ H16_B144/H16_B1446/ H16_B144/H16_B1446/ H16_B144/H16_B1446/ H16_B144/H16_B1446/ H16_B144/H16_B1446/ H16_B144/H16_B1456/ H16_B144/H16_B1456/ H16_B144/H16_B1456/ | unknown/unknown/ | 3hbcoa <-> ccoa + h2o | 3hbcoa <-> ccoa + h2o | 3hbcoa <-> ccoa + h2o |
|-----|----------|--|---|------------|---|--|---|---|---|
| 34 | 1DHDHF | Fluorene degradation | 3,4-dihydroxy-3,4- dihydrofluorene dehydrogenase | 1.3.1 | H16_B0731/H16_B0734 | unknown/unknown | c34dhdhf -> 34dhflu + h2 | c34dhdhf -> 34dhflu + h2 | c34dhdhf -> 34dhflu + h2 |
| 34 | 1DHFD | Fluorene degradation | 3,4- | 1.13.11 | H16_A0633/H16_B0223/ H16_B0757/H16_B1109/ H16_B1420/H16_B1836 | nown/unknown/unk | 34dhflu + o2 -> hodhiybe + h | 34dhflu + o2 -> hodhiybe + h | 34dhflu + o2 -> hodhiybe + h |
| 12 | 2DHFD | Fluorene degradation | 1,2- | 1.13.11 | H16_A0633/H16_B0223/ | pcaH2/unknown/unk nown/unknown/unk | 12dhflu + o2 -> hodhiyb2e + h | 12dhflu + o2 -> hodhiyb2e + h | 12dhflu + o2 -> hodhiyb2e + h |
| 2⊦ | HOHPHDB | Fluorene degradation | 2-Hydroxy-6-oxo-6- | 3.7.1.8 | H16_B0600 | | 2hohphd + h2o -> salcyl + op4en + h | 2hohphd + h2o -> salcyl + op4en + h | 2hohphd + h2o -> salcyl + op4en + h |
| 21- | HOHPHODB | Fluorene degradation | 2-Hydroxy-6-oxo-6- | 3.7.1.8 | H16_B0600 | bphD | 2hohphod + h2o -> 2hmuc + catech + h | 2hohphod + h2o -> 2hmuc + catech + h | 2hohphod + h2o -> 2hmuc + catech + h |
| BZ | ZOTD3 | Fluorobenzoate | benzoylhydrolase benzoate 1,2- | 1.14.12.10 | H16_A1961&H16_A196 | benC&benB&benA | 2flrbz + nadh + h + o2 -> 2fchdc + nad | 2firbz + nadh + h + o2 -> 2fchdc + nad | 2firbz + nadh + h + o2 -> 2fchdc + nad |
| | ZOTD4 | | benzoate 1,2- | 1.14.12.10 | H16_A1961&H16_A196 | | 2flrbz + nadh + h + o2 -> 6fchdc + nad | 2flrbz + nadh + h + o2 -> 6fchdc + nad | 2flrbz + nadh + h + o2 -> 6fchdc + nad |
| | ZOTD5 | degradation Fluorobenzoate | benzoate 1,2- | | H16_A1961&H16_A196 | | 3flrbz + nadh + o2 + h -> 3fchdc + nad | 3flrbz + nadh + o2 + h -> 3fchdc + nad | 3flrbz + nadh + o2 + h -> 3fchdc + nad |
| | ZOTD6 | degradation Fluorobenzoate | benzoate 1,2- | 1.14.12.10 | H16_A1961&H16_A196 | | 3flrbz + nadh + o2 + h -> 5fchdc + nad | 3flrbz + nadh + o2 + h -> 5fchdc + nad | 3firbz + nadh + o2 + h -> 5fchdc + nad |
| | | degradation Fluorobenzoate degradation | benzoate 1,2- dioxygenase | 1.14.12.10 | 28H16_A1963 | | 4firbz + nadh + h + o2 -> 4fchdc + nad | 4flrbz + nadh + h + o2 -> 4fchdc + nad | 4firbz + nadh + h + o2 -> 4fchdc + nad |
| 16 | 5DCDC2 | Fluorobenzoate degradation | carboxylate | 1.3.1.25 | H16_A1960 | benD | 3fchdc + nad -> 3flrcatech + nadh + co2 | 3fchdc + nad -> 3ffrcatech + nadh + co2 | 3fchdc + nad -> 3ffrcatech + nadh + co2 |
| 16 | 5DCDC3 | Fluorobenzoate degradation | carboxylate | 1.3.1.25 | H16_A1960 | benD | Sfchdc + nad -> 4flrcatech + nadh + co2 | 5fchdc + nad -> 4flrcatech + nadh + co2 | 5fchdc + nad -> 4flrcatech + nadh + co2 |
| 16 | 5DCDC4 | Fluorobenzoate degradation | dehydrogenase 1,6- dihydroxycyclohexa- 2,4-diene-1- carboxylate | 1.3.1.25 | H16_A1960 | benD | 4fchdc + nad -> 4flrcatech + nadh + co2 | 4fchdc + nad -> 4flrcatech + nadh + co2 | 4fchdc + nad -> 4flrcatech + nadh + co2 |
| CA | ATCHDG6 | Fluorobenzoate degradation | dehydrogenase | 1.13.11.1 | H16_A1964/H16_B0968 | catA/pcpA | 3flrcatech + o2 -> 2flcmuc + 2 h | 3flrcatech + o2 -> 2flcmuc + 2 h | 3flrcatech + o2 -> 2flcmuc + 2 h |
| CA | ATCHDG7 | Fluorobenzoate degradation | catechol 1.2- | 1.13.11.1 | H16_A1964/H16_B0968 | catA/pcpA | 4flrcatech + o2 -> 3flcmuc + 2 h | 4fircatech + o2 -> 3ficmuc + 2 h | 4fircatech + o2 -> 3ficmuc + 2 h |
| FI | .BZDD | Fluorobenzoate | fluorobenzene | 1.3.1 | H16_B0731/H16_B0734 | unknown/unknown | 4fchcd + nad -> 4flrcatech + nadh + h | 4fchcd + nad -> 4flrcatech + nadh + h | 4fchcd + nad -> 4flrcatech + nadh + h |
| | | degradation Fluorobenzoate | dehydrogenase | | | | | | |
| | CCIS5 | degradation Fluorobenzoate | cycloisomerase | 5.5.1.1 | H16_A1966/H16_B0536 H16_A2215/H16_A2739/ | unknown/unknown/ | 3flcmuc + h -> 4fmuclac | 3flcmuc + h -> 4fmuclac | 3flcmuc + h -> 4fmuclac |
| | MBLD6 | degradation Fluorobenzoate | enolidase carboxymethylenebut | 3.1.1.45 | H16_A3488 H16_A2215/H16_A2739/ | unknown | 4fmuclac + h2o -> 2mac + hf + 2 h | 4fmuclac + h2o -> 2mac + hf + 2 h | 4fmuclac + h2o -> 2mac + hf + 2 h |
| | MBLD7 | degradation | haloacetate | | H16_A3488 | unknown | 5fmuclac + h2o -> 2mac + hf + 2 h | 5fmuclac + h2o -> 2mac + hf + 2 h | 5fmuclac + h2o -> 2mac + hf + 2 h |
| HA | ACDH | degradation | dehalogenase | 3.8.1.3 | | | hf + glycolate + h <-> flac + h2o | hf + glycolate + h <-> flac + h2o | hf + glycolate + h <-> flac + h2o |
| FL | | Fluorobenzoate degradation | fluoroacetaldehyde:N AD+ oxidoreductase fluoroacetaldehyde:L- | 1.2.1.69 | | | flac + nadh + 2 h <-> flald + nad + h2o | flac + nadh + 2 h <-> flald + nad + h2o | flac + nadh + 2 h <-> flald + nad + h2o |
| | ALDTHR | Fluorobenzoate degradation | | 2.2.1.8 | | | flald + thr <-> acal + 4flthr | flald + thr <-> acal + 4flthr | flald + thr <-> acal + 4flthr |
| Dł | HFR1 | Folate Biosynthesis | reductase dihydropteroate | 1.5.1.3 | H16_A2704 | folA2 | dhf + 2 h + nadph <-> nadp + thf | dhf + h + nadph <-> nadp + thf | dhf + h + nadph <-> nadp + thf |
| DI | HPS2 | Folate Biosynthesis | synthase | 2.5.1.15 | H16_A2446 | folP | paba + ahhmd -> dhpt + ppi | paba + ahhmd -> dhpt + ppi + h | paba + ahhmd -> dhpt + ppi + h |
| G1 | TPCHI | | GTP cyclohydrolase I | | H16_B1967 | folE | gtp + h2o -> ahdt + formate + h | gtp + h2o -> ahdt + formate + h | gtp + h2o -> ahdt + formate + h |
| | GLUS1 | Folate Biosynthesis | 4-aminohanzoata | | H16_A2610 | folC | atp + dhpt + glu -> adp + dhf + pi | atp + dhpt + glu -> adp + dhf + h + pi | atp + dhpt + glu -> adp + dhf + h + pi |
| AE | BZS | Folate Biosynthesis | synthase 4-amino-4- | 4.1.3.38 | H16_A3087 | unknown | adchor -> paba + h + pyr | adchor -> paba + h + pyr | adchor -> paba + h + pyr |
| ΑĽ | DCMS | Folate Biosynthesis | deoxychorismate synthase | 2.6.1.85 | H16_A3087 | unknown | chor + gln -> adchor + glu | chor + gln -> adchor + glu | chor + gln -> adchor + glu |
| Dł | HNPTA | Folate Biosynthesis | dihydroneopterin aldolase | 4.1.2.25 | H16_A0259 | folB | dhnpt -> ahhmp + glal | dhnpt -> ahhmp + glal | dhnpt -> ahhmp + glal |
| DI | HNMPDP | Folate Biosynthesis | Dihydroneopterin monophosphate dephosphorylase | | H16_A0260/H16_A0711/ H16_A0728/H16_A0917/ H16_A0983/H16_A1118/ H16_A1282/H16_A1904/ H16_A2322/H16_A783/ H16_A2711/H16_A2943/ H16_A3250/H16_A3452/ H16_B0187/H16_B0193/ H16_B0187/H16_B0193/ H16_B0187/H16_B0193/ H16_B0538/H16_B1571/ H16_B1613/H16_B2325/H16_B2575/ | unknown/cpaF1/unk nown/unknown/cpaF 3/unknown/unknow n/prpR/unknown/un known/unknown/mr p/obg/unknown/ur D3/parA2/cpaF2/unk nown/poxR/uvrA2/u nknown/unknown/n | dhpmp + h2o -> dhnpt + pi | dhpmp + h2o -> dhnpt + pi | dhpmp + h2o -> dhnpt + pi |

| DHNTPP | Folate Biosynthesis | Dihydroneopterin triphosphate pyrophosphatase | 3.6.1 | H16. A0260/H16_A0711, H16. A0728/H16_A0917, H16. A09837, H16. A0982/H16. A118, H16. A1282/H16_A1294, H16. A2320/H16_A2683, H16. A3250/H16_A3466, H16. B0187/H16_80169, H16. B0187/H16_B0193/ H16_B1618/H16_B0193/ H16_B1618/H16_B0193/ H16_B1618/H16_B0193/ H16_B1618/H16_B0193/ H16_B1618/H16_B0193/ H16_B1618/H16_B0193/ H16_B1618/H16_B0193/ H16_B1618/H16_B0193/ | unknown/cpaF1/unk nown/unknown/cpaF 3/unknown/unknow n/prpR/unknown/un known/unknown/mr p/obg/unknown/uvr D3/parA2/cpaF2/unk nown/poxR/uvrA2/u nknown/unknown/n orR2/unknown/ | ahdt + h2o -> dhpmp + ppi | ahdt + h2o -> dhpmp + ppi + 2 h | ahdt + h2o -> dhpmp + ppi + 2 h |
|----------|---|---|------------|--|--|---|--|---|
| HMDPPK | Folate Biosynthesis | pyrophosphokinase | 2.7.6.3 | H16_A3082 | folK | ahhmp + atp -> ahhmd + amp | ahhmp + atp -> ahhmd + amp + h | ahhmp + atp -> ahhmd + amp + h |
| 6PYRTP | Folate Biosynthesis | 6-pyruvoyl tetrahydrobiopterin synthase | 4.2.3.12 | H16_A1924 | ptpS | ahdt -> pythp + pppi | ahdt -> pythp + pppi | ahdt -> pythp + pppi + h |
| AKLPP | Folate Biosynthesis | alkaline phosphatase | 3.1.3.1 | H16_A2182/H16_A2183/ H16_B0842 | unknown/unknown/ phoD | ahdt + 3 h2o -> dhnpt + 3 pi | ahdt + 3 h2o -> dhnpt + 3 pi + 3 h | ahdt + 3 h2o -> dhnpt + 3 pi + 2 h |
| DHPS1 | Folate Biosynthesis | dihydropteroate synthase | 2.5.1.15 | H16_A2446 | folP | ahhmp + paba -> dhpt + h2o | ahhmp + paba -> dhpt + h2o | ahhmp + paba -> dhpt + h2o |
| DHFR2 | Folate Biosynthesis | dihydrofolate | 1.5.1.3 | H16_A2704 | folA2 | dhf + nad <-> fl + nadh + h | dhf + nad <-> fl + nadh + h | dhf + nad <-> fl + nadh + h |
| DHFR3 | Folate Biosynthesis | dihydrofolate reductase | 1.5.1.3 | H16_A2704 | folA2 | $fl + nadh + h + h2 \rightarrow thf + nad$ | $fl + nadh + h + h2 \rightarrow thf + nad$ | $fl + nadh + h + h2 \rightarrow thf + nad$ |
| FPGLUS2 | Folate Biosynthesis | folylpolyglutamate synthase | 6.3.2.17 | H16_A2610 | folC | atp + thf + glu <-> adp + pi + thfglu | atp + thf + glu <-> adp + pi + thfglu + h | atp + thf + glu <-> adp + pi + thfglu + h |
| DHFR2p | Folate Biosynthesis | dihydrofolate reductase | 1.5.1.3 | H16_A2704 | folA2 | dhf + nadp <-> fl + nadph + 2 h | dhf + nadp <-> fl + nadph + h | dhf + nadp <-> fl + nadph + h |
| DHFR3p | Folate Biosynthesis | dihydrofolate reductase | 1.5.1.3 | H16_A2704 | folA2 | $fl + nadph + 2 h + h2 \rightarrow thf + nadp$ | $fl + nadph + h + h2 \rightarrow thf + nadp$ | $fl + nadph + h + h2 \rightarrow thf + nadp$ |
| METTHFD | Folate Metabolism | methylenetetrahydrof olate dehydrogenase (NADP) | | H16_A1370 | folD | metthf + nadp <-> h + methf + nadph | metthf + nadp <-> methf + nadph | metthf + nadp <-> methf + nadph |
| FTHFDF | Folate Metabolism | formyltetrahydrofolat e deformylase | 3.5.1.10 | H16_A2505/H16_B1956 | unknown/purU | fthf + h2o -> formate + h + thf | fthf + h2o -> formate + h + thf | fthf + h2o -> formate + h + thf |
| GLYAMT | Folate Metabolism | aminomethyltranefer | 2.1.2.10 | H16_A1567/H16_A3619 | gcvT2/gcvT1 | gly + nad + thf <-> co2 + metthf + nadh + nh4 | gly + nad + thf \leftarrow co2 + metthf + nadh + nh4 | gly + nad + thf <-> co2 + metthf + nadh + nh4 |
| METTHER | Folate Metabolism | olate reductase | 1.5.1.20 | H16_A0246 | unknown | h + metthf + nadh -> mthf + nad | h + metthf + nadh -> mthf + nad | h + metthf + nadh -> mthf + nad |
| | | (NADH) | | H16_A0679/H16_A0893/ | unknown/unknown/ | | | |
| GSDH | Fructose and Mannose metabolism | glucose/sorbosone dehydrogenase | 111 | H16_A1256/H16_A1828/ H16_A2460/H16_A2586/ H16_B0034/H16_B0572/ H16_B0663/H16_B0831/ H16_B1417/H16_B2561 | abmB/unknown/wec C/unknown/unknow n/unknown/unknow | sbt6p + nadp <-> sb1p + nadph + 2 h | sbt6p + nadp <-> sb1p + nadph + h | sbt6p + nadp <-> sb1p + nadph + h |
| HEXf | Fructose and Mannose metabolism | hexokinase (D- fructose:ATP) | 2.7.1.4 | H16_B1503 | frcK | atp + fru -> adp + f6p | atp + fru -> adp + f6p + h | atp + fru -> adp + f6p + h |
| MAN6PI | Fructose and Mannose metabolism | mannose-6- phosphate isomerase | 5.3.1.8 | H16_B1152 | unknown | man6p <-> f6p | man6p <-> f6p | man6p <-> f6p |
| PMANM | Fructose and Mannose metabolism | phosphomannomuta se | 5.4.2.8 | H16_A1847/H16_A2445/ H16_A2885 | manB1/manB3/manB 2 | man1p <-> man6p | man1p <-> man6p | man1p <-> man6p |
| MAN1PGT | Fructose and Mannose metabolism | mannose-1- phosphate guanylyltransferase (GDP) | 2.7.7.22 | H16_A1854/H16_A2905 | manC1/manC2 | gdp + man1p -> gdpmann + pi | gdp + man1p -> gdpmann + pi | gdp + man1p + h -> gdpmann + pi |
| GDPMAND | Fructose and Mannose metabolism | GDP-D-mannose dehydratase | 4.2.1.47 | H16_A2900 | unknown | gdpmann -> gdpddman + h2o | gdpmann -> gdpddman + h2o | gdpmann -> gdpddman + h2o |
| ALRTs | Fructose and Mannose metabolism | aldehyde reductase | 1.1.1.21 | H16_A3186 | unknown | sot + nadp <-> glc + nadph + 2 h | sot + nadp <-> glc + nadph + h | sot + nadp <-> glc + nadph + h |
| FRUP | Fructose and Mannose metabolism | phosphatase | 3.1.3 | H16_A0168/H16_A0520/ H16_B0594/H16_B1063 | | bf2p + h2o <-> fru + pi | bf2p + h2o <-> fru + pi | bf2p + h2o <-> fru + pi |
| F26BP | Fructose and Mannose | fructose-2,6- bisphosphatase | 3.1.3.46 | H16_B0760 | unknown | bf26p + h2o -> f6p + pi | bf26p + h2o -> f6p + pi | bf26p + h2o -> f6p + pi |
| UDPG4E | metabolism Galactose metabolism | UDPglucose 4- epimerase | 5.1.3.2 | H16_B0226/H16_B0283 | galE/unknown | udpg <-> udpgal | udpg <-> udpgal | udpg <-> udpgal |
| GALT1PD | Galactose | Galactitol-1- | 1.1.1.251 | | | qalt1p + nad <-> h + nadh + t6p | galtlp + nad <-> h + nadh + t6p | galt1p + nad <-> h + nadh + t6p |
| | metabolism Galactose | dehydrogenase | | | | glac + nadp + 2 h2o <-> galt + nadph + 2 h + | glac + nadp + 2 h2o <-> galt + nadph + h | |
| ALRTgp | metabolism Galactose | aldehyde reductase | | H16_A3186 | unknown | 02 | + o2 glac + nad + 2 h2o <-> galt + nadh + h + | glac + nadp + 2 h2o <-> galt + nadph + h + o2 |
| ALRTg | metabolism gamma- | aldehyde reductase catechol 1,2- | 1.1.1.21 | H16_A3186 | unknown | glac + nad + 2 h2o <-> galt + nadh + h + o2 | 02 | glac + nad + 2 h2o <-> galt + nadh + h + o2 |
| CATCHDG2 | Hexachlorocyclohe xane degradation gamma- | dioxygenase | 1.13.11.1 | H16_A1964/H16_B0968 | catA/pcpA | tchrocat + o2 -> tchccm + 2 h | tchrocat + o2 -> tchccm + h | tchrocat + o2 -> tchccm + h |
| CMBLD1 | Hexachlorocyclohe xane degradation | carboxymethylenebut enolidase | 3.1.1.45 | H16_A2215/H16_A2739/ H16_A3488 | unknown/unknown/ unknown | dchrocmo + h2o -> dchrooe + h | dchrocmo + h2o -> dchrooe + h | dchrocmo + h2o -> dchrooe + h |
| MACR1 | gamma- Hexachlorocyclohe xane degradation gamma- | maleylacetate reductase | 1.3.1.32 | H16_A1786/H16_B0970 | unknown/pcpE | dchrooe + 2 nadh + h -> coadip + hcl + 2 nad | dchrooe + 2 nadh + h -> coadip + hcl + 2 nad | dchrooe + 2 nadh + h -> coadip + hcl + 2 nad |
| CATOCS | Hexachlorocyclohe xane degradation gamma- | | | | | coadip + h2o -> chac + succ + h | coadip -> chac + succ + h | coadip + h2o -> chac + succ + h |
| HACDHG | Hexachlorocyclohe xane degradation | denalogenase | 3.8.1.3 | H16_A0197 | unknown | chac + h2o -> glycolate + hcl + h | chac + h2o -> glycolate + hcl + h | chac + h2o -> glycolate + hcl + h |
| BPDDO | gamma- Hexachlorocyclohe xane degradation gamma- | dioxygenase | 1.13.11.39 | H16_B0654 | bphC | chcatol + o2 -> chhmsald + h | chcatol + o2 -> chhmsald + h | chcatol + o2 -> chhmsald + h |
| CATCHDG3 | Hexachlorocyclohe xane degradation | catechol 1,2- dioxygenase | 1.13.11.1 | H16_A1964/H16_B0968 | catA/pcpA | chcatol + o2 -> chccm + 2 h | chcatol + o2 -> chccm + 2 h | chcatol + o2 -> chccm + 2 h |
| CMBLD2 | gamma- Hexachlorocyclohe xane degradation | carboxymethylenebut enolidase | 3.1.1.45 | H16_A2215/H16_A2739/ H16_A3488 | unknown/unknown/ unknown | tcmbo + h2o -> 2mac + h | tcmbo + h2o -> 2mac + h | tcmbo + h2o -> 2mac + h |
| UNSMONO | gamma- Hexachlorocyclohe xane degradation | unspecific monooxygenase | 1.14.14.1 | H16_B0939/H16_B1009 | cyp/unknown | parat + h2o -> parax + h2s | parat + h2o -> parax + h2s + h | parat + h2o -> parax + h2s + h |
| 4NPHP1 | gamma- Hexachlorocyclohe xane degradation | 4-nitrophenyl phosphatase | 3.1.3.2 | H16_B1238 | unknown | ntphp + h2o -> pnp + pi | ntphp + h2o -> pnp + pi | ntphp + h2o -> pnp + pi + h |
| 4NPHP2 | gamma- Hexachlorocyclohe xane degradation | 4-nitrophenyl phosphatase | 3.1.3.1 | H16_A2182/H16_A2183 | unknown/unknown | ntphp + h2o -> pnp + pi | ntphp + h2o -> pnp + pi | ntphp + h2o -> pnp + pi + h |
| FBMO8 | gamma- Hexachlorocyclohe xane degradation | flavin-binding monooxygenase | 1.14.13 | H16_A1145/H16_B0495/ H16_B1480/H16_B2135 | | pnp + o2 + nadph + h -> pbzq + no2 + nadp + $h2o$ | pnp + o2 + nadph -> pbzq + no2 + nadp + h2o | pnp + o2 + nadph + h -> pbzq + no2 + nadp + h2o |
| FBMO9 | gamma- Hexachlorocyclohe xane degradation | flavin-binding monooxygenase | 1.14.13 | H16_A1145/H16_B0495/ H16_B1480/H16_B2135 | | hqn + nadph + 2 h + o2 -> thbn + nadp + h2o | $hqn + nadph + h + o2 \rightarrow thbn + nadp + h2o$ | hqn + nadph + h + o2 -> thbn + nadp + h2o |

| PHE2MO4 | gamma- Hexachlorocyclohe | phenol 2- monooxygenase | 1.14.13.7 | H16_B0539&H16_B0540 &H16_B0541&H16_B05 42&H16_B0543&H16_B | poxA&poxB&poxC& | resoc + o2 + nadph + 2 h -> thbn + nadp + h2o | resoc + o2 + nadph + h -> thbn + nadp + h2o | resoc + o2 + nadph + h -> thbn + nadp + h2o |
|---------------|---|--|-----------|---|--|--|---|---|
| 4NOXDR | xane degradation gamma- Hexachlorocyclohe | | 1.14 | 0544 H16_B0730/H16_B0738/ | | nicatol + o2 + 3 h2 -> thbn + no2 + h2o + h | nicatol + o2 + 3 h2 -> thbn + no2 + h2o + | nicatol + o2 + 3 h2 -> thbn + no2 + h2o |
| HIOADI | xane degradation | | 1.14 | H16_B2129 H16_B0355/H16_B0367/ | | TICATO + 02 + 3 112 -> 01011 + 1102 + 1120 + 11 | h | TICATOL + 02 + 3 112 -> 01011 + 1102 + 1120 |
| GERCT | Geraniol degrdation | geranic acid CoA- transferase | 2.8.3 | H16_B0488/H16_B0655/ H16_B0656/H16_B0847/ H16_B0914 H16_A0866/H16_A0871/ H16_A1230/H16_A1519/ H16_A1700/H16_A1718/ | unknown/unknown/ unknown/ unknown/unknown/ unknown/unknown/ | gerana + coa + h -> tgercoa + h2o | gerana + coa + h -> tgercoa + h2o | gerana + coa + h -> tgercoa + h2o |
| CITNCL | Geraniol degrdation | citronellyl-CoA ligase | 6.2.1 | H16_A2252/H16_A2794/ H16_A2807/H16_A2978/ H16_B0174/H16_B0677/ H16_B0910/H16_B1148/ H16_B1264/H16_B1335/ H16_B1662/H16_B1709/ | unknown/unknown/ unknown/unknown/ unknown/unknown/ unknown/unknown/ unknown/unknown/ | citnl + coa + atp + h -> citnlcoa + amp + ppi | citnl + coa + atp -> citnlcoa + amp + ppi + h | citnl + coa + atp -> citnlcoa + amp + ppi + h |
| ACCOAA2 | Geraniol degrdation | acetyl-CoA acyltransferase | 2.3.1.16 | H16_B2522 H16_A0462/H16_A1290/ H16_B0200 | unknown/ unknown/unknown/ pcaF | 7m3o6ocoa + coa -> 5mh4ecoa + accoa | 7m3o6ocoa + coa -> 5mh4ecoa + accoa | 7m3o6ocoa + coa -> 5mh4ecoa + accoa |
| ENCOAR | Geraniol degrdation | enoyl-CoA reductase | 1.3.99 | | unknown/unknown/ | 5mh4ecoa + fad -> 2e5mhdcoa + fadh2 | 5mh4ecoa + fad + h -> 2e5mhdcoa + fadh2 | 5mh4ecoa + fad + h -> 2e5mhdcoa + fadh2 |
| ACCOAA3 | Geraniol degrdation | acetyl-CoA acyltransferase | 2.3.1.16 | H16_B0699 H16_A0462/H16_A1290/ H16_B0200 | unknown/ unknown/unknown/ pcaF | 5m3o4hcoa + coa -> 3mccoa + accoa | 5m3o4hcoa + coa -> 3mccoa + accoa | 5m3o4hcoa + coa -> 3mccoa + accoa |
| SUCSD2 | Glutamate metabolism | succinate- semialdehyde dehydrogenase | 1.2.1.16 | H16_B0982/H16_B1179/ H16_B1537/H16_B2057 | | h2o + nadp + sucsal -> 3 h + nadph + succ | h2o + nadp + sucsal -> 2 h + nadph + succ | h2o + nadp + sucsal -> 2 h + nadph + succ |
| GABAT1 | Glutamate | (NADP) 4-aminobutyrate | 2.6.1.19 | H16_B0981 | gabT | gaba + akg -> glu + sucsal | gaba + akg -> glu + sucsal | gaba + akg -> glu + sucsal |
| | metabolism Glutamate | transaminase carbamoyl- phosphate synthase | | H16_A2106/H16_A2452/ | | 2 atp + gln + h2o + hco3 -> 2 adp + cap + glu | | 2 atp + gln + h2o + hco3 -> 2 adp + cap + glu |
| CABPS | metabolism | (glutamine- hydrolysing) | 6.3.5.5 | H16_A2454 | carB1/carB2/carA | + h + pi | glu + 2 h + pi | + 2 h + pi |
| GLUR | Glutamate metabolism | glutamate racemase | 5.1.1.3 | H16_A2529 | murI | dglu <-> glu | dglu <-> glu | dglu <-> glu |
| GGLUCYSS | Glutamate metabolism | glutamylcysteine synthetase | 6.3.2.2 | H16_A0322 | gshA | atp + cys + glu -> adp + gcys + pi | atp + cys + glu -> adp + gcys + h + pi | atp + cys + glu -> adp + gcys + h + pi |
| GTHRDS | Glutamate metabolism | glutathione synthetase | 6.3.2.3 | H16_A0323 H16_A3430/H16_A3431/ | gshB | atp + gcys + gly -> adp + rgt + pi | atp + gcys + gly -> adp + rgt + h + pi | atp + gcys + gly -> adp + rgt + h + pi |
| GLUS | Glutamate metabolism | glutamate synthase | 1.4.1.13 | H16_B2192/H16_B2193/ H16_B2194 | gltD/gltB1/glxB/glxC /gltB2 | akg + gln + 2 h + nadph -> 2 glu + nadp | akg + gln + h + nadph -> 2 glu + nadp | akg + gln + h + nadph -> 2 glu + nadp |
| GLUDH2 | Glutamate Metabolism | dehydrogenase | 1.4.1.4 | H16_B1945 | gdhA2 | glu + h2o + nadp <-> akg + 2 h + nadph + nh4 | glu + h2o + nadp <-> akg + h + nadph + nh4 | glu + h2o + nadp <-> akg + h + nadph + nh4 |
| GLUDH1 | Glutamate Metabolism Glutamate | glutamate dehydrogenase glutamate | 1.4.1.3 | H16_A0471 | gdhA1 | glu + h2o + nadp <-> akg + 2 h + nadph + nh4 | glu + h2o + nadp <-> akg + h + nadph + nh4 glu + h2o + nad <-> akg + h + nadh + | glu + h2o + nadp <-> akg + h + nadph + nh4 |
| GLUDH3 | Metabolism Glutamate | dehydrogenase | 1.4.1.2 | | gudB | glu + h2o + nad <-> akg + h + nadh + nh4 | nh4 | glu + h2o + nad <-> akg + h + nadh + nh4 |
| GLUN1 | Metabolism Glutamate | glutaminase glutamate | 3.5.1.38 | H16_A1910/H16_A2280 | | gln + h2o -> glu + nh4 | gln + h2o -> glu + nh4 | gln + h2o -> glu + nh4 |
| GLUDCB | Metabolism Glutamate | Decarboxylase | 4.1.1.19 | H16_A2930 H16_A2335/H16_B0618/ | IdcC | glu + h -> gaba + co2 | glu + h -> gaba + co2 | glu + h -> gaba + co2 |
| GLNST1 | metabolism | glutamine synthetase NAD+ synthase | 6.3.1.2 | H16_B2191 | glna/glnA2/glnA3 | atp + glu + nh4 -> adp + gln + pi | atp + glu + nh4 -> adp + gln + h + pi | atp + glu + nh4 -> adp + gln + h + pi |
| NADSG | Glutamate Metabolism | | 6.3.5.1 | H16_A0749 | nadE | atp + dnad + gln + h2o + h -> amp + ppi + nad + glu | atp + dnad + gln + h2o -> amp + ppi + nad + glu + h | $ atp + dnad + gln + h2o -> amp + ppi + nad + \\ glu + h $ |
| GABAT2 | Glutamate Metabolism | 4-aminobutyrate transaminase aspartyl- | 2.6.1.19 | H16_B0981 | gabT | gaba + akg <-> glu + sucsal | gaba + akg <-> glu + sucsal | gaba + akg <-> glu + sucsal |
| GTADT1 | Glutamate metabolism | +PNA(Acn)/alutamul- | 6.3.5.7 | H16_A0108&H16_A011 1&H16_A0112&H16_A1 509&H16_A1882 | gatB&gatA1&gatC& gatA3&unknown | glutrna + gln + atp + $h2o \rightarrow glntrna + glu + pi$ + adp | glutrna + gln + atp + h2o -> glntrna + glu + pi + adp + h | glutrna + gln + atp + $h2o \rightarrow glntrna + glu + pi$ + $adp + h$ |
| MAAMPT | Glutathione Metabolism Glutathione | aminopeptidase | 3.4.11.2 | H16_A1000 | pepN | h2o + progly -> gly + pro | h2o + progly -> gly + pro atp + rot + sprmd -> adp + gtspmd + h + | h2o + progly -> gly + pro |
| GTSPMDS | Metabolism | ne synthetase | 6.3.1.8 | H16_A0042 | unknown | atp + rgt + sprmd -> adp + gtspmd + pi | atp + rgt + sprma -> aap + gtspma + n + pi | atp + rgt + sprmd -> adp + gtspmd + h + pi |
| GTHHR | Glutathione Metabolism | glutathione hydralase | 2.3.2.2 | H16_A0784/H16_A1098/ H16_A2780/H16_B0984 | | rgt + h2o -> cysgly + glu | rgt + h2o -> cysgly + glu | rgt + h2o -> cysgly + glu + h |
| ALAAPT | Glutathione Metabolism | alanyl aminopeptidase | 3.4.11.2 | H16_A1000 | pepN | cysgly + h2o -> cys + gly | cysgly + h2o -> cys + gly | cysgly + h2o + h -> cys + gly |
| GTTPX | Glutathione metabolism | glutathione peroxidase alcohol | 1.11.1.9 | H16_A0065 | unknown | h2o2 + 2 rgt <-> ogt + 2 h2o | h2o2 + 2 rgt <-> ogt + 2 h2o | h2o2 + 2 rgt <-> ogt + 2 h2o + 2 h |
| ALCDgl | Glycerolipid Metabolism | dehydrogenase (glycerol) | 1.1.1.21 | H16_A3186/H16_B2162 | unknown/unknown | t3 + h + nadh <-> gl + nad | t3 + h + nadh <-> gl + nad | t3 + h + nadh <-> gl + nad |
| GLYCK | Glycerolipid Metabolism | glycerol kinase | 2.7.1.30 | | | atp + gl -> adp + glyc3p | atp + gl -> adp + glyc3p + h | atp + gl -> adp + glyc3p + h |
| ALHD2 | Glycerolipid Metabolism | aldehyde dehydrogenase (NAD+) | 1.2.1.3 | H16_A0232/H16_A0745/ H16_A1114/H16_A1495/ H16_B0212/H16_B0421/ H16_B0737/H16_B0833/ H16_B1534/H16_B1735/ H16_B1751/H16_B1835/ H16_B1960/H16_B2444 | unknown/unknown/ unknown/unknown/ unknown/unknown/ unknown/unknown/ unknown/unknown/ | t3 + nad + h2o <-> glyc-R + nadh + 2 h | t3 + nad + h2o <-> glyc-R + nadh + 2 h | t3 + nad + h2o <-> glyc-R + nadh + 2 h |
| TAGL1 | Glycerolipid Metabolism | triacylglycerol lipase | 3.1.1.3 | H16_A1322 | unknown | | 0.007 c150 + 0.254 c160 + 0.175 c161 + 0.006 c170 + 0.007 c171 + 0.013 c180 + 0.112 c181 | dgr + h2o -> agl + 0.007 c120 + 0.419 c140 + 0.007 c150 + 0.254 c160 + 0.175 c161 + 0.006 c170 + 0.007 c171 + 0.013 c180 + 0.112 c181 dgr + h2o -> agl + 0.002 c120 + 0.414 c140 + |
| TAGL1_Nlimit | Glycerolipid Metabolism | triacylglycerol lipase | 3.1.1.3 | H16_A1322 | unknown | 0.001 c141 + 0.028 c150 + 0.01 c151 + 0.255 c160 + 0.06 c161 + 0.105 c170 + 0.008 c180 + 0.105 c181 + 0.012 c190 | 0.001 c141 + 0.028 c150 + 0.01 c151 + 0.255 c160 + 0.06 c161 + 0.105 c170 + 0.008 c180 + 0.105 c181 + 0.012 c190 | 0.001 c141 + 0.028 c150 + 0.01 c151 + 0.255 c160 + 0.06 c161 + 0.105 c170 + 0.008 c180 + 0.105 c181 + 0.012 c190 |
| TAGL2 | Glycerolipid Metabolism | triacylglycerol lipase | 3.1.1.3 | H16_A1322 | unknown | tgl + h2o -> 0.007 c120 + 0.419 c140 + 0.007 c150 + 0.254 c160 + 0.175 c161 + 0.006 c170 + 0.007 c171 + 0.013 c180 + 0.112 c181 tgl + h2o -> 0.002 c120 + 0.414 c140 + 0.001 | tgl + h2o -> 0.007 c120 + 0.419 c140 + 0.007 c150 + 0.254 c160 + 0.175 c161 + 0.006 c170 + 0.007 c171 + 0.013 c180 + 0.112 c181 tgl + h2o -> 0.002 c120 + 0.414 c140 + 0.001 | tgl + h2o -> 0.007 c120 + 0.419 c140 + 0.007 c150 + 0.254 c160 + 0.175 c161 + 0.006 c170 + 0.007 c171 + 0.013 c180 + 0.112 c181 tgl + h2o -> 0.002 c120 + 0.414 c140 + 0.001 |
| TAGL2_Nlimit | Glycerolipid Metabolism | triacylglycerol lipase | 3.1.1.3 | H16_A1322 | unknown | c141 + 0.028 c150 + 0.01 c151 + 0.255 c160 + | c141 + 0.028 c150 + 0.01 c151 + 0.255 c160 + 0.06 c161 + 0.105 c170 + 0.008 c180 + 0.105 c181 + 0.012 c190 | c141 + 0.028 c150 + 0.01 c151 + 0.255 c160 + 0.06 c161 + 0.105 c170 + 0.008 c180 + 0.105 c181 + 0.012 c190 |
| ALCDglp | Glycerolipid Metabolism | (glycerol) | 1.1.1.21 | H16_A3186/H16_B2162 | unknown/unknown | t3 + 2 h + nadph <-> gl + nadp | t3 + h + nadph <-> gl + nadp | t3 + h + nadph <-> gl + nadp |
| GL3PDp | Glycerophospholipi d Metabolism | glycerol-3-phosphate dehydrogenase (NADP) | 1.1.1.94 | H16_A0336 | gpsA | glyc3p + nadp <-> dhap + 2 h + nadph | glyc3p + nadp <-> dhap + h + nadph | glyc3p + nadp <-> dhap + h + nadph |
| ETHAML | Glycerophospholipi d Metabolism | Ethanolamine ammonia-lyase | 4.3.1.7 | H16_B0096 | eutB | etha -> acal + nh4 | etha -> acal + nh4 | etha -> acal + nh4 |
| G3POAT | Glycerophospholipi d Metabolism | glycerol-3-phosphate O-acyltransferase | 23.1.15 | | | glyc3p + 0.007 c120ACP + 0.419 c140ACP + 0.007 c150ACP + 0.254 c160ACP + 0.175 c161ACP + 0.006 c170ACP + 0.007 c171ACP + 0.013 c180ACP + 0.112 c181ACP -> agl3p + ACP | glyc3p + 0.007 c120ACP + 0.419 c140ACP + 0.007 c150ACP + 0.254 c160ACP + 0.175 c161ACP + 0.013 c180ACP + 0.112 c181ACP + 0.006 c170ACP + 0.007 c171ACP -> agl3p + ACP | glyc3p + 0.007 c120ACP + 0.419 c140ACP + 0.007 c150ACP + 0.254 c160ACP + 0.175 c161ACP + 0.006 c170ACP + 0.007 c171ACP + 0.013 c180ACP + 0.112 c181ACP -> agl3p + ACP |
| G3POAT_Nlimit | Glycerophospholipi d Metabolism | glycerol-3-phosphate O-acyltransferase | 23.1.15 | | | glyc3p + 0.002 c120ACP + 0.414 c140ACP + 0.001 c141ACP + 0.008 c150ACP + 0.01 c151ACP + 0.255 c160ACP + 0.06 c140ACP + 0.05 c170ACP + 0.008 c180ACP + 0.105 c181ACP + 0.002 c190ACP -> agl3p + ACP | glyc3p + 0.002 c120ACP + 0.414 c140ACP + | glyc3p + 0.002 c120ACP + 0.414 c140ACP + 0.001 c141ACP + 0.002 c150ACP + 0.01 c151ACP + 0.255 c160ACP + 0.06 c161ACP + 0.105 c170ACP + 0.006 c180ACP + 0.105 c181ACP + 0.012 c190ACP -> ag/3p + ACP |

| AG3POAT | Glycerophospholipi d Metabolism | acyltransferase | 2.3.1.51 | H16_A0519/ H16_A2911 | plsC1/plsC2 | 0.006 c170ACP + 0.007 c171ACP + 0.013 c180ACP + 0.112 c181ACP -> pa + ACP agl3p + 0.002 c120ACP + 0.414 c140ACP + 0.001 | 0.007 c150ACP + 0.254 c160ACP + 0.175 c161ACP + 0.013 c180ACP + 0.112 c181ACP + 0.006 c170ACP + 0.007 c171ACP -> pa + ACP agl3p + 0.002 c120ACP + 0.414 c140ACP + 0.001 | agl3p + 0.007 c120ACP + 0.419 c140ACP + 0.007 c150ACP + 0.254 c160ACP + 0.175 c161ACP + 0.006 c170ACP + 0.007 c171ACP + 0.013 c180ACP + 0.112 c181ACP - 9.0 a + ACP agl3p + 0.002 c120ACP + 0.414 c140ACP + 0.001 |
|----------------------|---|---|-----------|---|-------------------------------|---|--|---|
| AG3POAT_Nlin | d Metabolism | acyltransferase | 2.3.1.51 | H16_A0519/ H16_A2911 | plsC1/plsC2 | c141ACP + 0.028 c150ACP + 0.01 c151ACP + 0.255 c160ACP + 0.06 c161ACP + 0.105 c170ACP + 0.008 c180ACP + 0.105 c181ACP + 0.012 c190ACP -> pa + ACP | c141ACP + 0.028 c150ACP + 0.01 c151ACP + 0.255 c160ACP + 0.06 c161ACP + 0.105 c170ACP + 0.008 c180ACP + 0.105 c181ACP + 0.012 c190ACP -> pa + ACP | c141ACP + 0.028 c150ACP + 0.01 c151ACP + 0.255 c160ACP + 0.06 c161ACP + 0.105 c170ACP + 0.008 c180ACP + 0.105 c181ACP + 0.012 c190ACP -> pa + ACP |
| DGRK | Glycerophospholipi d Metabolism | diacyigiyceror kiriase | 2.7.1.107 | H16_A1027 | dgkA | dgr + atp -> adp + pa | dgr + atp -> adp + pa | dgr + atp -> adp + pa |
| PPTCT | Glycerophospholipi d Metabolism Glycerophospholipi | cytidylyltransferase i Phosphatidylglycerol | 2.7.7.41 | H16_A2088 | unknown | pa + ctp -> cdpdg + ppi | pa + ctp -> cdpdg + ppi | pa + ctp -> cdpdg + ppi |
| PPGS | d Metabolism | synthase i Phosphatidylserine | 2.7.8.5 | H16_A2546 | unknown | cdpdg + glyc3p -> cmp + pgp | cdpdg + glyc3p -> cmp + pgp | cdpdg + glyc3p -> cmp + pgp |
| PPSERS | d Metabolism | syntase | 2.7.8.8 | H16_A1039 | pssA | cdpdg + ser -> cmp + ps pc -> 2ag3pc + 0.007 c120 + 0.419 c140 + 0.007 | cdpdg + ser -> cmp + ps pc -> 2ag3pc + 0.007 c120 + 0.419 c140 + | cdpdg + ser -> cmp + ps pc -> 2ag3pc + 0.007 c120 + 0.419 c140 + 0.007 |
| PLIPASA1C | Glycerophospholipi d Metabolism | i Phospholipase A1 (phosphatidylcholine) | 3.1.1.32 | H16_A1139 | unknown | c150 + 0.254 c160 + 0.175 c161 + 0.006 c170 + 0.007 c171 + 0.013 c180 + 0.112 c181 | 0.007 c150 + 0.254 c160 + 0.175 c161 + 0.006 c170 + 0.007 c171 + 0.013 c180 + 0.112 c181 | 0.007 c171 + 0.013 c180 + 0.012 c181 1 pc -> 2ag3pc + 0.002 c120 + 0.414 c140 + 0.001 |
| PLIPASA1C_NIi mit | Glycerophospholipi d Metabolism | i Phospholipase A1 (phosphatidylcholine) | 3.1.1.32 | H16_A1139 | unknown | c141 + 0.028 c150 + 0.01 c151 + 0.255 c160 + 0.06 c161 + 0.105 c170 + 0.008 c180 + 0.105 c181 + 0.012 c190 | c141 + 0.028 c150 + 0.01 c151 + 0.255 c160 + 0.06 c161 + 0.105 c170 + 0.008 c180 + 0.105 c181 + 0.012 c190 | c141 + 0.028 c150 + 0.01 c151 + 0.255 c160 + 0.06 c161 + 0.105 c170 + 0.008 c180 + 0.105 c181 + 0.012 c190 |
| PLIPASA1S | Glycerophospholipi d Metabolism | i Phospholipase A1 (Phosphatidylserine) | 3.1.1.32 | H16_A1139 | unknown | 0.007 c171 + 0.013 c180 + 0.112 c181 | 0.007 c150 + 0.254 c160 + 0.175 c161 + 0.006 c170 + 0.007 c171 + 0.013 c180 + 0.112 c181 | ps -> 2ag3ps + 0.007 c120 + 0.419 c140 + 0.007 c150 + 0.254 c160 + 0.175 c161 + 0.006 c170 + 0.007 c171 + 0.013 c180 + 0.112 c181 ps -> 2ag3ps + 0.002 c120 + 0.414 c140 + 0.001 |
| PLIPASA1S_NIi mit | Glycerophospholipi d Metabolism | (Phosphatidylserine) | 3.1.1.32 | H16_A1139 | unknown | 0.06 c161 + 0.105 c170 + 0.008 c180 + 0.105 c181 + 0.012 c190 | c141 + 0.028 c150 + 0.01 c151 + 0.255 c160 + 0.06 c161 + 0.105 c170 + 0.008 c180 + 0.105 c181 + 0.012 c190 | c141 + 0.028 c150 + 0.01 c151 + 0.255 c160 + 0.06 c161 + 0.105 c170 + 0.008 c180 + 0.105 c181 + 0.012 c190 |
| PLIPASA1E | Glycerophospholipi d Metabolism | (pnospnatidyletnanoi amine) | 3.1.1.32 | H16_A1139 | unknown | pe -> 2ag3pe + 0.007 c120 + 0.419 c140 + 0.007 c150 + 0.254 c160 + 0.175 c161 + 0.006 c170 + 0.007 c171 + 0.013 c180 + 0.112 c181 pe -> 2ag3pe + 0.002 c120 + 0.414 c140 + | | pe -> 2ag3pe + 0.007 c120 + 0.419 c140 + 0.007 c150 + 0.254 c160 + 0.175 c161 + 0.006 c170 + 0.007 c171 + 0.013 c180 + 0.112 c181 pe -> 2ag3pe + 0.002 c120 + 0.414 c140 + |
| PLIPASA1E_Nli mit | Glycerophospholipi d Metabolism | (phosphatidylethanol amine) | 3.1.1.32 | H16_A1139 | unknown | 0.001 c141 + 0.028 c150 + 0.01 c151 + 0.255 | 0.001 c141 + 0.028 c150 + 0.01 c151 + 0.255 c160 + 0.06 c161 + 0.105 c170 + 0.008 c180 + 0.105 c181 + 0.012 c190 | 0.001 c141 + 0.028 c150 + 0.01 c151 + 0.255 c160 + 0.06 c161 + 0.105 c170 + 0.008 c180 + 0.105 c181 + 0.012 c190 |
| PGRPP | Glycerophospholipi d Metabolism | phosphatase phosphatase | 3.1.3.27 | H16_A3155 | рдрА | pgp + h2o -> pg + pi | pgp + h2o -> pg + pi | pgp + h2o -> pg + pi |
| GPPDPD1 | Glycerophospholipi d Metabolism | Glycerophosphodiest i er phosphodiesterase (Glycerophosphochol ine) | | H16_A0499/H16_A2326 | gdpD/ugpQ | g3pc + h2o -> choline + glyc3p | g3pc + h2o -> choline + glyc3p + h | g3pc + h2o -> choline + glyc3p + h |
| GPPDPD2 | Glycerophospholipi d Metabolism | Glycerophosphodiest i er phosphodiesterase (Glycerophosphoetha nolamine) | | H16_A0499/H16_A2326 | gdpD/ugpQ | g3pe + h2o -> etha + glyc3p | g3pe + h2o -> etha + glyc3p + h | g3pe + h2o -> etha + glyc3p + h |
| GPPDPD3 | Glycerophospholipi d Metabolism | Glycerophosphodiest i er phosphodiesterase (Glycerophosphoseri ne) | 3.1.4.46 | H16_A0499/H16_A2326 | gdpD/ugpQ | g3ps + h2o -> glyc3p + ser | g3ps + h2o -> glyc3p + ser + h | g3ps + h2o -> glyc3p + ser + h |
| GPPDPD4 | Glycerophospholipi d Metabolism | Glycerophosphodiest i er phosphodiesterase (Glycerophosphoglyc erol) | 31.4.46 | H16_A0499/H16_A2326 | gdpD/ugpQ | g3pg + h2o -> gl + glyc3p | g3pg + h2o -> gl + glyc3p + h | g3pg + h2o -> gl + glyc3p + h |
| GPPDPD5 | Glycerophospholipi d Metabolism | Glycerophosphodiest i er phosphodiesterase (Glycerophosphoinos itol) | | H16_A0499/H16_A2326 | gdpD/ugpQ | g3pi + h2o -> glyc3p + mi | g3pi + h2o -> glyc3p + mi + h | g3pi + h2o -> glyc3p + mi + h |
| CDPDGP | Glycerophospholipi d Metabolism | i CDP-diacylglycerol pyrophosphatase | 3.6.1.26 | H16_B2144 | unknown | cdpdg + h2o -> pa + cmp | cdpdg + h2o -> pa + cmp | cdpdg + h2o -> pa + cmp |
| PSERD | | Phoenhatidulcarina | 4.1.1.65 | H16_A1038 | psd | ps -> pe + co2 | ps -> pe + co2 | ps -> pe + co2 |
| CLPNS1 | Glycerophospholipi d Metabolism | | 2.7.8 | H16_A0458/H16_B1255 | unknown/unknown | 2 pg <-> clpn + gl | 2 pg <-> clpn + gl | 2 pg <-> clpn + gl |
| PPLDc | Glycerophospholipi d Metabolism | phospholipase D | 3.1.4.4 | H16_B0932/H16_B1107 | unknown/unknown | pc + h2o -> pa + choline | pc + h2o -> pa + choline | pc + h2o -> pa + choline |
| PPLDe | Glycerophospholipi d Metabolism | i phospholipase D | 3.1.4.4 | H16_B0932/H16_B1107 | unknown/unknown | pe + h2o -> pa + etha | pe + h2o -> pa + etha | pe + h2o -> pa + etha |
| PPLCc | Glycerophospholipi d Metabolism | i phospholipase C | 3.1.4.3 | H16_A2724/H16_B0534/ H16_B1067/H16_B1166 | | pc + h2o -> dgr + cholp | pc + h2o -> dgr + cholp | pc + h2o -> dgr + cholp |
| PPLCe | Glycerophospholipi d Metabolism | phospholipase C | 3.1.4.3 | H16_A2724/H16_B0534/ H16_B1067/H16_B1166 | plcN1/plcN2/plcN3/ | pe + h2o -> dgr + ethap | pe + h2o -> dgr + ethap | pe + h2o -> dgr + ethap |
| PPLCg | Glycerophospholipi d Metabolism | phospholipase C | 3.1.4.3 | H16_A2724/H16_B0534/ | plcN1/plcN2/plcN3/ | pg + h2o -> dgr + glyc3p | pg + h2o -> dgr + glyc3p | pg + h2o -> dgr + glyc3p |
| CLPNS2 | Glycerophospholipi | cardiolipin synthase | 2.7.8 | H16_B1067/H16_B1166 H16_A0458/H16_B1255 | | pg + cdpdg -> clpn + cmp | pg + cdpdg -> clpn + cmp | pg + cdpdg -> clpn + cmp |
| ETNP | | i ethanolaminenhornh | 2.7.8.1 | | | pe + cmp <-> cdpetn + dgr | pe + cmp <-> cdpetn + dgr | pe + cmp <-> cdpetn + dgr |
| | d metabolism | alveral-3-phosphate | | | | | | |
| GL3PD | Glycerophospholipi d Metabolism Glycine, Serine and | dehydrogenase (NADP) | 1.1.1.94 | H16_A0336 | gpsA | glyc3p + nad <-> dhap + h + nadh | glyc3p + nad <-> dhap + h + nadh | glyc3p + nad <-> dhap + h + nadh |
| HPYRR | threonine Metabolism Glycine, Serine and | reductase (NADH) | 1.1.1.29 | H16_B0611 | hprA | h + hpyr + nadh -> glyc-R + nad | h + hpyr + nadh -> glyc-R + nad | h + hpyr + nadh -> glyc-R + nad |
| HPYRRp | threonine Metabolism Glycine, Serine and | reductase (NADPH) | 1.1.1.81 | H16_A2132/H16_A3601 | ttuD2/ttuD1 | 2 h + hpyr + nadph -> glyc-R + nadp | h + hpyr + nadph -> glyc-R + nadp | h + hpyr + nadph -> glyc-R + nadp |
| THRDH | threonine Metabolism Glycine, Serine and | denydrogenase | 1.1.1.103 | H16_A1934 H16_A0185/H16_A3712 | tdh unknown/serA1/serA | nad + thr -> 2aobut + h + nadh | nad + thr -> 2aobut + h + nadh | nad + thr -> 2aobut + 2 h + nadh |
| PGLCED | threonine Metabolism Glycine, Serine and | phosphoglycerate dehydrogenase | 1.1.1.95 | H16_B0347/H16_B0466/ H16_B0824/H16_B0841/ H16_B1819 | 2/serA3/serA4/serA5 /serA6 | 3pg + nad -> 3php + h + nadh | 3pg + nad -> 3php + h + nadh | 3pg + nad -> 3php + h + nadh |
| GLYHMT | threonine Metabolism Glycine, Serine and | hydroxymethyltransfe rase | 2.1.2.1 | H16_A2834 | glyA | ser + thf <-> gly + h2o + metthf | ser + thf <-> gly + h2o + metthf | ser + thf <-> gly + h2o + metthf |
| GLYCAT | threonine Metabolism Glycine, Serine and | acetyltransferase | 2.3.1.29 | H16_B0819 | kbl | accoa + gly <-> 2aobut + coa | accoa + gly <-> 2aobut + coa | accoa + gly <-> 2aobut + coa + h |
| PSERT | threonine Metabolism Glycine, Serine and | transaminase | 2.6.1.52 | H16_A0791 | serC | 3php + glu -> akg + pser | 3php + glu -> akg + pser | 3php + glu -> akg + pser |
| GLYCEK2 | threonine Metabolism Glycine, Serine and | glycerate kinase | 2.7.1.31 | H16_B0612 | glxK | atp + glyc-R -> 2pg + adp | atp + glyc-R -> 2pg + adp + h | atp + glyc-R -> 2pg + adp + h |
| PSERP | threonine Metabolism | phosphatase (L- serine) | 3.1.3.3 | H16_A1452/H16_A3080, H16_B1164 | serB1/serB2/serB3 | h2o + pser -> pi + ser | h2o + pser -> pi + ser | h2o + pser -> pi + ser |
| SERD | Glycine, Serine and threonine Metabolism | L-serine deaminase | 4.3.1.17 | H16_A3622 | sdaA | ser -> nh4 + pyr | ser -> nh4 + pyr | ser -> nh4 + pyr |
| MNAO1 | Glycine, Serine and threonine Metabolism | monoamine oxidase | 1.4.3.4 | H16_A0831 | maoB | aact + h2o + o2 -> h2o2 + mtg + nh4 | aact + h2o + o2 -> h2o2 + mtg + nh4 | aact + h2o + o2 + h -> h2o2 + mtg + nh4 |

| ALDRm | Glycine, Serine and threonine Metabolism | aldose reductase (methylglyoxal) | 1.1.1 | H16_A0679/H16_A0893/ H16_A1256/H16_A1828/ H16_A2460/H16_A2586/ H16_B0034/H16_B0572/ H16_B0663/H16_B0831/ H16_B1417/H16_B2561 | unknown/unknown/ abmB/unknown/wec C/unknown/unknow n/unknown/unknow | 2 h + mtg + nadph -> acetol + nadp | h + mtg + nadph -> acetol + nadp | h + mtg + nadph -> acetol + nadp |
|----------|--|--|-----------------------|---|--|--|--|--|
| HSERD | Glycine, Serine and Threonine Metabolism | homoserine dehydrogenase (NADPH) | 1.1.1.3 | H16_A2266 | thrA | hser + nadp <-> aspsa + 2 h + nadph | hser + nadp <-> aspsa + h + nadph | hser + nadp <-> aspsa + h + nadph |
| ASPSAD | Glycine, Serine and Threonine Metabolism | l aspartate- semialdehyde dehydrogenase | 1.2.1.11 | H16_A2618 | asd | aspsa + nadp + pi <-> basp + 3 h + nadph | aspsa + nadp + pi <-> basp + h + nadph | aspsa + nadp + pi <-> basp + h + nadph |
| HSERK | Glycine, Serine and Threonine Metabolism | | 2.7.1.39 | H16_A2744/H16_A3212/ H16_A3213/H16_A3222 | | atp + hser -> adp + phser | atp + hser -> adp + phser + h | atp + hser -> adp + phser + h |
| ASPK | Glycine, Serine and Threonine Metabolism | aspartate kinase | 2.7.2.4 | H16_A1225 | lysC | asp + atp <-> basp + adp | asp + atp <-> basp + adp | asp + atp <-> basp + adp |
| THRAD2 | Glycine, Serine and Threonine Metabolism | L-allo-threonine aldolase | 4.1.2.5 | H16_A2762 | ItaA | athr -> acal + gly | athr -> acal + gly | athr -> acal + gly |
| THRAD1 | Glycine, Serine and Threonine Metabolism | threonine aldolase | 4.1.2.5 | H16_A2762 | ItaA | thr -> acal + gly | thr -> acal + gly | thr -> acal + gly |
| THRS | Glycine, Serine and Threonine Metabolism | threonine synthase | 4.2.3.1 | H16_A2265/H16_B0301 | thrC/unknown | h2o + phser -> pi + thr | h2o + phser -> pi + thr | h2o + phser -> pi + thr |
| AOBUTDO | Glycine, Serine and | L-2-amino-3- oxobutanoate decarboxylation (spontaneous) | | unknown | unknown | 2aobut + h -> aact + co2 | 2aobut + h -> aact + co2 | 2aobut + h -> aact + co2 |
| BETALDDH | Glycine, Serine and 1 Threonine Metabolism | | 1.2.1.8 | H16_B2130 | betB | bal + h2o + nad -> glyb + 2 h + nadh | bal + h2o + nad -> glyb + 2 h + nadh | bal + h2o + nad -> glyb + 2 h + nadh |
| BETALDDH | Glycine, Serine and Threonine | betaine-aldehyde dehydrogenase | 1.2.1.8 | H16_B2130 | betB | bal + h2o + nadp -> glyb + 3 h + nadph | bal + h2o + nadp -> glyb + 2 h + nadph | bal + h2o + nadp -> glyb + 2 h + nadph |
| SERDHT1 | Metabolism Glycine, Serine and Threonine | | 4.3.1.19 | H16_A0427/H16_B0554 | unknown/tdcB | ser -> nh4 + pyr | ser -> nh4 + pyr | ser -> nh4 + pyr |
| THRD_L | Metabolism Glycine, Serine and Threonine | threonine dehydratase | 4.3.1.19 | H16_A0427/H16_B0554 | unknown/tdcB | thr -> obut + nh4 | thr -> obut + nh4 | thr -> obut + nh4 |
| GLYD | Metabolism Glycine, Serine and Threonine | glycine | 1.4.4.2 | H16_A3621 | gcvP | gly + lipop -> sap + co2 | gly + lipop -> sap + co2 | gly + lipop -> sap + co2 |
| AMTF1 | Metabolism Glycine, Serine and Threonine | aminomethyltransfer | 2.1.2.10 | H16_A3619 | gcvT1 | sap + thf + h -> dlipop + metthf + nh4 | sap + thf + h -> dlipop + metthf + nh4 | sap + thf + h -> dlipop + metthf + nh4 |
| DLPD | Metabolism Glycine, Serine and Threonine | dihydrolipoamide | 1.8.1.4 | H16_A1377/H16_A2323/ | pdhL/odhL/lpdaA/un | | dlipop + nad -> lipop + nadh + h | dlipop + nad -> lipop + nadh + h |
| CHOLD1 | Metabolism Glycine, Serine and Threonine | dehydrogenase choline | | H16_A3724/H16_B1098 H16_A0233/H16_A1655/ H16_A3663/H16_A3737/ | | | choline + fad + h -> bal + fadh2 | choline + fad + h -> bal + fadh2 |
| | Metabolism Glycine, Serine and | dehydrogenase choline | | H16_B2131 H16_A0233/H16_A1655/ | host 2 (host 4.2 (host 4.4) | | | |
| CHOLD2 | Threonine Metabolism Glycine, Serine and | | 1.1.99.1 | H16_A3663/H16_A3737/ H16_B2131 | unknown/betA1 | bal + fad + h2o -> fadh2 + glyb + h | bal + fad + h2o -> fadh2 + glyb | bal + fad + h2o -> fadh2 + glyb |
| BETHM | Threonine Metabolism Glycine, Serine and | homocysteine S- methyltransferase I diaminobutyrate-2- | 2.1.1.5 | H16_A0150 | bhmT | glyb + hcys -> dimgly + met | glyb + hcys -> dimgly + met | glyb + hcys -> dimgly + met |
| DABOT | Threonine Metabolism Glycolysis/Glucone | oxoglutarate transaminase | 2.6.1.76 | H16_B1692 | unknown | glu + aspsa -> akg + 24dab | glu + aspsa -> akg + 24dab | glu + aspsa -> akg + 24dab |
| PGLCM | ogenesis Glycolysis/Glucone ogenesis | pnospnogiucomutase | 1.1.1.27 | H16_A0666 | ldh | g1p <-> g6p llac + nad <-> pyr + nadh + h | g1p <-> g6p llac + nad <-> pyr + nadh + h | g1p <-> g6p llac + nad <-> pyr + nadh + h |
| GA3PD | Glycolysis/Glucone ogenesis | glyceraldehyde-3- phosphate | 1.2.1.12 | H16_A3146/H16_B1386 | gapA/cbbG2 | g3p + nad + pi <-> 13pdg + nadh + 2 h | g3p + nad + pi <-> 13pdg + nadh + h | g3p + nad + pi <-> 13pdg + nadh + h |
| GLK | Glycolysis/Glucone ogenesis | dehydrogenase glucokinase | 2.7.1.2 | | glk | atp + glc -> adp + g6p | atp + glc -> adp + g6p + h | atp + glc -> adp + g6p + h |
| PYK | Glycolysis/Glucone ogenesis | pyruvate kinase | 2.7.1.40 | H16_A0567/H16_A3602/ H16_B0961 | pyk1/pyk2/pyk3 | adp + pep -> atp + pyr | adp + pep -> atp + pyr | adp + pep -> atp + pyr |
| PGK | ogenesis | phosphoglycerate kinase | 2.7.2.3 | H16_A0566/H16_B1385 | pgk/cbbK2 | 3pg + atp <-> 13pdg + adp | 3pg + atp <-> 13pdg + adp | 3pg + atp <-> 13pdg + adp |
| FBP | Glycolysis/Glucone ogenesis | bisphosphatase | 3.1.3.11 | H16_A0999/H16_B1390 | fbp/cbbF2 | fdp + h2o -> f6p + pi | fdp + h2o -> f6p + pi | fdp + h2o -> f6p + pi |
| APPS1 | Glycolysis/Glucone ogenesis | acylphosphatase fructose- | 3.6.1.7 | H16_A3325 | acyP | 13pdg + h2o -> 3pg + pi | 13pdg + h2o -> 3pg + pi + h | 13pdg + h2o -> 3pg + pi + h |
| FBA | Glycolysis/Glucone ogenesis | bisphosphate aldolase | 4.1.2.13 | H16_A0568/H16_B0278/ H16_B1384 | fba/fbaB/cbbA2 | fdp <-> dhap + g3p | fdp <-> dhap + g3p | fdp <-> dhap + g3p |
| ENO | Glycolysis/Glucone ogenesis | enoiase | 4.2.1.11 | H16_A1188 | eno | 2pg <-> h2o + pep | 2pg + h <-> h2o + pep | 2pg + h <-> h2o + pep |
| TPI | Glycolysis/Glucone ogenesis | triose-phosphate isomerase | 5.3.1.1 | H16_A1047 | tpiA | dhap <-> g3p | dhap <-> g3p | dhap <-> g3p |
| PGI | Glycolysis/Glucone ogenesis | glucose-6-phosphate isomerase | 5.3.1.9 | H16_A1502/H16_B1502 | pgi1/pgi2 | g6p <-> f6p | g6p <-> f6p | g6p <-> f6p |
| PGM | Glycolysis/Glucone ogenesis | phosphoglycerate mutase | 5.4.2.1 | H16_A0332/H16_A0493 | pgam1/pgam2 | 2pg <-> 3pg | 2pg <-> 3pg | 2pg <-> 3pg |
| PDH1 | Glycolysis/Glucone ogenesis | pyruvate dehydrogenase E1 | 1.2.4.1 | H16_A1374/H16_A1753/ H16_B0145/H16_B1300/ H16_B2233/H16_B2234 | pdhA1/pdhA2/acoB/ aceE/bkdA1/bkdA2 | pyr + lipo + h -> adlipo + co2 | pyr + lipo + h -> adlipo + co2 | pyr + lipo + h -> adlipo + co2 |
| PDH2 | Glycolysis/Glucone ogenesis | component | 2.3.1.12 | H16_B2233/H16_B2234 H16_A1375/H16_B0146 | | coa + adlipo -> accoa + dlipo | coa + adlipo -> accoa + dlipo | coa + adlipo -> accoa + dlipo |
| | | (dihydrolipoamide acetyltransferase) dihydrolipoamide | | H16 A1377/H16 A2323/ | rpdhL/odhL/lpdaA/un | dlipo + nad -> lipo + nadh + h | | |
| PDH3 | ogenesis Glyoxylate and | dehydrogenase tartronate | 1.8.1.4 | | known | dlipo + nad -> lipo + nadh + h | dlipo + nad -> lipo + nadh + h | dlipo + nad -> lipo + nadh + h |
| TARSAR | Dicarboxylate metabolism Glyoxylate and | semialdehyde reductase | 1.1.1.60 | H16_A3600 | unknown | h3op + h + nadh <-> glyc-R + nad | h3op + h + nadh <-> glyc-R + nad | h3op + h + nadh <-> glyc-R + nad |
| LCTAD1 | Dicarboxylate metabolism Glyoxylate and | lactaldehyde dehydrogenase | (1.2.1.22 in kegg) | H16_A1919 | unknown | h2o + llald + nad -> 2 h + llac + nadh | h2o + llald + nad -> 2 h + llac + nadh | h2o + llald + nad -> 2 h + llac + nadh |
| PGLYCP | Dicarboxylate metabolism Glyoxylate and | Phosphoglycolate phosphatase | 3.1.3.18 | H16_A0174/H16_A3318/ H16_B1387 | unknown/gph/cbbZ2 | 2ppg + h2o -> glycolate + pi | 2ppg + h2o -> glycolate + pi | 2ppg + h2o -> glycolate + pi |
| HPYRI | Dicarboxylate metabolism Glyoxylate and | hydroxypyruvate isomerase | 5.3.1.22 | H16_A1558/H16_A3599 | hyi1/hyi2 | hpyr <-> h3op | hpyr <-> h3op | hpyr <-> h3op |
| GLYCLTO | Dicarboxylate metabolism | Glycolate oxidase | 1.1.1.29 | H16_B0611 | hprA | glycolate + uq -> glx + uqh2 | glycolate + uq -> glx + uqh2 | glycolate + uq -> glx + uqh2 |
| GLCALDD | Glyoxylate and Dicarboxylate metabolism | Glycolaldehyde dehydrogenase | 1.2.1.21 | | | glal + h2o + nad -> glycolate + 2 h + nadh | glal + h2o + nad -> glycolate + 2 h + nadh | glal + h2o + nad -> glycolate + 2 h + nadh |
| GLYCEK1 | Glyoxylate and Dicarboxylate metabolism | glycerate kinase | 2.7.1.31 | H16_B0612 | glxK | atp + glyc-R -> 3pg + adp | atp + glyc-R -> 3pg + adp + h | atp + glyc-R -> 3pg + adp + h |

H16_A0679/H16_A0893/ unknown/unknown/

| GLOXCL | Glyoxylate and Dicarboxylate metabolism | glyoxalate carboligase | 4.1.1.47 | H16_A3598 | unknown | 2 glx + h -> h3op + co2 | 2 glx + h -> h3op + co2 | 2 glx + h -> h3op + co2 |
|----------|--|--|----------|--|--|--|--|---|
| GLYCDH | Glyoxylate and Dicarboxylate | Glycolate dehydrogenase | 1.1.1.29 | H16_B0611 | hprA | glx + h + nadh -> glycolate + nad | glx + h + nadh -> glycolate + nad | glx + h + nadh -> glycolate + nad |
| FDH | metabolism Glyoxylate and Dicarboxylate metabolism | formate dehydrogenase | 12.1.2 | (H16_A0640&H16_A064 1&H16_A0642&H16_A0 644/)H16_A2934&H16_ A2936&H16_A2937&H1 6_B1471)/H16_A3292/H 16_B1383/(H16_B1452& H16_B1453&H16_B1454 01)/(H16_B1700&H16_B17 01) | dsD)/(fdhC&fdhB1&f dhA1&fdhA2)/unkno wn/cbbB/(fdoG&fdo H&fdoI)/(fdwA&fdw | formate a god a cook a godb | formate + nad <-> co2 + nadh | formate + nad <-> co2 + nadh |
| ACFM1 | Glyoxylate and Dicarboxylate metabolism | arylformamidase | 3.5.1.9 | H16_A3005/H16_B1997 | unknown/unknown | forkn + h2o -> formate + kn + h | forkn + h2o -> formate + kn + h | forkn + h2o -> formate + kn + h |
| FMDF | Glyoxylate and Dicarboxylate metabolism | formylmethionine deformylase | 3.5.1.31 | H16_A3700 | def | formt + h2o -> formate + met | formt + h2o -> formate + met | formt + h2o -> formate + met |
| FMMS | Glyoxylate and Dicarboxylate metabolism | formamidase | 3.5.1.49 | H16_B0072/H16_B0476 | fmdA1/fmdA2 | fa + h2o -> formate + nh4 | fa + h2o -> formate + nh4 | fa + h2o -> formate + nh4 |
| FGDM | Glyoxylate and Dicarboxylate metabolism | N-formylglutamate deformylase | 3.5.1.68 | H16_A1109/H16_A1306/ H16_A3013/H16_A3649 | | forglu + h2o -> formate + glu | forglu + h2o -> formate + glu | forglu + h2o -> formate + glu |
| S2HAO | Glyoxylate and Dicarboxylate metabolism | (S)-2-hydroxy-acid oxidase | 1.1.3.15 | H16_A3094/H16_A3096/ H16_A3097 | glcD1/glcE/glcF | glycolate + o2 -> glx + h2o2 | glycolate + o2 -> glx + h2o2 | glycolate + o2 -> glx + h2o2 |
| HISTDH | Histidine Metabolism | histidinol dehydrogenase | 1.1.1.23 | H16_A1694/H16_A3416 | unknown/hisD | h2o + hisol + 2 nad -> 3 h + his + 2 nadh | h2o + hisol + 2 nad -> 3 h + his + 2 nadh | h2o + hisol + 2 nad -> 3 h + his + 2 nadh |
| ATPPRT | Histidine Metabolism | ATP phosphoribosyltransf erase | 2.4.2.17 | H16_A3417 | hisG | atp + prpp -> ppi + prbatp | atp + prpp -> ppi + prbatp + h | atp + prpp -> ppi + prbatp + h |
| HISTPT | Histidine Metabolism | histidinol-phosphate transaminase | 2.6.1.9 | H16_A0793/H16_A3415 | hisC1/hisC2 | glu + imACP -> akg + hisolp | glu + imACP -> akg + hisolp | glu + imACP -> akg + hisolp |
| HISTP | Histidine Metabolism | histidinol- phosphatase | 3.1.3.15 | | | h2o + hisolp -> hisol + pi | h2o + hisolp -> hisol + pi | h2o + hisolp -> hisol + pi |
| PRAMPCH | Histidine Metabolism | cyclonydrolase | 3.5.4.19 | H16_A3409 | hisI | h2o + prbamp + h -> prfp | h2o + prbamp -> prfp | h2o + prbamp -> prfp |
| PRATPPP | Histidine Metabolism | pyrophosphatase | 3.6.1.31 | H16_A3408 | hisE | h2o + prbatp -> ppi + prbamp | h2o + prbatp -> ppi + prbamp + h | h2o + prbatp -> ppi + prbamp + 2 h |
| IMGPDH | Histidine Metabolism | imidazoleglycerol- phosphate dehydratase 1-(5- | 4.2.1.19 | H16_A3414 | hisB | dimgp + h -> h2o + imACP | dimgp -> h2o + imACP | dimgp -> h2o + imACP |
| PRMIIZCI | Histidine Metabolism | phosphoribosyl)-5- [(5- phosphoribosylamino) methylideneamino)i midazole-4- carboxamide | 5.3.1.16 | H16_A3411 | hisA | prfp <-> prlp | prfp <-> prlp | prfp <-> prlp |
| IMG3PS | Histidine Metabolism | isomerase Imidazole-glycerol-3- phosphate synthase | | H16_A3410/H16_A3412 | hisF/hisH | gln + prlp -> aicar + dimgp + glu + 2 h | gln + prlp -> aicar + dimgp + glu + 2 h | gln + prlp -> aicar + dimgp + glu + h |
| HISAL | Histidine | histidine ammonia- | 4.3.1.3 | H16_A3018 | hutH | his -> urocan + nh4 | his -> urocan + nh4 | his -> urocan + nh4 |
| UROCH | metabolism Histidine | lyase urocanate hydratase | | H16_A0695/H16_A3017 | | urocan + h2o -> 4i5p + h | urocan + h2o -> 4i5p + h | urocan + h2o -> 4i5p + h |
| FBMO1 | metabolism Histidine metabolism | flavin-binding monooxygenase | 1.14.13 | H16_A1145/H16_B0495/ H16_B1480/H16_B2135 | unknown/unknown/ | 2 4i5p + o2 -> 2 ht5p | 2 4i5p + o2 + 2 h -> 2 ht5p | 2 4i5p + o2 + 2 h -> 2 ht5p |
| IMZPP | Histidine metabolism | imidazolonepropiona | 3.3.2./ | H16_A3015 | hutI | 4i5p + h2o -> nfglu | 4i5p + h2o + h -> nfglu | 4i5p + h2o + h -> nfglu |
| FORGD | Histidine metabolism | formimidoylglutamat e deiminase | 3.5.3.13 | H16_A3014 | hutF | nfglu + h2o -> forglu + nh4 | nfglu + h2o -> forglu + nh4 | nfglu + h2o -> forglu + nh4 |
| HTTOG | Histidine metabolism | lumping reaction | | | | ht5p + 2 h2o + h -> glu + nh4 + co2 | ht5p + 2 h2o + h -> glu + nh4 + co2 | ht5p + 2 h2o + h -> glu + nh4 + co2 |
| ALHD7 | Histidine metabolism | aldehyde dehydrogenase (NAD+) | 12.1.3 | H16_A0232/H16_A0745/ H16_A1114/H16_A1495/ H16_B0212/H16_B0421/ H16_B0737/H16_B0833/ H16_B1534/H16_B1735/ H16_B1751/H16_B1835/ H16_B1960/H16_B2444 | unknown/unknown/ unknown/unknown/ unknown/unknown/ unknown/unknown/ unknown/unknown/ | i4aa + nad + h2o -> i4ac + nadh + 2 h | i4aa + nad + h2o -> i4ac + nadh + 2 h | i4aa + nad + h2o -> i4ac + nadh + 2 h |
| MNAO2 | Histidine metabolism | monoamine oxidase malonate- | 1.4.3.4 | H16_A0831 | maoB | nmhis + h2o + o2 -> mlzac + nh4 + h2o2 | nmhis + h2o + o2 -> mlzac + nh4 + h2o2 | nmhis + h2o + o2 -> mlzac + nh4 + h2o2 |
| MSDHA | Inositol metabolism | semialdehyde dehydrogenase (acetylating) | 1.2.1.27 | H16_A0273/H16_A3664/ H16_B1191 | mmsA1/mmsA2/mm sA3 | 3opp + coa + nad -> accoa + co2 + nadh | 3opp + coa + nad -> accoa + co2 + nadh | 3opp + coa + nad -> accoa + co2 + nadh |
| MI1P | Inositol Phosphate Metabolism Lipopolysaccharide | myo-inositol 1- phosphatase UDP-N- | 3.1.3.25 | H16_A1214 | suhB | h2o + dmi1p -> mi + pi | h2o + dmi1p -> mi + pi | h2o + dmi1p -> mi + pi |
| UDPAGAT | Biosynthesis | acetylglucosamine acyltransferase Lipid A disaccaride | | H16_A2043 | IpxA | 3hmrsACP + udpnag <-> ACP + udpg2aa | 3hmrsACP + udpnag <-> ACP + udpg2aa | 3hmrsACP + udpnag <-> ACP + udpg2aa |
| LIPADSS | Biosynthesis Lipopolysaccharide | synthase Tetraacyldisaccharide | | H16_A2042 H16_A0606 | lpxB lpxK | lipidX + udpg23a -> lipidAds + udp atp + lipidAds -> adp + lipidA | lipidX + udpg23a + h -> lipidAds + udp atp + lipidAds -> adp + lipidA + 2 h | lipidX + udpg23a -> lipidAds + udp atp + lipidAds -> adp + lipidA + 2 h |
| KDOCTT | Biosynthesis Lipopolysaccharide | 4'kinase 3-deoxy-manno- octulosonate | 2.7.7.38 | H16_A0604 | kdsB | ctp + kdo -> ckdo + ppi | ctp + kdo -> ckdo + ppi + h | ctp + kdo -> ckdo + ppi + h |
| KDO8PP | Biosynthesis Lipopolysaccharide Biosynthesis | cytidylyltransferase 3-deoxy-manno- octulosonate-8- | 3.1.3.45 | H16_A0604 | KOSB | h2o + kdo8p -> kdo + pi | h2o + kdo8p -> kdo + pi | h2o + kdo8p -> kdo + pi |
| KDO8PS | Lipopolysaccharide Biosynthesis | phosphatase 2-dehydro-3- deoxyphosphooctona te aldolase (3-deoxy -D-manno- | 2.5.1.55 | H16_A1186 | kdsA | a5p + h2o + pep -> kdo8p + pi | a5p + h2o + pep -> h + kdo8p + pi | a5p + h2o + pep -> h + kdo8p + pi |
| ACMUED | Lipopolysaccharide | octulosonic -acid 8- phosphate synthase) ADP-D-glycero-D- | F1220 | U1C 40004 | hido. | | | ada da da da da cara da da cara da da cara da da cara |
| AGMHEP | Biosynthesis | manno-heptose epimerase Endotoxin Synthesis | 5.1.3.20 | H16_A0804 H16_A0228/H16_A0229/ | hldD unknown/unknown/ | adpdgdmhep -> adphep | adpdgdmhep -> adphep | adpdgdmhep -> adphep |
| EDOTXS1 | Biosynthesis Lipopolysaccharide | (lauroyl transferase) Endotoxin Synthesis | 2.3.1 | H16_B0917 | unknown | c120ACP + k2lipiv -> ACP + lk2lipiv | c120ACP + k2lipiv -> ACP + lk2lipiv | c120ACP + k2lipiv -> ACP + lk2lipiv |
| EDOTXS2 | Biosynthesis Lipopolysaccharide | (myristoyl transferase) D-glycero-D-manno- | 2.3.1 | | | lk2lipiv + c140ACP -> ACP + lipa | lk2lipiv + c140ACP -> ACP + lipa | Ik2lipiv + c140ACP -> ACP + lipa |
| GMHEPADT | Biosynthesis | hepose 1-phosphate adenyltransferase D-glycero-D-manno- | 2.7 | H16_A0803 | hldA | atp + dgdmh1p -> adpdgdmhep + ppi | atp + dgdmh1p -> adpdgdmhep + ppi | atp + dgdmh1p -> adpdgdmhep + ppi |
| GMHEPK | Lipopolysaccharide Biosynthesis | heptose 7-phosphate kinase D-glycero-D-manno- | 2.7 | H16_A0803 | hldA | atp + dgdmh7p -> adp + dgdmh17bp | $atp + dgdmh7p \rightarrow adp + dgdmh17bp + h$ | atp + dgdmh7p -> adp + dgdmh17bp + h |
| GMHEPBP | Lipopolysaccharide Biosynthesis | heptose 1,7- bisphosphate phosphatase | 3.1.1 | | | dgdmh17bp + h2o -> dgdmh1p + pi | dgdmh17bp + h2o -> dgdmh1p + pi | dgdmh17bp + h2o -> dgdmh1p + pi |
| DMOAT | Lipopolysaccharide Biosynthesis | 3-deoxy-D-manno- octulosonic acid transferase | 2.4.99 | H16_A2883 | kdtA | ckdo + lipidA -> cmp + kdolipid4 | ckdo + lipidA -> cmp + kdolipid4 + h | ckdo + lipidA -> cmp + kdolipid4 + h |

| | | 3-deoxy-D-manno- | | | | | | |
|---------|------------------------------------|--|--------------|---|--|---------------------------------------|---|---|
| DMOAT2 | Lipopolysaccharide Biosynthesis | octulosonic acid transferase | 2.4.99 | H16_A2883 | kdtA | ckdo + kdolipid4 -> cmp + k2lipiv | ckdo + kdolipid4 -> cmp + k2lipiv + h | ckdo + kdolipid4 -> cmp + k2lipiv + h |
| S7PISM | Lipopolysaccharide Biosynthesis | sedoheptulose 7- phosphate isomerase UDP-3-O-(3- | 5 | | | s7p -> dgdmh7p | s7p -> dgdmh7p | s7p -> dgdmh7p |
| U3HGAAT | Lipopolysaccharide Biosynthesis | hydroxymyristoyl)glu cosamine acyltransferase | 2.3.1 | H16_A2045 | lpxD | 3hmrsACP + u3hga -> ACP + h + udpg23a | 3hmrsACP + u3hga -> ACP + h + udpg23a | 3hmrsACP + u3hga -> ACP + udpg23a |
| U3AGDA | Lipopolysaccharide Biosynthesis | UDP-3-O- acetylglucosamine deacetylase | 3.5.1 | H16_A3266 | lpxC | h2o + udpg2aa -> ac + u3hga | h2o + udpg2aa -> ac + u3hga | h2o + udpg2aa -> ac + u3hga + h |
| UDPSH | Lipopolysaccharide Biosynthesis | UDP-sugar hydrolase | 3.6.1 | | | h2o + udpg23a -> lipidX + ump | h2o + udpg23a -> lipidX + ump + 2 h | h2o + udpg23a -> lipidX + ump + 2 h |
| DHDCR | Lysine Biosynthesis | reductase (NADPH) | | H16_A3141/H16_A3348 | dapB/unknown | dhdp + 2 h + nadph -> nadp + tdhdp | dhdp + h + nadph -> nadp + tdhdp | dhdp + h + nadph -> nadp + tdhdp |
| THDPSUC | Lysine Biosynthesis | e succinyiase | 2.3.1.117 | H16_A2066 | dapD | h2o + succoa + tdhdp -> coa + sl2a6o | h2o + succoa + tdhdp -> coa + sl2a6o | h2o + succoa + tdhdp -> coa + sl2a6o |
| SUCDPT | Lysine Biosynthesis | succinyldiaminopimel ate transaminase succinyl- | 2.6.1.17 | H16_A2065/H16_A3025 | unknown/argD | akg + sl26da <-> glu + sl2a6o | akg + sl26da <-> glu + sl2a6o | akg + sl26da <-> glu + sl2a6o |
| SUCDPDS | Lysine Biosynthesis | | 3.5.1.18 | H16_A2069 | dapE | h2o + sl26da -> 26dap-LL + succ | h2o + sl26da -> 26dap-LL + succ | h2o + sl26da -> 26dap-LL + succ |
| DAPMDC | Lysine Biosynthesis | decarboxyrase | 4.1.1.20 | H16_A3443 | lysA2 | 26dap-M + h -> co2 + lys | 26dap-M + h -> co2 + lys | 26dap-M + h -> co2 + lys |
| DHDPCS | Lysine Biosynthesis | syntnase | 4.2.1.52 | H16_A1204/H16_B0213/ H16_B0891/H16_B1831 | dapA1/dapA2/dapA3 /dapA4 | aspsa + pyr -> dhdp + h + 2 h2o | aspsa + pyr -> dhdp + h + 2 h2o | aspsa + pyr -> dhdp + h + 2 h2o |
| DAPME | Lysine Biosynthesis | epimerase | 5.1.1.7 | H16_A0227 | dapF | 26dap-LL <-> 26dap-M | 26dap-LL <-> 26dap-M | 26dap-LL <-> 26dap-M |
| GLUCD1 | Lysine degradation | dehydrogenase 2-oxoglutarate dehydrogenase E2 | 1.3.99.7 | H16_A2818 | gcdH | glutcoa + nad -> ccoa + nadh + co2 | glutcoa + nad -> ccoa + nadh + co2 | glutcoa + nad -> ccoa + nadh + co2 |
| OGDH2 | Lysine degradation | | 2.3.1.61 | H16_A2324 | odhB | coa + sgdhl <-> glutcoa + dlipoe | coa + sgdhl <-> glutcoa + dlipoe | coa + sgdhl <-> glutcoa + dlipoe |
| OGDH1 | Lysine degradation | | 1.2.4.2 | H16_A2325 H16_A0100/H16_A0142/ | odhA | 2oad + lipoe + h -> sgdhl + co2 | 2oad + lipoe + h -> sgdhl + co2 | 2oad + lipoe + h -> sgdhl + co2 |
| ENCOAH3 | Membrane Lipid Metabolism | enoyl-CoA hydratase | 42.1.17 | H16, A0179/H16, A0461, H16, A0464/H16, A0810, H16, A0865/H16, A0873, H16, A1101/H16, A14716, H16, A1101/H16, A14716, H16, A1719/H16, A1832, H16, A1885/H16, A1889, H16, A2189/H16, A2289, H16, A2189/H16, A2289, H16, A3311/H16, A2289, H16, A3311/H16, A3289, H16, A3311/H16, A3289, H16, B0382/H16, B0389/ H16, B0420/H16, B0419/ H16, B0420/H16, B0419/ H16, B0420/H16, B0419/ H16, B0420/H16, B0419/ H16, B0420/H16, B0419/ H16, B0420/H16, B0419/ H16, B1488/H16, B0419/ H16, B1449/H16, B0419/ H16, B1449/H16, B1440/ H16, B1441/H16, B1440/ H16, B2478/ | unknown/unknown/ | 3mccoa + h2o <-> 3hivcoa | 3mccoa + h2o <-> 3hivcoa | 3mccoa + h2o <-> 3hivcoa |
| ENCOAH4 | Membrane Lipid Metabolism | encyl-CoA hydratase | 42.1.17 | H16, A0100/H16, A0142, H16, A0179/H16, A0461/H16, A04801/H16, A04801/H16, A0810/H16, A04801/H16, A04801/H16, A1110/H16, A1110/H16, A1110/H16, A1110/H16, A1110/H16, A1110/H16, A1110/H16, A1180/H16, A1880/H16, A1880/H16, A3201/H16, A3301/H16, A3301/H16, A3301/H16, B0380/H16, B00380/H16, B0040/H16, B1430/H16, | u unknown/unknown/ u unknown/unknown/ u unknown/unknown/ u unknown/unknown/ u unknown/unknown/ | 2mp2ecoa + h2o -> 3hibcoa | 2mp2ecoa + h2o -> 3hibcoa | 2mp2ecoa + h2o -> 3hibcoa |
| ENCOAHS | Membrane Lipid Metabolism | encyl-CoA hydratase | 42.1.17 | H16, A0100/H16, A0142, H16, A0179/H16, A0461, H16, A0464/H16, A0810, H16, A0865/H16, A0810, H16, A0865/H16, A0810, H16, A1090/H16, A116, A116, A116, A116, A116, A1170, H16, B0015/H16, B0015/H16, B0015/H16, B0140, H16, B1146/H16, | unknown/unknown/ unknown/ unknown/unknown/ unknown/unknown/ unknown/unknown/ unknown/unknown/ unknown/unknown/ unknown/unknown/ unknown/unknown/ unknown/ unknown/unknown/ unknown/ unknown/unknown/ unknown/ unkno | 2m2ecoa + h2o -> s3h2mbcoa | 2m2ecoa + h2o -> s3h2mbcoa | 2m2ecca + h2o -> s3h2mbcoa |
| HACOAD2 | Membrane Lipid Metabolism | | 1.1.1.35 | H16_A0282/H16_A0602/ H16_A1102/H16_A1888/ H16_B0388/H16_B0724/ | H2/unknown/unkno | | s3h2mbcoa + nad <-> 2maaccoa + nadh + h | s3h2mbcoa + nad <-> 2maaccoa + nadh + h |
| HACOAD3 | Membrane Lipid | oxohexanoyl-CoA) 3-hydroxyacyl-CoA dehydrogenase (3- | 1.1.1.35 | H16_B1652 H16_A0282/H16_A0602/ H16_A1102/H16_A1888/ | wn / paaH1/unknown/paa / H2/unknown/unkno | hibut + nad <-> mmsa + nadh + h | hibut + nad <-> mmsa + nadh + h | hibut + nad <-> mmsa + nadh + h |
| | Metabolism | oxooctanoyl-CoA) | - | H16_B0388/H16_B0724/ H16_B1652 | wn/unknown/unkno wn | | | |

| | | | | | H16_A0100/H16_A0142/ | | | | |
|-------------------|----------------------------------|--|---|---|---|--|--|---|---|
| | | | | | H16_A0179/H16_A0461/ H16_A0464/H16_A0810/ | | | | |
| | | | | | H16_A0865/H16_A0873/ | | | | |
| | | | | | H16_A1101/H16_A1410/ H16_A1699/H16_A1716/ | | | | |
| | | | | | H16_A1719/H16_A1832/ | | | | |
| | | | | | H16_A1885/H16_A1889/ H16_A2138/H16_A2258/ | | | | |
| | | | | | H16_A2979/H16_A3201/ | unknown/unknown/ | | | |
| | | Membrane Lipid | | | H16_A3311/H16_A3593/ H16_A3594/H16_B0365/ | | | | |
| EN | NCOAH6 | Metabolism | enoyl-CoA hydratase | 4.2.1.17 | H16_B0382/H16_B0389/ | unknown/unknown/ | carpcoa + h2o -> hadpcoa | carpcoa + h2o -> hadpcoa | carpcoa + h2o -> hadpcoa |
| | | | | | H16_B0402/H16_B0419/ H16_B0420/H16_B0657/ | | | | |
| | | | | | H16_B0659/H16_B0698/ | unknown/unknown/ | | | |
| | | | | | H16_B0724/H16_B0756/ H16_B0848/H16_B0915/ | | | | |
| | | | | | H16_B1188/H16_B1346/ | unknown/unknown/ | | | |
| | | | | | H16_B1439/H16_B1738/ H16_B1741/H16_B1742/ | | | | |
| | | | | | H16_B1773/H16_B1905/ H16_B1914/H16_B2156/ | | | | |
| | | | | | | unknown/ | | | |
| | | | 3-hydroxyacyl-CoA | | H16_A0282/H16_A0602/ | | | | |
| HA | ACOAD4 | Membrane Lipid Metabolism | dehydrogenase (3- | 1.1.1.35 | H16_A1102/H16_A1888/ H16_B0388/H16_B0724/ | | hadpcoa + nad -> ooadpcoa + nadh + h | hadpcoa + nad -> ooadpcoa + nadh + h | hadpcoa + nad -> ooadpcoa + nadh + h |
| | | | oxodecanoyl-CoA) | | H16_B1652 | wn | | | |
| | | | | | H16_A0100/H16_A0142/ | | | | |
| | | | | | H16_A0179/H16_A0461/ H16_A0464/H16_A0810/ | | | | |
| | | | | | H16_A0865/H16_A0873/ | unknown/unknown/ | | | |
| | | | | | H16_A1101/H16_A1410/ H16_A1699/H16_A1716/ | | | | |
| | | | | | H16_A1719/H16_A1832/ H16_A1885/H16_A1889/ | | | | |
| | | | | | H16_A2138/H16_A2258/ | unknown/unknown/ | | | |
| | | | | | H16_A2979/H16_A3201/ H16_A3311/H16_A3593/ | | | | |
| FN | ICOAH7 | Membrane Lipid | enoyl-CoA hydratase | 42117 | H16_A3594/H16_B0365/ | unknown/unknown/ | 2e5mhdcoa + h2o -> 3h5m4ecoa | 2e5mhdcoa + h2o -> 3h5m4ecoa | 2e5mhdcoa + h2o -> 3h5m4ecoa |
| LIV | 4COAIII | Metabolism | enoyi-cox nyuratase | 4.2.1.17 | H16_B0382/H16_B0389/ H16_B0402/H16_B0419/ | | 2e3111lacoa + 1120 -> 3113114ecoa | Zesimidcoa + 1120 -> Sitsimecoa | Zesimucoa + 1120 -> Sitsimecoa |
| | | | | | H16_B0420/H16_B0657/ | unknown/unknown/ | | | |
| | | | | | H16_B0659/H16_B0698/ H16_B0724/H16_B0756/ | | | | |
| | | | | | H16_B0848/H16_B0915/ | unknown/unknown/ | | | |
| | | | | | H16_B1188/H16_B1346/ H16_B1439/H16_B1738/ | | | | |
| | | | | | H16_B1741/H16_B1742/ | unknown/unknown/ | | | |
| | | | | | H16_B1773/H16_B1905/ H16_B1914/H16_B2156/ | | | | |
| | | | | | | unknown/ | | | |
| | | Membrane Lipid | 3-hydroxyacyl-CoA | | H16_A0282/H16_A0602/ H16_A1102/H16_A1888/ | | | | |
| HA | ACOAD5 | Metabolism | dehydrogenase (3- oxododecanoyl-CoA) | | H16_B0388/H16_B0724/ | | 3h5m4ecoa + nad -> 5m3o4hcoa + nadh + h | 3h5m4ecoa + nad -> 5m3o4hcoa + nadh + h | 3h5m4ecoa + nad -> 5m3o4hcoa + nadh + h |
| | | Membrane Lipid | 3-hydroxy-myristoyl- | | H16_B1652 | wn | c120ACP + 2 h + malACP + nadph + h -> | c120ACP + 2 h + malACP + nadph -> | c120ACP + 2 h + malACP + nadph -> |
| 3H | HMYSAS | Metabolism | ACP synthesis | | | | 3hmrsACP + ACP + co2 + nadp | 3hmrsACP + ACP + co2 + nadp | 3hmrsACP + ACP + co2 + nadp |
| FA | LDHD | Methane Metabolism | formaldehyde dehydrogenase | 1.1.1.284 | H16_B1195 | adhC | hmgth + nad <-> fmgt + h + nadh | hmgth + nad <-> fmgt + h + nadh | hmgth + nad <-> fmgt + h + nadh |
| | | Methionine | 2-keto-4- | | | | | | |
| 2K | MBT | Metabolism | methylthiobutyrate transamination | 2.6.1.57 | H16_A1151/H16_B1081 | tyrB1/tyrB2 | 2kmb + glu -> akg + met | 2kmb + glu -> akg + met | 2kmb + glu -> akg + met |
| M | ETS | Methionine | methionine synthase | 2.1.1.13 | H16_A0151 | metH | mthf + hcys -> met + thf | mthf + hcys -> met + thf | mthf + hcys -> met + thf |
| | FTADT | Metabolism Methionine | methionine | | H16 A0230/H16 A1975 | | | | |
| M | ETADT | Metabolism | adenosyltransferase S- | 2.5.1.6 | H16_A0230/H16_A1975 | metK1/metK2 | atp + h2o + met + h -> sam + pi + ppi | atp + h2o + met -> sam + pi + ppi + h | atp + h2o + met -> sam + pi + ppi + 2 h |
| AE | OHCYSNS | Methionine | adenosylhomocysteir | 3.2.2.9 | H16_A3337 | pfs | sah + h2o -> ad + srlh | sah + h2o -> ad + srlh | sah + h2o + h -> ad + srlh |
| | | Metabolism Methionine | e nucleosidase cystathionine | | | | | | |
| CY | TTS1 | Metabolism | gamma-synthase | 2.5.1.48 | H16_A2606 | metB | cys + oslhser -> llct + h + succ | cys + oslhser -> llct + h + succ | cys + oslhser -> llct + h + succ |
| CY | STBL1 | Methionine Metabolism | cystathionine b-lyase | 4.4.1.8 | H16_A1447 | metC | llct + h2o -> hcys + nh4 + pyr | llct + h2o -> hcys + nh4 + pyr | llct + h2o -> hcys + nh4 + pyr |
| 1.0 | AO2 | Methionine | L-amino-acid oxidase | 1/122 | H16_A0845/H16_A0856 | 1201/1202 | met + h2o + o2 -> 2kmb + nh4 + h2o2 | met + h2o + o2 -> 2kmb + nh4 + h2o2 | met + h2o + o2 -> 2kmb + nh4 + h2o2 |
| | | metabolism Methionine | adenosylhomocysteir | | | | | | |
| AE | DHC1 | metabolism | ase | 3.3.1.1 | H16_A0244 | ahcY | sah + h2o <-> adn + hcys | sah + h2o <-> adn + hcys | sah + h2o <-> adn + hcys + h |
| CY | /TTS2 | Methionine metabolism | cystathionine gamma-synthase | 2.5.1.48 | H16_A2606 | metB | oslhser + h2o <-> obut + succ + nh4 + h | oslhser + h2o <-> obut + succ + nh4 + h | oslhser + h2o <-> obut + succ + nh4 + h |
| CY | TTS3 | Methionine | cystathionine | 2.5.1.48 | H16_A2606 | metB | oahser + cys <-> llct + ac + h | oahser + cys <-> llct + ac + h | oahser + cys <-> llct + ac + h |
| | | metabolism Methionine | gamma-synthase cystathionine | | | | • | | • |
| CY | /TTS4 | metabolism | gamma-synthase | 2.5.1.48 | H16_A2606 | metB | oahser + h2s -> hcys + ac + h | oahser + h2s -> hcys + ac | oahser + h2s -> hcys + ac |
| OA | AHSL1 | Methionine metabolism | O-acetylhomoserine (thiol)-lyase | 2.5.1.49 | H16_A1313/H16_B2229 | metY1/metY2 | oahser + tsul + rthio -> hcys + so3 + othio + ac + h | oahser + tsul + rthio -> hcys + so3 + othio + ac + h | oahser + tsul + rthio -> hcys + so3 + othio + ac + h |
| CY | TTS5 | Methionine | cystathionine | 2.5.1.48 | H16_A2606 | metB | oslhser + h2s <-> hcys + succ + h | oslhser + h2s <-> hcys + succ | oslhser + h2s <-> hcys + succ |
| ше | SERA | metabolism Methionine | gamma-synthase homoserine O- | 2.3.1.31 | H16_A0211 | metX | accoa + hser <-> coa + oahser | accoa + hser <-> coa + oahser | accoa + hser <-> coa + oahser |
| nà | -LIVI | metabolism | acetyltransferase 5- | 2.3.1.31 | | tA | accod - liser <-> cod + Odliser | account fisch size coal# Odliser | account fiser see coa + daliser |
| | | Methionine | | | | | | | |
| M | TTGH | | methyltetrahydropter | | | | | | |
| | | metabolism | methyltetrahydropter oyltriglutamate | | H16_B1581 | metE | Smtglu + hcys -> tglu + met | 5mtglu + hcys -> tglu + met | Smtglu + hcys -> tglu + met |
| | | | methyltetrahydropter | | H16_B1581 | metE | 5mtglu + hcys -> tglu + met | Smtglu + hcys -> tglu + met | 5mtglu + hcys -> tglu + met |
| N/T | TDDD6 | metabolism Naphthalene and | methyltetrahydropter oyltriglutamate homocysteine | 2.1.1.14 | H16_A0633/H16_B0223/ | pcaH2/unknown/unk | | Smtglu + hcys -> $tglu$ + met $phentrc + nadh + h + o2 -> c34dhphe +$ | |
| Nī | TPPD6 | metabolism Naphthalene and Anthracene degradation | methyltetrahydropter oyltriglutamate homocysteine methyltransferase | 2.1.1.14 | H16_A0633/H16_B0223/ | pcaH2/unknown/unk | Smtglu + hcys -> tglu + met $phentrc + nadh + h + o2 -> c34dhphe + nad$ | , , | Smtglu + hcys -> tglu + met $phentrc + nadh + h + o2 -> c34dhphe + nad$ |
| | TPPD6 | Naphthalene and Anthracene degradation Naphthalene and | methyltetrahydropter oyltriglutamate homocysteine methyltransferase 2-nitropropane dioxygenase chlorophenol 4- | 2.1.1.14 | H16_A0633/H16_B0223/ H16_B0757/H16_B1109/ H16_B1420/H16_B1836 H16_A1145/H16_B0495/ | pcaH2/unknown/unk nown/unknown/unk nown/unknown unknown/unknown/ | phentrc + nadh + h + o2 -> c34dhphe + nad phentrc + o2 + nadh + h -> pheth12o + h2o + | phentrc + nadh + h + o2 -> c34dhphe + nad phentrc + o2 + nadh + h -> pheth12o + | phentrc + nadh + h + o2 -> c34dhphe + nad phentrc + o2 + nadh + h -> pheth12o + h2o + |
| | | Naphthalene and Anthracene degradation Naphthalene and Anthracene degradation | methyltetrahydropter oyltriglutamate homocysteine methyltransferase 2-nitropropane dioxygenase | 2.1.1.14 | H16_A0633/H16_B0223/ H16_B0757/H16_B1109/ H16_B1420/H16_B1836 | pcaH2/unknown/unk nown/unknown/unk nown/unknown unknown/unknown/ | phentrc + nadh + h + o2 -> c34dhphe + nad phentrc + o2 + nadh + h -> pheth12o + h2o + | phentrc + nadh + h + o2 -> c34dhphe + nad | phentrc + nadh + h + o2 -> c34dhphe + nad |
| FB | MO12 | Maphthalene and Anthracene degradation Naphthalene and Anthracene degradation Naphthalene and | methyltetrahydropter oyltriglutamate homocysteine methyltransferase 2-nitropropane dioxygenase chlorophenol 4- monooxygenase chlorophenol 4- | 2.1.1.14 1.13.11 1.14.13 | H16_A0633/H16_B0223/ H16_B0757/H16_B1109/ H16_B1420/H16_B1836 H16_A1145/H16_B0495/ H16_B1480/H16_B2135 H16_A1145/H16_B0495/ | pcaH2/unknown/unk nown/unknown/unk nown/unknown unknown/unknown/ unknown/unknown unknown/unknown/ | phentrc + nadh + h + o2 -> c34dhphe + nad phentrc + o2 + nadh + h -> pheth12o + h2o + nad | phentrc + nadh + h + o2 -> c34dhphe + nad phentrc + o2 + nadh + h -> pheth12o + | phentrc + nadh + h + o2 -> c34dhphe + nad $phentrc + o2 + nadh + h -> pheth12o + h2o + nad$ |
| FB | | Maphthalene and Anthracene degradation Naphthalene and Anthracene degradation Naphthalene and Anthracene degradation | methyltetrahydropter oyltriglutamate- homocysteine methyltransferase 2-nitropropane dioxygenase chlorophenol 4- monooxygenase | 2.1.1.14 | H16_A0633/H16_B0223/ H16_B0757/H16_B1109/ H16_B1420/H16_B1836 H16_A1145/H16_B0495/ H16_B1480/H16_B2135 | pcaH2/unknown/unk nown/unknown/unk nown/unknown unknown/unknown/ unknown/unknown unknown/unknown/ | phentrc + nadh + h + o2 -> c34dhphe + nad phentrc + o2 + nadh + h -> pheth12o + h2o + | phentrc + nadh + h + o2 -> c34dhphe + nad phentrc + o2 + nadh + h -> pheth12o + h2o + nad | phentrc + nadh + h + o2 -> c34dhphe + nad phentrc + o2 + nadh + h -> pheth12o + h2o + |
| FB FB | MO12 | metabolism Naphthalene and Anthracene degradation Naphthalene and Anthracene degradation Naphthalene and Anthracene | methyltetrahydropter oyltriglutamate homocysteine methyltransferase 2-nitropropane dioxygenase chlorophenol 4- monooxygenase chlorophenol 4- chlorophenol 4- chlorophenol 4- | 2.1.1.14 1.13.11 1.14.13 | H16_A0633/H16_B0223/ H16_B0757/H16_B1109/ H16_B1420/H16_B1836 H16_A1145/H16_B0495/ H16_B1480/H16_B2135 H16_A1145/H16_B0495/ H16_B1480/H16_B2135 H16_A1145/H16_B0495/ | pcaH2/unknown/unk nown/unknown/unk nown/unknown unknown/unknown/ unknown/unknown unknown/unknown/ unknown/unknown unknown/unknown/ | phentrc + nadh + h + o2 -> c34dhphe + nad phentrc + o2 + nadh + h -> pheth12o + h2o + nad phentrc + o2 + nadh + h -> phatol + h2o + nad phentrc + o2 + nadh + h -> pheth910o + h2o + | phentrc + nadh + h + o2 -> c34dhphe + nad phentrc + o2 + nadh + h -> pheth12o + h2o + nad phentrc + o2 + nadh + h -> phatol + h2o + nad phentrc + o2 + nadh + h -> pheth910o + | phentrc + nadh + h + o2 -> c34dhphe + nad phentrc + o2 + nadh + h -> pheth12o + h2o + nad phentrc + o2 + nadh + h -> phatol + h2o + nad phentrc + o2 + nadh + h -> pheth910o + h2o + |
| FB FB | MO12 MO13 | metabolism Naphthalene and Anthracene degradation | methyltetrahydropter oyltriglutamate homocysteine methyltransferase 2-nitropropane dioxygenase chlorophenol 4- monooxygenase chlorophenol 4- monooxygenase | 2.1.1.14 1.13.11 1.14.13 | H16_A0633/H16_B0223/ H16_B0757/H16_B1109/ H16_B1420/H16_B1836 H16_A1145/H16_B0495/ H16_B1480/H16_B2135 H16_A1145/H16_B0495/ H16_B1480/H16_B2135 H16_A1145/H16_B0495/ H16_B1480/H16_B2135 | pcaH2/unknown/unk nown/unknown/unk nown/unknown unknown/unknown/ unknown/unknown/ unknown/unknown/ unknown/unknown/ unknown/unknown/ unknown/unknown/ | phentrc + nadh + h + o2 -> c34dhphe + nad phentrc + o2 + nadh + h -> pheth12o + h2o + nad phentrc + o2 + nadh + h -> phatol + h2o + nad phentrc + o2 + nadh + h -> pheth910o + h2o + | phentrc + nadh + h + o2 -> c34dhphe + nad phentrc + o2 + nadh + h -> pheth12o + h2o + nad phentrc + o2 + nadh + h -> phatol + h2o + nad phentrc + o2 + nadh + h -> pheth910o + h2o + nad | phentrc + nadh + h + o2 -> c34dhphe + nad phentrc + o2 + nadh + h -> pheth12o + h2o + nad phentrc + o2 + nadh + h -> phatol + h2o + nad |
| FB FB | MO12 MO13 | metabolism Naphthalene and Anthracene degradation Naphthalene and Anthracene degradation Naphthalene and Anthracene degradation Naphthalene and Anthracene and Anthracene and Anthracene | methyltetrahydropter oyltriglutamate homocysteine methyltransferase 2-nitropropane dioxygenase chlorophenol 4- monooxygenase chlorophenol 4- chlorophenol 4- chlorophenol 4- | 21.1.14 113.11 114.13 114.13 114.13 | H16, A0633/H16, B0223/ H16, B0757/H16, B1109/ H16, B1420/H16, B1836 H16, A1145/H16, B0495/ H16, B1480/H16, B2135 H16, A1145/H16, B0495/ H16, B1480/H16, B2135 H16, A10578/H16, B0295/ H16, B1480/H16, B2135 | pcaH2/unknown/unk nown/unknown/unk nown/unknown unknown/unknown/ unknown/unknown unknown/unknown unknown/unknown unknown/unknown/ unknown/unknown/ unknown/unknown/ unknown/unknown/ | phentrc + nadh + h + o2 -> c34dhphe + nad phentrc + o2 + nadh + h -> pheth12o + h2o + nad phentrc + o2 + nadh + h -> phatol + h2o + nad phentrc + o2 + nadh + h -> pheth910o + h2o + nad hnaptho + nadh + o2 + 2 h -> napth12d + co2 | phentrc + nadh + h + o2 -> c34dhphe + nad phentrc + o2 + nadh + h -> pheth12o + h2o + nad phentrc + o2 + nadh + h -> phatol + h2o + nad phentrc + o2 + nadh + h -> pheth910o + h2o + nad hnaptho + nadh + o2 + 2 h -> napth12d + | phentrc + nadh + h + o2 -> c34dhphe + nad phentrc + o2 + nadh + h -> pheth12o + h2o + nad phentrc + o2 + nadh + h -> phath12 + h2o + nad phentrc + o2 + nadh + h -> phath910o + h2o + nad hnaptho + nadh + o2 + 2 h -> napth12d + co2 |
| FB FB | MO12 MO13 MO14 | metabolism Naphthalene and Anthracene degradation | methyltetrahydropter cyltrigitutamate homocysteine methyltransferase 2-nitropropane dioxygenase chlorophenol 4- monooxygenase chlorophenol 4- monooxygenase chlorophenol 4- monooxygenase | 21.1.14 113.11 114.13 114.13 114.13 | H16_A0633/H16_B0223/ H16_B075/H16_B1120/ H16_B1420/H16_B1836 H16_A1145/H16_B0495/ H16_B1480/H16_B2135 H16_A1145/H16_B0495/ H16_B1480/H16_B2135 H16_A1145/H16_B0495/ H16_B1480/H16_B2135 H16_A0578/H16_A0922/ H16_A1785/H16_B0750/ H16_B0876 | pcaH2/unknown/ | phentrc + nadh + h + o2 -> c34dhphe + nad phentrc + o2 + nadh + h -> pheth12o + h2o + nad phentrc + o2 + nadh + h -> phatol + h2o + nad phentrc + o2 + nadh + h -> pheth910o + h2o + nad hnaptho + nadh + o2 + 2 h -> napth12d + co2 + nad + h2o | phentrc + nadh + h + o2 -> c34dhphe + nad phentrc + o2 + nadh + h -> pheth12o + h2o + nad phentrc + o2 + nadh + h -> phatol + h2o + nad phentrc + o2 + nadh + h -> pheth910o + h2o + nad | phentrc + nadh + h + o2 -> c34dhphe + nad phentrc + o2 + nadh + h -> pheth12o + h2o + nad phentrc + o2 + nadh + h -> phatol + h2o + nad phentrc + o2 + nadh + h -> pheth910o + h2o + nad |
| FB FB | MO12 MO13 MO14 | metabolism Naphthalene and Anthracene degradation Naphthalene and Anthracene dagradation Naphthalene and Anthracene dagradation Naphthalene and Anthracene | methyltetrahydropter oyltrigitutamate- homocysteine methyltransferase 2-nitropropane dioxygenase chlorophenol 4- monooxygenase chlorophenol 4- monooxygenase salicylate hydroxylase 2-nitropropane | 21.1.14 113.11 114.13 114.13 114.13 | H16_A0633/H16_B0223/ H16_B075/H16_B1136/ H16_B1420/H16_B1836 H16_A1145/H16_B0495/ H16_B1480/H16_B2135 H16_A1145/H16_B0495/ H16_B1480/H16_B2135 H16_A1145/H16_B0495/ H16_A1745/H16_B0495/ H16_A1745/H16_B0750/ H16_A1745/H16_B0750/ H16_B0876/ H16_B0876/ H16_B0876/ H16_B0876/ H16_B0877/H16_B0223/ | pcaH2/unknown/ | phentrc + nadh + h + o2 -> c34dhphe + nad phentrc + o2 + nadh + h -> pheth12o + h2o + nad phentrc + o2 + nadh + h -> phatol + h2o + nad phentrc + o2 + nadh + h -> pheth910o + h2o + nad hnaptho + nadh + o2 + 2 h -> napth12d + co2 + nad + h2o | phentrc + nadh + h + o2 -> c34dhphe + nad phentrc + o2 + nadh + h -> pheth12o + h2o + nad phentrc + o2 + nadh + h -> phatol + h2o + nad phentrc + o2 + nadh + h -> pheth910o + h2o + nad hnaptho + nadh + o2 + 2 h -> napth12d + | phentrc + nadh + h + o2 -> c34dhphe + nad phentrc + o2 + nadh + h -> pheth12o + h2o + nad phentrc + o2 + nadh + h -> phath12 + h2o + nad phentrc + o2 + nadh + h -> phath910o + h2o + nad hnaptho + nadh + o2 + 2 h -> napth12d + co2 |
| FB FB | MO12 MO13 MO14 ALCH1 | metabolism Naphthalene and Anthracene degradation | methyltertahydropter oyltrigitutamate- homocysteine methyltransferase 2-nitropropane dioxygenase chlorophenol 4- monooxygenase chlorophenol 4- monooxygenase salicylate hydroxylase 2-nitropropane dioxygenase | 21.1.14 113.11 114.13 114.13 114.13 | H16_A0633/H16_B0223/ H16_B075/H16_B1136/ H16_B1420/H16_B1836 H16_A1145/H16_B0495/ H16_B1480/H16_B2135 H16_A1145/H16_B0495/ H16_B1480/H16_B2135 H16_A1145/H16_B0495/ H16_B1480/H16_B2135 H16_A0578/H16_A0922/ H16_A1785/H16_B0750/ H16_B0875/ H16_B0875/H16_B0223/ H16_B0875/H16_B10575/ H16_B0875/H16_B10575/ H16_B0875/H16_B10575/ H16_B0875/H16_B1136/ H16_B0875/H16_B1136/ H16_B18270/H16_B1136/ | pcaH2/unknown/ | phentrc + nadh + h + o2 -> c34dhphe + nad phentrc + o2 + nadh + h -> pheth12o + h2o + nad phentrc + o2 + nadh + h -> phatol + h2o + nad phentrc + o2 + nadh + h -> pheth910o + h2o + nad hnaptho + nadh + o2 + 2 h -> napth12d + co2 + nad + h2o | phentrc + nadh + h + o2 -> c34dhphe + nad phentrc + o2 + nadh + h -> pheth12o + h2o + nad phentrc + o2 + nadh + h -> phath01 + h2o + nad phentrc + o2 + nadh + h -> pheth910o + h2o + nad hnaptho + nadh + o2 + 2 h -> napth12d + co2 + nad + h2o | phentrc + nadh + h + o2 -> c34dhphe + nad phentrc + o2 + nadh + h -> pheth12o + h2o + nad phentrc + o2 + nadh + h -> phatol + h2o + nad phentrc + o2 + nadh + h -> phatol + h2o + nad phentrc + o2 + nadh + h -> pheth910o + h2o + nad hnaptho + nadh + o2 + 2 h -> napth12d + co2 + nad + h2o |
| FB FB SA | MO12 MO13 MO14 ALCH1 | metabolism Naphthalene and Anthracene degradation Naphthalene and Naphthalene and Nathracene degradation Naphthalene Anthracene degradation Naphtha | methyltetrahydropter oyltriglutamate homocysteine methyltransferase 2-nitropropane dioxygenase chlorophenol 4- monooxygenase chlorophenol 4- monooxygenase chlorophenol 4- monooxygenase 2-nitropropane dioxygenase | 21.1.14 113.11 114.13 114.13 114.13.1 113.11 | H16_A0633/H16_B0223/ H16_B075/H16_B1129/ H16_B1420/H16_B1836 H16_A1145/H16_B0495/ H16_B1480/H16_B2135 H16_A1145/H16_B0495/ H16_B1480/H16_B2135 H16_A0578/H16_B0235/ H16_A0578/H16_B0795/ H16_B0876 H | pcaH2/unknown/ | phentrc + nadh + h + o2 -> c34dhphe + nad phentrc + o2 + nadh + h -> pheth12o + h2o + nad phentrc + o2 + nadh + h -> phatol + h2o + nad phentrc + o2 + nadh + h -> pheth910o + h2o + nad hnaptho + nadh + o2 + 2 h -> napth12d + co2 + nad + h2o | phentrc + nadh + h + o2 -> c34dhphe + nad phentrc + o2 + nadh + h -> pheth12o + h2o + nad phentrc + o2 + nadh + h -> phath01 + h2o + nad phentrc + o2 + nadh + h -> pheth910o + h2o + nad hnaptho + nadh + o2 + 2 h -> napth12d + co2 + nad + h2o | phentrc + nadh + h + o2 -> c34dhphe + nad phentrc + o2 + nadh + h -> pheth12o + h2o + nad phentrc + o2 + nadh + h -> phatol + h2o + nad phentrc + o2 + nadh + h -> phatol + h2o + nad phentrc + o2 + nadh + h -> pheth910o + h2o + nad hnaptho + nadh + o2 + 2 h -> napth12d + co2 + nad + h2o |
| FB FB SA | MO12 MO13 MO14 ALCH1 TPPD7 | metabolism Naphthalene and Anthracene degradation degradation Naphthalene and Anthracene degradation | methyltetrahydropter oyltrigitutamate homocysteine methyltransferase 2-nitropropane dioxygenase chlorophenol 4- monooxygenase chlorophenol 4- monooxygenase chlorophenol 4- monooxygenase salicylate hydroxylase 2-nitropropane dioxygenase 2-nitropropane dioxygenase | 21.1.14 113.11 114.13 114.13 114.13.1 113.11 | H16, A0633/H16, B0223/ H16, B0757/H16, B1109/ H16, B1420/H16, B1836 H16, A1145/H16, B0495/ H16, B1480/H16, B2135 H16, A1145/H16, B0495/ H16, B1480/H16, B2135 H16, A0578/H16, B0495/ H16, B1480/H16, B2135 H16, A0578/H16, B0750/ H16, B1480/H16, B0750/ H16, B0750/H16, B0750/ H16, B0876/ H16, A0633/H16, B0223/ H16, B0757/H16, B1109/ H16, B1420/H16, B1836 H16, A0633/H16, B10223/ H16, B0757/H16, B1109/ H16, B1420/H16, B1836 | pcaH2/unknown/ | phentrc + nadh + h + o2 -> c34dhphe + nad phentrc + o2 + nadh + h -> pheth12o + h2o + nad phentrc + o2 + nadh + h -> phatol + h2o + nad phentrc + o2 + nadh + h -> pheth910o + h2o + nad hnaptho + nadh + o2 + 2 h -> napth12d + co2 + nad + h2o 12anthcd + o2 -> carvnapc + 2 h | phentrc + nadh + h + o2 -> c34dhphe + nad phentrc + o2 + nadh + h -> pheth12o + h2o + nad phentrc + o2 + nadh + h -> phatol + h2o + nad phentrc + o2 + nadh + h -> pheth910o + h2o + nad hnaptho + nadh + o2 + 2 h -> napth12d + co2 + nad + h2o 12anthcd + o2 -> carvnapc + 2 h | phentrc + nadh + h + o2 -> c34dhphe + nad phentrc + o2 + nadh + h -> pheth12o + h2o + nad phentrc + o2 + nadh + h -> phatol + h2o + nad phentrc + o2 + nadh + h -> phatol + h2o + nad phentrc + o2 + nadh + h -> pheth910o + h2o + nad hnaptho + nadh + o2 + 2 h -> napth12d + co2 + nad + h2o 12anthcd + o2 -> carvnapc + 2 h |
| FB FB SA NTI | MO12 MO13 MO14 ALCH1 TPPD7 | metabolism Naphthalene and Anthracene degradation Naphth | methyltertahydropter oyltrigiutamate- homocysteine methyltransferase 2-nitropropane dioxygenase chlorophenol 4- monooxygenase chlorophenol 4- monooxygenase chlorophenol 4- monooxygenase 2-nitropropane dioxygenase 2-nitropropane dioxygenase 2-nitropropane dioxygenase 2-nitropropane | 21.1.14 113.11- 114.13- 114.13- 114.13- 114.13- 114.13.1 113.11- | H16, A0633/H16, B0223/ H16, B0757/H16, B1109/ H16, B1420/H16, B1836 H16, A1145/H16, B0495/ H16, B1480/H16, B2135 H16, A1145/H16, B0495/ H16, B1480/H16, B2135 H16, A0578/H16, B0495/ H16, B1480/H16, B2135 H16, A0578/H16, B0750/ H16, B0876 H16, A053/H16, B1036/ H16, B0575/H16, B1036/ H16, B0575/H16, B1036/ H16, B0575/H16, B1036/ H16, B0575/H16, B1036/ H16, B1420/H16, B1836 H16, A0633/H16, B0223/ H16, B0575/H16, B1036/ H16, B1420/H16, B1836 H16, A0633/H16, B0233/ H16, B0575/H16, B1836 H16, B0633/H16, B1836 | pcaH2/unknown/ | phentrc + nadh + h + o2 -> c34dhphe + nad phentrc + o2 + nadh + h -> pheth12o + h2o + nad phentrc + o2 + nadh + h -> phatol + h2o + nad phentrc + o2 + nadh + h -> pheth910o + h2o + nad hnaptho + nadh + o2 + 2 h -> napth12d + co2 + nad + h2o 12anthcd + o2 -> carvnapc + 2 h | phentrc + nadh + h + o2 -> c34dhphe + nad phentrc + o2 + nadh + h -> pheth12o + h2o + nad phentrc + o2 + nadh + h -> phatol + h2o + nad phentrc + o2 + nadh + h -> pheth910o + h2o + nad hnaptho + nadh + o2 + 2 h -> napth12d + co2 + nad + h2o 12anthcd + o2 -> carvnapc + 2 h | phentrc + nadh + h + o2 -> c34dhphe + nad phentrc + o2 + nadh + h -> pheth12o + h2o + nad phentrc + o2 + nadh + h -> phatol + h2o + nad phentrc + o2 + nadh + h -> phatol + h2o + nad phentrc + o2 + nadh + h -> pheth910o + h2o + nad hnaptho + nadh + o2 + 2 h -> napth12d + co2 + nad + h2o 12anthcd + o2 -> carvnapc + 2 h |
| FB FB SA NTI | MO12 MO13 MO14 ALCH1 TPPD7 | metabolism Naphthalene and Anthracene degradation Naphthalene and Anthracene | methyltertahydropter oyltrigiutamate homocysteine methyltransferase chlorophenol 4- monoovygenase chlorophenol 4- monoovygenase chlorophenol 4- monoovygenase chlorophenol 4- monoovygenase salicylate hydroxylase 2-nitropropane dioxygenase 2-nitropropane dioxygenase 2-nitropropane dioxygenase | 21.1.14 113.11- 114.13- 114.13- 114.13- 114.13- 114.13.1 113.11- | H16_A0633/H16_B0223/ H16_B075/H16_B1136/ H16_B1420/H16_B1136 H16_A1145/H16_B0495/ H16_B1480/H16_B2135 H16_A1145/H16_B0495/ H16_B1480/H16_B2135 H16_A1145/H16_B0495/ H16_A0578/H16_A0922/ H16_A1785/H16_B0736/ H16_B0876/ H16_B0876/ H16_B0876/ H16_B083/H16_B0233/ H16_B075/H16_B1109/ H16_B075/H16_B1109/ H16_B075/H16_B1109/ H16_B075/H16_B0123/ H16_B075/H16_B1109/ H16_B075/H16_B1109/ H16_B075/H16_B1109/ H16_B075/H16_B1109/ H16_B1420/H16_B1836 | pcaH2/unknown/unk nown/unknown/unk nown/unknown unknown/unknown unknown/unknown unknown/unknown unknown/unknown unknown/unknown unknown/unknown unknown/unknown/ unknown/unknown/ unknown/unknown/ unknown/unknown/ unknown/unknown/ unknown/unknown/ unknown/unknown/ unknown/unknown/ unknown/unknown/ unknown/unknown/ unknown/unknown/ unknown/unknown/ unknown/unknown/ unknown | phentrc + nadh + h + o2 -> c34dhphe + nad phentrc + o2 + nadh + h -> pheth12o + h2o + nad phentrc + o2 + nadh + h -> phatol + h2o + nad phentrc + o2 + nadh + h -> pheth910o + h2o + nad hnaptho + nadh + o2 + 2 h -> napth12d + co2 + nad + h2o 12anthcd + o2 -> carvnapc + 2 h 12anthcd + o2 -> carvnapc + 2 h 3h2napth + o2 -> cmcdopp + h | phentrc + nadh + h + o2 -> c34dhphe + nad phentrc + o2 + nadh + h -> pheth12o + h2o + nad phentrc + o2 + nadh + h -> phatol + h2o + nad phentrc + o2 + nadh + h -> pheth910o + h2o + nad hnaptho + nadh + o2 + 2 h -> napth12d + co2 + nad + h2o 12anthcd + o2 -> carvnapc + 2 h 12anthcd + o2 -> hnapoxen + h | phentrc + nadh + h + o2 -> c34dhphe + nad phentrc + o2 + nadh + h -> pheth12o + h2o + nad phentrc + o2 + nadh + h -> phath12 + h2o + nad phentrc + o2 + nadh + h -> pheth910o + h2o + nad hnaptho + nadh + o2 + 2 h -> napth12d + co2 + nad + h2o 12anthcd + o2 -> carvnapc + 2 h 12anthcd + o2 -> hnapoxen + h |
| FB FB SA NT NT NT | MO12 MO13 MO14 ALCH1 TPPD7 | metabolism Naphthalene and Anthracene degradation Naphthalene and Anthracene dagradation Naphthalene and Anthracene dagradation Naphthalene and Anthracene dagradation | methyltertahydropter oyltrigiutamate- homocysteine methyltransferase 2-nitropropane dioxygenase chlorophenol 4- monooxygenase chlorophenol 4- monooxygenase chlorophenol 4- monooxygenase 2-nitropropane dioxygenase 2-nitropropane dioxygenase 2-nitropropane dioxygenase 2-nitropropane | 211.14 1.13.11 1.14.13 1.14.13 1.14.13.1 1.13.11 1.13.11 1.13.11 | H16_A0633/H16_B0223/ H16_B075/H16_B1109/ H16_B1420/H16_B1836 H16_A1145/H16_B0495/ H16_B1480/H16_B2135 H16_A1145/H16_B0495/ H16_B1480/H16_B2135 H16_A0578/H16_B02135 H16_A0578/H16_B0750/ H16_B0876/ H16_A0633/H16_B0223/ H16_B075/H16_B1109/ H16_B1420/H16_B1836 H16_A0633/H16_B0223/ H16_B075/H16_B1109/ H16_B1420/H16_B1836 H16_A0633/H16_B0223/ H16_B075/H16_B1109/ H16_B1420/H16_B1836 H16_A0633/H16_B0223/ H16_B075/H16_B1109/ H16_B1420/H16_B1836 H16_A0633/H16_B0223/ H16_B075/H16_B1109/ H16_B1420/H16_B1836 H16_A0633/H16_B0223/ H16_B075/H16_B1109/ H16_B1420/H16_B1836 | pcaH2/unknown/unk nown/unknown/unk nown/unknown unknown/unknown unknown/unknown unknown/unknown unknown/unknown unknown/unknown unknown/unknown unknown/unknown unknown/unknown unknown/unknown/unk nown/unknown/unk nown/unknown/unk nown/unknown/unk nown/unknown/unk nown/unknown/unk nown/unknown/unk nown/unknown/unk nown/unknown/unk nown/unknown/unk nown/unknown/unk nown/unknown/unk nown/unknown/unk nown/unknown/unk nown/unknown/unk nown/unknown/unk nown/unknown/unk nown/unknown/unk | phentrc + nadh + h + o2 -> c34dhphe + nad phentrc + o2 + nadh + h -> pheth12o + h2o + nad phentrc + o2 + nadh + h -> phatol + h2o + nad phentrc + o2 + nadh + h -> pheth910o + h2o + nad hnaptho + nadh + o2 + 2 h -> napth12d + co2 + nad + h2o 12anthcd + o2 -> carvnapc + 2 h 12anthcd + o2 -> carvnapc + 2 h 3h2napth + o2 -> cmcdopp + h | phentrc + nadh + h + o2 -> c34dhphe + nad phentrc + o2 + nadh + h -> pheth12o + h2o + nad phentrc + o2 + nadh + h -> phatol + h2o + nad phentrc + o2 + nadh + h -> pheth910o + h2o + nad hnaptho + nadh + o2 + 2 h -> napth12d + co2 + nad + h2o 12anthcd + o2 -> carvnapc + 2 h 12anthcd + o2 -> hnapoxen + h | phentrc + nadh + h + o2 -> c34dhphe + nad phentrc + o2 + nadh + h -> pheth12o + h2o + nad phentrc + o2 + nadh + h -> phath12 + h2o + nad phentrc + o2 + nadh + h -> pheth910o + h2o + nad hnaptho + nadh + o2 + 2 h -> napth12d + co2 + nad + h2o 12anthcd + o2 -> carvnapc + 2 h 12anthcd + o2 -> hnapoxen + h |
| FB FB SA NT NT NT | MO12 MO13 MO14 ALCH1 TPPD7 TPPD8 | metabolism Naphthalene and Anthracene degradation Naphthalene and Anthracene | methyltetrahydropter oyltrigitutamate- homocysteine homocysteine chlorophenol 4- monooxygenase chlorophenol 4- monooxygenase chlorophenol 4- monooxygenase salicylate hydroxylase 2-nitropropane dioxygenase 2-nitropropane dioxygenase 2-nitropropane dioxygenase 2-nitropropane | 211.14 1.13.11 1.14.13 1.14.13 1.14.13.1 1.13.11 1.13.11 1.13.11 | H16, A0633/H16, B0223/ H16, B075/H16, B1109/ H16, B1420/H16, B1836 H16, A1145/H16, B0495/ H16, B1480/H16, B2135 H16, A1145/H16, B0495/ H16, B1480/H16, B2135 H16, A1145/H16, B0495/ H16, B1480/H16, B2135 H16, A0578/H16, A0922/ H16, A1785/H16, B0750/ H16, B075/H16, B1109/ H16, B142/0/H16, B1836 H16, A0633/H16, B0223/ H16, B0757/H16, B1109/ H16, B142/0/H16, B1836 H16, A0633/H16, B0223/ H16, B0757/H16, B1109/ H16, B142/0/H16, B1836 | pcaH2/unknown/unk nown/unknown/unk nown/unknown unknown/unknown unknown/unknown unknown/unknown unknown/unknown unknown/unknown unknown/unknown unknown/unknown unknown/unknown unknown/unknown/unk nown/unknown/unk nown/unknown/unk nown/unknown/unk nown/unknown/unk nown/unknown/unk nown/unknown/unk nown/unknown/unk nown/unknown/unk nown/unknown/unk nown/unknown/unk nown/unknown/unk nown/unknown/unk nown/unknown/unk nown/unknown/unk nown/unknown/unk nown/unknown/unk nown/unknown/unk | phentrc + nadh + h + o2 -> c34dhphe + nad phentrc + o2 + nadh + h -> pheth12o + h2o + nad phentrc + o2 + nadh + h -> phatol + h2o + nad phentrc + o2 + nadh + h -> pheth910o + h2o + nad phentrc + o2 + nadh + h -> pheth910o + h2o + nad hnaptho + nadh + o2 + 2 h -> napth12d + co2 + nad + h2o 12anthcd + o2 -> carvnapc + 2 h 12anthcd + o2 -> hnapoxen + h 3h2napth + o2 -> cmcdopp + h | phentrc + nadh + h + o2 -> c34dhphe + nad phentrc + o2 + nadh + h -> pheth12o + h2o + nad phentrc + o2 + nadh + h -> phatol + h2o + nad phentrc + o2 + nadh + h -> pheth910o + h2o + nad hnaptho + nadh + o2 + 2 h -> napth12d + co2 + nad + h2o 12anthcd + o2 -> carvnapc + 2 h 12anthcd + o2 -> chnapoxen + h 3h2napth + o2 -> cmcdopp + h | phentrc + nadh + h + o2 -> c34dhphe + nad phentrc + o2 + nadh + h -> pheth12o + h2o + nad phentrc + o2 + nadh + h -> phath01 + h2o + nad phentrc + o2 + nadh + h -> phath01 + h2o + nad phentrc + o2 + nadh + h -> pheth910o + h2o + nad hnaptho + nadh + o2 + 2 h -> napth12d + co2 + nad + h2o 12anthcd + o2 -> carvnapc + 2 h 12anthcd + o2 -> hnapoxen + h 3h2napth + o2 -> cmcdopp + h |

| | Naphthalene and | | | | | | | |
|---------|---|---|------------|---|-------------------------------------|---|--|--|
| FBMO15 | Anthracene degradation | chlorophenol 4- monooxygenase | 1.14.13 | H16_A1145/H16_B0495/ H16_B1480/H16_B2135 | | salcyl + nadh + o2 + h -> gensa + nad + h2o | salcyl + nadh + o2 + h -> gensa + nad + h2o | salcyl + nadh + o2 + h -> gensa + nad + h2o |
| FBMO15p | Naphthalene and Anthracene degradation | chlorophenol 4- monooxygenase | 1.14.13 | H16_A1145/H16_B0495/ H16_B1480/H16_B2135 | | salcyl + nadph + o2 + 2 h -> gensa + nadp + h2o | salcyl + nadph + o2 + h -> gensa + nadp + $h2o$ | salcyl + nadph + o2 + h -> gensa + nadp + h2o |
| SALCH2 | Naphthalene and Anthracene degradation | salicylate hydroxylase | 1.14.13.1 | H16_A0578/H16_A0922/ H16_A1785/H16_B0750/ H16_B0876 | | salcyl + o2 + nadh + 2 h -> catech + co2 + nad + h2o | salcyl + o2 + nadh + 2 h -> catech + co2 + nad + $h2o$ | salcyl + o2 + nadh + 2 h -> catech + co2 + nad + $h2o$ |
| ANOXDR | Naphthalene and Anthracene degradation | Oxidoreductase | 1.14 | H16_B0730/H16_B0738/ H16_B2129 | unknown/unknown/ unknown | aniline + o2 + h + h2 -> catech + nh4 | aniline + o2 + h + h2 -> catech + nh4 | aniline + o2 + h + h2 -> catech + nh4 |
| NITOXDR | Naphthalene and Anthracene degradation | Oxidoreductase | 1.14 | H16_B0730/H16_B0738/ H16_B2129 | unknown/unknown/ unknown | nitbz + o2 + h2 -> catech + no2 + h | nitbz + o2 + h2 -> catech + no2 + h | nitbz + o2 + h2 -> catech + no2 + h |
| PHE2MO5 | Naphthalene and Anthracene degradation | phenol 2- monooxygenase | 1.14.13.7 | H16_B0539&H16_B0540 &H16_B0541&H16_B05 42&H16_B0543&H16_B 0544 | | phenol + o2 + nadph + 2 h -> catech + nadp + h2o | phenol + o2 + nadph + h -> catech + nadp + h2o | phenol + o2 + nadph + h -> catech + nadp + h2o |
| PHOXDR | Naphthalene and Anthracene | Oxidoreductase | 1.14 | H16_B0730/H16_B0738/ H16_B2129 | unknown/unknown/ unknown | pheborn + o2 + 2.5 h2 -> phenol + 3 h2o | pheborn + o2 + 2.5 h2 -> phenol + 3 h2o | pheborn + o2 + 2.5 h2 -> phenol + 3 h2o |
| ANTOXDR | degradation Naphthalene and Anthracene | Oxidoreductase | 1.14 | H16_B0730/H16_B0738/ H16_B2129 | unknown/unknown/ unknown | anthrc + o2 + h2 -> anthr910d | anthrc + o2 + h2 -> anthr910d | anthrc + o2 + h2 -> anthr910d |
| NACMNP | degradation Nicotinate and Nicotinamide | | 2.4.2.11 | H16_A2589 | pncB | atp + h2o + nac + prpp + h -> adp + nacn + pi + ppi | nac + prpp -> nacn + ppi | atp + h2o + nac + prpp -> adp + nacn + pi + ppi + h |
| NACNDP | Micotinate and Nicotinamide | pyrophosphorylase nicotinate-nucleotide diphosphorylase | 2.4.2.19 | H16_A3037/H16_B0560 | nadC/unknown | 2 h + prpp + qa <-> co2 + nacn + ppi | h + nmn + 03 co 202 + nacn + nni | |
| NACNDP | metabolism Nicotinate and | (carboxylating) | 2.4.2.19 | H16_A3U3//H16_BU56U | nadc/unknown | 2 n + prpp + qa <-> co2 + nacn + ppi | h + prpp + qa <-> co2 + nacn + ppi | h + prpp + qa <-> co2 + nacn + ppi |
| NADK | Nicotinamide metabolism Nicotinate and | NAD kinase nicotinamide- | 2.7.1.23 | H16_A1132/H16_B0143 | unknown/acoX | atp + nad -> adp + nadp | atp + nad -> adp + nadp + h | atp + nad -> adp + nadp + h |
| NAMNAT | Nicotinamide metabolism Nicotinate and | nucleotide adenylyltransferase | 2.7.7.18 | H16_A0913 | nadD | atp + namn -> nad + ppi | atp + namn -> nad + ppi | atp + namn -> nad + ppi |
| NACM | Nicotinamide metabolism | nicotinamidase | 3.5.1.19 | H16_A1527 | pncA | h2o + nam -> nac + nh4 | h2o + nam -> nac + nh4 | h2o + nam -> nac + nh4 |
| NADDP1 | Nicotinate and Nicotinamide metabolism | NAD diphosphatase | 3.6.1.22 | H16_A2761 | unknown | h2o + nad -> amp + namn | h2o + nad -> amp + namn + 2 h | h2o + nad -> amp + namn + 2 h |
| ASPOX2 | metabolism | L-aspartate oxidase | 1.4.3.16 | H16_A3036 | nadB | asp + o2 <-> h + h2o2 + iasp | asp + o2 <-> h + h2o2 + iasp | asp + o2 <-> h + h2o2 + iasp |
| QULS | Nicotinate and Nicotinamide metabolism | quinolinate synthase | | H16_A3038 | nadA (2.5.1.72) | dhap + iasp <-> 2 h2o + pi + qa | dhap + iasp <-> 2 h2o + pi + qa | dhap + iasp <-> 2 h2o + pi + qa |
| NTNAT | Nicotinate and Nicotinamide metabolism | nicotinate-nucleotide adenylyltransferase | 2.7.7.18 | H16_A0913 | nadD | atp + nacn <-> dnad + ppi + h | atp + nacn <-> dnad + ppi + h | atp + nacn <-> dnad + ppi + h |
| NTD13 | Nicotinate and Nicotinamide metabolism | 5'-nucleotidase | 3.1.3.5 | H16_A2376 | surE | namn + h2o -> namd + pi | namn + h2o -> namd + pi | namn + h2o -> namd + pi |
| NTD14 | Nicotinate and Nicotinamide metabolism | 5'-nucleotidase | 3.1.3.5 | H16_A2376 | surE | nacn + h2o -> nacd + pi | nacn + h2o -> nacd + pi | nacn + h2o -> nacd + pi |
| NADDP2 | Nicotinate and Nicotinamide metabolism | NAD diphosphatase | 3.6.1.22 | H16_A2761 | unknown | dnad + h2o + h -> amp + nacn | dnad + h2o -> amp + nacn + h | dnad + h2o -> amp + nacn + h |
| NODOX1 | Nitrogen Metabolism | nitric oxide dioxygenase | 1.14.12.17 | H16_A3533 | hmp2 | nadh + 2 no + 2 o2 -> h + nad + 2 no3 | nadh + 2 no + 2 o2 -> h + nad + 2 no3 | nadh + 2 no + 2 o2 -> h + nad + 2 no3 |
| NODOX2 | Nitrogen Metabolism | nitric ovide | 1.14.12.17 | H16_A3533 | hmp2 | nadph + 2 no + 2 o2 -> nadp + 2 no3 | nadph + 2 no + 2 o2 -> nadp + 2 no3 + h | nadph + 2 no + 2 o2 -> nadp + 2 no3 + h |
| NO3RUQ1 | Nitrogen Metabolism | Nitrate reductase | 1.7.99.4 | H16_B0776/H16_B2265/ H16_B2266/H16_B2267/ | unknown/narG2/nar H2/narJ2/narI2 | 2 h + no3 + uqh2 -> 2 h_e + h2o + no2 + uq | no3 + uqh2 + 2 h -> h2o + no2 + uq + 2 h_e | 2 h + no3 + uqh2 -> 2 h_e + h2o + no2 + uq |
| CYNTL | Nitrogen | cyanate lyase | 4.2.1.104 | H16_B2268 H16_B0046 | cynS | cynt + hco3 -> co2 + cabm | cynt + h + hco3 -> co2 + cabm | cynt + h + hco3 -> co2 + cabm |
| NADFRBO | | NADH:flavorubredoxi | | H16_B2323 | norB2 | h + nadh + 2 no -> h2o + n2o + nad | h + nadh + 2 no -> h2o + n2o + nad | h + nadh + 2 no -> h2o + n2o + nad |
| | Metabolism Nitrogen | n oxidoreductase cytochrome cd1 | | | | | | |
| CNITRT | metabolism Nitrogen | (NirS) | 1.7.2.1 | H16_B2277 H16_B0777&H16_B0778 | nirS unknown&nasE&nas | no2 + fadh2 + h -> no + h2o + fad | no2 + fadh2 + h -> no + h2o + fad | no2 + fadh2 + h -> no + h2o + fad |
| NITRT | metabolism | | 1.7.1.4 | &H16_B0779&H16_B09 48 | D&unknown | no2 + 3 nadh + 5 h -> 3 nad + nh4 + 2 h2o | no2 + 3 nadh + 5 h -> 3 nad + nh4 + 2 h2o | no2 + 3 nadh + 5 h -> 3 nad + nh4 + 2 h2o |
| NITORT | Nitrogen metabolism Nucleotide Salvage | reductase | 1.7.99.6 | PHG252 | nosZ | n2o + fadh2 -> n2 + fad + h2o | n2o + fadh2 -> n2 + fad + h2o + h | n2o + fadh2 -> n2 + fad + h2o + h |
| ADNK3 | Pathway Nucleotide Salvage | (GTP) | 2.7.4.3 | H16_A0603 | adk | amp + gtp <-> adp + gdp | amp + gtp + h <-> adp + gdp | amp + gtp <-> adp + gdp |
| ADNK4 | Pathway | (ITP) dTDP-4- | 2.7.4.3 | H16_A0603 | adk | amp + itp <-> adp + idp | amp + itp + h <-> adp + idp | amp + itp <-> adp + idp |
| TDPDRHR | Nucleotide sugars metabolism | | 1.1.1.133 | H16_A1850/H16_A2908 | rfbD/unknown | dtdp4d6dm + 2 h + nadph -> dtdprmn + nadp | dtdp4d6dm + h + nadph -> dtdprmn + nadp | dtdp4d6dm + h + nadph -> dtdprmn + nadp |
| UDPG6D | Nucleotide sugars metabolism | LIDPolycore 6- | 1.1.1.22 | H16_A0802 | ugd | h2o + 2 nad + udpg -> 3 h + 2 nadh + udpglcur | h2o + 2 nad + udpg -> 3 h + 2 nadh + udpglcur | h2o + 2 nad + udpg -> 3 h + 2 nadh + udpglcur |
| G1PTT1 | Nucleotide sugars metabolism | glucose-1-phosphate thymidylyltransferase | 2.7.7.24 | H16_A1864 | rfbA | dttp + g1p -> dtdpglu + ppi | dttp + g1p -> dtdpglu + ppi | dttp + g1p -> dtdpglu + ppi |
| UG1PUT | Nucleotide sugars metabolism | uriuyiyitialisielase | 2.7.7.9 | H16_A2752 | galU | g1p + utp -> ppi + udpg | glp + utp -> ppi + udpg | glp + utp -> ppi + udpg |
| TDPGLUD | Nucleotide sugars metabolism | (irreversible) dTDPglucose 4,6- dehydratase | 4.2.1.46 | H16_A1851/H16_A2909/ H16_B1642 | rfbB2/unknown/unkn | dtdpglu -> dtdp4d6dg + h2o | dtdpglu -> dtdp4d6dg + h2o | dtdpglu -> dtdp4d6dg + h2o |
| TDPDRHE | Nucleotide sugars metabolism | dTDP-4- | 5.1.3.13 | H16_A1848/H16_A2906 | | dtdp4d6dg -> dtdp4d6dm | dtdp4d6dg -> dtdp4d6dm | dtdp4d6dg -> dtdp4d6dm |
| G1PTT2 | Nucleotide sugars metabolism | alusasa 1 nhasabata | 2.7.7.33 | H16_A2893 | rfbF | dttp + g1p -> dtdpglu + ppi | dttp + g1p -> dtdpglu + ppi | dttp + g1p -> dtdpglu + ppi |
| UDPG4E1 | | UDP-glucose 4- | 5.1.3.2 | H16_B0226/H16_B0283 | galE/unknown | dtdpglu <-> dtdpgal | dtdpglu <-> dtdpgal | dtdpglu <-> dtdpgal |
| UDPG4E2 | | epimerase UDP-glucose 4- | 5.1.3.2 | H16_B0226/H16_B0283 | galE/unknown | udpg <-> udpgal | udpg <-> udpgal | udpg <-> udpgal |
| AMTF2 | | epimerase aminomethyltransfer | 2.1.2.10 | H16_A1567/H16_A3619 | | methf + h2o -> 5fthf + h | methf + h2o -> 5fthf + h | methf + h2o -> 5fthf + h |
| | by Folate One carbon pool | ase 5- | | | | | | |
| FORTF | by Folate | formyltetrahydrofolat e cyclo-ligase L-Lactate | 6.3.3.2 | H16_A0249 | unknown | Sfthf + atp + h -> adp + pi + methf | 5fthf + atp -> adp + pi + methf | Sfthf + atp -> adp + pi + methf |
| LACDHq | Oxidative Phosphorylation | | 1.1.2.3 | H16_B0460/H16_B1817 | lldA/lldD | llac + uq -> pyr + uqh2 | llac + uq -> pyr + uqh2 | llac + uq -> pyr + uqh2 |
| DLDHDq | Oxidative Phosphorylation | D-lactate | 1.1.2.4 | H16_A3091 | dld | lac + uq -> pyr + uqh2 | lac + uq -> pyr + uqh2 | lac + uq -> pyr + uqh2 |
| | Oxidative | glycerol-3-phosphate | | | | glyc3p + uq -> dhap + uqh2 | Short and the state | |
| GL3PDq | Phosphorylation | dehydrogenase (ubiquinone-8) | 1.1.99.5 | H16_A2508/H16_B1198 | unknown/unknown | glycsp + uq -> unap + uqnz | glyc3p + uq -> dhap + uqh2 | glyc3p + uq -> dhap + uqh2 |

| | Oxidative | hydrogenase | | | | | | |
|---|--|--|---|---|---|---|---|---|
| HYDGq | Phosphorylation | (ubiquinone-8: 2 protons) formate | 1.18.99.1 | | | 2 h + h2 + uq -> 2 h_e + uqh2 | 2 h + uq + h2 -> uqh2 + 2 h_e | 2 h + h2 + uq -> 2 h_e + uqh2 |
| FDHGq | Oxidative Phosphorylation | dehydrogenase (quinone-8) | 1.2.2.1 | | | formate + h + uq -> co2 + uqh2 | formate + 3 h + uq -> co2 + uqh2 + 2 h_e | formate + h + uq -> co2 + uqh2 |
| POX | Oxidative Phosphorylation | pyruvate oxidase | 1.2.2.2 | H16_A3123 | unknown | h2o + pyr + uq -> ac + co2 + uqh2 | h2o + pyr + uq -> ac + co2 + uqh2 | h2o + pyr + uq -> ac + co2 + uqh2 |
| SUCCD1 | Oxidative Phosphorylation | succinate dehydrogenase | 1.3.99.1 | | sdhB&sdhA&sdhD& sdhC&unknown | uq + succ -> fum + uqh2 | uq + succ -> fum + uqh2 | uq + succ -> fum + uqh2 |
| | | | | H16_A0850&H16_A085 1&H16_A0852&H16_A1 | pntAa1&pntAb1&pn | | | |
| NADPTH | Oxidative Phosphorylation | NAD(P) transhydrogenase | 1.6.1.2 | 264&H16_A1265&H16_ A1266&H16_A3128&H1 | tB1&pntAa2&pntAb 2&pntB2&pntAa3&p | 2 h_e + nadh + nadp -> 3 h + nad + nadph | nadh + nadp + 2 h_e -> 2 h + nad + nadph | 2 h_e + nadh + nadp -> 2 h + nad + nadph |
| | | | | 6_A3130&H16_A3131& H16_B1714&H16_B1715 | nts3&pnts4&pntA4 | | | |
| | | NADH | | H16_A0251/H16_A1050/ H16_A1051/H16_A1052/ H16_A1053/H16_A1054/ | unknown/nuoA/nuo | 4 h + nadh + uq -> 3 h_e + nad + uqh2 | | |
| NADHHq1 | Oxidative Phosphorylation | dehydrogenase (ubiquinone-8 & 3 | 1.6.5.3 | H16_A1055/H16_A1056/ H16_A1057/H16_A1058/ | B/nuoC/nuoD/nuoE/ nuoF/nuoG/nuoH/nu | 4 h + nadh + uq -> 3 h_e + nad + uqh2 | 4 h + nadh + uq -> nad + uqh2 + 3 h_e | 4 h + nadh + uq -> 3 h_e + nad + uqh2 |
| | | protons) | | H16_A1059/H16_A1060/ H16_A1061/H16_A1062/ | oI/nuoJ/nuoK/nuoL/ nuoM/nuoN/ | | | |
| | | | | H16 A0251/H16 A1050/ | | | | |
| | Oxidative | NADH | | H16_A1053/H16_A1054/ H16_A1055/H16_A1056/ | unknown/nuoA/nuo B/nuoC/nuoD/nuoE/ | h + nadh + uq -> nad + uqh2 | | |
| NADHHq2 | Phosphorylation | dehydrogenase (ubiquinone-8) | 1.6.5.3 | H16_A1057/H16_A1058/ H16_A1059/H16_A1060/ | nuoF/nuoG/nuoH/nu oI/nuoJ/nuoK/nuoL/ | h + nadh + uq -> nad + uqh2 | h + nadh + uq -> nad + uqh2 | h + nadh + uq -> nad + uqh2 |
| | | | | H16_A1061/H16_A1062/ | , , | | | |
| NO3RUQ2 | Oxidative Phosphorylation | Nitrate reductase (Ubiquinol-8) | 1.7.99.4 | H16_B0776/H16_B2265/ H16_B2266/H16_B2267/ H16_B2268 | unknown/narG2/nar H2/narJ2/narI2 | 2 h + no3 + uqh2 -> 2 h_e + h2o + no2 + uq | 2 h + no3 + uqh2 -> h2o + no2 + uq + 2 h_e | 2 h + no3 + uqh2 -> 2 h_e + h2o + no2 + uq |
| ****** | Oxidative | thioredoxin | | H16_A0753/H16_A1199/ | unknown/trxB1/unkn | | | |
| THIORp | Phosphorylation | reductase (NADPH) | 1.8.1.9 | H16_B1092/H16_B1422 | | 2 h + nadph + othio -> nadp + rthio | h + nadph + othio -> nadp + rthio | h + nadph + othio -> nadp + rthio |
| | Oxidative | ATP synthase (four | | H16_A3636&H16_A363 7&H16_A3638&H16_A3 | | | | |
| ATPSYN | Phosphorylation | protons for one ATP) | 3.6.3.14 | 639&H16_A3640&H16_ A3641&H16_A3642&H1 6_A3643&H16_B2371 | | adp + 4 h_e + pi <-> atp + 4 h + h2o | adp + pi + 4 h_e <-> atp + 3 h + h2o | adp + 4 h_e + pi <-> atp + 3 h + h2o |
| | Oxidative | gamma- butyrobetainyl-CoA: | | | | | | |
| BTCRNCT | Phosphorylation | carnitine CoA transferase | | H16_A2078/H16_B2438 | unknown/unknown | bbtcoa + cm <-> crncoa + gbbtn | bbtcoa + cm <-> crncoa + gbbtn | bbtcoa + crn <-> crncoa + gbbtn |
| CTBTCRNCT | Oxidative Phosphorylation | crotonobetainyl-CoA: carnitine CoA | | H16_A2078/H16_B2438 | unknown/unknown | crn + ctbtcoa <-> crncoa + ctbt | crn + ctbtcoa <-> crncoa + ctbt | cm + ctbtcoa <-> cmcoa + ctbt |
| CRNCDH | Oxidative Phosphorylation | transferase Carnityl-CoA dehydratse | | H16_A2078/H16_B2438 | unknown/unknown | crncoa <-> ctbtcoa + h2o | crncoa <-> ctbtcoa + h2o | crncoa <-> ctbtcoa + h2o |
| CYTCOBD | Oxidative Phosphorylation | cytochrome oxidase bd (ubiquinol-8: 2 | | | | 2 h + 0.5 o2 + uqh2 -> 2 h_e + h2o + uq | 2 h + 0.5 o2 + uqh2 -> h2o + uq + 2 h_e | 2 h + 0.5 o2 + uqh2 -> 2 h_e + h2o + uq |
| | Oxidative | protons) cytochrome oxidase | | | | | | |
| CYTCOBO3 | Phosphorylation Oxidative | bo3 (ubiquinol-8: 4 protons) NAD | | | | 4 h + 0.5 o2 + uqh2 -> 4 h_e + h2o + uq | 4 h + 0.5 o2 + uqh2 -> h2o + uq + 4 h_e | 4 h + 0.5 o2 + uqh2 -> 4 h_e + h2o + uq |
| NADTRHG NITRR | Phosphorylation Oxidative | transhydrogenase nitrite Reductase | | | | h + nad + nadph -> nadh + nadp | nad + nadph -> nadh + nadp | nad + nadph -> nadh + nadp |
| INTLINE | Phosphorylation | | | | | | | |
| 0.16680 | Oxidative | (NADH) succinate | EC- | | | 5 h + 3 nadh + no2 -> 2 h2o + 3 nad + nh4 | 5 h + 3 nadh + no2 -> 2 h2o + 3 nad + nh4 | 5 h + 3 nadh + no2 -> 2 h2o + 3 nad + nh4 |
| SUCCD2 | Oxidative phosphorylation | succinate dehydrogenase | Undetermi ned | | | fadh2 + uq -> fad + uqh2 | fadh2 + uq -> fad + uqh2 + h | fadh2 + uq -> fad + uqh2 + h |
| SUCCD2 DP2R | Oxidative phosphorylation | succinate dehydrogenase | Undetermi | | | | | |
| | Oxidative phosphorylation Pantothenate and | succinate dehydrogenase 2-dehydropantoate 2-reductase 3-methyl-2- oxobutanoate hydroxymethyltransfe | Undetermined 1.1.1.169 | H16_A1715/H16_B1719/ H16_B1769 | | fadh2 + uq -> fad + uqh2 | fadh2 + uq -> fad + uqh2 + h | fadh2 + uq -> fad + uqh2 + h |
| DP2R | Oxidative phosphorylation Pantothenate and CoA biosynthesis Pantothenate and CoA biosynthesis Pantothenate and | succinate dehydrogenase 2-dehydropantoate 2-reductase 3-methyl-2- oxobutanoate hydroxymethyltransfer rase dephospho-CoA | Undetermined 1.1.1.169 | H16_A1715/H16_B1719/ H16_B1769 | apbA1/apbA2/apbA3 | fadh2 + uq -> fad + uqh2 dhpant + 2 h + nadph -> nadp + pant | fadh2 + uq -> fad + uqh2 + h dhpant + h + nadph -> nadp + pant | fadh2 + uq -> fad + uqh2 + h dhpant + h + nadph -> nadp + pant |
| DP2R MOBHMT | Oxidative phosphorylation Pantothenate and CoA biosynthesis Pantothenate and CoA biosynthesis | succinate dehydrogenase 2-dehydropantoate 2-reductase 3-methyl-2- oxobutanoate hydroxymethyltransfer rase dephospho-CoA kinase pantothenate kinase | Undetermined 1.1.1.169 2.1.2.11 2.7.1.24 | H16_A1715/H16_B1719/ H16_B1769 H16_A3084 H16_A3258 | apbA1/apbA2/apbA3 | fadh2 + uq -> fad + uqh2 dhpant + 2 h + nadph -> nadp + pant 3mob + h2o + metthf -> dhpant + thf | $fadh2 + uq \rightarrow fad + uqh2 + h$ $dhpant + h + nadph \rightarrow nadp + pant$ $3mob + h2o + methf \rightarrow dhpant + thf$ | fadh2 + uq -> fad + uqh2 + h dhpant + h + nadph -> nadp + pant 3mob + h2o + metthf -> dhpant + thf |
| DP2R MOBHMT DPCOAK | Oxidative phosphorylation Pantothenate and CoA biosynthesis Pantothenate and CoA biosynthesis Pantothenate and CoA biosynthesis Pantothenate and CoA biosynthesis Pantothenate and | succinate dehydrogenase 2-dehydrogenase 2-dehydropantoate 2-reductase 3-methyl-2-oxobutanoate hydroxymethyltransferase dephospho-CoA kinase pantetheine-phosphate | Undetermined 1.1.1.169 2.1.2.11 2.7.1.24 | H16_A1715/H16_B1719/ H16_B1769 H16_A3084 H16_A3258 | apbA1/apbA2/apbA3 panB coaE | fadh2 + uq -> fad + uqh2 dhpant + 2 h + nadph -> nadp + pant 3mob + h2o + metthf -> dhpant + thf atp + dpcoa -> adp + coa | fadh2 + uq -> fad + uqh2 + h dhpant + h + nadph -> nadp + pant 3mob + h2o + metthf -> dhpant + thf atp + dpcoa -> adp + coa + h | fadh2 + uq -> fad + uqh2 + h dhpant + h + nadph -> nadp + pant 3mob + h2o + metthf -> dhpant + thf atp + dpcoa -> adp + coa + h |
| DP2R MOBHMT DPCOAK PNTOK1 | Oxidative phosphorylation Pantothenate and CoA biosynthesis Pantothenate and Pantothenate a | succinate dehydrogenase 2-dehydrogenase 2-dehydrogenase 2-reductase 3-methyl-2- oxobutanoate hydroxymethyltransferase dephospho-CoA kinase pantetheine-phosphate adenylytransferase aderylytransferase acyl-carrier protein | Undetermined 1.1.1.169 2.1.2.11 2.7.1.24 2.7.1.33 | H16_A1715/H16_B1719/ H16_B1769 H16_A3084 H16_A3258 H16_A0136 | apbA1/apbA2/apbA3 panB coaE unknown | fadh2 + uq -> fad + uqh2 dhpant + 2 h + nadph -> nadp + pant 3mob + h2o + metthf -> dhpant + thf atp + dpcoa -> adp + coa atp + pnto -> 4ppnto + adp | fadh2 + uq -> fad + uqh2 + h dhpant + h + nadph -> nadp + pant 3mob + h2o + methf -> dhpant + thf atp + dpcoa -> adp + coa + h atp + pnto -> 4ppnto + adp + h | fadh2 + uq -> fad + uqh2 + h dhpant + h + nadph -> nadp + pant 3mob + h2o + metthf -> dhpant + thf atp + dpcoa -> adp + coa + h atp + pnto -> 4ppnto + adp + h |
| DP2R MOBHMT DPCOAK PNTOK1 PTHPAT ACPS | Oxidative phosphorylation Pantothenate and CoA biosynthesis Pantothenate and Pantothenate a | succinate dehydrogenase 2-dehydrogenase 2-dehydrogenase 2-reductase 3-methyl-2- oxobutanoate hydroxymethyl-zo- oxobutanoate hydroxymethyltransferase dephospho-CoA kinase pantetheine-phosphate adenylytransferase acyl-carrier protein synthase | Undetermined 11.1.169 2.1.2.11 2.7.1.24 2.7.1.33 2.7.7.3 | H16_A1715/H16_B1719/ H16_B1769 H16_A3084 H16_A3258 H16_A0136 H16_A0367 | apbA1/apbA2/apbA3 pan8 coaE unknown unknown acpS | fadh2 + uq -> fad + uqh2 dhpant + 2 h + nadph -> nadp + pant 3mob + h2o + metthf -> dhpant + thf atp + dpcoa -> adp + coa atp + pnto -> 4ppnto + adp atp + 4ppnte -> dpcoa + ppi apoACP + coa -> ACP + pap | fadh2 + uq -> fad + uqh2 + h dhpant + h + nadph -> nadp + pant 3mob + h2o + metthf -> dhpant + thf atp + dpcoa -> adp + coa + h atp + pnto -> 4ppnto + adp + h atp + 4ppnte -> dpcoa + ppi apoACP + coa -> ACP + pap + h | fadh2 + uq -> fad + uqh2 + h dhpant + h + nadph -> nadp + pant 3mob + h2o + metthf -> dhpant + thf atp + dpcoa -> adp + coa + h atp + pnto -> 4ppnto + adp + h atp + 4ppnte -> dpcoa + ppi apoACP + coa -> ACP + pap + h |
| DP2R MOBHMT DPCOAK PNTOK1 PTHPAT ACPS PPTCDC | Oxidative phosphorylation Pantothenate and CoA biosynthesis Pantothenate and CoA poisynthesis Pantothenate and CoA poisynthesis Pantothenate and CoA poisynthesis Pantothenate and CoA poisynthesis Pantothenate and Pantothenate a | succinate dehydrogenase 2-dehydrogenase 2-dehydrogenase 2-reductase 3-methyl-2- oxobutanoate hydroxymethyl-zo- oxobutanoate hydroxymethyltransferase dephospho-CoA kinase pantetheine-phosphate adenylytransferase acyl-carrier protein synthase | Undetermined 11.1.169 2.1.2.11 2.7.1.24 2.7.1.33 2.7.7.3 4.1.1.36 | H16_A1715/H16_B1719/ H16_B1769 H16_A3084 H16_A3258 H16_A0136 H16_A0367 H16_A2551 H16_A3048 | apbA1/apbA2/apbA3 panB coaE unknown unknown acpS | fadh2 + uq -> fad + uqh2 dhpant + 2 h + nadph -> nadp + pant 3mob + h2o + methf -> dhpant + thf atp + dpcoa -> adp + coa atp + pnto -> 4ppnto + adp atp + 4ppnte -> dpcoa + ppi apoACP + coa -> ACP + pap 4ppcys + h -> co2 + 4ppnte | fadh2 + uq -> fad + uqh2 + h dhpant + h + nadph -> nadp + pant 3mob + h2o + methf -> dhpant + thf atp + dpcoa -> adp + coa + h atp + pnto -> 4ppnto + adp + h atp + 4ppnte -> dpcoa + ppi | fadh2 + uq -> fad + uqh2 + h dhpant + h + nadph -> nadp + pant 3mob + h2o + metthf -> dhpant + thf atp + dpcoa -> adp + coa + h atp + pnto -> 4ppnto + adp + h atp + 4ppnte -> dpcoa + ppi apoACP + coa -> ACP + pap + h 4ppcys + h -> co2 + 4ppnte |
| DP2R MOBHMT DPCOAK PNTOK1 PTHPAT ACPS | Oxidative phosphorylation Pantothenate and CoA biosynthesis | succinate dehydrogenase 2-dehydrogenase 2-dehydrogenase 2-dehydrogenase 3-methyl-2-oxobutanoate hydroxymethyltransferase dephospho-CoA kinase pantetheine-phosphate adenylyfransferase aderylyfransferase acyl-carrier protein synthase pantetheine-phosphopantothenot loysteine decarboxylase pantothenate synthase pantothenate synthase pantothenate synthase | Undetermined 11.1.169 2.1.2.11 2.7.1.24 2.7.1.33 2.7.7.3 4.1.1.36 6.3.2.1 | H16. A1715/H16. B1719/ H16. B1769 H16. A3084 H16. A3136 H16. A0136 H16. A0367 H16. A2551 | apbA1/apbA2/apbA3 pan8 coaE unknown unknown acpS | fadh2 + uq -> fad + uqh2 dhpant + 2 h + nadph -> nadp + pant 3mob + h2o + metthf -> dhpant + thf atp + dpcoa -> adp + coa atp + pnto -> 4ppnto + adp atp + 4ppnte -> dpcoa + ppi apoACP + coa -> ACP + pap 4ppcys + h -> co2 + 4ppnte bala + atp + pant -> amp + pnto + ppi | fadh2 + uq -> fad + uqh2 + h dhpant + h + nadph -> nadp + pant 3mob + h2o + metthf -> dhpant + thf atp + dpcoa -> adp + coa + h atp + pnto -> 4ppnto + adp + h atp + 4ppnte -> dpcoa + ppi apoACP + coa -> ACP + pap + h 4ppcys + h -> co2 + 4ppnte bala + atp + pant -> amp + pnto + ppi + 2 h 4ppnto + ctp + cys -> 4ppcys + cmp + ppi | fadh2 + uq -> fad + uqh2 + h dhpant + h + nadph -> nadp + pant 3mob + h2o + metthf -> dhpant + thf atp + dpcoa -> adp + coa + h atp + pnto -> 4ppnto + adp + h atp + 4ppnte -> dpcoa + ppi apoACP + coa -> ACP + pap + h 4ppcys + h -> co2 + 4ppnte bala + atp + pant -> amp + pnto + ppi + 2 h 4ppnto + ctp + cys -> 4ppcys + cmp + ppi + 2 |
| DP2R MOBHMT DPCOAK PNTOK1 PTHPAT ACPS PPTCDC PANTOS | Oxidative phosphorylation Pantothenate and CoA biosynthesis | succinate dehydrogenase 2-dehydrogenase 2-dehydrogenase 2-reductase 3-methyl-2- oxobutanoate hydroxymethyltransfer rase dephospho-CoA kinase pantetheine-phosphate adenylytransferase acyl-carrier protein synthase phosphopantothenot loysteine decarboxylase pantothenate synthase phosphopantothenosphosphopantothenosphosphopantothenosphosphopantothenosphosphopantothenosphosphopantothenosphosphopantothenosphosphopantothenosphosphopantothenosphosphopantothenosphosphopantothenosphosphopantothenosphosphopantothenosphosphopantothenosphosphopantothenosphosphopantothenosphosphosphopantothenosphosphosphopantothenosphosphosphopantothenosphosphosphosphosphosphosphosphosphosph | Undetermined 11.1.169 2.1.2.11 2.7.1.24 2.7.1.33 2.7.7.3 2.7.8.7 4.1.1.36 6.3.2.1 6.3.2.5 | H16_A1715/H16_B1719/ H16_B1769 H16_A3084 H16_A3258 H16_A0136 H16_A0367 H16_A2551 H16_A3048 H16_A2959 | apbA1/apbA2/apbA3 panB coaE unknown unknown acpS dfp unknown | fadh2 + uq -> fad + uqh2 dhpant + 2 h + nadph -> nadp + pant 3mob + h2o + methf -> dhpant + thf atp + dpcoa -> adp + coa atp + pnto -> 4ppnto + adp atp + 4ppnte -> dpcoa + ppi apoACP + coa -> ACP + pap 4ppcys + h -> co2 + 4ppnte | fadh2 + uq -> fad + uqh2 + h dhpant + h + nadph -> nadp + pant 3mob + h2o + methf -> dhpant + thf atp + dpcoa -> adp + coa + h atp + pnto -> 4ppnto + adp + h atp + 4ppnte -> dpcoa + ppi apoACP + coa -> ACP + pap + h 4ppcys + h -> co2 + 4ppnte bala + atp + pant -> amp + pnto + ppi + 2 h | fadh2 + uq -> fad + uqh2 + h dhpant + h + nadph -> nadp + pant 3mob + h2o + metthf -> dhpant + thf atp + dpcoa -> adp + coa + h atp + pnto -> 4ppnto + adp + h atp + 4ppnte -> dpcoa + ppi apoACP + coa -> ACP + pap + h 4ppcys + h -> co2 + 4ppnte bala + atp + pant -> amp + pnto + ppi + 2 h |
| DP2R MOBHMT DPCOAK PNTOK1 PTHPAT ACPS PPTCDC PANTOS PPNTCL | Oxidative phosphorylation Pantothenate and CoA biosynthesis | succinate dehydrogenase 2-dehydrogenase 2-dehydrogenase 2-dehydrogenase 3-methyl-2- oxobutanoate hydroxymethyltransferase dephospho-CoA kinase pantothenate kinase pantetheine-phosphate adenylytransferase acyl-carrier protein synthase phosphopantothenoylcysteine decarboxylase pantothenate synthase synthase phosphopantothenoylcysteine decarboxylase pantothenate synthase phosphopantothenate synthase phosphopantothenate c-cysteine ligase | Undetermined 11.1.169 2.7.1.24 2.7.1.33 2.7.7.3 2.7.8.7 4.1.1.36 6.3.2.1 6.3.2.5 2.7.1.33 | H16_A1715/H16_B1719/ H16_B1769 H16_A3084 H16_A3258 H16_A0136 H16_A0367 H16_A2551 H16_A3048 H16_A2959 H16_A3048 | apbA1/apbA2/apbA3 panB coaE unknown unknown acpS dfp unknown dfp | fadh2 + uq -> fad + uqh2 dhpant + 2 h + nadph -> nadp + pant 3mob + h2o + metthf -> dhpant + thf atp + dpcoa -> adp + coa atp + pnto -> 4ppnto + adp atp + 4ppnte -> dpcoa + ppi apoACP + coa -> ACP + pap 4ppcys + h -> co2 + 4ppnte bala + atp + pant -> amp + pnto + ppi 4ppnto + ctp + cys -> 4ppcys + cmp + ppi | fadh2 + uq -> fad + uqh2 + h dhpant + h + nadph -> nadp + pant 3mob + h2o + metthf -> dhpant + thf atp + dpcoa -> adp + coa + h atp + pnto -> 4ppnto + adp + h atp + 4ppnte -> dpcoa + ppi apoACP + coa -> ACP + pap + h 4ppcys + h -> co2 + 4ppnte bala + atp + pant -> amp + pnto + ppi + 2 h 4ppnto + ctp + cys -> 4ppcys + cmp + ppi + 2 h | fadh2 + uq -> fad + uqh2 + h dhpant + h + nadph -> nadp + pant 3mob + h2o + metthf -> dhpant + thf atp + dpcoa -> adp + coa + h atp + pnto -> 4ppnto + adp + h atp + 4ppnte -> dpcoa + ppi apoACP + coa -> ACP + pap + h 4ppcys + h -> co2 + 4ppnte bala + atp + pant -> amp + pnto + ppi + 2 h 4ppnto + ctp + cys -> 4ppcys + cmp + ppi + 2 h |
| DP2R MO8HMT DPCOAK PNTOK1 PTHPAT ACPS PPTCDC PANTOS PPNTCL PNTOK2 | Oxidative phosphorylation Pantothenate and CoA biosynthesis Pantothenate and CoB biosynthesis Pentose and glucuronate | succinate dehydrogenase 2-dehydrogenase 2-dehydrogenase 2-reductase 3-methyl-2- oxobutanoate hydroxymethyltransfer rase dephospho-CoA kinase pantothenate kinase pantothenate kinase pantothenate kinase pantothenate synthase decarboxylaransferase acyt-carrier protein synthase decarboxylase pantothenate synthase pantothenate synthase pantothenate synthase pantothenate cysteine ligase pantothenate kinase pantothenate kinase pantothenate synthase pantothenate synthase pantothenate kinase pantothenate kinas | Undetermined 11.1.169 21.2.11 2.7.1.24 2.7.1.33 2.7.8.7 4.1.1.36 6.3.2.1 6.3.2.5 2.7.1.33 2.7.1.33 | H16, A1715/H16, B1719/ H16, B1769 H16, A3084 H16, A3084 H16, A0136 H16, A0367 H16, A2551 H16, A3048 H16, A3048 H16, A3048 H16, A3048 H16, A3048 | apbA1/apbA2/apbA3 panB coaE unknown unknown acpS dfp unknown dfp unknown unknown | fadh2 + uq -> fad + uqh2 dhpant + 2 h + nadph -> nadp + pant 3mob + h2o + metthf -> dhpant + thf atp + dpcoa -> adp + coa atp + pnto -> 4ppnto + adp atp + 4ppnte -> dpcoa + ppi apoACP + coa -> ACP + pap 4ppcys + h -> co2 + 4ppnte bala + atp + pant -> amp + pnto + ppi 4ppnto + ctp + cys -> 4ppcys + cmp + ppi atp + pantcys -> adp + 4ppcys | fadh2 + uq -> fad + uqh2 + h dhpant + h + nadph -> nadp + pant 3mob + h2o + metthf -> dhpant + thf atp + dpcoa -> adp + coa + h atp + pnto -> 4ppnto + adp + h atp + 4ppnte -> dpcoa + ppi apoACP + coa -> ACP + pap + h 4ppcys + h -> co2 + 4ppnte bala + atp + pant -> amp + pnto + ppi + 2 h 4ppnto + ctp + cys -> 4ppcys + cmp + ppi + 2 h atp + pantoys -> adp + 4ppcys + h | fadh2 + uq -> fad + uqh2 + h dhpant + h + nadph -> nadp + pant 3mob + h2o + metthf -> dhpant + thf atp + dpcoa -> adp + coa + h atp + pnto -> 4ppnto + adp + h atp + 4ppnto -> dpcoa + ppi apoACP + coa -> ACP + pap + h 4ppcys + h -> co2 + 4ppnte bala + atp + pant -> amp + pnto + ppi + 2 h 4ppnto + ctp + cys -> 4ppcys + cmp + ppi + 2 h atp + pantcys -> adp + 4ppcys + h |
| DP2R MOBHMT DPCOAK PNTOK1 PTHPAT ACPS PPTCDC PANTOS PPNTCL PNTOK2 PNTOK3 ALTRNH | Oxidative phosphorylation Pantothenate and CoA biosynthesis Pentose and glucuronate interconversion Pentose and | succinate dehydrogenase 2-dehydrogenase 2-dehydrogenase 2-dehydrogenase 3-methyl-2-oxobutanoate hydroxymethyl-2-oxobutanoate hydroxymethyltransferase dephospho-CoA kinase pantetheine-phosphate adenylytransferase acyl-carrier protein synthase phosphopantothenot loysteine decarboxydise pantothenate synthase pantothenate synthase pantothenate c-cysteine ligase pantothenate kinase pantothenate kinase pantothenate kinase altronate hydrolase | Undetermined 1111169 27124 27.133 27.7.3 27.8.7 411.36 63.21 6.32.5 27.133 27.133 4.21.7 | H16. A1715/H16. B1719/ H16. B1769 H16. A3084 H16. A3084 H16. A0136 H16. A0367 H16. A2551 H16. A3048 H16. A3048 H16. A3048 H16. A3048 H16. A3048 H16. A3048 H16. A3048 | apbA1/apbA2/apbA3 pan8 coaE unknown unknown acpS dfp unknown dfp unknown unknown unknown | fadh2 + uq -> fad + uqh2 dhpant + 2 h + nadph -> nadp + pant 3mob + h2o + metthf -> dhpant + thf atp + dpcoa -> adp + coa atp + opcoa -> adp + coa atp + 4ppnte -> dpcoa + ppi apoACP + coa -> ACP + pap 4ppcys + h -> co2 + 4ppnte bala + atp + pant -> amp + pnto + ppi 4ppnto + ctp + cys -> 4ppcys + cmp + ppi atp + pantcys -> adp + 4ppcys atp + ptt -> adp + 4ppnte dalt -> kdg + h2o | fadh2 + uq -> fad + uqh2 + h dhpant + h + nadph -> nadp + pant 3mob + h2o + metthf -> dhpant + thf atp + dpcoa -> adp + coa + h atp + pnto -> dponto + adp + h atp + 4ppnte -> dpcoa + ppi apoACP + coa -> ACP + pap + h 4ppcys + h -> co2 + 4ppnte bala + atp + pant -> amp + pnto + ppi + 2 h 4ppnto + ctp + cys -> 4ppcys + cmp + ppi + 2 h atp + pantcys -> adp + 4ppcys + h atp + pntcys -> adp + 4ppcys + h atp + ptt -> adp + 4ppnte + h dalt -> kdg + h2o | fadh2 + uq -> fad + uqh2 + h dhpant + h + nadph -> nadp + pant 3mob + h2o + metthf -> dhpant + thf atp + dpcoa -> adp + coa + h atp + optoa -> dppnto + adp + h atp + 4ppnto -> dpcoa + ppi apoACP + coa -> ACP + pap + h 4ppcys + h -> co2 + 4ppnte bala + atp + pant -> amp + pnto + ppi + 2 h 4ppnto + ctp + cys -> 4ppcys + cmp + ppi + 2 h atp + pantcys -> adp + 4ppcys + h atp + patrcys -> adp + 4ppcys + h atp + ptt -> adp + 4ppnte + h dalt -> kdg + h2o |
| DP2R MOBHMT DPCOAK PNTOK1 PTHPAT ACPS PPTCDC PANTOS PPNTCL PNTOK2 PNTOK3 | Oxidative phosphorylation Pantothenate and CoA biosynthesis Pantothenate and CoB Biosynthesis Pantothenate and CoB Biosynthesis Pantothenate and Glucuronate interconversion | succinate dehydrogenase 2-dehydrogenase 2-dehydrogenase 2-reductase 3-methyl-2- oxobutanoate hydroxymethyltransfer rase dephospho-CoA kinase pantetheine-phosphate adenylytransferase acyl-carrier protein synthase phosphopantothenoy loysteine decarboxydase pantothenate synthase phosphopantothenate synthase phosphopantothenate synthase phosphopantothenate acyl-carrier protein synthase phosphopantothenate synthase phosphopantothenate synthase phosphopantothenate kinase pantothenate kinase | Undetermined 1111169 27124 27.133 27.7.3 27.8.7 411.36 63.21 6.32.5 27.133 27.133 4.21.7 | H16_A1715/H16_B1719/ H16_B1769 H16_A3084 H16_A0136 H16_A0136 H16_A0367 H16_A2551 H16_A3048 H16_A2959 H16_A3048 H16_A0136 H16_A0136 | apbA1/apbA2/apbA3 panB coaE unknown unknown acpS dfp unknown dfp unknown unknown | fadh2 + uq -> fad + uqh2 dhpant + 2 h + nadph -> nadp + pant 3mob + h2o + methf -> dhpant + thf atp + dpcoa -> adp + coa atp + pnto -> 4ppnto + adp atp + 4ppnte -> dpcoa + ppi apoACP + coa -> ACP + pap 4ppcys + h -> co2 + 4ppnte bala + atp + pant -> amp + pnto + ppi 4ppnto + ctp + cys -> 4ppcys + cmp + ppi atp + pantcys -> adp + 4ppcys atp + pntcys -> adp + 4ppcys atp + ptt -> adp + 4ppnte | fadh2 + uq -> fad + uqh2 + h dhpant + h + nadph -> nadp + pant 3mob + h2o + methf -> dhpant + thf atp + dpcoa -> adp + coa + h atp + pnto -> 4ppnto + adp + h atp + 4ppnte -> dpcoa + ppi apoACP + coa -> ACP + pap + h 4ppcys + h -> co2 + 4ppnte bala + atp + pant -> amp + pnto + ppi + 2 h 4ppnto + ctp + cys -> 4ppcys + cmp + ppi +2 h atp + pantcys -> adp + 4ppcys + h atp + pantcys -> adp + 4ppcys + h atp + ptt -> adp + 4ppnte + h | fadh2 + uq -> fad + uqh2 + h dhpant + h + nadph -> nadp + pant 3mob + h2o + metthf -> dhpant + thf atp + dpcoa -> adp + coa + h atp + pnto -> 4ppnto + adp + h atp + 4ppnte -> dpcoa + ppi apoACP + coa -> ACP + pap + h 4ppcys + h -> co2 + 4ppnte bala + atp + pant -> amp + pnto + ppi + 2 h 4ppnto + ctp + cys -> 4ppcys + cmp + ppi + 2 h atp + pantcys -> adp + 4ppcys + h atp + pantcys -> adp + 4ppcys + h atp + pntt -> adp + 4ppnte + h |
| DP2R MOBHMT DPCOAK PNTOK1 PTHPAT ACPS PPTCDC PANTOS PPNTCL PNTOK2 PNTOK3 ALTRNH | Oxidative phosphorylation Pantothenate and CoA biosynthesis Pantothenate and CoB iosynthesis Pantothenate and CoB iosynthesis Pentose and glucuronate interconversion | succinate dehydrogenase 2-dehydrogenase 2-dehydrogenase 2-dehydrogenase 3-methyl-2-oxobutanoate hydroxymethyl-2-oxobutanoate hydroxymethyltransferase dephospho-CoA kinase pantetheine-phosphate adenylytransferase acyl-carrier protein synthase phosphopantothenot loysteine decarboxydise pantothenate synthase pantothenate synthase pantothenate c-cysteine ligase pantothenate kinase pantothenate kinase pantothenate kinase altronate hydrolase | Undetermined 111169 27124 27133 277.3 278.7 41136 6321 27133 4217 11121 | H16. A1715/H16. B1719/ H16. B1769 H16. A3084 H16. A3084 H16. A0136 H16. A0367 H16. A2551 H16. A3048 H16. A3048 H16. A3048 H16. A3048 H16. A3048 H16. A3048 H16. A3048 | apbA1/apbA2/apbA3 pan8 coaE unknown unknown acpS dfp unknown dfp unknown unknown unknown | fadh2 + uq -> fad + uqh2 dhpant + 2 h + nadph -> nadp + pant 3mob + h2o + metthf -> dhpant + thf atp + dpcoa -> adp + coa atp + opcoa -> adp + coa atp + 4ppnte -> dpcoa + ppi apoACP + coa -> ACP + pap 4ppcys + h -> co2 + 4ppnte bala + atp + pant -> amp + pnto + ppi 4ppnto + ctp + cys -> 4ppcys + cmp + ppi atp + pantcys -> adp + 4ppcys atp + ptt -> adp + 4ppnte dalt -> kdg + h2o | fadh2 + uq -> fad + uqh2 + h dhpant + h + nadph -> nadp + pant 3mob + h2o + metthf -> dhpant + thf atp + dpcoa -> adp + coa + h atp + pnto -> dponto + adp + h atp + 4ppnte -> dpcoa + ppi apoACP + coa -> ACP + pap + h 4ppcys + h -> co2 + 4ppnte bala + atp + pant -> amp + pnto + ppi + 2 h 4ppnto + ctp + cys -> 4ppcys + cmp + ppi + 2 h atp + pantcys -> adp + 4ppcys + h atp + pntcys -> adp + 4ppcys + h atp + ptt -> adp + 4ppnte + h dalt -> kdg + h2o | fadh2 + uq -> fad + uqh2 + h dhpant + h + nadph -> nadp + pant 3mob + h2o + metthf -> dhpant + thf atp + dpcoa -> adp + coa + h atp + optoa -> dppnto + adp + h atp + 4ppnto -> dpcoa + ppi apoACP + coa -> ACP + pap + h 4ppcys + h -> co2 + 4ppnte bala + atp + pant -> amp + pnto + ppi + 2 h 4ppnto + ctp + cys -> 4ppcys + cmp + ppi + 2 h atp + pantcys -> adp + 4ppcys + h atp + patrcys -> adp + 4ppcys + h atp + ptt -> adp + 4ppnte + h dalt -> kdg + h2o |
| DP2R MOBHMT DPCOAK PNTOK1 PTHPAT ACPS PPTCDC PANTOS PPNTCL PNTOK2 PNTOK3 ALTRNH ALRTX | Oxidative phosphorylation Pantothenate and CoA biosynthesis Pantothenate and CoB biosynthesis Pantothenate and CoB biosynthesis Pantothenate and CoB biosynthesis Pantothenate and CoB biosynthesis Pentose and glucuronate interconversion Pentose and glucuronate interconversion Pentose and glucuronate interconversion Pentose and glucuronate pentose and glucuronate interconversion Pentose and glucuronate glucuronate glucuronate glucuronate | succinate dehydrogenase 2-dehydrogenase 2-dehydrogenase 2-dehydrogenase 3-methyl-2-oxobutanoate hydroxymethyltransferase dephospho-CoA kinase pantothenate kinase pantothenate kinase pantothenate kinase pantothenate synthase phosphopantothenot cysteine decarboxylase pantothenate synthase pantothenate synthase pantothenate kinase pantothenate kinase pantothenate kinase pantothenate kinase pantothenate kinase altronate hydrolase aldehyde reductase aldehyde reductase | Undetermined 111169 27124 27.133 27.7.3 27.8.7 41136 6321 6325 27.133 27.133 421.7 11121 11121 | H16_A1715/H16_B1719/ H16_B1769 H16_A3084 H16_A3258 H16_A0136 H16_A0367 H16_A2551 H16_A2959 H16_A3048 H16_A3048 H16_A0136 H16_A0136 H16_A0136 H16_A0136 H16_A0136 | apbA1/apbA2/apbA3 pan8 coaE unknown unknown acpS dfp unknown dfp unknown unknown unknown | fadh2 + uq -> fad + uqh2 dhpant + 2 h + nadph -> nadp + pant 3mob + h2o + metthf -> dhpant + thf atp + dpcoa -> adp + coa atp + pnto -> 4ppnto + adp atp + 4ppnte -> dpcoa + ppi apoACP + coa -> ACP + pap 4ppcys + h -> co2 + 4ppnte bala + atp + pant -> amp + pnto + ppi 4ppnto + ctp + cys -> 4ppcys + cmp + ppi atp + pantcys -> adp + 4ppcys atp + ptt -> adp + 4ppnte dalt -> kdg + h2o xylt + nadp <-> xyl + nadph + 2 h | fadh2 + uq -> fad + uqh2 + h dhpant + h + nadph -> nadp + pant 3mob + h2o + metthf -> dhpant + thf atp + dpcoa -> adp + coa + h atp + pnto -> dpcoa + ppi apoACP + coa -> ACP + pap + h 4ppcys + h -> co2 + 4ppnte bala + atp + pant -> amp + pnto + ppi + 2 h 4ppnto + ctp + cys -> 4ppcys + cmp + ppi + 2 h atp + pantcys -> adp + 4ppcys + h atp + pantcys -> adp + 4ppcys + h atp + patt -> adp + 4ppnte + h dalt -> kdg + h2o xyft + nadp <-> xyft + nadph + h | fadh2 + uq -> fad + uqh2 + h dhpant + h + nadph -> nadp + pant 3mob + h2o + metthf -> dhpant + thf atp + dpcoa -> adp + coa + h atp + pnto -> 4ppnto + adp + h atp + 4ppnte -> dpcoa + ppi apoACP + coa -> ACP + pap + h 4ppcys + h -> co2 + 4ppnte bala + atp + pant -> amp + pnto + ppi + 2 h 4ppnto + ctp + cys -> 4ppcys + cmp + ppi + 2 h atp + pantcys -> adp + 4ppcys + h atp + patt -> adp + 4ppnte + h datt -> kdg + h2o xyft + nadp <-> xyft + nadph + h |
| DP2R MOBHMT DPCOAK PNTOK1 PTHPAT ACPS PPTCDC PANTOS PPNTCL PNTOK2 PNTOK2 PNTOK3 ALTRNH ALRTx ALRTap | Oxidative phosphorylation Pantothenate and CoA biosynthesis Pantothenate and CoB biosynthesis Pantothenate and CoB biosynthesis Pantothenate and CoB biosynthesis Pantothenate and CoB biosynthesis Pantothenate and GoB biosynthesis Pantothenate and glucuronate interconversion Pentose Phosphate Pentose Phosphate | succinate dehydrogenase 2-dehydrogenase 2-dehydrogenase 2-dehydrogenase 3-methyl-2- oxobutanoate hydroxymethylransferase dephospho-CoA kirase adehydroxymethylransferase acyl-carrier protein synthase pantetheine-phosphate adenylytransferase acyl-carrier protein synthase phosphopantothenot loysteine decarboxydase pantothenate synthase phosphopantothenate synthase aldrohydransferase aldrohydransferase aldrohydransferase aldrohydransferase aldrohydransferase aldrohydr reductase aldehyde reductase aldehyde reductase aldehyde reductase | Undetermined 1111169 27124 27133 27.87 41136 6321 6325 27133 4217 111121 111121 111121 | H16_A1715/H16_B1719/ H16_B1769 H16_A3084 H16_A3086 H16_A0136 H16_A0367 H16_A3048 H16_A3048 H16_A3048 H16_A3048 H16_A3136 H16_A3136 H16_A3136 H16_A3186 H16_A3186 | apbA1/apbA2/apbA3 panB coaE unknown unknown acpS dfp unknown dfp unknown unknown unknown unknown unknown | fadh2 + uq -> fad + uqh2 dhpant + 2 h + nadph -> nadp + pant 3mob + h2o + metthf -> dhpant + thf atp + dpcoa -> adp + coa atp + pnto -> 4ppnto + adp atp + 4ppnte -> dpcoa + ppi apoACP + coa -> ACP + pap 4ppcys + h -> co2 + 4ppnte bala + atp + pant -> amp + pnto + ppi 4ppnto + ctp + cys -> 4ppcys + cmp + ppi atp + pantcys -> adp + 4ppcys atp + ptt -> adp + 4ppnte dalt -> kdg + h2o xylt + nadp <-> xyl + nadph + 2 h arbt + nadp <-> larabinose + nadph + 2 h arbt + nad <-> larabinose + nadph + h | fadh2 + uq -> fad + uqh2 + h dhpant + h + nadph -> nadp + pant 3mob + h2o + metthf -> dhpant + thf atp + dpcoa -> adp + coa + h atp + pnto -> dponto + adp + h atp + 4ppnte -> dpcoa + ppi apoACP + coa -> ACP + pap + h 4ppcys + h -> co2 + 4ppnte bala + atp + pant -> amp + pnto + ppi + 2 h 4ppnto + ctp + cys -> 4ppcys + cmp + ppi + 2 h atp + pantys -> adp + 4ppcys + h atp + ptt -> adp + 4ppnte + h dalt -> kdg + h2o xyft + nadp -> xyfl + nadph + h arbt + nadp -> larabinose + nadph + h arbt + nad -> larabinose + nadh + h | fadh2 + uq -> fad + uqh2 + h dhpant + h + nadph -> nadp + pant 3mob + h2o + metthf -> dhpant + thf atp + dpcoa -> adp + coa + h atp + dpcoa -> adp + coa + h atp + 4ppnte -> dpcoa + ppi apoACP + coa -> ACP + pap + h 4ppcys + h -> co2 + 4ppnte bala + atp + pant -> amp + pnto + ppi + 2 h 4ppnto + ctp + cys -> 4ppcys + cmp + ppi + 2 h atp + pantcys -> adp + 4ppcys + h atp + patt -> adp + 4ppnte + h dalt -> kdg + h2o xyft + nadp <-> xyf + nadph + h arbt + nadp <-> larabinose + nadph + h arbt + nadp <-> larabinose + nadh + h |
| DP2R MOBHMT DPCOAK PNTOK1 PTHPAT ACPS PPTCDC PANTOS PPNTCL PNTOK2 PNTOK3 ALTRNH ALRTx ALRTap ALRTa GLCNK | Oxidative phosphorylation Pantothenate and CoA biosynthesis Pantothenate and Jucuronate interconversion Pentose and glucuronate interconversion Pentose Phosphate Pathway | succinate dehydrogenase 2-dehydrogenase 2-dehydrogenase 2-dehydrogenase 2-dehydropantoate 2-reductase 3-methyl-2- oxobutanoate hydroxymethyltransfer rase dephospho-CoA kinase pantothenate kinase pantothenate kinase pantothenate phosphate adenylytransferase acyl-carrier protein synthase decarboxydase pantothenate synthase pantothenate synthase pantothenate kinase pantothenate kinase pantothenate kinase altronate hydrolase aldehyde reductase aldehyde reductase aldehyde reductase aldehyde reductase 2-dehydro-3- | Undetermined 111169 27124 27133 277.3 278.7 41136 6321 27133 421.7 11121 11121 27112 | H16_A1715/H16_B1719/ H16_B1769 H16_A3084 H16_A3084 H16_A0136 H16_A0367 H16_A2551 H16_A2959 H16_A3048 H16_A3048 H16_A1136 H16_A0136 H16_A1366 H16_A3186 H16_A3186 H16_A3186 H16_A3186 | apbA1/apbA2/apbA3 pan8 coaE unknown unknown acpS dfp unknown unknown unknown unknown unknown unknown unknown unknown | fadh2 + uq -> fad + uqh2 dhpant + 2 h + nadph -> nadp + pant 3mob + h2o + metthf -> dhpant + thf atp + dpcoa -> adp + coa atp + pnto -> 4ppnto + adp atp + 4ppnte -> dpcoa + ppi apoACP + coa -> ACP + pap 4ppcys + h -> co2 + 4ppnte bala + atp + pant -> amp + pnto + ppi 4ppnto + ctp + cys -> 4ppcys + cmp + ppi atp + pattcys -> adp + 4ppcys atp + ptt -> adp + 4ppnte dalt -> kdg + h2o xylt + nadp <-> xyl + nadph + 2 h arbt + nad <-> larabinose + nadph + 2 h arbt + nad <-> larabinose + nadh + h atp + gluc -> d6pgc + adp | fadh2 + uq -> fad + uqh2 + h dhpant + h + nadph -> nadp + pant 3mob + h2o + metthf -> dhpant + thf atp + dpcoa -> adp + coa + h atp + pnto -> dponto + adp + h atp + 4ppnte -> dpcoa + ppi apoACP + coa -> ACP + pap + h 4ppcys + h -> co2 + 4ppnte bala + atp + pant -> amp + pnto + ppi + 2 h 4ppnto + ctp + cys -> 4ppcys + cmp + ppi + 2 h atp + pantcys -> adp + 4ppcys + h atp + pantcys -> adp + 4ppcys + h atp + pantcys -> adp + 4ppnte + h dalt -> kdg + h2o xyft + nadp <-> xyft + nadph + h arbt + nad <-> larabinose + nadph + h arbt + nad <-> larabinose + nadh + h atp + gluc -> d6pgc + adp + h | fadh2 + uq -> fad + uqh2 + h dhpant + h + nadph -> nadp + pant 3mob + h2o + metthf -> dhpant + thf atp + dpcoa -> adp + coa + h atp + pnto -> 4ppnto + adp + h atp + 4ppnte -> dpcoa + ppi apoACP + coa -> ACP + pap + h 4ppcys + h -> co2 + 4ppnte bala + atp + pant -> amp + pnto + ppi + 2 h 4ppnto + ctp + cys -> 4ppcys + cmp + ppi + 2 h atp + pattcys -> adp + 4ppcys + h atp + patt -> adp + 4ppcys + h atp + ptt -> adp + 4ppnte + h dalt -> kdg + h2o xyft + nadp <-> xyft + nadph + h arbt + nad <-> larabinose + nadph + h arbt + nad <-> larabinose + nadh + h atp + gluc -> d6pgc + adp + h |
| DP2R MOBHMT DPCOAK PNTOK1 PTHPAT ACPS PPTCDC PANTOS PPNTCL PNTOK2 PNTOK3 ALTRNH ALRTx ALRTap | Oxidative phosphorylation Pantothenate and CoA biosynthesis Pantothenate and CoB biosynthesis Pantothenate and CoB biosynthesis Pantothenate and CoB biosynthesis Pantothenate and CoB biosynthesis Pantothenate and GoB biosynthesis Pentose and glucuronate interconversion Pentose and glucuronate interconversion Pentose and glucuronate interconversion Pentose and glucuronate Pentose Phosphate Pathway | succinate dehydrogenase 2-dehydrogenase 2-dehydrogenase 2-dehydrogenase 3-methyl-2- oxobutanoate 1-reductase 3-methyl-2- oxobutanoate hydroxymethyltransfer rase dephospho-CoA kirase 2-dehydroxymethyltransferase adehydransferase acyl-carrier protein synthase pantetheine-phosphate adenylyttransferase acyl-carrier protein synthase acyl-carrier protein synthase acyl-carrier protein synthase phosphopantothenate synthase phosphopantothenate e-cysteine ligase pantothenate kinase altronate hydrolase altronate hydrolase aldehyde reductase aldehyde reductase aldehyde reductase 2-dehydro-3-deoxygluconokinase 2-dehydro-3-deoxygluconokinase | Undetermined 111169 27124 27133 277.3 278.7 41136 6321 27133 421.7 11121 11121 27112 | H16_A1715/H16_B1719/ H16_B1769 H16_A3084 H16_A3086 H16_A0136 H16_A0367 H16_A3048 H16_A3048 H16_A3048 H16_A3048 H16_A3136 H16_A3136 H16_A3136 H16_A3186 H16_A3186 | apbA1/apbA2/apbA3 panB coaE unknown unknown acpS dfp unknown dfp unknown unknown unknown unknown unknown | fadh2 + uq -> fad + uqh2 dhpant + 2 h + nadph -> nadp + pant 3mob + h2o + metthf -> dhpant + thf atp + dpcoa -> adp + coa atp + pnto -> 4ppnto + adp atp + 4ppnte -> dpcoa + ppi apoACP + coa -> ACP + pap 4ppcys + h -> co2 + 4ppnte bala + atp + pant -> amp + pnto + ppi 4ppnto + ctp + cys -> 4ppcys + cmp + ppi atp + pantcys -> adp + 4ppcys atp + ptt -> adp + 4ppnte dalt -> kdg + h2o xylt + nadp <-> xyl + nadph + 2 h arbt + nadp <-> larabinose + nadph + 2 h arbt + nad <-> larabinose + nadph + h | fadh2 + uq -> fad + uqh2 + h dhpant + h + nadph -> nadp + pant 3mob + h2o + metthf -> dhpant + thf atp + dpcoa -> adp + coa + h atp + pnto -> dponto + adp + h atp + 4ppnte -> dpcoa + ppi apoACP + coa -> ACP + pap + h 4ppcys + h -> co2 + 4ppnte bala + atp + pant -> amp + pnto + ppi + 2 h 4ppnto + ctp + cys -> 4ppcys + cmp + ppi + 2 h atp + pantys -> adp + 4ppcys + h atp + ptt -> adp + 4ppnte + h dalt -> kdg + h2o xylt + nadp -> xyl + nadph + h arbt + nadp -> larabinose + nadph + h arbt + nad -> larabinose + nadh + h | fadh2 + uq -> fad + uqh2 + h dhpant + h + nadph -> nadp + pant 3mob + h2o + metthf -> dhpant + thf atp + dpcoa -> adp + coa + h atp + dpcoa -> adp + coa + h atp + 4ppnte -> dpcoa + ppi apoACP + coa -> ACP + pap + h 4ppcys + h -> co2 + 4ppnte bala + atp + pant -> amp + pnto + ppi + 2 h 4ppnto + ctp + cys -> 4ppcys + cmp + ppi + 2 h atp + pantcys -> adp + 4ppcys + h atp + patt -> adp + 4ppnte + h dalt -> kdg + h2o xyft + nadp <-> xyf + nadph + h arbt + nadp <-> larabinose + nadph + h arbt + nadp <-> larabinose + nadh + h |
| DP2R MOBHMT DPCOAK PNTOK1 PTHPAT ACPS PPTCDC PANTOS PPNTCL PNTOK2 PNTOK3 ALTRNH ALRTx ALRTap ALRTa GLCNK | Oxidative phosphorylation Pantothenate and CoA biosynthesis Pantothenate and CoB biosynthesis Pantothenate and CoB biosynthesis Pantothenate and CoB biosynthesis Pentote and glucuronate interconversion Pentose and glucuronate interconversion Pentose and glucuronate interconversion Pentose and glucuronate interconversion Pentose Posphate Pentose Phosphate Pentose Phosphate Pentose Phosphate | succinate dehydrogenase 2-dehydrogenase 2-dehydrogenase 2-dehydrogenase 3-methyl-2- oxobutanoate 1-reductase 3-methyl-2- oxobutanoate hydroxymethyltransfer rase dephospho-CoA kirase 2-dehydroxymethyltransferase adehydransferase acyl-carrier protein synthase pantetheine-phosphate adenylyttransferase acyl-carrier protein synthase acyl-carrier protein synthase acyl-carrier protein synthase phosphopantothenate synthase phosphopantothenate e-cysteine ligase pantothenate kinase altronate hydrolase altronate hydrolase aldehyde reductase aldehyde reductase aldehyde reductase 2-dehydro-3-deoxygluconokinase 2-dehydro-3-deoxygluconokinase | Undetermined 111169 27124 27133 2773 2787 41136 6321 27133 4217 11121 11121 27112 27145 53113 | H16_A1715/H16_B1719/ H16_B1769 H16_A3084 H16_A3084 H16_A0136 H16_A0367 H16_A2551 H16_A2959 H16_A3048 H16_A3048 H16_A1136 H16_A0136 H16_A1366 H16_A3186 H16_A3186 H16_A3186 H16_A3186 | apbA1/apbA2/apbA3 pan8 coaE unknown unknown acpS dfp unknown unknown unknown unknown unknown unknown unknown unknown | fadh2 + uq -> fad + uqh2 dhpant + 2 h + nadph -> nadp + pant 3mob + h2o + metthf -> dhpant + thf atp + dpcoa -> adp + coa atp + pnto -> 4ppnto + adp atp + 4ppnte -> dpcoa + ppi apoACP + coa -> ACP + pap 4ppcys + h -> co2 + 4ppnte bala + atp + pant -> amp + pnto + ppi 4ppnto + ctp + cys -> 4ppcys + cmp + ppi atp + pattcys -> adp + 4ppcys atp + ptt -> adp + 4ppnte dalt -> kdg + h2o xylt + nadp <-> xyl + nadph + 2 h arbt + nad <-> larabinose + nadph + 2 h arbt + nad <-> larabinose + nadh + h atp + gluc -> d6pgc + adp | fadh2 + uq -> fad + uqh2 + h dhpant + h + nadph -> nadp + pant 3mob + h2o + metthf -> dhpant + thf atp + dpcoa -> adp + coa + h atp + pnto -> dponto + adp + h atp + 4ppnte -> dpcoa + ppi apoACP + coa -> ACP + pap + h 4ppcys + h -> co2 + 4ppnte bala + atp + pant -> amp + pnto + ppi + 2 h 4ppnto + ctp + cys -> 4ppcys + cmp + ppi + 2 h atp + pantcys -> adp + 4ppcys + h atp + pantcys -> adp + 4ppcys + h atp + pantcys -> adp + 4ppnte + h dalt -> kdg + h2o xyft + nadp <-> xyft + nadph + h arbt + nad <-> larabinose + nadph + h arbt + nad <-> larabinose + nadh + h atp + gluc -> d6pgc + adp + h | fadh2 + uq -> fad + uqh2 + h dhpant + h + nadph -> nadp + pant 3mob + h2o + metthf -> dhpant + thf atp + dpcoa -> adp + coa + h atp + pnto -> 4ppnto + adp + h atp + 4ppnte -> dpcoa + ppi apoACP + coa -> ACP + pap + h 4ppcys + h -> co2 + 4ppnte bala + atp + pant -> amp + pnto + ppi + 2 h 4ppnto + ctp + cys -> 4ppcys + cmp + ppi + 2 h atp + pattcys -> adp + 4ppcys + h atp + patt -> adp + 4ppcys + h atp + ptt -> adp + 4ppnte + h dalt -> kdg + h2o xyft + nadp <-> xyft + nadph + h arbt + nad <-> larabinose + nadph + h arbt + nad <-> larabinose + nadh + h atp + gluc -> d6pgc + adp + h |
| DP2R MOBHMT DPCOAK PNTOK1 PTHPAT ACPS PPTCDC PANTOS PPNTCL PNTOK2 PNTOK2 PNTOK3 ALTRNH ALRTx ALRTap ALRTa GLCNK DDGLCNK | Oxidative phosphorylation Pantothenate and CoA biosynthesis Pantothenate and CoB biosynthesis Pantothenate and glucuronate interconversion Pentose Phosphate Pathway Pentose Phosphate Pathway Pentose Phosphate Pathway Pentose Phosphate Pathway | succinate dehydrogenase 2-dehydrogenase 2-dehydrogenase 2-dehydrogenase 2-dehydrogenase 3-methyl-2- oxobutanoate hydroxymethyltransfer rase dephospho-CoA kinase pantetheine-phosphate adenylytransferase acyl-carrier protein synthase phosphopantothenot loysteine decarboxylase pantothenate synthase phosphopantothenate synthase phosphopantothenate kinase altronate hydrolase aldehyde reductase aldehyde reductase aldehyde reductase 2-dehydro-3-deoxygluconokinase 2-dehydro-3-deoxygluconokinase 2-dehydro-3-phosphate somerase ribose-1,5- | Undetermined 111169 27124 27133 27.87 41136 6321 6325 27133 27.131 11121 11121 11121 11121 27112 271.45 53113 | H16_A1715/H16_B1719/ H16_B1769 H16_A3084 H16_A3084 H16_A0136 H16_A0367 H16_A2551 H16_A3048 H16_A2959 H16_A3048 H16_A0136 H16_A0136 H16_A0136 H16_A0136 H16_A1186 H16_A3186 H16_A3186 H16_A3186 H16_A3186 H16_A3179 H16_B1212 | apbA1/apbA2/apbA3 panB coaE unknown unknown acpS dfp unknown dfp unknown unknown unknown unknown unknown unknown unknown unknown unknown | fadh2 + uq -> fad + uqh2 dhpant + 2 h + nadph -> nadp + pant 3mob + h2o + metthf -> dhpant + thf atp + dpcoa -> adp + coa atp + pnto -> 4ppnto + adp atp + 4ppnte -> dpcoa + ppi apoACP + coa -> ACP + pap 4ppcys + h -> co2 + 4ppnte bala + atp + pant -> amp + pnto + ppi 4ppnto + ctp + cys -> 4ppcys + cmp + ppi atp + pantcys -> adp + 4ppcys atp + ptt -> adp + 4ppnte dalt -> kdg + h2o xylt + nadp <-> xyl + nadph + 2 h arbt + nad <-> larabinose + nadph + 2 h arbt + nad <-> larabinose + nadph + h atp + gluc -> d6pgc + adp kdg + atp -> kdpg + adp | fadh2 + uq -> fad + uqh2 + h dhpant + h + nadph -> nadp + pant 3mob + h2o + metthf -> dhpant + thf atp + dpcoa -> adp + coa + h atp + pnto -> dpcoa + ppi apoACP + coa -> ACP + pap + h 4ppcys + h -> co2 + 4ppnte bala + atp + pant -> amp + pnto + ppi + 2 h 4ppnto + ctp + cys -> 4ppcys + cmp + ppi + 2 h atp + pantcys -> adp + 4ppcys + h atp + pantcys -> adp + 4ppcys + h atp + pantcys -> adp + 4ppcys + h atp + pantcys -> adp + 4ppcys + h atp + pantcys -> adp + appcys + h atp + pantcys -> adp + appcys + h atp + pantcys -> adp + appcys + h atp + pantcys -> adp + appcys + h atp + pantcys -> adp + appcys + h atp + pantcys -> adp + appcys + h atp + pantcys -> adp + appcys + h atp + pantcys -> adp + appcys + h atp + pantcys -> adp + appcys + h atp + pantcys -> adp + appcys + h atp + pantcys -> adp + adph + h arbt + nadp -> larabinose + nadph + h atp + gluc -> d6pgc + adp + h kdg + atp -> kdpg + adp + h | fadh2 + uq -> fad + uqh2 + h dhpant + h + nadph -> nadp + pant 3mob + h2o + metthf -> dhpant + thf atp + dpcoa -> adp + coa + h atp + dpcoa -> dpp + coa + h atp + 4ppnte -> dpcoa + ppi apoACP + coa -> ACP + pap + h 4ppys + h -> co2 + 4ppnte bala + atp + pant -> amp + pnto + ppi + 2 h 4ppnto + ctp + cys -> 4ppys + cmp + ppi + 2 h atp + pantcys -> adp + 4ppys + h atp + pantcys -> adp + 4ppys + h atp + ptt -> adp + 4ppnte + h dalt -> kdg + h2o xyft + nadp <-> xyf + nadph + h arbt + nad <-> larabinose + nadph + h arbt + nad <-> larabinose + nadph + h atp + gluc -> d6pgc + adp + h kdg + atp -> kdpg + adp + h |
| DP2R MOBHMT DPCOAK PNTOK1 PTHPAT ACPS PPTCDC PANTOS PPNTCL PNTOK2 PNTOK3 ALTRNH ALRTx ALRTap ALRTa GLCNK DDGLCNK ABSPI R158PK | Oxidative phosphorylation Pantothenate and CoA biosynthesis Pantothenate and Jucuronate interconversion Pentose and glucuronate interconversion Pentose and glucuronate interconversion Pentose and glucuronate interconversion Pentose Phosphate Pathway Pentose Phosphate Pathway Pentose Phosphate Pathway Pentose Phosphate Pathway | succinate dehydrogenase 2-dehydrogenase 2-dehydrogenase 2-dehydrogenase 2-dehydrogenase 3-methyl-2- oxobutanoate hydroxymethyltransferase dephospho-CoA kinase pantetheine-phosphate adenylytransferase acyl-carrier protein synthase phosphopantothenot loysteine decarboxydise pantothenate synthase phosphopantothenate synthase phosphopantothenate synthase phosphopantothenate synthase addenyldransferase alderyldransferase aldronate hydrolase aldehyde reductase aldehyde reductase aldehyde reductase 2-dehydro-3-deoxygluconokinase 2-dehydro-3-deoxygluconokinase arabinose-5-phosphate isomerase | Undetermined 111169 221211 27124 27133 277.87 41136 6322 27133 421.7 11121 11121 27112 27112 27145 533113 27.423 | H16_A1715/H16_B1719/ H16_B1769 H16_A3084 H16_A3084 H16_A0367 H16_A0367 H16_A2551 H16_A2959 H16_A3048 H16_A3048 H16_A3186 H16_A3186 H16_A3186 H16_A3186 H16_A3186 H16_A3186 H16_A3189 H16_A3189 H16_A3189 H16_A3189 H16_A3189 H16_A3189 H16_A3189 H16_A3189 H16_A3189 | apbA1/apbA2/apbA3 pan8 coaE unknown unknown acpS dfp unknown dfp unknown unknown unknown unknown unknown unknown unknown unknown | fadh2 + uq -> fad + uqh2 dhpant + 2 h + nadph -> nadp + pant 3mob + h2o + metthf -> dhpant + thf atp + dpcoa -> adp + coa atp + pnto -> 4ppnto + adp atp + 4ppnte -> dpcoa + ppi apoACP + coa -> ACP + pap 4ppcys + h -> co2 + 4ppnte bala + atp + pant -> amp + pnto + ppi 4ppnto + ctp + cys -> 4ppcys + cmp + ppi atp + pattcys -> adp + 4ppcys atp + ptt -> adp + 4ppnte dalt -> kdg + h2o xylt + nadp <-> xyl + nadph + 2 h arbt + nad <-> larabinose + nadph + 2 h arbt + nad <-> larabinose + nadh + h atp + gluc -> d6pgc + adp kdg + atp -> kdpg + adp ri5p <-> aSp atp + r15bp -> adp + prpp | fadh2 + uq -> fad + uqh2 + h dhpant + h + nadph -> nadp + pant 3mob + h2o + metthf -> dhpant + thf atp + dpcoa -> adp + coa + h atp + pnto -> dppnto + adp + h atp + 4ppnte -> dpcoa + ppi apoACP + coa -> ACP + pap + h 4ppcys + h -> co2 + 4ppnte bala + atp + pant -> amp + pnto + ppi + 2 h 4ppnto + ctp + cys -> 4ppcys + cmp + ppi + 2 h atp + pantys -> adp + 4ppcys + h atp + pantys -> adp + 4ppcys + h atp + pantys -> adp + 4ppnte + h dalt -> kdg + h2o xylt + nadp <-> xyl + nadph + h arbt + nad <-> larabinose + nadph + h arbt + nad <-> larabinose + nadph + h kdg + atp -> kdpg + adp + h kdg + atp -> kdpg + adp + h kdg + atp -> kdpg + adp + prpp | fadh2 + uq -> fad + uqh2 + h dhpant + h + nadph -> nadp + pant 3mob + h2o + metthf -> dhpant + thf atp + dpcoa -> adp + coa + h atp + pnto -> 4ppnto + adp + h atp + 4ppnto -> dpcoa + ppi apoACP + coa -> ACP + pap + h 4ppcys + h -> co2 + 4ppnte bala + atp + pant -> amp + pnto + ppi + 2 h 4ppnto + ctp + cys -> 4ppcys + cmp + ppi + 2 h atp + pantcys -> adp + 4ppcys + h atp + patt -> adp + 4ppcys + h atp + ptt -> adp + 4ppnte + h dalt -> kdg + h2o xyft + nadp <-> xyft + nadph + h arbt + nad <-> larabinose + nadph + h arbt + nad <-> larabinose + nadph + h atp + gluc -> d6pgc + adp + h kdg + atp -> kdpg + adp + h kdg + atp -> kdpg + adp + h kdg + atp -> kdpg + adp + prpp |
| DP2R MOBHMT DPCOAK PNTOK1 PTHPAT ACPS PPTCDC PANTOS PPNTCL PNTOK2 PNTOK3 ALTRNH ALRTx ALRTap ALRTa GLCNK DDGLCNK ABSPI | Oxidative phosphorylation Pantothenate and CoA biosynthesis Pantothenate and CoB biosynthesis Pantothenate and CoB biosynthesis Pantothenate and CoB biosynthesis Pentose and glucuronate interconversion Pentose and glucuronate interconversion Pentose and glucuronate interconversion Pentose Phosphate Pathway | succinate dehydrogenase 2-dehydrogenase 2-dehydrogenase 2-dehydrogenase 2-dehydrogenase 3-methyl-2-oxobutanoate hydroxymethyltransferase dephospho-CoA kirase dephospho-CoA kirase pantetheine-phosphate adenylytransferase acyl-carrier protein synthase phosphopantothenot loysteine decarboxydase pantothenate synthase phosphopantothenate synthase aldrohydramate kirase aldrohydramate kirase aldrohydramate kirase aldrehyde reductase aldehyde reductase aldehyde reductase aldehyde reductase 2-dehydro-3-deoxygluconokinase 2-dehydro-3-deoxygluconokinase 2-arabinose-5-phosphate isomerase phosphorphosphophosphorphosphate synthetase | Undetermined 111169 27124 27133 278.7 41136 6321 6325 27133 421.7 11121 11121 27112 27145 53113 27.423 27.61 | H16_A1715/H16_B1719/ H16_B1769 H16_A3084 H16_A3084 H16_A0136 H16_A0367 H16_A2551 H16_A3048 H16_A2959 H16_A3048 H16_A0136 H16_A0136 H16_A0136 H16_A13186 H16_A3186 H16_A3186 | apbA1/apbA2/apbA3 panB coaE unknown unknown acpS dfp unknown dfp unknown unknown unknown unknown unknown unknown unknown unknown unknown | fadh2 + uq -> fad + uqh2 dhpant + 2 h + nadph -> nadp + pant 3mob + h2o + metthf -> dhpant + thf atp + dpcoa -> adp + coa atp + pnto -> 4ppnto + adp atp + 4ppnte -> dpcoa + ppi apoACP + coa -> ACP + pap 4ppcys + h -> co2 + 4ppnte bala + atp + pant -> amp + pnto + ppi 4ppnto + ctp + cys -> 4ppcys + cmp + ppi atp + pantcys -> adp + 4ppcys atp + ptt -> adp + 4ppnte dalt -> kdg + h2o xylt + nadp <-> xyl + nadph + 2 h arbt + nad <-> larabinose + nadph + 2 h arbt + nad <-> dfopgc + adp kdg + atp -> kdpg + adp riSp <-> aSp atp + r1Sbp -> adp + prpp atp + r5p <-> amp + prpp | fadh2 + uq -> fad + uqh2 + h dhpant + h + nadph -> nadp + pant 3mob + h2o + metthf -> dhpant + thf atp + dpcoa -> adp + coa + h atp + pnto -> 4ppnto + adp + h atp + 4ppnte -> dpcoa + ppi apoACP + coa -> ACP + pap + h 4ppcys + h -> co2 + 4ppnte balla + atp + pant -> amp + pnto + ppi + 2 h 4ppnto + ctp + cys -> 4ppcys + cmp + ppi + 2 h atp + pantcys -> adp + 4ppcys + h atp + ptt -> adp + 4ppnte + h dalt -> kdg + h2o xylt + nadp <-> xyl + nadph + h arbt + nad <-> larabinose + nadph + h arbt + nad <-> larabinose + nadph + h kdg + atp -> kdpg + adp + h kdg + atp -> kdpg + adp + h riSp <-> aSp atp + riSbp + h -> adp + prpp atp + riSp <-> amp + prpp + h | fadh2 + uq -> fad + uqh2 + h dhpant + h + nadph -> nadp + pant 3mob + h2o + metthf -> dhpant + thf atp + dpcoa -> adp + coa + h atp + dpcoa -> dpp + coa + h atp + pnto -> dpponto + adp + h atp + 4ppnte -> dpcoa + ppi apoACP + coa -> ACP + pap + h 4ppcys + h -> co2 + 4ppnte bala + atp + pant -> amp + pnto + ppi + 2 h 4ppnto + ctp + cys -> 4ppys + cmp + ppi + 2 h atp + pantcys -> adp + 4ppres + h atp + patt -> adp + 4ppnte + h dalt -> kdg + h2o xyft + nadp <-> xyft + nadph + h arbt + nad <-> larabinose + nadph + h atp + gluc -> dfopgc + adp + h kdg + atp -> kdpg + adp + h kdg + atp -> kdpg + adp + h rlSp <-> aSp atp + r1Sbp -> adp + prpp atp + r5p <-> amp + prpp + h |
| DP2R MOBHMT DPCOAK PNTOK1 PTHPAT ACPS PPTCDC PANTOS PPNTCL PNTOK2 PNTOK3 ALTRNH ALRTx ALRTap ALRTa GLCNK DDGLCNK ABSPI R158PK | Oxidative phosphorylation Pantothenate and CoA biosynthesis Pantothenate and Jucuronate interconversion Pentose and glucuronate interconversion Pentose and glucuronate interconversion Pentose Phosphate Pathway | succinate dehydrogenase 2-dehydrogenase 2-dehydrogenase 2-dehydrogenase 2-dehydrogenase 3-methyl-2-oxobutanoate hydroxymethyltransferase dephospho-CoA kinase pantetheine-phosphate adenylytransferase acyl-carrier protein synthase phosphopantothenot lcysteine decarboxylase pantothenate synthase phosphopantothenate synthase phosphopantothenate synthase pantothenate kinase pantothenate kinase pantothenate kinase pantothenate kinase pathopantothenate synthase phosphopantothenate synthase phosphopantothenate kinase pantothenate kinase phosphopantothenate sinase phosphopantonkinase aldehyde reductase cheonygluconokinase arabinose 5-phosphate isomerase ribose-1,5-bisphophokinase phosphoribosylyprophosphate synthetase phosphoribosylyprophosphate synthetase phosphoribosylyprophosphate phosphoribosylyprophosphate 2-dehydrogenase | Undetermined 111169 27124 27133 277.87 41136 6321 27133 4217 11121 11121 27112 27145 53113 27.423 27.423 27.423 27.423 27.423 | H16_A1715/H16_B1719/ H16_B1769 H16_A3084 H16_A3084 H16_A0367 H16_A0367 H16_A2551 H16_A2959 H16_A3048 H16_A3048 H16_A3186 H16_A3186 H16_A3186 H16_A3186 H16_A3186 H16_A3186 H16_A3189 H16_A3189 H16_A3189 H16_A3189 H16_A3189 H16_A3189 H16_A3189 H16_A3189 H16_A3189 | apbA1/apbA2/apbA3 pan8 coaE unknown unknown acpS dfp unknown dfp unknown unknown unknown unknown unknown unknown unknown unknown | fadh2 + uq -> fad + uqh2 dhpant + 2 h + nadph -> nadp + pant 3mob + h2o + metthf -> dhpant + thf atp + dpcoa -> adp + coa atp + pnto -> 4ppnto + adp atp + 4ppnte -> dpcoa + ppi apoACP + coa -> ACP + pap 4ppcys + h -> co2 + 4ppnte bala + atp + pant -> amp + pnto + ppi 4ppnto + ctp + cys -> 4ppcys + cmp + ppi atp + pattcys -> adp + 4ppcys atp + ptt -> adp + 4ppnte dalt -> kdg + h2o xylt + nadp <-> xyl + nadph + 2 h arbt + nad <-> larabinose + nadph + 2 h arbt + nad <-> larabinose + nadh + h atp + gluc -> d6pgc + adp kdg + atp -> kdpg + adp ri5p <-> aSp atp + r15bp -> adp + prpp | fadh2 + uq -> fad + uqh2 + h dhpant + h + nadph -> nadp + pant 3mob + h2o + metthf -> dhpant + thf atp + dpcoa -> adp + coa + h atp + pnto -> dppnto + adp + h atp + 4ppnte -> dpcoa + ppi apoACP + coa -> ACP + pap + h 4ppcys + h -> co2 + 4ppnte bala + atp + pant -> amp + pnto + ppi + 2 h 4ppnto + ctp + cys -> 4ppcys + cmp + ppi + 2 h atp + pantys -> adp + 4ppcys + h atp + pantys -> adp + 4ppcys + h atp + pantys -> adp + 4ppnte + h dalt -> kdg + h2o xylt + nadp <-> xyl + nadph + h arbt + nad <-> larabinose + nadph + h arbt + nad <-> larabinose + nadph + h kdg + atp -> kdpg + adp + h kdg + atp -> kdpg + adp + h kdg + atp -> kdpg + adp + prpp | fadh2 + uq -> fad + uqh2 + h dhpant + h + nadph -> nadp + pant 3mob + h2o + metthf -> dhpant + thf atp + dpcoa -> adp + coa + h atp + pnto -> 4ppnto + adp + h atp + 4ppnto -> dpcoa + ppi apoACP + coa -> ACP + pap + h 4ppcys + h -> co2 + 4ppnte bala + atp + pant -> amp + pnto + ppi + 2 h 4ppnto + ctp + cys -> 4ppcys + cmp + ppi + 2 h atp + pantcys -> adp + 4ppcys + h atp + patt -> adp + 4ppcys + h atp + ptt -> adp + 4ppnte + h dalt -> kdg + h2o xyft + nadp <-> xyft + nadph + h arbt + nad <-> larabinose + nadph + h arbt + nad <-> larabinose + nadph + h atp + gluc -> d6pgc + adp + h kdg + atp -> kdpg + adp + h kdg + atp -> kdpg + adp + h kdg + atp -> kdpg + adp + prpp |
| DP2R MOBHMT DPCOAK PNTOK1 PTHPAT ACPS PPTCDC PANTOS PPNTCL PNTOK2 PNTOK2 PNTOK3 ALTRNH ALRTx ALRTap ALRTa GLCNK DDGLCNK ABSPI R15BPK PRPPS | Oxidative phosphorylation Pantothenate and CoA biosynthesis Pantothenate and Jucuronate interconversion Pentose and glucuronate interconversion Pentose and glucuronate interconversion Pentose Phosphate Pathway | succinate dehydrogenase 2-dehydrogenase 2-dehydrogenase 2-dehydrogenase 3-methyl-2- coxobutanoate 1-dehydrogenase 1-dehydrogenase 1-dehydrogenase 1-dehydrogenase 2-dehydrogenase 2-dehydrogen | Undetermined 111169 27124 27133 277.87 41136 6321 27133 4217 11121 11121 27112 27145 53113 27.423 27.423 27.423 27.423 27.423 | H16_A1715/H16_B1719/ H16_B1769 H16_A3084 H16_A3084 H16_A0136 H16_A0367 H16_A2551 H16_A3048 H16_A0368 H16_A0136 H16_A0136 H16_A0136 H16_A0136 H16_A0136 H16_A01391 H16_B1212 H16_B1212 H16_B0391 H16_B0372 H16_B0372 H16_B0372 H16_B0372 H16_B0372 H16_B0373 | apbA1/apbA2/apbA3 pan8 coaE unknown unknown acpS dfp unknown dfp unknown unknown unknown unknown unknown unknown unknown unknown unknown patt kdgk gutQ phnN prsA kguD | fadh2 + uq -> fad + uqh2 dhpant + 2 h + nadph -> nadp + pant 3mob + h2o + metthf -> dhpant + thf atp + dpcoa -> adp + coa atp + pnto -> 4ppnto + adp atp + 4ppnte -> dpcoa + ppi apoACP + coa -> ACP + pap 4ppcys + h -> co2 + 4ppnte bala + atp + pant -> amp + pnto + ppi 4ppnto + ctp + cys -> 4ppcys + cmp + ppi atp + pantcys -> adp + 4ppcys atp + ptt -> adp + 4ppnte dalt -> kdg + h2o xylt + nadp <-> xyl + nadph + 2 h arbt + nad <-> larabinose + nadph + 2 h arbt + nad <-> dfopgc + adp kdg + atp -> kdpg + adp riSp <-> aSp atp + r1Sbp -> adp + prpp atp + r5p <-> amp + prpp | fadh2 + uq -> fad + uqh2 + h dhpant + h + nadph -> nadp + pant 3mob + h2o + metthf -> dhpant + thf atp + dpcoa -> adp + coa + h atp + pnto -> 4ppnto + adp + h atp + 4ppnte -> dpcoa + ppi apoACP + coa -> ACP + pap + h 4ppcys + h -> co2 + 4ppnte balla + atp + pant -> amp + pnto + ppi + 2 h 4ppnto + ctp + cys -> 4ppcys + cmp + ppi + 2 h atp + pantcys -> adp + 4ppcys + h atp + ptt -> adp + 4ppnte + h dalt -> kdg + h2o xylt + nadp <-> xyl + nadph + h arbt + nad <-> larabinose + nadph + h arbt + nad <-> larabinose + nadph + h kdg + atp -> kdpg + adp + h kdg + atp -> kdpg + adp + h riSp <-> aSp atp + riSbp + h -> adp + prpp atp + riSp <-> amp + prpp + h | fadh2 + uq -> fad + uqh2 + h dhpant + h + nadph -> nadp + pant 3mob + h2o + metthf -> dhpant + thf atp + dpcoa -> adp + coa + h atp + dpcoa -> dpp + coa + h atp + pnto -> dpponto + adp + h atp + 4ppnte -> dpcoa + ppi apoACP + coa -> ACP + pap + h 4ppcys + h -> co2 + 4ppnte bala + atp + pant -> amp + pnto + ppi + 2 h 4ppnto + ctp + cys -> 4ppys + cmp + ppi + 2 h atp + pantcys -> adp + 4ppres + h atp + patt -> adp + 4ppnte + h dalt -> kdg + h2o xyft + nadp <-> xyft + nadph + h arbt + nad <-> larabinose + nadph + h atp + gluc -> dfopgc + adp + h kdg + atp -> kdpg + adp + h kdg + atp -> kdpg + adp + h rlSp <-> aSp atp + r1Sbp -> adp + prpp atp + r5p <-> amp + prpp + h |

| | Pentose Phosphate | | | | | | | |
|----------|-------------------------------|--|------------|---|-----------------------------------|---|---|--|
| TRKT1 | , | | 2.2.1.1 | H16_A3147/H16_B1388 | tktA/cbbT2 | r5p + xu5p <-> g3p + s7p | r5p + xu5p <-> g3p + s7p | r5p + xu5p <-> g3p + s7p |
| TRKT2 | Pentose Phosphate Pathway | transketolase | 2.2.1.1 | H16_A3147/H16_B1388 | tktA/cbbT2 | e4p + xu5p <-> f6p + g3p | e4p + xu5p <-> f6p + g3p | e4p + xu5p <-> f6p + g3p |
| TRADL | Pentose Phosphate Pathway | transatuolase | 2.2.1.2 | H16_A2346 | tal | g3p + s7p <-> e4p + f6p | g3p + s7p <-> e4p + f6p | g3p + s7p <-> e4p + f6p |
| PGL | Pentose Phosphate Pathway | 6- phosphogluconolact onase | 3.1.1.31 | H16_B2565 | pgl | 6pgl + h2o -> d6pgc + h | 6pgl + h2o -> d6pgc + h | 6pgl + h2o -> d6pgc + h |
| EDA | Pentose Phosphate Pathway | 2-dehydro-3-deoxy- phosphogluconate aldolase | 4.1.2.14 | H16_B1213 | eda | kdpg -> g3p + pyr | kdpg -> g3p + pyr | kdpg -> g3p + pyr |
| EDD | Pentose Phosphate Pathway | 6-phosphogluconate dehydratase | 4.2.1.12 | H16_A1178/H16_B2567 | edd1/edd2 | d6pgc -> kdpg + h2o | d6pgc -> kdpg + h2o | d6pgc -> kdpg + h2o |
| RPE | Pentose Phosphate Pathway | ribulose 5-phosphate 3-epimerase | 5.1.3.1 | H16_A3317/H16_B1391 | rpe/cbbE2 | rlSp <-> xuSp | rl5p <-> xu5p | rlSp <-> xuSp |
| RPI | Pentose Phosphate Pathway | ribose-5-phosphate isomerase | 5.3.1.6 | H16_A2345 | rpiA | r5p <-> rl5p | rSp <-> rlSp | rSp <-> rlSp |
| GLTN2 | Pentose Phosphate Pathway | gluconolactonase | 3.1.1.17 | H16_A3012/H16_B0345/ H16_B1441 | gnl1/gnl2/gnl3 | g15l + h2o -> gluc + h | g15l + h2o -> gluc + h | g15l + h2o -> gluc + h |
| PPG2DGp | Pentose Phosphate Pathway | phosphogluconate 2- dehydrogenase | 1.1.1.43 | H16_B1813 | kguD | d6pgc + nadp -> 2dhglcn6p + nadph + 2 h | d6pgc + nadp -> 2dhglcn6p + nadph + h | d6pgc + nadp -> 2dhglcn6p + nadph + h |
| PAMPPT | Peptidoglycan Biosynthesis | phospho-N- acetylmuramoyl- pentapeptide- transferase (meso- 2,6-diaminopimelate) | | H16_A3276 | mraY | udcpp + ugmda -> uagmda + ump | udcpp + ugmda -> uagmda + ump | udcpp + ugmda -> uagmda + ump |
| UDCPDP | Peptidoglycan Biosynthesis | undecaprenyl- diphosphatase UDP-N- | 3.6.1.27 | H16_A2871 | bacA | h2o + udcpdp -> pi + udcpp | h2o + udcpdp -> 2 h + pi + udcpp | h2o + udcpdp -> h + pi + udcpp |
| UAMAGDS | Peptidoglycan Biosynthesis | acetylmuramoyl-L- alanyl-D-glutamyl- meso-2,6- diaminopimelate synthetase UDP-N- | 6.3.2.13 | H16_A3278 | murE | 26dap-M + atp + uamag -> adp + pi + ugmd | 26dap-M + atp + uamag -> adp + h + pi + ugmd | 26dap-M + atp + uamag -> adp + 2 h + pi + ugmd |
| UAMAGDAS | Peptidoglycan Biosynthesis | acetylmuramoyl-L- alanyl-D-glutamyl- meso-2,6- diaminopimeloyl-D- alanyl-D-alanine synthetase | 6.3.2.10 | H16_A3277 | murF | alaala + atp + ugmd -> adp + pi + ugmda | alaala + atp + ugmd -> adp + h + pi + ugmda | alaala + atp + ugmd -> adp + pi + ugmda |
| UACMAS | Peptidoglycan Biosynthesis | UDP-N- acetylmuramoyl-L- alanine synthetase | 6.3.2.8 | H16_A3167/H16_A3272 | murC1/murC2 | ala + atp + udpnam -> adp + pi + uama | ala + atp + udpnam -> adp + h + pi + uama | ala + atp + udpnam -> adp + h + pi + uama |
| UACMAGS | Peptidoglycan Biosynthesis | UDP-N- acetylmuramoyl-L- alanyl-D-glutamate synthetase UDP-N- acetylglucosamine- | 6.3.2.9 | H16_A3275 | murD | atp + dglu + uama -> adp + pi + uamag | atp + dglu + uama -> adp + h + pi + uamag | atp + dglu + uama -> adp + h + pi + uamag |
| UAGMPUT | Peptidoglycan Biosynthesis | undecaprenol N- acetylglucosamine | 2.4.1.227 | H16_A3273 | murG | udpnag + uagmda -> uaagmda + udp | udpnag + uagmda -> uaagmda + udp | udpnag + uagmda -> uaagmda + udp + h |
| GLNST2 | Peptidoglycan Biosynthesis | transferase glutamine synthetase | 6.3.1.2 | H16_A2335/H16_B0618/ H16_B2191 | glna/glnA2/glnA3 | uaagmda + atp + nh4 -> uaagmmda + adp + pi | uaagmda + atp + nh4 -> uaagmmda + adp + pi + h | uaagmda + atp + nh4 -> uaagmmda + adp + pi + h |
| NACMAA | Peptidoglycan Biosynthesis | N-acetylmuramoyl-L- alanine amidase UDP-N- | 3.5.1.28 | H16_A0597/H16_A3236 | amiC/unknown | acala + h2o -> acmur + ala | acala + h2o -> acmur + ala | acala + h2o -> acmur + ala |
| UNAMPLA | Peptidoglycan Biosynthesis | acetylmuramoylpenta peptide-lysine N6- alanyltransferase | 2.3.2.10 | | | 5 gly + uaagmmda -> uaagmm5da + 5 h2o | 5 gly + uaagmmda -> uaagmm5da + 5 h2o | 5 gly + uaagmmda -> uaagmm5da + 5 h2o |
| PGPS | Peptidoglycan Biosynthesis | peptidoglycan precursor synthesis | | | | uaagmm5da -> udcpdp + ppeptido | uaagmm5da -> udcpdp + ppeptido | uaagmm5da -> udcpdp + ppeptido |
| DALAT | Peptidoglycan Biosynthesis | D-alanine transaminase aldehyde | 2.6.1.21 | H16_A2521 | dat | ppeptido + dala -> PEPTIDO + dala_e | ppeptido + dala -> PEPTIDO + dala_e | ppeptido + dala -> PEPTIDO + dala_e |
| ALHD3 | Phenylalanine metabolism | dehydrogenase (phenylacetaldehyde, NAD) | 1.2.1.39 | H16_B1358/H16_B1939 | paaK2/feaB | h2o + nad + pacald -> 2 h + nadh + pac | h2o + nad + pacald -> 2 h + nadh + pac | h2o + nad + pacald -> 2 h + nadh + pac |
| OXP4EH | Phenylalanine metabolism | 2-oxopent-4-enoate hydratase | 4.2.1.80 | H16_A0143/H16_B0548/ H16_B0597/H16_B0884 | | h2o + op4en -> hopt | h2o + op4en -> hopt | h2o + op4en -> hopt |
| PHEACL | Phenylalanine metabolism | phenylacetate-CoA ligase | 6.2.1.30 | H16_A0291/H16_A3313 | unknown | atp + coa + h + pac -> amp + phaccoa + ppi | atp + coa + pac -> amp + phaccoa + ppi + h | atp + coa + pac -> amp + phaccoa + ppi + h |
| 3HCINNMH | Phenylalanine metabolism | 3-hydroxycinnamate hydroxylase | 1.14.13 | H16_B1546 | unknown | 3hcinnm + h + nadh + o2 -> dhcinnm + h2o + nad | 3hcinnm + h + nadh + o2 -> dhcinnm + h2o + nad | 3hcinnm + h + nadh + o2 -> dhcinnm + h2o + nad |
| 3HPPPNH | Phenylalanine metabolism | 3-(3-hydroxy- phenyl)propionate hydroxylase | 1.14.13 | H16_B1546 | unknown | $3hpppn + h + nadh + o2 \rightarrow dhpppn + h2o + nad$ | 3hpppn + h + nadh + o2 -> dhpppn + h2o + nad | $3hpppn + h + nadh + o2 \rightarrow dhpppn + h2o + nad$ |
| CINNMDO | Phenylalanine metabolism | Cinnamate dioxygenase 4-hydroxy-2- | | H16_A1632/H16_B0800 | - | cinnm + h + nadh + o2 -> cenchddd + nad | cinnm + h + nadh + o2 -> cenchddd + nad | cinnm + h + nadh + o2 -> cenchddd + nad |
| 4H2OPNTA | Phenylalanine metabolism | oxopentanoate aldolase | 4.1.3.39 | H16_A1807/H16_B0552/ H16_B0595 | mhpE2/mhpE1/bpHI | hopt -> acal + pyr | hopt -> acal + pyr | hopt -> acal + pyr |
| PPPNDO | Phenylalanine metabolism | Phenylpropanoate Dioxygenase | 1.14.12.19 | H16_A1632&H16_B0800 | nagH&unknown | h + nadh + o2 + pppn -> cechddd + nad | h + nadh + o2 + pppn -> cechddd + nad | h + nadh + o2 + pppn -> cechddd + nad |
| НРРН | Phenylalanine metabolism | hippurate hydrolase | 3.5.1.32 | H16_A0073/H16_A3299, H16_B0605/H16_B1473 | | benzot + gly -> nppr + n2o | benzot + gly -> hppr + h2o | benzot + gly -> hppr + h2o |
| CNTOB | Phenylalanine metabolism | unclear reaction | | | | cinnm + 2 h2o + nad -> benzot + ac + nadh + 2 h | + 2 h | $\begin{array}{l} cinnm + 2 \ h2o + nad \rightarrow benzot + ac + nadh + 2 \\ h \end{array}$ |
| AMDS1 | Phenylalanine metabolism | amidase 4- | | H16_A1469/H16_B1874/ H16_B2459 | unknown/unknown/ aimE | pheact + h2o -> pac + nh4 | pheact + h2o -> pac + nh4 | pheact + h2o -> pac + nh4 |
| 4HPHED2 | Phenylalanine metabolism | hydroxyphenylpyruva te dioxygenase | 1.13.11.27 | H16_B1083 | hpd | phpyr + o2 -> 2hpa + co2 | phpyr + o2 -> 2hpa + co2 | phpyr + o2 -> 2hpa + co2 |
| MNAO9 | Phenylalanine metabolism | monoamine oxidase | 1.4.3.4 | H16_A0831 | maoB | peamn + o2 + h2o -> pacald + nh4 + h2o2 | peamn + o2 + h2o -> pacald + nh4 + h2o2 | peamn + o2 + h2o -> pacald + nh4 + h2o2 |
| DATA3 | Phenylalanine metabolism | D-alanine transaminase | | H16_A2521 H16_A0770/H16_A0817, | dat / | phpyr + dglu <-> dphe + akg | phpyr + dglu <-> dphe + akg | phpyr + dglu <-> dphe + akg |
| DAAD2 | Phenylalanine metabolism | D-Amino acid dehydrogenase | 1.4.99.1 | H16_A0770/H16_A0817/ H16_A1505/H16_B0508/ H16_B1893 | dadA2/dadA1/dadA 5/dadA6/dadA7 | dphe + h2o + fad -> phpyr + nh4 + fadh2 | dphe + h2o + fad + h -> phpyr + nh4 + fadh2 | dphe + h2o + fad + h -> phpyr + nh4 + fadh2 |
| LAAO5 | Phenylalanine metabolism | L-amino-acid oxidase | 1.4.3.2 | H16_A0845/H16_A0856 | lao1/lao2 | phe + h2o + o2 -> phpyr + nh4 + h2o2 | phe + h2o + o2 -> phpyr + nh4 + h2o2 | phe + h2o + o2 -> phpyr + nh4 + h2o2 |
| ASPAM6 | Phenylalanine metabolism | aspartate aminotransferase | 2.6.1.1 | H16_A2857 | unknown | phe + akg <-> phpyr + glu | phe + akg <-> phpyr + glu | phe + akg <-> phpyr + glu |

| ACTF3 | Phenylalanine metabolism | acetyltransferase | 2.3.1 | H16, A0039/H16, A0240/ H16, A0269/H16, A0659/ H16, A1315/H16, A1564/ H16, A1563/H16, A1807/ H16, A3759/H16, A3071/ H16, A3033/H16, A3212/ H16, B0018/H16, B0021/ H16, B0018/H16, B0032/ H16, B178/H16, B1292/ H16, B1407/H16, B1899/H16, B1899/H16, B1899/H16, B1899/H16, B1899/H16, B1899/H16 | unknown/unknown/ unknown/unknown/ unknown/unknown/ unknown/unknown/ unknown/unknown/ unknown/pat/unkno wn/unknown/whpb/ unknown/unknown/ phnT/unknown/unkn own/unknown/unkn | phaccoa + gly -> pheacgly + coa + h | phaccoa + gly -> pheacgly + coa + h | phaccoa + gly -> pheacgly + coa + h |
|--------------|--|---|-----------|---|--|--|--|--|
| SHKDH | Phenylalanine, Tyrosine and Tryptophan biosynthesis | shikimate dehydrogenase | 1.1.1.25 | H16_A3161 | aroE | dhsk + 2 h + nadph <-> nadp + sme | dhsk + h + nadph <-> nadp + sme | dhsk + h + nadph <-> nadp + sme |
| PPNDHG | Phenylalanine, Tyrosine and Tryptophan biosynthesis Phenylalanine, | prephenate dehydrogenase | 1.3.1.12 | H16_A0794 | tyrA | nad + phen -> 4hpp + co2 + nadh | nad + phen -> 4hpp + co2 + nadh | nad + phen -> 4hpp + co2 + nadh |
| ANTPRT | Tyrosine and Tryptophan biosynthesis Phenylalanine, | anthranilate phosphoribosyltransf erase 3-phosphoshikimate | 2.4.2.18 | H16_A0356/H16_A3321 | trpD2/trpD1 | an + prpp -> ppi + npran | an + prpp -> ppi + npran + h | an + prpp -> ppi + npran + h |
| PSHKCVT | Tyrosine and Tryptophan biosynthesis Phenylalanine, | 1. | 2.5.1.19 | H16_A0795 | aroA | pep + skm5p <-> 3psme + pi | pep + skm5p <-> 3psme + h + pi | pep + skm5p <-> 3psme + h + pi |
| TYRTA1 | Tyrosine and Tryptophan biosynthesis Phenylalanine, | tyrosine transaminase | 2.6.1.9 | H16_A0793/H16_A3415 | hisC1/hisC2 | akg + tyr <-> 4hpp + glu | akg + tyr <-> 4hpp + glu | akg + tyr <-> 4hpp + glu |
| TYRTA2 | Tyrosine and Tryptophan biosynthesis Phenylalanine, | tyrosine transaminase | 2.6.1.57 | H16_A1151/H16_B1081 | tyrB1/tyrB2 | akg + tyr <-> 4hpp + glu | akg + tyr <-> 4hpp + glu | akg + tyr <-> 4hpp + glu |
| PHETA1 | Tyrosine and Tryptophan biosynthesis Phenylalanine, | phenylalanine transaminase | 2.6.1.58 | | | akg + phe <-> glu + phpyr | akg + phe <-> glu + phpyr | akg + phe <-> glu + phpyr |
| PHETA2 | Tyrosine and Tryptophan biosynthesis Phenylalanine, | phenylalanine transaminase | 2.6.1.57 | H16_A1151/H16_B1081 | tyrB1/tyrB2 | akg + phe <-> glu + phpyr | akg + phe <-> glu + phpyr | akg + phe <-> glu + phpyr |
| SHKK | Tyrosine and Tryptophan biosynthesis Phenylalanine, | | 2.7.1.71 | H16_A3435 | aroL | atp + sme -> adp + skm5p | atp + sme -> adp + skm5p + h | atp + sme -> adp + skm5p + h |
| IG3PS | Tyrosine and Tryptophan biosynthesis Phenylalanine, | indole-3-glycerol- phosphate synthase 3-deoxy-7- | 4.1.1.48 | H16_A3322 | trpC | 2cpr5p + h -> 3ig3p + co2 + h2o | 2cpr5p + h -> 3ig3p + co2 + h2o | 2cpr5p + h -> 3ig3p + co2 + h2o |
| DOXPHS | Tyrosine and Tryptophan biosynthesis Phenylalanine, | phosphoheptulonate synthase | 2.5.1.54 | H16_A1122/H16_B1076 | aroG1/aroG2 | e4p + h2o + pep -> 3ddah7p + pi | e4p + h2o + pep -> 3ddah7p + h + pi | e4p + h2o + pep -> 3ddah7p + h + pi |
| ANTHS | Tyrosine and Tryptophan biosynthesis Phenylalanine, | anthranilate synthase | 4.1.3.27 | H16_A3319 & H16_A3320 | trpE&trpG | chor + gln -> an + glu + h + pyr | chor + gln -> an + glu + h + pyr | chor + gln -> an + glu + h + pyr |
| DHQND | Tyrosine and Tryptophan biosynthesis Phenylalanine, | 3-dehydroquinate dehydratase | 4.2.1.10 | H16_A3170/H16_B0465 | aroQ1/aroQ2 | dqt -> dhsk + h2o | dqt -> dhsk + h2o | dqt -> dhsk + h2o |
| TRPS1 | Tyrosine and Tryptophan biosynthesis Phenylalanine, | tryptophan synthase | 4.2.1.20 | 4 | trpA&trpB | 3ig3p + ser -> g3p + h2o + trp | 3ig3p + ser -> g3p + h2o + trp | 3ig3p + ser -> g3p + h2o + trp |
| TRPS2 | Tyrosine and Tryptophan biosynthesis Phenylalanine, Tyrosine and | tryptophan synthase | 4.2.1.20 | H16_A2612&H16_A261 4 H16_A2612&H16_A261 | trpA&trpB | indole + ser -> h2o + trp | indole + ser -> h2o + trp | indole + ser -> h2o + trp |
| TRPS3 | Tryptophan biosynthesis Phenylalanine, Tyrosine and | tryptophan synthase prephenate | 4.2.1.20 | 4 | trpA&trpB | 3ig3p -> g3p + indole | 3ig3p -> g3p + indole | 3ig3p -> g3p + indole |
| PPNDHT | Tryptophan biosynthesis Phenylalanine, Tyrosine and | dehydratase | | | pheA | h + phen -> co2 + h2o + phpyr | h + phen -> co2 + h2o + phpyr | h + phen -> co2 + h2o + phpyr |
| CHORS | Tryptophan biosynthesis Phenylalanine, Tyrosine and | chorismate synthase phosphoribosylanthr | | | aroC | 3psme -> chor + pi | 3psme -> chor + pi | 3psme -> chor + pi |
| PRANTI | Tryptophan biosynthesis Phenylalanine, Tyrosine and | anilate isomerase | 5.3.1.24 | | trpF | npran -> 2cpr5p | npran -> 2cpr5p | npran -> 2cpr5p |
| CHORM | Tryptophan biosynthesis Phenylalanine, Tyrosine and | chorismate mutase 3-dehydroquinate | 5.4.99.5 | | pheA | chor -> phen | chor -> phen | chor -> phen |
| DHQTS QDPQ1 | Tryptophan biosynthesis Phenylalanine, Tyrosine and | synthase quinate dehydrogenase | 4.2.3.4 | H16_A3434 | aroB | 3ddah7p -> dqt + pi sme + pqq <-> dhsk + pqqh2 | 3ddah7p -> dqt + pi | 3ddah7p -> dqt + pi |
| QDPQ2 | Tryptophan biosynthesis Phenylalanine, Tyrosine and | (pyrroloquinoline- quinone) quinate dehydrogenase | | | quiA quiA | | sme + pqq <-> dhsk + pqqh2 | sme + pqq <-> dhsk + pqqh2 |
| PHEA4H | Tryptophan biosynthesis Phenylalanine, Tyrosine and | (pyrroloquinoline- quinone) | | | phhA | dhsk + pqqh2 + h2o <-> qt + pqq | dhsk + pqqh2 + h2o <-> qt + pqq | dhsk + pqqh2 + h2o <-> qt + pqq |
| TYRTM | Tryptophan biosynthesis Phenylalanine, Tyrosine and | hydroxylase aromatic-amino-acid | 2.6.1.57 | H16_A3678 H16_A1151/H16_B1081 | • | tethbp + phe + o2 -> dhbpt + tyr + h2o phen + asp -> oaa + ag | tethbp + phe + o2 -> dhbpt + tyr + h2o | tethbp + phe + o2 -> dhbpt + tyr + h2o phen + asp -> oaa + ag |
| CPPPGO | Tryptophan biosynthesis Porphyrin and Chlorophyll | transaminase coproporphyrinogen oxidase (O2 | 1.3.3.3 | | tyrB1/tyrB2 hemF | pnen + asp -> oaa + ag cpp + 2 h + o2 -> 2 co2 + 2 h2o + pphg | phen + asp -> oaa + ag cpp + 2 h + o2 -> 2 co2 + 2 h2o + pphg | pnen + asp -> oaa + ag cpp + 2 h + o2 -> 2 co2 + 2 h2o + pphg |
| PPHGO | metabolism Porphyrin and Chlorophyll | required) | 1.3.3.4 | | unknown/unknown | | 3 o2 + 2 pphg -> 6 h2o + 2 ppix | 3 o2 + 2 pphg -> 6 h2o + 2 ppix |
| PPHGOx | metabolism Porphyrin and Chlorophyll metabolism | protonomhyrinogen | 1.3.3.4 | H16_A2891/H16_B2453 | unknown/unknown | 3 fum + pphg -> ppix + 3 succ | 3 fum + pphg -> ppix + 3 succ | 3 fum + pphg -> ppix + 3 succ |
| UPPMT | Porphyrin and Chlorophyll metabolism | uroporphyrinogen methyltransferase | 2.1.1.107 | H16_A2919/H16_A2994/ H16_B2285 | hemXD/cysG/nirE | 2 sam + uppg3 -> 2 sah + dscl + h | 2 sam + uppg3 -> 2 sah + dscl + h | 2 sam + uppg3 -> 2 sah + dscl + h |
| | | | | | | | | |

H16_A0039/H16_A0240/ unknown/unknown/

| CBIAT1 | Porphyrin and Chlorophyll | Cobinamide adenyltransferase | 2.5.1.17 | H16_A2969/H16_A3090 | btuR/unknown | atp + cbi <-> adcba + pppi | atp + cbi <-> adcba + pppi | atp + cbi <-> adcba + pppi + h |
|---------|--|--|-----------|--|--|--|--|---|
| UPPDC1 | metabolism Porphyrin and Chlorophyll | uroporphyrinogen decarboxylase (uroporphyrinogen | 4.1.1.37 | H16_A3633 | hemE | 4 h + uppg3 -> 4 co2 + cpp | 4 h + uppg3 -> 4 co2 + cpp | 4 h + uppg3 -> 4 co2 + cpp |
| PPBINGS | metabolism Porphyrin and Chlorophyll | III) porphobilinogen | 4.2.1.24 | H16_A3453 | hemB | 2 5aop -> h + 2 h2o + pbg | 2 Saop -> h + 2 h2o + pbg | 2 5aop + h -> 2 h2o + pbg |
| HMBS | metabolism Porphyrin and Chlorophyll | hydroxymethylbilane | 2.5.1.16 | H16_A2920 | hemC | h2o + 4 pbg -> hmb + 4 nh4 | h2o + 4 pbg -> hmb + 4 nh4 | h2o + 4 pbg -> hmb + 4 nh4 |
| FERCLT | metabolism Porphyrin and Chlorophyll | synthase ferrochelatase | 4.99.1.1 | H16_A1134 | hemH | fe2 + ppix -> pth + 2 h | fe2 + ppix -> pth + 2 h | fe2 + ppix -> pth + 2 h |
| | metabolism Porphyrin and | glutamate-1- | | | | | | |
| GLU1SAT | Chlorophyll metabolism | semialdehyde aminotransferase | 5.4.3.8 | H16_A0734 | hemL | glu1sa <-> 5aop | glu1sa <-> 5aop | glu1sa <-> 5aop + h |
| GLUTRS | Porphyrin and Chlorophyll metabolism | Glutamyl-tRNA synthetase | 6.1.1.17 | H16_A2403/H16_A2716 | gltX1/gltX2 | atp + glu + h + trnaglu -> amp + glutrna + ppi | atp + glu + trnaglu -> amp + glutrna + ppi + h | atp + glu + trnaglu -> amp + glutrna + ppi + h |
| ACOBPGT | Porphyrin and Chlorophyll metabolism | Adenosyl cobinamide phosphate guanyltransferase | | H16_A2962 | cobU | adcbap + gtp -> agdpcba + ppi | adcbap + gtp -> agdpcba + ppi | adcbap + gtp -> agdpcba + ppi |
| ADCOBK | Porphyrin and Chlorophyll metabolism | Adenosyl cobinamide kinase | 2.7.1.156 | H16_A2962 | cobU | adcba + atp -> adcbap + adp | adcba + atp -> adcbap + adp + h | adcba + atp -> adcbap + adp + h |
| ADCOBPS | Porphyrin and Chlorophyll metabolism | Adenosylcobalamin 5'-phosphate synthase | 2.7.8.26 | H16_A2967 | cobS1 | agdpcba + rdmbzi + h -> adocbl + gmp | agdpcba + rdmbzi -> adocbl + gmp + h | agdpcba + rdmbzi -> adocbl + gmp + h |
| GLUTRR | Porphyrin and Chlorophyll metabolism | glutamyl-tRNA reductase | 1.2.1.70 | H16_A3339 | hemA | glutrna + 2 h + nadph -> glu1sa + nadp + trnaglu | glutrna + h + nadph -> glu1sa + nadp + trnaglu | glutrna + h + nadph -> glu1sa + nadp + tmaglu |
| HEMEOS | Porphyrin and Chlorophyll metabolism | Heme O synthase | 2.5.1 | H16_A0352 | ctaB | frdp + h2o + pth + 2 h -> hemeO + ppi | frdp + h2o + pth + h -> hemeO + ppi | frdp + h2o + pth + h -> hemeO + ppi |
| UPPDC2 | Porphyrin and Chlorophyll metabolism | uroporphyrinogen decarboxylase | 4.1.1.37 | H16_A3633 | hemE | uppg1 + 4 h -> cppi + 4 co2 | uppg1 + 4 h -> cppi + 4 co2 | uppg1 + 4 h -> cppi + 4 co2 |
| SRHCC | Porphyrin and Chlorophyll metabolism | sirohydrochlorin cobaltochelatase | 4.99.1.3 | H16_A2993 | cbiX | shcl + cobalt2 -> cobtpc + 2 h | shcl + cobalt2 -> cobtpc + 2 h | shcl + cobalt2 -> cobtpc + 2 h |
| PHEMEAS | Porphyrin and Chlorophyll metabolism | putative hemeA synthase | | H16_A0351 | ctaA | hemeO + h2o -> hemeA + 2 h2 | hemeO + h2o -> hemeA + 2 h2 | hemeO + h2o -> hemeA + 2 h2 |
| CBIAT2 | Porphyrin and Chlorophyll metabolism | Cobinamide adenyltransferase | 2.5.1.17 | H16_A2969/H16_A3090 | btuR/unknown | cobacd + atp -> acda + pppi | cobacd + atp -> acda + pppi | cobacd + atp -> acda + pppi + h |
| ADNCOS | Porphyrin and Chlorophyll metabolism | adenosylcobyric acid synthase | 6.3.5.10 | H16_A2961 | cbiP | acda + 4 gln + 4 atp + 4 h2o + h -> acha + 4 glu + 4 pi + 4 adp | acda + 4 gln + 4 atp + 4 h2o -> acha + 4 glu + 4 pi + 4 adp + 3 h | acda + 4 gln + 4 atp + 4 h2o -> acha + 4 glu + 4 pi + 4 adp + 3 h |
| COBBP1 | Porphyrin and Chlorophyll metabolism | cobalamin biosynthetic protein CobC | 6.3.1.10 | H16_A2963/H16_A2964 | cbiB/cobD | atp + acha + amppo -> adp + pi + adcba + h | atp + acha + amppo -> adp + pi + adcba + 2 h | atp + acha + amppo -> adp + pi + adcba + 2 h |
| COBBP2 | Porphyrin and Chlorophyll metabolism | cobalamin biosynthetic protein CobC | 6.3.1.10 | H16_A2963/H16_A2964 | cbiB/cobD | acha + dlap2oop + atp -> adcbap + adp + pi + h | acha + d1ap2oop + atp -> adcbap + adp + $pi + 2h$ | acha + d1ap2oop + atp -> adcbap + adp + pi + 2 h |
| PPNAK | Propanoate metabolism | Propionate kinase | 2.7.2.1 | H16_A0670/H16_B1630 | ackA2/ackA | adp + ppap <-> atp + ppa | adp + ppap <-> atp + ppa | adp + ppap <-> atp + ppa |
| MICITL | Propanoate metabolism | methylisocitrate lyase | 4.1.3.30 | H16_A1905 | prpB | micit <-> pyr + succ | micit <-> pyr + succ | micit <-> pyr + succ |
| MCITDH | Propanoate metabolism | 2-methylcitrate dehydratase | 4.2.1.79 | H16_A1909/H16_B0681/ H16_B1436/H16_B1444 | | 2mcit -> maco + h2o | 2mcit -> maco + h2o | 2mcit -> maco + h2o |
| OBUTFL | Propanoate metabolism | 2-Oxobutanoate formate lyase | 2.3.1.54 | | | obut + coa -> formate + ppcoa | obut + coa -> formate + ppcoa | obut + coa -> formate + ppcoa |
| PACTF | Propanoate | Phosphate acetyltransferase | 2.3.1.8 | H16_B1631/H16_B1871 | pta1/pta2 | pi + ppcoa -> coa + ppap + h | pi + ppcoa -> coa + ppap | pi + ppcoa -> coa + ppap |
| MCDCX | metabolism Propanoate | malonyl-CoA | 4.1.1.9 | H16_A2981 | mcd | malcoa + h -> accoa + co2 | malcoa + h -> accoa + co2 | malcoa + h -> accoa + co2 |
| WEDEA | metabolism | decarboxylase | 4.1.1.5 | H16_A0866/H16_A0871/ H16_A1230/H16_A1519/ H16_A1700/H16_A1718/ H16_A2252/H16_A2794/ | / unknown/unknown/ / unknown/unknown/ / unknown/unknown/ | matca + 11 - 2 accos + Co2 | Tillecoa + 11 -> accoa + co2 | matos + ii -> accos + coz |
| HIBCH | Propanoate metabolism | 3-hydroxyisobutyryl- CoA hydrolase | 6.2.1 | H16_A2807/H16_A2978/ H16_B0174/H16_B0677/ H16_B0910/H16_B1148/ H16_B1264/H16_B1335/ H16_B1662/H16_B1709/ | unknown/unknown/ unknown/unknown/ unknown/unknown/ unknown/unknown/ unknown/unknown/ | 3hpcoa + pi + adp <-> 3hpp + coa + atp + h | 3hpcoa + pi + adp <-> 3hpp + coa + atp | 3hpcoa + pi + adp <-> 3hpp + coa + atp |
| ENCOAH2 | Propanoate metabolism | encyl-CoA hydratase | 421.17 | H16, B2522 H16, A0100/H16, A0142, H16, A0179/H16, A0141, H16, A0179/H16, A0461, H16, A0179/H16, A0813, H16, A0161, H16, A0865, H16, A01867, H16, A0161, A016 | ulmkonvr/unkcowr/ unknown/uknowr/ unknown/uknown/ unknown/unknown/ | 3hpcoa <-> ppecoa + h2o | 3hpcoa <-> ppecoa + h2o | 3hpcoa <-> ppecoa + h2o |

| ACOADH2 | Propanoate metabolism | acyl-CoA dehydrogenase | 13.99.3 | HLE, BUS3-Sh/HLE, BUS3-BM, HLE, BUS3-Sh/HLE, | own/unknown/unkn own/unknown/abmD /unknown/unknown/unknown/ unknown/unknown/ | fad + ppcoa <-> fadh2 + ppecoa | fad + ppcoa + h <-> fadh2 + ppecoa | fad + ppcoa + h <-> fadh2 + ppecoa |
|---|---|--|---|--|---|---|--|--|
| BKAR1 | Propanoate metabolism | beta-ketoacyl-ACP reductase | 1.3.1 | - ' | unknown/unknown | ppcoa + nadp <-> ppecoa + nadph + 2 h | ppcoa + nadp <-> ppecoa + nadph + h | ppcoa + nadp <-> ppecoa + nadph + h |
| ACCSYN1 | Propanoate metabolism | acetyl-CoA synthetase | 6.2.1.1 | H16_A1197/H16_A1616/ H16_A2525/H16_B0386/ H16_B0696/H16_B0834/ H16_B1102/ | acoE/unknown/unkn | ppcoa + amp <-> ppald + coa | ppcoa + amp + h <-> ppald + coa | ppcoa + amp + h <-> ppald + coa |
| ACCSYN2 | Propanoate metabolism | acetyl-CoA synthetase | 6.2.1.1 | H16_A1197/H16_A1616/ H16_A2525/H16_B0386/ H16_B0696/H16_B0834/ H16_B1102/ | acoE/unknown/unkn | ppald + ppi <-> ppa + atp + h | ppald + ppi <-> ppa + atp | ppald + ppi <-> ppa + atp |
| PPCSYN1 | Propanoate metabolism | propionyl-CoA | 6.2.1.17 | H16_A2462 | prpE | ppcoa + amp <-> ppald + coa | ppcoa + amp + h <-> ppald + coa | ppcoa + amp + h <-> ppald + coa |
| PPCSYN2 | Propanoate | synthetase propionyl-CoA | 6.2.1.17 | H16_A2462 | prpE | ppald + ppi <-> ppa + atp + h | ppald + ppi <-> ppa + atp | ppald + ppi <-> ppa + atp |
| PPCCX | metabolism Propanoate | synthetase propionyl-CoA | 6.4.1.3 | H16_A0177/H16_A1973/ | unknown/unknown/ | atp + ppcoa + hco3 -> adp + pi + mmcoa-S + h | atp + ppcoa + hco3 -> adp + pi + mmcoa-S | atp + ppcoa + hco3 -> adp + pi + mmcoa-S + h |
| | metabolism Propanoate | carboxylase 2-methylcitrate | | _ | pccB | | + h | |
| 2MCITS | metabolism | synthase | 2.3.3.5 | H16_A1906/H16_A2636 | prpC1/prpC2 | ppcoa + oaa + h2o <-> 2mcit + coa + h | ppcoa + oaa + h2o <-> 2mcit + coa + h | ppcoa + oaa + h2o <-> 2mcit + coa + h |
| MMSDH | Propanoate metabolism | methylmalonate- semialdehyde | 1.2.1.27 | H16_A0273/H16_A3664/ H16_B1191 | mmsA1/mmsA2/mm sA3 | mmsa + coa + nad -> ppcoa + co2 + nadh | mmsa + coa + nad -> ppcoa + co2 + nadh | mmsa + coa + nad -> ppcoa + co2 + nadh |
| L-LACD4 | Propanoate metabolism | dehydrogenase L-lactate | 1.1.1.27 | H16_A0666 | ldh | 2hba + nad -> obut + nadh + h | 2hba + nad -> obut + nadh + h | 2hba + nad -> obut + nadh + h |
| ACPCD | Propanoate metabolism | dehydrogenase 1- aminocyclopropane- 1-carboxylate | 3.5.99.7 | H16_B1365 | acd | acpc + h2o <-> obut + nh4 | acpc + h2o <-> obut + nh4 | acpc + h2o <-> obut + nh4 |
| PCT2 | Propanoate | deaminase propionate CoA- | 2.8.3.1 | 1116 42710 | | ladara con con la laca con | Indiana company and the company | Indexes a second library second |
| | metabolism Propanoate | transferase | 2.8.3.1 | H16_A2718 | pct | lactcoa + ppa <-> llac + ppcoa malcoa + h2o + nadp <-> 3oppcoa + o2 + | lactcoa + ppa <-> llac + ppcoa malcoa + h2o + nadp <-> 3oppcoa + o2 + | lactcoa + ppa <-> llac + ppcoa malcoa + h2o + nadp <-> 3oppcoa + o2 + |
| MCTOP | metabolism Propanoate | unclear reaction | | | | nadph + h | nadph | nadph |
| OPTHP | metabolism | unclear reaction | | | | 3oppcoa + nadph + 2 h <-> 3hpcoa + nadp | 3oppcoa + nadph + h <-> 3hpcoa + nadp | 3oppcoa + nadph + h <-> 3hpcoa + nadp |
| ALHD16 | Propanoate metabolism | aldehyde dehydrogenase (NAD+) | 1.2.1.3 | H16_A0232/H16_A0745/ H16_A1114/H16_A1495/ H16_B0212/H16_B0421/ H16_B0737/H16_B0833/ H16_B1534/H16_B1735/ H16_B1751/H16_B1835/ H16_B1960/H16_B2444 | unknown/unknown/ unknown/unknown/ unknown/unknown/ unknown/unknown/ unknown/unknown/ | 2p1a + nad + h2o -> ppn + nadh + 2 h | 2p1a + nad + h2o -> ppn + nadh + 2 h | 2p1a + nad + h2o -> ppn + nadh + 2 h |
| 2MCITDT | Propanoate metabolism | 2-methylisocitrate dehydratase | 4.2.1.99 | H16_A1907 | acnM | maco + h2o <-> micit | maco + h2o <-> micit | maco + h2o <-> micit |
| | | | | | | | | |
| IMPCH | | IMP cyclohydrolase | | H16_A0501 | purH | h2o + imp <-> fprica | h2o + imp <-> fprica | h2o + imp <-> fprica |
| IMPCH PRAIZC2 | Purine and Pyrimidine | IMP cyclohydrolase phosphoribosylamino imidazole | | H16_A0501 | purH | h2o + imp <-> fprica cair <-> caiz | | |
| | Purine and Pyrimidine Biosynthesis Purine and Pyrimidine | IMP cyclohydrolase phosphoribosylamino | | H16_A0501 | purH | cair <-> caiz | h2o + imp <-> fprica | h2o + imp <-> fprica |
| PRAIZC2 | Purine and Pyrimidine Biosynthesis Purine and | IMP cyclohydrolase phosphoribosylamino imidazole carboxylase GAR transformylase- T GTP diphosphokinase | | H16_A0501 H16_A0955/H16_A1337 | | cair <-> caiz | h2o + imp <-> fprica $cair <-> caiz$ $atp + formate + gar -> adp + fgam + h +$ | h2o + imp <-> fprica cair <-> caiz |
| PRAIZC2 GARTFT | Purine and Pyrimidine Biosynthesis Purine and Pyrimidine Biosynthesis | IMP cyclohydrolase phosphoribosylamino imidazole carboxylase GAR transformylase-T GTP diphosphokinase guanosine-5'- triphosphate,3'- diphosphate | 2.1.2 2.7.6.5 | | | cair <-> caiz atp + formate + gar -> adp + fgam + pi | h2o + imp <-> fprica $cair <-> caiz$ $atp + formate + gar -> adp + fgam + h + pi$ | h2o + imp <-> fprica cair <-> caiz atp + formate + gar -> adp + fgam + pi |
| PRAIZC2 GARTFT GTPDPK | Purine and Pyrimidine Biosynthesis Purine and Pyrimidine Biosynthesis Purine metabolism | IMP cyclohydrolase phosphoribosylamino imidazole carboxylase GAR transformylase-T GTP diphosphokinase guanosine-5'- triphosphate,3'- diphosphate diphosphatase Ureidoglycolate | 21.2 27.6.5 3.6.1.11 3.5.3.19 | H16_A0955/H16_A1337 H16_A2436 H16_B2455 | spoT1/spoT2 ppx unknown | cair <>> caiz atp + formate + gar -> adp + fgam + pi atp + gtp -> amp + pppgpp pppgpp + h2o -> pi + ppgpp | h2o + imp <-> fprica cair <-> caiz atp + formate + gar -> adp + fgam + h + pi atp + gtp -> amp + pppgpp + 2 h | h2o + imp <-> fprica cair <-> caiz atp + formate + gar -> adp + fgam + pi atp + gtp -> amp + pppgpp + h |
| GARTET GTPDPK GSTDPDP | Purine and Pyrimidine Biosynthesis Purine and Pyrimidine Biosynthesis Purine metabolism | IMP cyclohydrolase phosphoribosylamino imidazole carboxylase GAR transformylase-T GTP diphosphokinase guanosine-5'- triphosphate, 3'- diphosphate diphosphatase Ureidoglycolate hydrolase xanthine dehydrogenase | 21.2 27.6.5 3.6.1.11 3.5.3.19 | H16_A0955/H16_A1337 H16_A2436 | spoT1/spoT2 ppx unknown | cair <-> caiz atp + formate + gar -> adp + fgam + pi atp + gtp -> amp + pppgpp pppgpp + h2o -> pi + ppgpp | h2o + imp <-> fprica cair <-> caiz atp + formate + gar -> adp + fgam + h + pi atp + gtp -> amp + pppgpp + 2 h pppgpp + h2o -> h + pi + ppgpp | h2o + imp <>> fprica cair <>> caiz atp + formate + gar -> adp + fgam + pi atp + gtp -> amp + pppgpp + h pppgpp + h2o -> h + pi + ppgpp |
| GARTET GTPDPK GSTDPDP URGLYCH | Purine and Pyrimidine Biosynthesis Purine and Pyrimidine Biosynthesis Purine metabolism Purine metabolism | IMP cyclohydrolase phosphoribosylamino imidazole carboxylase GAR transformylase-T GTP diphosphokinase guanosine-5'- triphosphate3'- diphosphatase Ureidoglycolate hydrolase xanthine dehydrogenase ribonucleoside-diphosphate | 21.2 2.7.6.5 3.6.1.11 3.5.3.19 | H16_A0955/H16_A1337 H16_A2436 H16_B2455 H16_A1016/H16_A1017/ H16_A3371/H16_B1897/ | spoT1/spoT2 ppx unknown xdhB1/xdhA1/coxL5/ | cair <-> caiz atp + formate + gar -> adp + fgam + pi atp + gtp -> amp + pppgpp pppgpp + h2o -> pi + ppgpp 2 h + h2o + urdglyc -> co2 + glx + 2 nh4 | h2o + imp <-> fprica cair <-> caiz atp + formate + gar -> adp + fgam + h + pi atp + gtp -> amp + pppgpp + 2 h pppgpp + h2o -> h + pi + ppgpp 2 h + h2o + urdglyc -> co2 + glx + 2 nh4 | h2o + imp <-> fprica cair <-> caiz atp + formate + gar -> adp + fgam + pi atp + gtp -> amp + pppgpp + h pppgpp + h2o -> h + pi + ppgpp 2 h + h2o + urdglyc -> co2 + glx + 2 nh4 |
| GARTET GTPDPK GSTDPDP URGLYCH XANDH | Purine and Pyrimidine Biosynthesis Purine and Pyrimidine Biosynthesis Purine metabolism Purine metabolism Purine metabolism | IMP cyclohydrolase phosphoribosylamino imidazole carboxylase GAR transformylase-T GTP dilphoribosylamino imidazole sunosine-5'- triphosphate,3'- diphosphate,3'- diphosphate,3'- diphosphate warnine dehydrogenase ribonucleoside-diphosphate (reductase (ADP) ribonucleoside-diphosphate (Tibonucleoside-diphosphate reductase (ADP) ribonucleoside-inibonucleoside-inibonucleoside-inibonucleoside-inibonucleoside-inibonucleoside-inibonucleoside- | 21.2 27.6.5 3.6.1.11 3.5.3.19 1.17.1.4 | H16_A0955/H16_A1337 H16_A2436 H16_B2455 H16_A1016/H16_A1017/ H16_B3371/H16_B1898 H16_A3230/(H16_A3234 &H16_A3290/H16_A3234 | spoT1/spoT2 ppx unknown xdhB1/xdhA1/coxL5/ | cair <> caiz atp + formate + gar -> adp + fgam + pi atp + gtp -> amp + pppgpp pppgpp + h2o -> pi + ppgpp 2 h + h2o + urdglyc -> co2 + glx + 2 nh4 h2o + nad + xan -> h + nadh + urate | h2o + imp <-> fprica cair <-> caiz atp + formate + gar -> adp + fgam + h + pi atp + gtp -> amp + pppgpp + 2 h pppgpp + h2o -> h + pi + ppgpp 2 h + h2o + urdglyc -> co2 + glx + 2 nh4 h2o + nad + xan -> h + nadh + urate | h2o + imp <>> fprica cair <>> caiz atp + formate + gar -> adp + fgam + pi atp + gtp -> amp + pppgpp + h pppgpp + h2o -> h + pi + ppgpp 2 h + h2o + urdglyc -> co2 + glx + 2 nh4 h2o + nad + xan -> 2 h + nadh + urate |
| GARTET GTPDPK GSTDPDP URGLYCH XANDH RNDPR1 | Purine and Pyrimidine Biosynthesis Purine and Pyrimidine Biosynthesis Purine metabolism Purine metabolism Purine metabolism | IMP cyclohydrolase phosphoribosylamino imidazole carboxylase GAR transformylase-T GTP dilphoribosylamino imidazole guanosine-5'- triphosphate,3'- diphosphate,3'- diphosphate,3'- diphosphate bydrolase hydrolase xanthine dehydrogenase ribonucleoside-diphosphate reductase (ADP) ribonucleoside-diphosphate reductase (GDP) ribonucleoside-diphosphate reductase (CDP) | 212 27.6.5 3.6.1.11 3.5.3.19 1.17.1.4 | H16_A0955/H16_A1337 H16_A2436 H16_B2455 H16_A1016/H16_A1017/ H16_A3371/H16_B1897/ H16_A2390/(H16_A3234 &H16_A2390/(H16_A3234) H16_A2390/(H16_A3234) | spoT1/spoT2 ppx unknown xdhB1/xdhA1/coxL5/ xdhA2/xdhB2 nrdJ/(nrdB&nrdA) | cair <-> caiz atp + formate + gar -> adp + fgam + pi atp + gtp -> amp + pppgpp pppgpp + h2o -> pi + ppgpp 2 h + h2o + urdglyc -> co2 + glx + 2 nh4 h2o + nad + xan -> h + nadh + urate adp + rthio -> dadp + h2o + othio | h2o + imp <-> fprica cair <-> caiz atp + formate + gar -> adp + fgam + h + pi atp + gtp -> amp + pppgpp + 2 h pppgpp + h2o -> h + pi + ppgpp 2 h + h2o + urdglyc -> co2 + glx + 2 nh4 h2o + nad + xan -> h + nadh + urate adp + rthio -> dadp + h2o + othio | h2o + imp <-> fprica cair <-> caiz atp + formate + gar -> adp + fgam + pi atp + gtp -> amp + pppgpp + h pppgpp + h2o -> h + pi + ppgpp 2 h + h2o + urdglyc -> co2 + glx + 2 nh4 h2o + nad + xan -> 2 h + nadh + urate adp + rthio -> dadp + h2o + othio |
| GARTET GTPDPK GSTDPDP URGLYCH XANDH RNDPR1 RNDPR2 | Purine and Pyrimidine Biosynthesis Purine and Pyrimidine Biosynthesis Purine metabolism Purine metabolism Purine metabolism Purine metabolism Purine metabolism | IMP cyclohydrolase phosphoribosylamino imidazole carboxylase GAR transformylase-T GTF diphosphoribosylamino imidazole carboxylase GAR transformylase-T Ureidoglycolate hydrolase diphosphates wanthine dehydrogenase ribonucleoside-diphosphate reductase (APP) ribonucleoside-diphosphate reductase (GPP) ribonucleoside-diphosphate reductase (UPP) | 21.2 2.7.6.5 3.6.1.11 3.5.3.19 117.1.4 117.4.1 | H16_A0955/H16_A1337 H16_A2436 H16_B2455 H16_A1016/H16_A1017/ H16_B3371/H16_B1897/ H16_B3390/(H16_A3234 &H16_A2390/(H16_A3234 &H16_A2390/(H16_A3234 &H16_A2390/(H16_A3234) H16_A2390/(H16_A3234) | spoT1/spoT2 ppx unknown xdh81/xdh41/coxL5/ xdh42/xdh82 nrdJ/(nrdB&nrdA) nrdJ/(nrdB&nrdA) | cair <-> caiz atp + formate + gar -> adp + fgam + pi atp + gtp -> amp + pppgpp pppgpp + h2o -> pi + ppgpp 2 h + h2o + urdglyc -> co2 + glx + 2 nh4 h2o + nad + xan -> h + nadh + urate adp + rthio -> dadp + h2o + othio gdp + rthio -> dgdp + h2o + othio | h2o + imp <-> fprica cair <-> caiz atp + formate + gar -> adp + fgam + h + pi atp + gtp -> amp + pppgpp + 2 h pppgpp + h2o -> h + pi + ppgpp 2 h + h2o + urdglyc -> co2 + glx + 2 nh4 h2o + nad + xan -> h + nadh + urate adp + rthio -> dadp + h2o + othio gdp + rthio -> dgdp + h2o + othio | h2o + imp <>> fprica cair <-> caiz atp + formate + gar -> adp + fgam + pi atp + gtp -> amp + pppgpp + h pppgpp + h2o -> h + pi + ppgpp 2 h + h2o + urdglyc -> co2 + glx + 2 nh4 h2o + nad + xan -> 2 h + nadh + urate adp + rthio -> dadp + h2o + othio gdp + rthio -> dgdp + h2o + othio |
| GARTET GTPDPK GSTDPDP URGLYCH XANDH RNDPR1 RNDPR2 RNDPR3 | Purine and Pyrimidine Biosynthesis Purine and Pyrimidine Biosynthesis Purine metabolism | IMP cyclohydrolase phosphoribosylamino imidazole carboxylase GAR transformylase-T GP GIP diphosphoribosylamino imidazole carboxylase GAR transformylase-T triphosphate,3"- diphosphate guanosine-5"- triphosphate,3"- diphosphate diphosphates wanthine dehydroglase ribonucleoside-diphosphate reductase (ADP) ribonucleoside-diphosphate reductase (GDP) ribonucleoside-diphosphate reductase (CDP) ribonucleoside-diphosphate reductase (CDP) ribonucleoside-diphosphate reductase (UDP) purine-nucleoside-diphosphate reductase (UDP) purine-nucleoside-phosphorylase (Adenosine) | 212 27.6.5 3.6.1.11 3.5.3.19 117.1.4 117.4.1 117.4.1 117.4.1 | H16_A0955/H16_A1337 H16_A2436 H16_B2455 H16_A1016/H16_A1017/H16_A3371/H16_B1898 H16_A2390/(H16_A3234 &H16_A2390/(H16_A3234 &H16_A2390/(H16_A3234 &H16_A2390/(H16_A3234) H16_A2390/(H16_A3234) H16_A2390/(H16_A3234) H16_A2390/(H16_A3234) | spoT1/spoT2 ppx unknown xdh81/xdh41/coxL5/ xdhA2/xdh82 nrdJ/(nrd8&unrdA) nrdJ/(nrd8&unrdA) nrdJ/(nrd8&unrdA) | cair <-> caiz atp + formate + gar -> adp + fgam + pi atp + gtp -> amp + pppgpp pppgpp + h2o -> pi + ppgpp 2 h + h2o + urdglyc -> co2 + glx + 2 nh4 h2o + nad + xan -> h + nadh + urate adp + rthio -> dadp + h2o + othio gdp + rthio -> dcdp + h2o + othio cdp + rthio -> dcdp + h2o + othio | h2o + imp <-> fprica cair <-> caiz atp + formate + gar -> adp + fgam + h + pi atp + gtp -> amp + pppgpp + 2 h pppgpp + h2o -> h + pi + ppgpp 2 h + h2o + urdglyc -> co2 + glx + 2 nh4 h2o + nad + xan -> h + nadh + urate adp + rthio -> dadp + h2o + othio gdp + rthio -> dcdp + h2o + othio cdp + rthio -> dcdp + h2o + othio | h2o + imp <>> fprica cair <>> caiz atp + formate + gar >> adp + fgam + pi atp + gtp >> amp + pppgpp + h pppgpp + h2o -> h + pi + ppgpp 2 h + h2o + urdglyc -> co2 + glx + 2 nh4 h2o + nad + xan -> 2 h + nadh + urate adp + rthio -> dadp + h2o + othio gdp + rthio -> dgdp + h2o + othio cdp + rthio -> dcdp + h2o + othio |
| GARTET GTPDPK GSTDPDP URGLYCH XANDH RNDPR1 RNDPR2 RNDPR3 RNDPR4 | Purine and Pyrimidine Biosynthesis Purine and Pyrimidine Biosynthesis Purine metabolism | IMP cyclohydrolase phosphoribosylamino imidazole carboxylase GAR transformylase-T GFB diphosphokinase guanosine-5'- triphosphate,3'- diphosphate guanosine-5'- triphosphate,3'- diphosphate diphosphate wanthine dehydrogense ribonucleoside-diphosphate reductase (ADP) ribonucleoside-diphosphate reductase (GDP) ribonucleoside-diphosphate reductase (CDP) ribonucleoside-diphosphate reductase (CDP) ribonucleoside-diphosphate reductase (CDP) ribonucleoside-diphosphate productase (DP) ribonucleoside-diphosphate pribonucleoside-diphosphate productase (DP) ribonucleoside-phosphosphosphate (DP) purine-nucleoside phosphorylase (Qeboxylane) (Qeboxyl | 212 27.6.5 3.6.1.11 3.5.3.19 117.1.4 117.4.1 117.4.1 117.4.1 | H16_A0955/H16_A1337 H16_A2436 H16_B2455 H16_A1016/H16_A1017/H16_B1897/H16_B1898 H16_A2390/H16_A3234 &H16_A2390/H16_A3234 &H16_A2390/H16_A3234 &H16_A2390/H16_A3234 &H16_A2390/H16_A3234 &H16_A2390/H16_A3234 | spoT1/spoT2 ppx unknown xdh81/xdhA1/coxL5/ xdhA2/xdh82 nrdJ/(nrd8&nrdA) nrdJ/(nrd8&nrdA) nrdJ/(nrd8&nrdA) | cair <-> caiz atp + formate + gar -> adp + fgam + pi atp + gtp -> amp + pppgpp pppgpp + h2o -> pi + ppgpp 2 h + h2o + urdglyc -> co2 + glx + 2 nh4 h2o + nad + xan -> h + nadh + urate adp + rthio -> dadp + h2o + othio gdp + rthio -> dcdp + h2o + othio cdp + rthio -> dcdp + h2o + othio rthio + udp -> dudp + h2o + othio | h2o + imp <-> fprica cair <-> caiz atp + formate + gar -> adp + fgam + h + pi atp + gtp -> amp + pppgpp + 2 h pppgpp + h2o -> h + pi + ppgpp 2 h + h2o + urdglyc -> co2 + glx + 2 nh4 h2o + nad + xan -> h + nadh + urate adp + rthio -> dadp + h2o + othio gdp + rthio -> dddp + h2o + othio cdp + rthio -> dcdp + h2o + othio rthio + udp -> dudp + h2o + othio | h2o + imp <>> fprica cair <>> caiz atp + formate + gar -> adp + fgam + pi atp + gtp -> amp + pppgpp + h pppgpp + h2o -> h + pi + ppgpp 2 h + h2o + urdglyc -> co2 + glx + 2 nh4 h2o + nad + xan -> 2 h + nadh + urate adp + rthio -> dadp + h2o + othio gdp + rthio -> dgdp + h2o + othio cdp + rthio -> dcdp + h2o + othio rthio + udp -> dudp + h2o + othio |
| GARTET GTPDPK GSTDPDP URGLYCH XANDH RNDPR1 RNDPR2 RNDPR3 RNDPR4 PUNPP1 | Purine and Pyrimidine Biosynthesis Purine and Pyrimidine Biosynthesis Purine metabolism | IMP cyclohydrolase phosphoribosylamino imidazole carboxylase GAR transformylase-T GF diphosphoribosylamino imidazole carboxylase GAR transformylase-T triphosphate,3'-diphosphate,3'-diphosphatese upreidosylocolate hydrolase hydrolase xanthine dethydrogenase ribonucleoside-diphosphate reductase (AP) ribonucleoside-diphosphate reductase (CP) ribonucleoside-diphosphate reductase (CP) ribonucleoside-diphosphate reductase (CP) pribonucleoside-diphosphate reductase (CP) pribonucleoside-diphosphate reductase (CP) pribonucleoside-diphosphate (Adenosine) purine-nucleoside phosphorylase (Adenosine) purine-nucleoside phosphorylase (Adenosine) purine-nucleoside phosphorylase (Deoxyadenosine) purine-nucleoside phosphorylase (De | 212- 27.65 36.111 35.319 1.17.14 1.17.41 1.17.41 1.17.41 | H16_A0955/H16_A1337 H16_A2436 H16_B2455 H16_A1016/H16_A1017/H16_A3371/H16_B1898 H16_A2390/(H16_A3234 &H16_A2390/(H16_A3234 &H16_A2390/(H16_A3234 &H16_A2390/(H16_A3234) H16_A2390/(H16_A3234) H16_A2390/(H16_A3234) H16_A2390/(H16_A3234) H16_A2012 H16_A2012 | spoT1/spoT2 ppx unknown xdhB1/xdhA1/coxL5/ xdhA2/xdhB2 nrdJ/(nrdB&nrdA) nrdJ/(nrdB&nrdA) nrdJ/(nrdB&nrdA) nrdJ/(nrdB&nrdA) deoA | cair <-> caiz atp + formate + gar -> adp + fgam + pi atp + gtp -> amp + pppgpp pppgpp + h2o -> pi + ppgpp 2 h + h2o + urdglyc -> co2 + glx + 2 nh4 h2o + nad + xan -> h + nadh + urate adp + rthio -> dadp + h2o + othio gdp + rthio -> dgdp + h2o + othio cdp + rthio -> dcdp + h2o + othio rthio + udp -> dudp + h2o + othio adn + pi <-> ad + r1p | h2o + imp <-> fprica cair <-> caiz atp + formate + gar -> adp + fgam + h + pi atp + gtp -> amp + pppgpp + 2 h pppgpp + h2o -> h + pi + ppgpp 2 h + h2o + urdglyc -> co2 + glx + 2 nh4 h2o + nad + xan -> h + nadh + urate adp + rthio -> dadp + h2o + othio gdp + rthio -> dgdp + h2o + othio cdp + rthio -> dcdp + h2o + othio rthio + udp -> dudp + h2o + othio adh + pi <-> ad + r1p | h2o + imp <>> fprica cair <>> caiz atp + formate + gar -> adp + fgam + pi atp + gtp -> amp + pppgpp + h pppgpp + h2o -> h + pi + ppgpp 2 h + h2o + urdglyc -> co2 + glx + 2 nh4 h2o + nad + xan -> 2 h + nadh + urate adp + rthio -> dadp + h2o + othio gdp + rthio -> dgdp + h2o + othio cdp + rthio -> dcdp + h2o + othio rthio + udp -> dudp + h2o + othio adn + pi <-> ad + r1p |
| GARTET GTPDPK GSTDPDP URGLYCH XANDH RNDPR1 RNDPR2 RNDPR3 RNDPR4 PUNPP1 | Purine and Pyrimidine Biosynthesis Purine and Pyrimidine Biosynthesis Purine metabolism | IMP cyclohydrolase phosphoribosylamino imidazole carboxylase GAR transformylase-T GP GIP diphosphoribosylamino imidazole carboxylase GAR transformylase-T triphosphate,3"-diphosphate guanosine-5"-triphosphate,3"-diphosphate diphosphates wanthine dehydrogenase ribonucleoside-diphosphate reductase (AP) ribonucleoside-diphosphate reductase (GP) ribonucleoside-diphosphate reductase (CP) ribonucleoside-diphosphate reductase (CP) purine-nucleoside-diphosphate reductase (UP) purine-nucleoside-diphosphate productase (UP) purine-nucleoside-diphosphate reductase (UP) purine-nucleoside-phosphorylase (Ceoxyadenosine) purine-nucleoside phosphorylase (Geoxyadenosine) purine-nucleoside phosphorylase (Geoxyadenosine) purine-nucleoside phosphorylase (Gounosine) purine-nucleosid | 212- 27.65 36.111 35.319 117.14 117.41 117.41 117.41 24.24 24.24 | H16_A0955/H16_A1337 H16_A2436 H16_B2455 H16_A1016/H16_A1017/H16_B3897 H16_A327/H16_B1897 H16_A2390/(H16_A3234 &H16_A2390/(H16_A3234 &H16_A2390/(H16_A3234 &H16_A2390/(H16_A3234 &H16_A2390/(H16_A3234 &H16_A235) H16_A2390/(H16_A3234 &H16_A235) H16_A2301/(H16_A3234 &H16_A2315) H16_A2012 H16_A2012 H16_A2012 | spoT1/spoT2 ppx unknown xdh81/xdh41/coxL5/ xdh42/xdh82 nrdJ/(nrd8&nrdA) nrdJ/(nrd8&nrdA) nrdJ/(nrd8&nrdA) deoA deoA | cair <-> caiz atp + formate + gar -> adp + fgam + pi atp + gtp -> amp + pppgpp pppgpp + h2o -> pi + ppgpp 2 h + h2o + urdglyc -> co2 + glx + 2 nh4 h2o + nad + xan -> h + nadh + urate adp + rthio -> dadp + h2o + othio gdp + rthio -> dgdp + h2o + othio rthio + udp -> dudp + h2o + othio rthio + udp -> dudp + h2o + othio adn + pi <-> ad + r1p da + pi <-> dr1p + ad | h2o + imp <-> fprica cair <-> caiz atp + formate + gar -> adp + fgam + h + pi atp + gtp -> amp + pppgpp + 2 h pppgpp + h2o -> h + pi + ppgpp 2 h + h2o + urdglyc -> co2 + glx + 2 nh4 h2o + nad + xan -> h + nadh + urate adp + rthio -> dadp + h2o + othio gdp + rthio -> dcdp + h2o + othio cdp + rthio -> dcdp + h2o + othio rthio + udp -> dudp + h2o + othio adn + pi <-> ad + r1p da + pi <-> ad + r1p da + pi <-> dr1p + ad | h2o + imp <-> fprica cair <-> caiz atp + formate + gar -> adp + fgam + pi atp + gtp -> amp + pppgpp + h pppgpp + h2o -> h + pi + ppgpp 2 h + h2o + urdglyc -> co2 + glx + 2 nh4 h2o + nad + xan -> 2 h + nadh + urate adp + rthio -> dadp + h2o + othio gdp + rthio -> ddpp + h2o + othio cdp + rthio -> dddp + h2o + othio rthio + udp -> dudp + h2o + othio adn + pi <-> ad + r1p da + pi <-> dr1p + ad |
| GARTET GTPDPK G5TDPDP URGLYCH XANDH RNDPR1 RNDPR2 RNDPR3 RNDPR4 PUNPP1 PUNPP2 PUNPP3 | Purine and Pyrimidine Biosynthesis Purine and Pyrimidine Biosynthesis Purine metabolism | IMP cyclohydrolase phosphoribosylamino imidazole carboxylase GAR transformylase-T GTP diphosphoribosylamino imidazole carboxylase GAR transformylase-T triphosphate,3 - diphosphate,3 - diphosphate,3 - diphosphate diphosphate wanthine dehydroglase ribonucleoside-diphosphate reductase (ADP) ribonucleoside-diphosphate reductase (CDP) ribonucleoside-diphosphate reductase (CDP) ribonucleoside-diphosphate reductase (CDP) ribonucleoside-diphosphate productase (DP) ribonucleoside-diphosphate productase (DP) purine-nucleoside-phosphorylase (Adenosine) purine-nucleoside-phosphorylase (Guancine) purine-nucleoside-phosphorylase (Guancine) purine-nucleoside-phosphorylase (Cuancine) purine-nucleoside-phosphorylase (Cuancine) purine-nucleoside-phosphorylase (Cuancine) purine-nucleoside-phosphorylase (Cuancine) purine-nucleoside-phosphorylase (Inosine) (Cooxyguanosine) purine-nucleoside-phosphorylase (Inosine) (Inosine) (Inosine) | 212- 27.65 36111 35319 117.14 117.41 117.41 117.41 24.24 24.24 | H16_A0955/H16_A1337 H16_A2436 H16_B2455 H16_A1016/H16_A1017/H16_B3897 H16_A327/H16_B1897 H16_A2390/(H16_A3234 &H16_A2390/(H16_A3234 &H16_A2390/(H16_A3234 &H16_A2390/(H16_A3234 &H16_A235) H16_A2390/(H16_A3234 &H16_A235) H16_A2301/H16_A3234 &H16_A2351 H16_A2012 H16_A2012 H16_A2012 | spoT1/spoT2 ppx unknown xdh81/xdhA1/coxt.5/ xdhA2/xdh82 nrdJ/(nrd8&nrdA) nrdJ/(nrd8&nrdA) nrdJ/(nrd8&nrdA) deoA deoA deoA | cair <-> caiz atp + formate + gar -> adp + fgam + pi atp + gtp -> amp + pppgpp pppgpp + h2o -> pi + ppgpp 2 h + h2o + urdglyc -> co2 + glx + 2 nh4 h2o + nad + xan -> h + nadh + urate adp + rthio -> dadp + h2o + othio gdp + rthio -> dcdp + h2o + othio cdp + rthio -> dcdp + h2o + othio rthio + udp -> dudp + h2o + othio adn + pi <-> ad + r1p da + pi <-> dr1p + ad gn + pi <-> gn + r1p | h2o + imp <-> fprica cair <-> caiz atp + formate + gar -> adp + fgam + h + pi atp + gtp -> amp + pppgpp + 2 h pppgpp + h2o -> h + pi + ppgpp 2 h + h2o + urdglyc -> co2 + glx + 2 nh4 h2o + nad + xan -> h + nadh + urate adp + rthio -> dadp + h2o + othio gdp + rthio -> dddp + h2o + othio cdp + rthio -> dcdp + h2o + othio rthio + udp -> dudp + h2o + othio adn + pi <-> ad + r1p da + pi <-> ad + r1p da + pi <-> gn + r1p | h2o + imp <>> fprica cair <>> caiz atp + formate + gar >> adp + fgam + pi atp + gtp >> amp + pppgpp + h pppgpp + h2o -> h + pi + ppgpp 2 h + h2o + urdglyc -> co2 + glx + 2 nh4 h2o + nad + xan -> 2 h + nadh + urate adp + rthio -> dadp + h2o + othio gdp + rthio -> dgdp + h2o + othio cdp + rthio -> dddp + h2o + othio rthio + udp -> dudp + h2o + othio adn + pi <-> ad + r1p da + pi <-> da + r1p da + pi <-> gn + r1p |
| GARTET GTPDPK GSTDPDP URGLYCH XANDH RNDPR1 RNDPR2 RNDPR3 RNDPR4 PUNPP1 PUNPP2 PUNPP3 | Purine and Pyrimidine Biosynthesis Purine and Pyrimidine Biosynthesis Purine metabolism | IMP cyclohydrolase phosphoribosylamino imidazole carboxylase GAR transformylase-T GTP GTP diphosphoribosylamino imidazole carboxylase GAR transformylase-T GTP diphosphate, 3'-diphosphate guanosine-5'-triphosphate, 3'-diphosphate diphosphatese vanthine dehydrogenase ribonucleoside-diphosphate reductase (AP) ribonucleoside-diphosphate reductase (GDP) ribonucleoside-diphosphate reductase (GDP) ribonucleoside-diphosphate reductase (GDP) purine-nucleoside-diphosphate reductase (GDP) purine-nucleoside-phosphorylase (Adenosine) purine-nucleoside phosphorylase (Deoxyadenosine) purine-nucleoside phosphorylase (Deoxyanosine) purine-nucleoside phosphorylase (Deoxyinosine) (Deoxyinosine) | 212- 2765 36111 35319 117.14 117.41 117.41 117.41 242.4 242.4 242.4 | H16_A0955/H16_A1337 H16_A2436 H16_B2455 H16_A1016/H16_A1017/H16_B1897 H16_A3371/H16_B1897/H16_B1898 H16_A2390/(H16_A3234 BH16_A2390/(H16_A3234 BH16_A2390/(H16_A3234 BH16_A2390/(H16_A3234 BH16_A2390/(H16_A3234 BH16_A235) H16_A2390/(H16_A3234 BH16_A235) H16_A2012 H16_A2012 H16_A2012 H16_A2012 | spoT1/spoT2 ppx unknown xdhB1/xdhA1/coxL5/ xdhA2/xdhB2 nrdJ/(nrdB&nrdA) nrdJ/(nrdB&nrdA) nrdJ/(nrdB&nrdA) deoA deoA deoA deoA | cair <-> caiz atp + formate + gar -> adp + fgam + pi atp + gtp -> amp + pppgpp pppgpp + h2o -> pi + ppgpp 2 h + h2o + urdglyc -> co2 + glx + 2 nh4 h2o + nad + xan -> h + nadh + urate adp + rthio -> dadp + h2o + othio gdp + rthio -> ddqp + h2o + othio cdp + rthio -> dddp + h2o + othio rthio + udp -> dudp + h2o + othio adn + pi <-> ad + r1p da + pi <-> dr1p + ad gsn + pi <-> gn + r1p dg + pi <-> dr1p + gn | h2o + imp <-> fprica cair <-> caiz atp + formate + gar -> adp + fgam + h + pi atp + gtp -> amp + pppgpp + 2 h pppgpp + h2o -> h + pi + ppgpp 2 h + h2o + urdglyc -> co2 + glx + 2 nh4 h2o + nad + xan -> h + nadh + urate adp + rthio -> dadp + h2o + othio gdp + rthio -> ddpp + h2o + othio cdp + rthio -> dcdp + h2o + othio rthio + udp -> dudp + h2o + othio adn + pi <-> ad + r1p da + pi <-> dr1p + ad gsn + pi <-> gn + r1p dd + pi <-> dr1p + gn | h2o + imp <>> fprica cair <>> caiz atp + formate + gar -> adp + fgam + pi atp + gtp -> amp + pppgpp + h pppgpp + h2o -> h + pi + ppgpp 2 h + h2o + urdglyc -> co2 + glx + 2 nh4 h2o + nad + xan -> 2 h + nadh + urate adp + rthio -> dadp + h2o + othio gdp + rthio -> dgdp + h2o + othio cdp + rthio -> dcdp + h2o + othio rthio + udp -> dudp + h2o + othio adn + pi <-> ad + r1p da + pi <-> dr1p + ad gsn + pi <-> gn + r1p dg + pi <-> dr1p + gn |
| GARTET GTPDPK GSTDPDP URGLYCH XANDH RNDPR1 RNDPR2 RNDPR3 RNDPR4 PUNPP1 PUNPP2 PUNPP3 PUNPP3 | Purine and Pyrimidine Biosynthesis Purine and Pyrimidine Biosynthesis Purine metabolism | IMP cyclohydrolase phosphorbosylamino imidazole carboxylase GAR transformylase-T GF GIP diphosphorboshate. Striphosphate. Striphosphate reductase (GDP) ritionucleoside-diphosphate reductase (GDP) ritionucleoside-diphosphate. Striphosphorylase (GDP) purine-nucleoside-phosphorylase (Deoxyadenosine) purine-nucleoside phosphorylase (Geonosine) purine-nucleoside phosphorylase (Ceoxyadenosine) purine-nucleoside phosphorylase (Ceoxyadenosine) purine-nucleoside phosphorylase (Ceoxyadenosine) purine-nucleoside phosphorylase (Inosine) purine-nucleoside purine-nucleoside phosphorylase (Inosine) purine-nucleoside phosphorylase (Inosine) purine-nucleoside purine-nucleoside phosphorylase (Inosine) purine-nucleoside purine-nucleoside purine-nucleoside purine-nucleoside purine-nucleoside phosphorylase (Inosine) purine-nucleoside phosphorylase (Inosine) purine-nucleoside phosphorylase (Inosine) purine-nucleoside purine-nucleoside phosphorylase (Inosine) | 212- 2765 36111 35319 11714 11741 11741 11741 2424 2424 2424 | H16_A0955/H16_A1337 H16_A2436 H16_B2455 H16_A1016/H16_A1017/H16_B1897 H16_A3371/H16_B1897 H16_A2390/(H16_A3234 8H16_A2325) H16_A2390/(H16_A3234 8H16_A2325) H16_A2390/(H16_A3234 8H16_A2325) H16_A2390/(H16_A3234 8H16_A2325) H16_A2012 H16_A2012 H16_A2012 H16_A2012 H16_A2012 H16_A2012 H16_A2012 H16_A2012 | spoT1/spoT2 ppx unknown xdh81/xdh81/coxL5/ xdh82/xdh82 nrdJ/(nrd8&nrdA) nrdJ/(nrd8&nrdA) nrdJ/(nrd8&nrdA) deoA deoA deoA deoA | cair <-> caiz atp + formate + gar -> adp + fgam + pi atp + gtp -> amp + pppgpp pppgpp + h2o -> pi + ppgpp 2 h + h2o + urdglyc -> co2 + glx + 2 nh4 h2o + nad + xan -> h + nadh + urate adp + rthio -> dadp + h2o + othio gdp + rthio -> dgdp + h2o + othio cdp + rthio -> dddp + h2o + othio rthio + udp -> dudp + h2o + othio adn + pi <-> ad + r1p da + pi <-> dr1p + ad gsn + pi <-> gn + r1p dg + pi <-> hyxn + r1p dg + pi <-> hyxn + r1p | h2o + imp <-> fprica cair <-> caiz atp + formate + gar -> adp + fgam + h + pi atp + gtp -> amp + pppgpp + 2 h pppgpp + h2o -> h + pi + ppgpp 2 h + h2o + urdglyc -> co2 + glx + 2 nh4 h2o + nad + xan -> h + nadh + urate adp + rthio -> dadp + h2o + othio gdp + rthio -> dcdp + h2o + othio rthio + udp -> dudp + h2o + othio rthio + udp -> dudp + h2o + othio adn + pi <-> ad + r1p da + pi <-> ad + r1p da + pi <-> gn + r1p dg + pi <-> gn + r1p dg + pi <-> hyxn + r1p | h2o + imp <-> fprica cair <-> caiz atp + formate + gar -> adp + fgam + pi atp + gtp -> amp + pppgpp + h pppgpp + h2o -> h + pi + ppgpp 2 h + h2o + urdglyc -> co2 + glx + 2 nh4 h2o + nad + xan -> 2 h + nadh + urate adp + rthio -> dadp + h2o + othio gdp + rthio -> dddp + h2o + othio cdp + rthio -> dddp + h2o + othio rthio + udp -> dudp + h2o + othio rthio + udp -> dudp + h2o + othio adn + pi <-> ad + r1p da + pi <-> dr1p + ad gsn + pi <-> gn + r1p dg + pi <-> dr1p + gn ins + pi <-> hyxn + r1p |
| GARTET GTPDPK GSTDPDP URGLYCH XANDH RNDPR1 RNDPR2 RNDPR3 RNDPR4 PUNPP1 PUNPP2 PUNPP3 PUNPP5 PUNPP6 | Purine and Pyrimidine Biosynthesis Purine and Pyrimidine Biosynthesis Purine metabolism | IMP cyclohydrolase phosphorhosylamino imidazole carboxylase GAR transformylase-T GF diphosphorhosylamino imidazole carboxylase GAR transformylase-T GF diphosphate, 3"- diphosphate, 3"- diphosphate diphosphates wanthine dehydrogenase ribonucleoside-diphosphate reductase (ADP) ribonucleoside-diphosphate reductase (CDP) ribonucleoside-diphosphate reductase (CDP) ribonucleoside-diphosphate reductase (CDP) ribonucleoside-diphosphate reductase (CDP) purine-nucleoside-diphosphate reductase (CDP) purine-nucleoside-diphosphorylase (Adenosine) purine-nucleoside phosphorylase (Deoxydenosine) purine-nucleoside phosphorylase (Cuanosine) purine-nucleoside phosphorylase (Cuanosine) purine-nucleoside phosphorylase (Deoxydenosine) purine-nucleoside phosphorylase (Deoxydenosine) purine-nucleoside phosphorylase (Deoxydenosine) purine-nucleoside phosphorylase (Deoxydenosine) purine-nucleoside phosphorylase (Rosine) (Cooxydenosine) (Cooxydenosin | 212- 27.65 36.111 35.319 117.14 117.41 117.41 117.41 24.24 24.24 24.24 24.24 24.24 24.24 | H16_A0955/H16_A1337 H16_A2436 H16_B2455 H16_A1016/H16_A1017/H16_B1897 H16_A3371/H16_B1897 H16_A3290/(H16_A3234 8H16_A2325) H16_A2390/(H16_A3234 8H16_A2235) H16_A2230/(H16_A3234 8H16_A3235) H16_A2230/(H16_A3234 8H16_A3235) H16_A2012 | spoT1/spoT2 ppx unknown xdh81/xdhA1/coxL5/ xdhA2/xdh82 nrdJ/(nrd8&nrdA) nrdJ/(nrd8&nrdA) nrdJ/(nrd8&nrdA) deoA deoA deoA deoA deoA | cair <-> caiz atp + formate + gar -> adp + fgam + pi atp + gtp -> amp + pppgpp pppgpp + h2o -> pi + ppgpp 2 h + h2o + urdglyc -> co2 + glx + 2 nh4 h2o + nad + xan -> h + nadh + urate adp + rthio -> dadp + h2o + othio gdp + rthio -> dcdp + h2o + othio cdp + rthio -> dcdp + h2o + othio rthio + udp -> dudp + h2o + othio adn + pi <-> ad + r1p da + pi <-> dr1p + ad gsn + pi <-> dr1p + gn ins + pi <-> hyxn + r1p din + pi <-> hyxn + r1p din + pi <-> dr1p + hyxn | h2o + imp <-> fprica cair <-> caiz atp + formate + gar -> adp + fgam + h + pi atp + gtp -> amp + pppgpp + 2 h pppgpp + h2o -> h + pi + ppgpp 2 h + h2o + urdglyc -> co2 + glx + 2 nh4 h2o + nad + xan -> h + nadh + urate adp + rthio -> dadp + h2o + othio gdp + rthio -> ddqp + h2o + othio cdp + rthio -> dcdp + h2o + othio rthio + udp -> dudp + h2o + othio adn + pi <-> ad + r1p da + pi <-> dr1p + ad gsn + pi <-> gn + r1p dg + pi <-> land + r1p dg + pi <-> hyxm + r1p din + pi <-> hyxm + r1p din + pi <-> hyxm + r1p din + pi <-> dr1p + hyxn | h2o + imp <>> fprica cair <>> caiz atp + formate + gar >> adp + fgam + pi atp + gtp >> amp + pppgpp + h pppgpp + h2o -> h + pi + ppgpp 2 h + h2o + urdglyc -> co2 + glx + 2 nh4 h2o + nad + xan -> 2 h + nadh + urate adp + rthio -> dadp + h2o + othio gdp + rthio -> dgdp + h2o + othio cdp + rthio -> dddp + h2o + othio rthio + udp -> dudp + h2o + othio adn + pi <-> ad + r1p da + pi <-> ad + r1p da + pi <-> dr1p + ad gsn + pi <-> gn + r2p dg + pi <-> byan + r1p dig + pi <-> byan + r1p dig + pi <-> co2 + glx + 2 nh4 dig + pi <-> dr1p + gn ins + pi <-> hyan + r1p din + pi <-> dr1p + hyan |
| GARTET GTPDPK GSTDPDP URGLYCH XANDH RNDPR1 RNDPR2 RNDPR3 RNDPR4 PUNPP1 PUNPP2 PUNPP3 PUNPP5 PUNPP6 PUNPP7 | Purine and Pyrimidine Biosynthesis Purine and Pyrimidine Biosynthesis Purine metabolism | IMP cyclohydrolase phosphoribosylamino imidazole carboxylase GAR transformylase-T GP GIP diphosphoribosylamino imidazole carboxylase GAR transformylase-T GP diphosphate, 3"- diphosphate, 3"- diphosphate, 3"- diphosphate within edehydrogenase ribonucleoside-diphosphate reductase (ADP) ribonucleoside-diphosphate reductase (GDP) ribonucleoside-diphosphate reductase (GDP) ribonucleoside-diphosphate reductase (CDP) ribonucleoside-diphosphate reductase (CDP) purine-nucleoside-diphosphate reductase (CDP) purine-nucleoside-phosphorylase (Loeoxylaminosphorylase (Deoxylaminosphorylase vanthine phosphoribosyltransferase erase | 212- 2765 36111 35319 11714 11741 11741 11741 2424 2424 2424 | H16_A0955/H16_A1337 H16_A2436 H16_B2455 H16_A1016/H16_A1017/H16_B1897 H16_A3371/H16_B1897 H16_A3290/(H16_A3234 8H16_A2325) H16_A2390/(H16_A3234 8H16_A2235) H16_A2230/(H16_A3234 8H16_A3235) H16_A2230/(H16_A3234 8H16_A3235) H16_A2012 | spoT1/spoT2 ppx unknown xdhB1/xdhA1/coxL5/ xdhA2/xdhB2 nrdJ/(nrdB&nrdA) nrdJ/(nrdB&nrdA) nrdJ/(nrdB&nrdA) deoA deoA deoA deoA deoA deoA | cair <-> caiz atp + formate + gar -> adp + fgam + pi atp + gtp -> amp + pppgpp pppgpp + h2o -> pi + ppgpp 2 h + h2o + urdglyc -> co2 + glx + 2 nh4 h2o + nad + xan -> h + nadh + urate adp + rthio -> dadp + h2o + othio gdp + rthio -> ddqp + h2o + othio cdp + rthio -> dcdp + h2o + othio rthio + udp -> dudp + h2o + othio adn + pi <-> ad + r1p da + pi <-> dr1p + ad gsn + pi <-> pn + r1p dg + pi <-> dr1p + gn ins + pi <-> hyxn + r1p din + pi <-> dr1p + hyxn pi + xtsine <-> r1p + xan | h2o + imp <-> fprica cair <-> caiz atp + formate + gar -> adp + fgam + h + pi atp + gtp -> amp + pppgpp + 2 h pppgpp + h2o -> h + pi + ppgpp 2 h + h2o + urdglyc -> co2 + glx + 2 nh4 h2o + nad + xan -> h + nadh + urate adp + rthio -> dadp + h2o + othio gdp + rthio -> ddqp + h2o + othio cdp + rthio -> dcdp + h2o + othio rthio + udp -> dudp + h2o + othio adn + pi <-> dr1p + ad gsn + pi <-> gn + r1p dg + pi <-> gn + r1p din + pi <-> hyxn + r1p din + pi <-> dr1p + hyxn pi + xtsine <-> r1p + xan | h2o + imp <>> fprica cair <>> caiz atp + formate + gar -> adp + fgam + pi atp + gtp -> amp + pppgpp + h pppgpp + h2o -> h + pi + ppgpp 2 h + h2o + urdglyc -> co2 + glx + 2 nh4 h2o + nad + xan -> 2 h + nadh + urate adp + rthio -> dadp + h2o + othio gdp + rthio -> ddpp + h2o + othio cdp + rthio -> dcdp + h2o + othio rthio + udp -> dudp + h2o + othio adn + pi <-> ad + r1p da + pi <-> dr1p + ad gsn + pi <-> gn + r1p dg + pi <-> hyxn + r1p din + pi <-> hyxn + r1p din + pi <-> dr1p + hyxn pi + xtsine <-> r1p + xan |

| HYXNPRT | Purine metabolism | hypoxanthine phosphoribosyltransf | 2.4.2.8 | H16_A3242 | hprT | hyxn + prpp -> imp + ppi | hyxn + prpp -> imp + ppi + h | hyxn + prpp -> imp + ppi + h |
|---------------|--|--|----------|---|--------------------|--|--|--|
| | | erase (Hypoxanthine) | | | | | | |
| ADNK DADNK | Purine metabolism Purine metabolism | deoxiadenidate | 2.7.1.20 | H16_A0603 | adk | adn + atp -> adp + amp atp + damp <-> adp + dadp | adn + atp -> adp + amp + h atp + damp + h <-> adp + dadp | adn + atp -> adp + amp + h atp + damp <-> adp + dadp |
| ADNK1 | Purine metabolism | kinase | 2.7.4.3 | H16_A0603 | adk | amp + atp <-> 2 adp | amp + atp + h <-> 2 adp | amp + atp <-> 2 adp |
| NUDPK1 | | nucleoside- | 2.7.4.6 | H16_A2368 | ndk | atp + gdp <-> adp + gtp | atp + gdp <-> adp + gtp | atp + gdp <-> adp + gtp |
| | | (ATP:GDP) nucleoside- | | | | | | 3 · · 3 |
| NUDPK5 | Purine metabolism | diphosphate kinase (ATP:dGDP) | 2.7.4.6 | H16_A2368 | ndk | atp + dgdp <-> adp + dgtp | atp + dgdp <-> adp + dgtp | atp + dgdp <-> adp + dgtp |
| AUUDDIVO | Durley weeks by the street | nucleoside- | 2746 | H1C 42260 | - 40 | and a dealer and a dele | and the state of t | and a dealer and a dealer |
| NUDPK8 | Purine metabolism | (ATP:dADP) | 2.7.4.0 | H16_A2368 | ndk | atp + dadp <-> adp + datp | atp + dadp <-> adp + datp | atp + dadp <-> adp + datp |
| DGNK | Purine metabolism | KITIASE (UGIVIF.ATF) | 2.7.4.8 | H16_A0953 | gmk | atp + dgmp <-> adp + dgdp | atp + dgmp + h <-> adp + dgdp | atp + dgmp <-> adp + dgdp |
| GKN | Purine metabolism | guanylate kinase (GMP:ATP) | 2.7.4.8 | H16_A0953 | gmk | atp + gmp <-> adp + gdp | atp + gmp + h <-> adp + gdp | atp + gmp <-> adp + gdp |
| NUTD10 | Purine metabolism | 5'-nucleotidase (XMP) | 3.1.3.5 | H16_A2376 | surE | h2o + xmp -> pi + xtsine | h2o + xmp -> pi + xtsine | h2o + xmp -> pi + xtsine |
| NUTD11 | Purine metabolism | 5'-nucleotidase (IMP) | 3.1.3.5 | H16_A2376 | surE | h2o + imp -> ins + pi | h2o + imp -> ins + pi | h2o + imp -> ins + pi |
| NUTD6 | Purine metabolism | 5'-nucleotidase (dAMP) | 3.1.3.5 | H16_A2376 | surE | damp + h2o -> da + pi | damp + h2o -> da + pi | damp + h2o -> da + pi |
| NUTD7 | Purine metabolism | 5'-nucleotidase | 3.1.3.5 | H16_A2376 | surE | amp + h2o -> adn + pi | amp + h2o -> adn + pi | amp + h2o -> adn + pi |
| NUTD8 | Purine metabolism | 5'-nucleotidase | 3.1.3.5 | H16_A2376 | surE | dgmp + h2o -> dg + pi | dgmp + h2o -> dg + pi | dgmp + h2o -> dg + pi |
| NUTD9 | Purine metabolism | (dGMP) 5'-nucleotidase | 3.1.3.5 | H16_A2376 | | gmp + h2o -> gsn + pi | gmp + h2o -> gsn + pi | gmp + h2o -> gsn + pi |
| | | (GMP) Nucleoside | | | | 2b | 2h 2 b. | 3p |
| NUTPTP1 | Purine metabolism | triphosphate tripolyhydrolase Nucleoside | 3.1.5.1 | H16_A3433 | dgt | dgtp + h2o -> dg + pppi | dgtp + h2o -> dg + pppi | dgtp + h2o -> dg + pppi + h |
| NUTPTP2 | Purine metabolism | triphosphate tripolyhydrolase | 3.1.5.1 | H16_A3433 | dgt | gtp + h2o -> gsn + pppi | gtp + h2o -> gsn + pppi | gtp + h2o -> gsn + pppi + h |
| AMPNS | Purine metabolism | AMP nucleosidase | 3.2.2.4 | H16_B0070 H16_A1013 | | amp + h2o -> ad + r5p | amp + h2o -> ad + r5p | amp + h2o -> ad + r5p qn + h + h2o -> nh4 + xan |
| GNDA ADNA | Purine metabolism Purine metabolism | Adenosine | 3.5.4.3 | H16_A1013 H16_A1014/H16_B2033 | - | gn + h + h2o -> nh4 + xan adn + h + h2o -> ins + nh4 | gn + h + h2o -> nh4 + xan adn + h + h2o -> ins + nh4 | gn + n + n2o -> nn4 + xan adn + h + h2o -> ins + nh4 |
| ADPRDP | Purine metabolism | deaminase ADPribose | 3.6.1.13 | H16 A1404 | | adprib + h2o -> amp + r5p | adprib + h2o -> amp + r5p + 2 h | adprib + h2o -> amp + r5p + 2 h |
| | | diphosphatase nucleoside- | | | | | | |
| NUTP1 | Purine metabolism | triphosphatase (ATP) | 3.6.1.15 | H16_A0948 | unknown | atp + h2o -> adp + pi | atp + h2o -> adp + h + pi | atp + h2o -> adp + h + pi |
| NUTP2 | Purine metabolism | nucleoside- triphosphatase (GTP) | 3.6.1.15 | H16_A0948 | unknown | gtp + h2o -> gdp + pi | gtp + h2o -> gdp + pi + h | gtp + h2o -> gdp + pi + h |
| ADNCYC | Purine metabolism | adenylate cyclase | 4.6.1.1 | H16_A0674/H16_A0827/ H16_A1791/H16_A1809/ H16_B0376 | | atp -> camp + ppi | atp -> camp + ppi + h | atp -> camp + ppi + h |
| DANDA | Purine metabolism | Deoxyadenosine deaminase | 3.5.4.4 | H16_B0376 H16_A1014/H16_B2033 | | da + h + h2o -> din + nh4 | da + h + h2o -> din + nh4 | da + h + h2o -> din + nh4 |
| BNTP | Purine metabolism | bis(5'-nucleosidyl)- | 3.6.1.17 | H16_A3406 | unknown | gp4g + h2o -> gtp + gmp | gp4g + h2o -> gtp + gmp + h | gp4g + h2o -> gtp + gmp + 2 h |
| | | tetraphosphatase hypoxanthine | | H16_A1016/H16_A1017/ | xdhR1/xdhA1/coxl5/ | | | |
| HYXND | Purine metabolism | dehydrogenase | 1.17.1.4 | H16_A3371/H16_B1897/ H16_B1898 | xdhA2/xdhB2 | h2o + hyxn + nad -> h + nadh + xan | h2o + hyxn + nad -> h + nadh + xan | h2o + hyxn + nad -> h + nadh + xan |
| IMPDH | | IMP dehydrogenase phosphoribosylglycin | | H16_A2030 | - | h2o + imp + nad -> h + nadh + xmp | h2o + imp + nad -> h + nadh + xmp | h2o + imp + nad -> h + nadh + xmp |
| PRGNFT | Purine metabolism | amide formyltransferase | 2.1.2.2 | H16_A3042 | purN | fthf + gar <-> fgam + h + thf | fthf + gar <-> fgam + h + thf | fthf + gar <-> fgam + thf |
| PRAZCFT | Purine metabolism | phosphoribosylamino imidazolecarboxamid | 2.1.2.3 | H16_A0501 | purH | fthf + aicar <-> fprica + thf | fthf + aicar <-> fprica + thf | fthf + aicar <-> fprica + thf |
| | | e formyltransferase | | | | | | |
| GLUPRPAT | Purine metabolism | glutamine phosphoribosyldipho | 2.4.2.14 | H16_A2607 | purF | gln + h2o + prpp -> glu + ppi + pram | gln + h2o + prpp -> glu + ppi + pram + h | gln + h2o + prpp -> glu + ppi + pram + 2 h |
| | | sphate amidotransferase | | | | | | |
| ADSUCL1 | Purine metabolism | adenylsuccinate lyase | 4.3.2.2 | H16_A3124 | purB | asuc <-> amp + fum | asuc <-> amp + fum | asuc <-> amp + fum |
| ADSUCL2 | Purine metabolism | adenylsuccinate lyase | | H16_A3124 | purB | saicar <-> aicar + fum | saicar <-> aicar + fum + h | saicar <-> aicar + fum + h |
| PRASUCS | Purine metabolism | phosphoribosylamino imidazolesuccinocarb | | H16_A0569 | purC | cair + asp + atp -> saicar + adp + h + pi | cair + asp + atp -> saicar + adp + h + pi | cair + asp + atp -> saicar + adp + pi |
| PRAIZS | Purine metabolism | oxamide synthase phosphoribosylamino | 6221 | H16_A3077 | purM | atp + fpram -> adp + air + pi | atp + fpram -> adp + air + h + pi | atp + fpram -> adp + air + h + pi |
| | | imidazole synthase phosphoribosylglycin | | | | | | |
| PRGCS | Purine metabolism | adenvlosuccinate | | H16_A0915 | purD | atp + gly + pram <-> adp + gar + pi | atp + gly + pram <-> adp + gar + h + pi | atp + gly + pram <-> adp + gar + h + pi |
| ADSUCS | Purine metabolism | synthase | 6.3.4.4 | H16_A2354/H16_B1994 | | asp + gtp + imp -> asuc + gdp + h + pi atp + gln + h2o + xmp -> amp + glu + gmp + | asp + gtp + imp -> asuc + gdp + 2 h + pi atp + gln + h2o + xmp -> amp + glu + | asp + gtp + imp -> asuc + gdp + 2 h + pi atp + gln + h2o + xmp -> amp + glu + gmp + 3 |
| GMPS | Purine metabolism | GMP synthase phosphoribosylformy | 6.3.5.2 | H16_A2028 | | h + ppi | gmp + 3 h + ppi | h + ppi |
| PRFGAS | Purine metabolism | Iglycinamidine | 6.3.5.3 | H16_A1511 | | atp + fgam + gln + h2o -> adp + fpram + glu + pi | $atp + fgam + gln + h2o -> adp + fpram + \\ glu + h + pi$ | atp + fgam + gln + h2o -> adp + fpram + glu + 2 h + pi |
| PRAIZC1 | Purine metabolism | synthase phosphoribosylamino imidazole | | H16_A0570/H16_A0571 | purE/purK | air + co2 <-> caiz + h | air + co2 <-> caiz + h | air + co2 <-> caiz + h |
| | | carboxylase adenine | | | | | | |
| ADPRT2 | Purine metabolism | phosphoribosyltransf erase adenine | 2.4.2.7 | H16_A0395 | apt | aicar + ppi <-> 5a4ic + prpp | aicar + ppi + h <-> 5a4ic + prpp | aicar + ppi + h <-> 5a4ic + prpp |
| ADPRT3 | Purine metabolism | phosphoribosyltransf erase | 2.4.2.7 | H16_A0395 | apt | gmp + ppi <-> gn + prpp | gmp + ppi + h <-> gn + prpp | gmp + ppi + h <-> gn + prpp |
| NUDPK9 | Purine metabolism | nucleoside- diphosphate kinase (ATP:GDP) | 2.7.4.6 | H16_A2368 | ndk | atp + didp <-> adp + ditp | atp + didp <-> adp + ditp | atp + didp <-> adp + ditp |
| NUDPK10 | Purine metabolism | nucleoside- diphosphate kinase (ATP:GDP) | 2.7.4.6 | H16_A2368 | ndk | atp + idp <-> adp + itp | atp + idp <-> adp + itp | atp + idp <-> adp + itp |
| ADPRT4 | Purine metabolism | adenine phosphoribosyltransf erase | 2.4.2.8 | H16_A3242 | hprT | amp + ppi <-> ad + prpp | amp + ppi + h <-> ad + prpp | amp + ppi + h <-> ad + prpp |
| PYK1 | Purine metabolism | | 2.7.1.40 | H16_A0567/H16_A3602/ H16_B0961 | pyk1/pyk2/pyk3 | datp + pyr <-> dadp + pep | datp + pyr <-> dadp + pep | datp + pyr <-> dadp + pep |
| PYK2 | Purine metabolism | pyruvate kinase | 2.7.1.40 | H16_A0567/H16_A3602/ H16_B0961 | pyk1/pyk2/pyk3 | gtp + pyr <-> gdp + pep | gtp + pyr <-> gdp + pep | gtp + pyr <-> gdp + pep |
| PYK3 | Purine metabolism | ., | 2.7.1.40 | H16_A0567/H16_A3602/ | | dgtp + pyr <-> dgdp + pep | dgtp + pyr <-> dgdp + pep | dgtp + pyr <-> dgdp + pep |
| ADNK2 | Purine metabolism | adenylate kinase | 2.7.4.3 | H16_B0961 H16_A0603 | adk | atp + damp <-> adp + dadp | atp + damp + h <-> adp + dadp | atp + damp <-> adp + dadp |
| BTPT1 | Purine metabolism | bis(5'-nucleosidyl)- tetraphosphatase | 3.6.1.17 | H16_A3406 | unknown | xp4g + h2o -> xtp + xmp | xp4g + h2o + h -> xtp + xmp | xp4g + h2o -> xtp + xmp |
| BTPT2 | Purine metabolism | his(5'-nucleosidyl)- | 3.6.1.17 | H16_A3406 | unknown | appppa + h2o -> atp + amp | appppa + h2o -> atp + amp + h | appppa + h2o -> atp + amp + 2 h |
| ADNCYC1 | Purine metabolism | adenylate cyclase | 4.6.1.1 | H16_A0674/H16_A0827/ H16_A1791/H16_A1809/ | nown/unknown/cycR | gtp -> cgmp + ppi | gtp -> cgmp + ppi + h | gtp -> cgmp + ppi + h |
| AADT1 | Purine metabolism | ATP | 2.7.7.53 | H16_B0376 | 2 unknown | | | |
| UUNII | rume metabolism | adenylyltransferase | | H16_A1656 | G-IKHOWH | aps + atp -> so4 + appppa + h | aps + atp -> so4 + appppa + h | aps + atp -> so4 + appppa |

| AADT2 | Purine metabolism | ATP | 2.7.7.53 | H16_A1656 | unknown | adp + atp -> pi + appppa | adp + atp -> pi + appppa + h | adp + atp + h -> pi + appppa |
|----------|--|--|----------|--|------------------|---|---|--|
| SADT1 | Purine metabolism | sulfate | 2.7.7.4 | H16_A2995&H16_A299 6&H16_B0626&H16_B0 | cysN1&cysD&cysN2 | atp + so4 + h -> ppi + aps | atp + so4 -> ppi + aps | atp + so4 -> ppi + aps |
| | | adenyiyitransierase | | 627 H16_A1081/H16_A1083, H16_A1084 | oxcysnz | | | |
| UREA | Purine metabolism | | 3.5.1.5 | | | urea + h2o + 2 h -> co2 + 2 nh4 | urea + h2o + 2 h -> co2 + 2 nh4 | urea + h2o + 2 h -> co2 + 2 nh4 |
| ALLTC | Purine metabolism | phenylacrylic acid | 3.5.3.4 | H16_B2460 | unknown | alltt + h2o <-> urdglyc + urea | alltt + h2o <-> urdglyc + urea | alltt + h2o <-> urdglyc + urea |
| PAAD2 | Purine metabolism Putative | decarboxylase allantoin transport in | 4.1.1 | H16_B2447 | unknown | a4ic + h -> amdz + co2 | a4ic + h -> amdz + co2 | a4ic + 2 h -> amdz + co2 |
| ALLTNtr | Transporters | via proton symport | | | | alltn_e + h_e <-> alltn + h | alltn_e + h_e <-> alltn + h | alltn_e + h_e <-> alltn + h |
| ARGORNt | Putative Transporters | arginine/ornithine antiporter acetoacetate | | | | arg_e + orn <-> arg + orn_e | arg_e + orn <-> arg + orn_e | arg_e + om <-> arg + orn_e |
| ACACt | Putative Transporters | transport via proton symport | | | | acac_e + h_e <-> acac + h | acac_e + h_e <-> acac + h | acac_e + h_e <-> acac + h |
| BUTtr | Putative Transporters | Butyrate transport via proton symport, reversible | | | | 1boh_e + h_e <-> 1boh + h | 1boh_e + h_e <-> 1boh + h | 1boh_e + h_e <-> 1boh + h |
| CYNTt | Putative Transporters | Cyanate transport via proton symport | | | | cynt_e + h_e -> cynt + h | cynt_e + h_e -> cynt + h | cynt_e + h_e -> cynt + h |
| GALCTtr | Putative Transporters | D-galactarte transport via proton | | | | dgal_e + h_e <-> dgal + h | dgal_e + h_e <-> dgal + h | dgal_e + h_e <-> dgal + h |
| PPPNtr | Putative Transporters | symport, reversible 3-phenylpropionate transport via proton symport, reversible | | | | h_e + pppn_e <-> h + pppn | h_e + pppn_e <-> h + pppn | h_e + pppn_e <-> h + pppn |
| HPPPNtr | Putative Transporters | 3-(3- hydroxyphenyl)propi onate transport via proton symport, | | | | 3hpppn_e + h_e <-> 3hpppn + h | 3hpppn_e + h_e <-> 3hpppn + h | 3hpppn_e + h_e <-> 3hpppn + h |
| HCINNMtr | Putative Transporters | reversible 3-hydroxycinnamic acid transport via proton symport, reversible | | | | 3hcinnm_e + h_e <-> 3hcinnm + h | 3hcinnm_e + h_e <-> 3hcinnm + h | 3hcinnm_e + h_e <-> 3hcinnm + h |
| GLUABUTt | Putative Transporters | 4- aminobutyrate/gluta mate antiport | | | | gaba + glu_e <-> gaba_e + glu | gaba + glu_e <-> gaba_e + glu | gaba + glu_e <-> gaba_e + glu |
| ALAtr | Putative Transporters | L-alanine reversible transport via proton symport | | | | ala_e + h_e <-> ala + h | ala_e + h_e <-> ala + h | ala_e + h_e <-> ala + h |
| URAtr | Putative Transporters | uracil transport in via proton symport, | | | | h_e + ura_e <-> h + ura | h_e + ura_e <-> h + ura | h_e + ura_e <-> h + ura |
| GLYBtr | Putative | reversible Glycine betaine transport via proton | | | | glyb_e + h_e <-> glyb + h | glyb_e + h_e <-> glyb + h | glyb_e + h_e <-> glyb + h |
| CHLabc | Transporters Putative | symport, reversible choline transport via | | | | atp + choline_e + h2o -> adp + choline + pi | | atp + choline_e + h2o -> adp + choline + h |
| GLYBabc | Transporters Putative | ABC system Glycine betaine transport via ABC | | | | atp + glyb_e + h2o -> adp + glyb + pi | + pi atp + glvb e + h2o -> adp + glvb + h + pi | + pi $atp + glyb_e + h2o \rightarrow adp + glyb + h + pi$ |
| TARTRt | Transporters Putative | system Tartrate/succinate | | | | succ + tartr e <-> succ e + tartr | succ + tartr e <-> succ e + tartr | succ + tartr e <-> succ e + tartr |
| | Transporters Putative | antiporter Succinate transport | | | | | | |
| SUCCabc | Transporters Putative | via ABC system | | | | atp + h2o + succ_e -> adp + pi + succ | atp + h2o + succ_e -> adp + h + pi + succ | atp + h2o + succ_e -> adp + h + pi + succ |
| GUAt2 | Transporters Putative | guanine transport in via proton symport | | | | gn_e + h_e -> gn + h | gn_e + h_e -> gn + h | gn_e + h_e -> gn + h |
| XANt2 | Transporters Pyrimidine | xanthine transport in via proton symport | | | | h_e + xan_e -> h + xan | h_e + xan_e -> h + xan | h_e + xan_e -> h + xan |
| THMDS | metabolism | thymidylate synthase | 2.1.1.45 | H16_A2703 | thyA | dump + metthf -> dhf + dtmp | dump + metthf -> dhf + dtmp | dump + metthf -> dhf + dtmp |
| THMDPP | Pyrimidine metabolism | thymidine phosphorylase uracil | 2.4.2.4 | H16_A2012 | deoA | pi + thymd <-> dr1p + thym | pi + thymd <-> dr1p + thym | pi + thymd <-> dr1p + thym |
| URAPRT | Pyrimidine metabolism | phosphoribosyltransf erase | 2.4.2.9 | H16_A0918/H16_A2914 | upp1/unknown | prpp + ura -> ppi + ump | prpp + ura -> ppi + ump + h | prpp + ura -> ppi + ump + h |
| CYTDK1 | Pyrimidine metabolism Pyrimidine | cytidylate kinase (CMP) cytidylate kinase | | H16_A0797 | cmk | atp + cmp <-> adp + cdp | atp + cmp + h <-> adp + cdp | atp + cmp <-> adp + cdp |
| CYTDK2 | metabolism | (dCMP) | 2.7.4.14 | H16_A0797 | cmk | atp + dcmp <-> adp + dcdp | atp + dcmp + h <-> adp + dcdp | atp + dcmp <-> adp + dcdp |
| UMPK | Pyrimidine metabolism | UMP kinase | 2.7.4.14 | H16_A0797 | cmk | atp + ump <-> adp + udp | atp + ump + h <-> adp + udp | atp + ump <-> adp + udp |
| NUDPK2 | Pyrimidine metabolism | nucleoside- diphosphate kinase (ATP:UDP) | 2.7.4.6 | H16_A2368 | ndk | atp + udp <-> adp + utp | atp + udp <-> adp + utp | atp + udp <-> adp + utp |
| NUDPK3 | Pyrimidine metabolism | nucleoside- diphosphate kinase (ATP:CDP) | 2.7.4.6 | H16_A2368 | ndk | atp + cdp <-> adp + ctp | atp + cdp <-> adp + ctp | atp + cdp <-> adp + ctp |
| NUDPK4 | Pyrimidine metabolism | nucleoside- diphosphate kinase | 2.7.4.6 | H16_A2368 | ndk | atp + dtdp <-> adp + dttp | atp + dtdp <-> adp + dttp | atp + dtdp <-> adp + dttp |
| NUDPK6 | Pyrimidine metabolism | (ATP:dTDP) nucleoside- diphosphate kinase | 2.7.4.6 | H16_A2368 | ndk | atp + dudp <-> adp + dutp | atp + dudp <-> adp + dutp | atp + dudp <-> adp + dutp |
| NILIDDK7 | Pyrimidine | (ATP:dUDP) nucleoside- | 2746 | H16 A2368 | nelle | atp + dcdp <-> adp + dctp | ata i dada ada i data | ato i dado e e ado i dato |
| NUDPK7 | metabolism Pyrimidine | diphosphate kinase (ATP:dCDP) | | _ | ndk | | atp + dcdp <-> adp + dctp | atp + dcdp <-> adp + dctp |
| DTMPK | metabolism | dTMP kinase | 2.7.4.9 | H16_A1569 | tmk | atp + dtmp <-> adp + dtdp | atp + dtmp + h <-> adp + dtdp | atp + dtmp <-> adp + dtdp |
| NUTD1 | Pyrimidine metabolism | 5'-nucleotidase (dUMP) | 3.1.3.5 | H16_A2376 | surE | dump + h2o -> du + pi | dump + h2o -> du + pi | dump + h2o -> du + pi |
| NUTD2 | Pyrimidine metabolism | 5'-nucleotidase (UMP) | 3.1.3.5 | H16_A2376 | surE | h2o + ump -> pi + uri | h2o + ump -> pi + uri | h2o + ump -> pi + uri |
| NUTD3 | Pyrimidine | 5'-nucleotidase | 3.1.3.5 | H16_A2376 | surE | dcmp + h2o -> dc + pi | dcmp + h2o -> dc + pi | dcmp + h2o -> dc + pi |
| NUTD4 | metabolism Pyrimidine | (dCMP) 5'-nucleotidase | 3.1.3.5 | H16_A2376 | surE | cmp + h2o -> cytd + pi | cmp + h2o -> cytd + pi | cmp + h2o -> cytd + pi |
| NUTD5 | metabolism Pyrimidine | (CMP) 5'-nucleotidase | 3.1.3.5 | H16_A2376 | surE | dtmp + h2o -> pi + thymd | dtmp + h2o -> pi + thymd | dtmp + h2o -> pi + thymd |
| CTDA | metabolism Pyrimidine | (dTMP) Cytosine deaminase | 3.5.4.1 | H16_B1593 | codA | ct + h + h2o -> nh4 + ura | ct + h + h2o -> nh4 + ura | ct + h + h2o -> nh4 + ura |
| DCTPDA1 | metabolism Pyrimidine | dCTP deaminase | 3.5.4.13 | H16_A2931 | dcd | dctp + h + h2o -> dutp + nh4 | dctp + h + h2o -> dutp + nh4 | dctp + h + h2o -> dutp + nh4 |
| | metabolism Pyrimidine | | | | | | | |
| DCTPDA2 | metabolism Pyrimidine | | 3.5.4.13 | H16_A2931 | dcd | ctp + h + h2o -> utp + nh4 | ctp + h + h2o -> utp + nh4 | ctp + h + h2o -> utp + nh4 |
| DUTPDP | metabolism Pyrimidine | dUTP diphosphatase deoxyuridine | | H16_A3049 | dut | dutp + h2o -> dump + ppi | dutp + h2o -> dump + ppi + 2 h | dutp + h2o -> dump + ppi + 2 h |
| DOURIP | metabolism | phosphorylase | 2.4.2.4 | H16_A2012 | deoA | du + pi <-> dr1p + ura | du + pi <-> dr1p + ura | du + pi <-> dr1p + ura |
| URIDK1 | Pyrimidine metabolism | (dUMP) | 2.7.4.9 | H16_A1569 | tmk | atp + dump <-> adp + dudp | atp + dump + h <-> adp + dudp | atp + dump <-> adp + dudp |
| DOROAD | Pyrimidine metabolism | dihydoorotic acid dehydrogenase | 1.3.3.1 | H16_A1401 | pyrD | doroa + o2 -> oroa + h2o2 | doroa + o2 -> oroa + h2o2 | doroa + o2 -> oroa + h2o2 |
| ASPCBT | Pyrimidine metabolism | aspartate carbamoyltransferase | 2.1.3.2 | H16_A2913 | ругВ | asp + cap -> caasp + h + pi | asp + cap -> caasp + h + pi | asp + cap -> caasp + h + pi |
| OROPRT | Pyrimidine | orotate phosphoribosyltransf | 2.4.2.10 | H16_A0224 | pyrE | omp + ppi <-> oroa + prpp | omp + ppi + h <-> oroa + prpp | omp + ppi + h <-> oroa + prpp |
| DHORT | metabolism Pyrimidine | erase dihydroorotase | 3.5.2.3 | H16_A0479 | pyrC | doroa + h2o <-> caasp + h | doroa + h2o <-> caasp + h | doroa + h2o <-> caasp + h |
| | metabolism | , 50101036 | | | +7 | | comp i ii | |

| OMPDC | Pyrimidine | orotidine-5'- phosphate | 4.1.1.23 | H16_A3157 | pyrF | h + omp -> co2 + ump | h + omp -> co2 + ump | h + omp -> co2 + ump |
|----------|--------------------------------|---|-----------|---|--|--|--|--|
| | metabolism Pyrimidine | decarboxylase CTP synthase | | _ | ., | atp + gln + h2o + utp -> adp + ctp + glu + h + | | atp + qln + h2o + utp -> adp + ctp + qlu + 2 h |
| CTPS | metabolism | (glutamine) | 6.3.4.2 | | | pi | + 2 h + pi | + pi |
| URIDK2 | Pyrimidine metabolism | | 2.7.4.22 | H16_A2053 | unknown | atp + ump <-> adp + udp | atp + ump + h <-> adp + udp | atp + ump <-> adp + udp |
| BTPT3 | Pyrimidine metabolism | bis(5'-nucleosidyl)- tetraphosphatase | 3.6.1.17 | H16_A3406 | unknown | up4g + h2o -> utp + ump | up4g + h2o -> utp + ump + h | up4g + h2o -> utp + ump + 2 h |
| PDRS | Pyrimidine metabolism | pseudouridylate synthase | 4.2.1.70 | H16_A3057 | truA2 | ura + r5p <-> puri5p + h2o | ura + r5p <-> puri5p + h2o | ura + r5p <-> puri5p + h2o |
| DHPM | Pyrimidine | dihydropyrimidinase | 3.5.2.2 | H16_A0068/H16_A3075 | unknown/unknown | 56dhu + h2o <-> 3urdpp + h | 56dhu + h2o <-> 3urdpp + h | 56dhu + h2o <-> 3urdpp + h |
| BUDPP1 | metabolism Pyrimidine | beta- | 3.5.1.6 | H16_A1475 | unknown | 3urdpp + h2o + 2 h -> bala + co2 + nh4 | 3urdpp + h2o + 2 h -> bala + co2 + nh4 | 3urdpp + h2o + 2 h -> bala + co2 + nh4 |
| | metabolism Pyrimidine | ureidopropionase | | | | dcmp + h2o + h -> dump + nh4 | | |
| DCDA | metabolism Pyrimidine | | 3.5.4.12 | H16_B0797 | unknown | | dcmp + h2o + h -> dump + nh4 | dcmp + h2o + h -> dump + nh4 |
| CYTDA | metabolism Pyrimidine | cytosine deaminase | 3.5.4.1 | H16_A0782/H16_B1593 | ssnA/codA | 5mc + h2o + h <-> thym + nh4 | 5mc + h2o + h <-> thym + nh4 | 5mc + h2o + h <-> thym + nh4 |
| DHPMD | metabolism | dihydropyrimidinase | 3.5.2.2 | H16_A0068/H16_A3075 | unknown/unknown | 56dht + h2o <-> 3udsb + h | 56dht + h2o <-> 3udsb + h | 56dht + h2o <-> 3udsb + h |
| BUDPP2 | Pyrimidine metabolism | beta- ureidopropionase | 3.5.1.6 | H16_A1475 | unknown | 3udsb + h2o + 2 h -> 3aibt + co2 + nh4 | 3udsb + h2o + 2 h -> 3aibt + co2 + nh4 | 3udsb + h2o + 2 h -> 3aibt + co2 + nh4 |
| ALHD1 | Pyruvate Metabolism | aldehyde dehydrogenase (acetaldehyde, NAD) | 12.13 | H16_A0232/H16_A0745, H16_A1114/H16_A1495, H16_B0212/H16_B0421/ H16_B0737/H16_B0833/ H16_B1534/H16_B1735/ H16_B1751/H16_B1835/ H16_B1960/H16_B2444 | unknown/unknown/ unknown/unknown/ unknown/unknown/ unknown/unknown/ unknown/unknown/ | acal + h2o + nad -> ac + 2 h + nadh | acal + h2o + nad -> ac + 2 h + nadh | acal + h2o + nad -> ac + 2 h + nadh |
| PPS | Pyruvate Metabolism | phosphoenolpyruvat e synthase | 2.7.9.2 | H16_A2038 | ppsA | atp + h2o + pyr -> amp + pep + pi | atp + h2o + pyr -> amp + 2 h + pep + pi | atp + h2o + pyr -> amp + h + pep + pi |
| ALDRD1 | Pyruvate | aldehyde reductase | 1.1.1.21 | H16_A3186/H16_B2162 | unknown/unknown | h + mtg + nadh -> dlald + nad | h + mtg + nadh -> dlald + nad | h + mtg + nadh -> dlald + nad |
| ALDRD2 | Metabolism Pyruvate | aldehyde reductase | 1.1.1.21 | H16 A3186/H16 B2162 | unknown/unknown | 2 h + dlald + nadph <-> 12ppd-R + nadp | h + dlald + nadph <-> 12ppd-R + nadp | h + dlald + nadph <-> 12ppd-R + nadp |
| HAGTH | Metabolism Pyruvate | hydroxyacylglutathio | 3.1.2.6 | H16_A0190/H16_A1980, | gloB1/unknown/unk | h2o + ltg -> rgt + h + lac | h2o + ltg -> rgt + h + lac | h2o + ltg -> rgt + h + lac |
| | Metabolism | ne hydrolase | | H16_A3582/H16_A3623, | | | | |
| MGXS | Pyruvate Metabolism | methylglyoxal synthase | 4.2.3.3 | H16_A0932 | mgsA | dhap -> mtg + pi | dhap -> mtg + pi | dhap -> mtg + pi |
| LGTTHL | Pyruvate Metabolism | lactoylglutathione lyase | 4.4.1.5 | H16_A0274/H16_A0517, H16_A2179/H16_B1143/ H16_B2255 | unknown/gloA1/unk nown/gloA2/gloA5 | rgt + mtg -> ltg | rgt + mtg -> Itg | rgt + mtg -> ltg |
| ALCDet | Pyruvate Metabolism | alcohol dehydrogenase (ethanol) | 1.1.1.1 | H16_A0757/H16_A3330, H16_B0517/H16_B1433/ H16_B1699/H16_B1745/ | wn/adhP/unknown/u nknown/unknown/u | | eth + nad <-> acal + h + nadh | eth + nad <-> acal + h + nadh |
| DLDHD | Pyruvate Metabolism | D-lactate | 1.1.1.28 | H16_B1834/H16_B2470 H16_A1681/H16_A1682 | | lac + nad <-> h + nadh + pyr | lac + nad <-> h + nadh + pyr | lac + nad <-> h + nadh + pyr |
| ACALDDH | Pyruvate | acetaldehyde | 1.2.1.10 | H16_A1806/H16_A2747, | | acal + coa + nad <-> accoa + h + nadh | acal + coa + nad <-> accoa + h + nadh | acal + coa + nad <-> accoa + h + nadh |
| | Metabolism Pyruvate | (acetylating) | | H16_B0551/H16_B0596 | | | | |
| LCTAD2 | Metabolism Pyruvate | dehydrogenase | 1.2.1.22 | H16_A1919 | unknown | mtg + nad + h2o <-> pyr + nadh + 2 h | mtg + nad + h2o <-> pyr + nadh + 2 h | mtg + nad + h2o <-> pyr + nadh + 2 h |
| PTA | Metabolism | phosphotransacetylas e | 2.3.1.8 | H16_B1631/H16_B1871 | pta1/pta2 | accoa + pi <-> actp + coa + h | accoa + pi <-> actp + coa | accoa + pi <-> actp + coa |
| ACKA | Pyruvate Metabolism | acetate kinase | 2.7.2.1 | H16_A0670/H16_B1630 | ackA2/ackA | ac + atp <-> actp + adp | ac + atp <-> actp + adp | ac + atp <-> actp + adp |
| PCT1 | Pyruvate Metabolism | propionate CoA- transferase | 2.8.3.1 | H16_A2718 | pct | accoa + ppa <-> ac + ppcoa | accoa + ppa <-> ac + ppcoa | accoa + ppa <-> ac + ppcoa |
| APPS2 | Pyruvate | acylphosphatase | 3.6.1.7 | H16_A3325 | acyP | actp + h2o -> ac + pi | actp + h2o -> ac + pi + h | actp + h2o -> ac + pi + h |
| | Metabolism | ** ' | | H16_A1616/H16_A2525 | | | | · |
| ACS | Pyruvate Metabolism | acetyl-CoA synthetase | 6.2.1.1 | H16_B0386/H16_B0591/ H16_B0696/H16_B0834/ H16_B1102 | | ac + atp + coa + h -> accoa + amp + ppi | ac + atp + coa -> accoa + amp + ppi + h | ac + atp + coa -> accoa + amp + ppi + h |
| PYC | Pyruvate metabolism | pyruvate carboxylase | 6.4.1.1 | H16_A1251/H16_A2142 | pyc/accA2 | atp + pyr + hco3 <-> adp + oaa + pi + h | atp + pyr + hco3 <-> adp + oaa + pi + h | atp + pyr + hco3 <-> adp + oaa + pi + h |
| PAAD1 | Pyruvate Metabolism | phenylacrylic acid decarboxylase | 4.1.1 | H16_B2447 | unknown | hedc + h -> pyr + co2 | hedc + h -> pyr + co2 | hedc + h -> pyr + co2 |
| ALHD1p | Pyruvate Metabolism | aldehyde dehydrogenase (acetaldehyde, NAD) | 12.1.3 | H16_B1534/H16_B1735/ | unknown/unknown/ unknown/unknown/ unknown/unknown/ unknown/unknown/ | acal + h2o + nadp -> ac + 3 h + nadph | acal + h2o + nadp -> ac + 2 h + nadph | acal + h2o + nadp -> ac + 2 h + nadph |
| | Rivoflavin | 5-amino-6-(5- | | H16_B1751/H16_B1835/ H16_B1960/H16_B2444 | | | | |
| A6PRAUR | metabolism | phosphoribosylamino)uracil reductase | 1.1.1.193 | H16_A2848 | ribD | a6rp5p + 2 h + nadph -> a6rp5p2 + nadp | a6rp5p + h + nadph -> a6rp5p2 + nadp | a6rp5p + h + nadph -> a6rp5p2 + nadp |
| FLVRp | Rivoflavin Metabolism | | 1.5.1.30 | H16_A2352/H16_B0671 | unknown/unknown | 2 h + nadph + ribflav -> nadp + rbflvrd | 2 h + nadph + ribflav -> nadp + rbflvrd | 2 h + nadph + ribflav -> nadp + rbflvrd |
| FLVR | Rivoflavin Metabolism | flavin reductase (NAD) | 1.5.1.30 | H16_A2352/H16_B0671 | unknown/unknown | h + nadh + ribflav -> nad + rbflvrd | 2 h + nadh + ribflav -> nad + rbflvrd | 2 h + nadh + ribflav -> nad + rbflvrd |
| RBFS1 | Rivoflavin metabolism | . , | 2.5.1.9 | H16_A2855 | ribH | a6rp + db4p -> dmlz + 2 h2o + pi | a6rp + db4p -> dmlz + h + 2 h2o + pi | a6rp + db4p -> dmlz + h + 2 h2o + pi |
| RBFS2 | Rivoflavin | riboflavin synthase | 2.5.1.9 | H16_A2849 | ribC | 2 dmlz -> a6rp + ribflav | 2 dmlz + h -> a6rp + ribflav | 2 dmlz + h -> a6rp + ribflav |
| APPT | metabolism Rivoflavin | | 3.1.3.2 | H16_A0767/H16_B1238 | | fmn + h2o -> ribflay + pi | fmn + h2o -> ribflav + pi | fmn + h2o -> ribflay + pi |
| | metabolism Rivoflavin | | | | | | • | |
| RBFK | metabolism Rivoflavin | riboflavin kinase FMN | 2.7.1.26 | H16_A3045 | unknown | atp + ribflav -> adp + fmn | atp + ribflav -> adp + fmn + h | atp + ribflav -> adp + fmn + h |
| FMNANT | metabolism | adenylyltransferase diaminohydroxyphos | 2.7.7.2 | H16_A3045 | unknown | atp + fmn -> fad + ppi | atp + fmn -> fad + ppi | atp + fmn -> fad + ppi |
| DHPPRAP | Rivoflavin metabolism | phoribosylaminopryri midine deaminase (25drapp) 3,4-Dihydroxy-2- | 3.5.4.26 | H16_A2848 | ribD | 25drapp + h + h2o -> a6rp5p + nh4 | 25drapp + h + h2o -> a6rp5p + nh4 | 25drapp + h + h2o -> a6rp5p + nh4 |
| DHB4PS | Rivoflavin metabolism | | 4.1.2 | H16_A2854/H16_B0632/ H16_B1223 | ribBA/unknown/unk nown | rl5p -> db4p + formate + h | rlSp -> db4p + formate + h | rl5p -> db4p + formate + h |
| GTPCHII | Rivoflavin metabolism | GTP cyclohydrolase II | 3.5.4.25 | H16_B1576 | ribA | gtp + 3 h2o -> 25drapp + formate + ppi + h | gtp + 3 h2o -> 25drapp + formate + ppi + 3 | gtp + 3 h2o -> 25drapp + formate + ppi + 3 h |
| NNDMBZPT | Rivoflavin metabolism | Nicotinate-nucleotide dimethylbenzimidazo le | | H16_A2968 | cobT1 | dmbzid + nacn -> 5prdmbz + 2 h + nac | dmbzid + nacn -> 5prdmbz + h + nac | dmbzid + nacn -> Sprdmbz + h + nac |
| | Rivoflavin | phosphoribosyltransf erase pyrimidine | | H16_A0520/H16_A0786, H16_A2434/H16_A2577, | | | | |
| PMPP | metabolism | phosphatase alpha-ribazole 5- | 3.1.3 | H16_B0594/H16_B1063/ H16_B2398 H16_A0520/H16_A0786/ | wn/unknown/unkno wn unknown/unknown/s | a6rp5p2 + h2o -> a6rp + pi | a6rp5p2 + h2o -> a6rp + pi | a6rp5p2 + h2o -> a6rp + pi |
| RZSPP | Rivoflavin metabolism | phosphate phosphatase | | H16_A2434/H16_A2577, H16_B0594/H16_B1063/ H16_B2398 | | 5prdmbz + h2o -> pi + rdmbzi | 5prdmbz + h2o -> pi + rdmbzi | Sprdmbz + h2o -> pi + rdmbzi |
| SELNPS | Selenoamino acid | Selenophosphate | 2.7.9.3 | H16_B0295 | selD | atp + h2o + seld -> amp + pi + selnp | atp + h2o + seld -> amp + pi + selnp + 2 h | atp + h2o + seld -> amp + pi + selnp + h |
| CYSGS1 | metabolism Selenoamino acid | synthase cystathionine | 2.5.1.48 | H16_A2606 | metB | ahser + scys -> sllct + ac + h | ahser + scys -> sllct + ac + h | ahser + scys -> sllct + ac + h |
| | metabolism | gamma-synthase | | | | | · 4. | - |

| | Selenoamino acid | cystathionine | | | | | | |
|----------|--|---|---------------------|---|---|---|---|---|
| CYSGS2 | metabolism Selenoamino acid | gamma-synthase | | H16_A2606 | metB | shser + scys -> sllct + succ + h | shser + scys -> sllct + succ + h | shser + scys -> sllct + succ + h |
| CYSTBL3 | metabolism | lyase | | H16_A1447 | metC | sllct + h2o -> shcys + nh4 + pyr | sllct + h2o -> shcys + nh4 + pyr | sllct + h2o -> shcys + nh4 + pyr |
| ADHC2 | Selenoamino acid metabolism | adenosylhomocystein ase S- | 3.3.1.1 | H16_A0244 | ahcY | seadseh + h2o -> adn + shcys | seadseh + h2o -> adn + shcys | seadseh + h2o + h -> adn + shcys |
| SADMET | Selenoamino acid metabolism | adenosylmethionine synthetase | 2.5.1.6 | H16_A0230/H16_A1975 | metK1/metK2 | atp + smet + h2o + h -> pi + ppi + seasmet | atp + smet + h2o -> pi + ppi + seasmet + 2 h | atp + smet + h2o -> pi + ppi + seasmet + 3 h |
| METTRSS | Selenoamino acid metabolism | methionyd-tPNA | 6.1.1.10 | H16_A2945 | metG | atp + smet + trnamet -> amp + ppi + selmtma | atp + smet + trnamet -> amp + ppi + selmtrna | atp + smet + trnamet -> amp + ppi + selmtrna |
| CYSST4 | Selenoamino acid metabolism | cysteine synthase | 2.5.1.47 | H16_A0807 | cysK1 | aser + seld -> scys + ac | aser + seld -> scys + ac | aser + seld -> scys + ac |
| SULFR | Selenoamino acid metabolism | sulfite reductase (NADPH) | | H16_A1639&H16_A299 9&H16_B2500 | cysI2&cysI1&unkno wn | selt + 3 nadp + 7 h2 -> seld + 3 nadph + 3 h2o + 7 h | selt + 3 nadp + 7 h2 -> seld + 3 nadph + 3 h2o + 4 h | selt + 3 nadp + 7 h2 -> seld + 3 nadph + 3 h2o + 4 h |
| ADSLFK2 | Selenoamino acid metabolism | adenylyl-sulfate | | H16_B0626 | cysN2 | atp + aseInt + h -> adp + ppadsel | atp + aseInt -> adp + ppadsel | atp + aseInt -> adp + ppadsel + h |
| G1PCYTF | | glucose-1-phosphate cytidylyltransferase | 2.7.7.33 | H16_A2893 | rfbF | ctp + g1p <-> ppi + cdpglc | ctp + g1p <-> ppi + cdpglc | ctp + g1p <-> ppi + cdpglc |
| CDPGD | Starch and sucrose metabolism | CDP-alucose 4.6- | 4.2.1.45 | H16_A2896 | unknown | cdpglc -> cdpddglc + h2o | cdpglc -> cdpddglc + h2o | cdpglc -> cdpddglc + h2o |
| TRHPS | Starch and sucrose | alpha,alpha- trehalose-phosphate | 2.4.1.15 | H16_A0430 | unknown | g6p + udpg -> tre6p + udp | g6p + udpg -> tre6p + udp | g6p + udpg -> tre6p + udp + h |
| | metabolism Starch and sucrose | synthase (UDP- forming) | | | | | | |
| AMMALT1 | metabolism Starch and sucrose | (maltotriose) | | H16_B1561 | malQ | mlt + mlttr -> glc + mltttr | mlt + mlttr -> glc + mltttr | mlt + mlttr -> glc + mltttr |
| AMMALT2 | metabolism | (maltotetraose) | 2.4.1.25 | H16_B1561 | malQ | mlt + mltttr -> glc + maltpt | mlt + mltttr -> glc + maltpt | mlt + mlttr -> glc + maltpt |
| AMMALT3 | Starch and sucrose metabolism | (maltopentaose) | 2.4.1.25 | H16_B1561 | malQ | mlt + maltpt -> glc + mlthx | mlt + maltpt -> glc + mlthx | mlt + maltpt -> glc + mlthx |
| AMMALT4 | Starch and sucrose metabolism | Amylomaltase (maltohexaose) | 2.4.1.25 | H16_B1561 | malQ | mlt + mlthx -> glc + malthp | mlt + mlthx -> glc + malthp | mlt + mlthx -> glc + malthp |
| TRH6PP | Starch and sucrose metabolism | trehalose- phosphatase | 3.1.3.12 | H16_A0428 | otsB | h2o + tre6p -> pi + tre | h2o + tre6p -> pi + tre | h2o + tre6p -> pi + tre |
| TREHL | Starch and sucrose metabolism | alpha,alpha-trehalase | 3.2.1.28 | H16_B2096 | treA | h2o + tre -> 2 glc | h2o + tre -> 2 glc | h2o + tre -> 2 glc |
| GLCGP | Starch and sucrose metabolism | glycogen phosphorylase | 2.4.1.1 | H16_B1562 | glgP | glycogen + pi -> g1p | glycogen + pi -> g1p | glycogen + pi -> g1p |
| GLCBRAN | Starch and sucrose metabolism | 1,4-alpha-glucan | 2.4.1.18 | H16_B1559 | glgB | glycogen -> bglycogen | glycogen -> bglycogen | glycogen -> bglycogen |
| MLTGCT | Starch and sucrose | bglycogen) maltose alpha-D- | 549916 | H16 B1558/H16 B1564 | unknown/treY | tre e <-> mlt e | tre e <-> mlt e | tre e <-> mlt e |
| NITL4 | metabolism Styrene | glucosyltransferase | | | nit | | | pheacnit + 2 h2o -> pac + nh4 |
| | degradation Styrene | | | H16_A1125 H16_A1469/H16_B1874/ | | pheacnit + 2 h2o -> pac + nh4 | pheacnit + 2 h2o -> pac + nh4 | |
| AMDS4 | degradation Styrene | amidase phenylacetaldehyde | | H16_B2459 | aimE | pheact + h2o -> pac + nh4 | pheact + h2o -> pac + nh4 | pheact + h2o -> pac + nh4 |
| PHEALDD | degradation | dehydrogenase | 1.2.1.39 | H16_B1358/H16_B1939 | | pacald + nad + h2o -> pac + nadh + 2 h | pacald + nad + h2o -> pac + nadh + 2 h | pacald + nad + h2o -> pac + nadh + 2 h |
| NTPPD5 | Styrene degradation | 2-nitropropane dioxygenase | | H16_A0633/H16_B0223/ H16_B0757/H16_B1109/ H16_B1420/H16_B1836 | nown/unknown/unk | styrene + o2 + nadh + h -> strcg + nad | styrene + o2 + nadh + h -> strcg + nad | styrene + o2 + nadh + h -> strcg + nad |
| CATCHD3 | Styrene degradation | catechol 2,3- dioxygenase | 1.13.11.2 | H16_B0546 | unknown | 3vcat + o2 -> 2h6ot + h | 3vcat + o2 -> 2h6ot + h | 3vcat + o2 -> 2h6ot + h |
| ALPNIT | Styrene degradation | aliphatic nitrilase | 3.5.5.7 | H16_A1956 | unknown | aconit + 2 h2o -> propen + nh4 | aconit + 2 h2o -> propen + nh4 | aconit + 2 h2o -> propen + nh4 |
| AMDS5 | Styrene degradation | amidase | | H16_A1469/H16_B1874/ H16_B2459 | unknown/unknown/ aimE | aclm + h2o -> propen + nh4 | aclm + h2o -> propen + nh4 | aclm + h2o -> propen + nh4 |
| PCT3 | Styrene | propionate CoA- | | H16_A2718 | pct | lactcoa + ac -> llac + accoa | lactcoa + ac -> llac + accoa | lactcoa + ac -> llac + accoa |
| PAC2H | degradation Styrene degradation | transferase phenylacetate 2- hydroxylase | 1.14.13 | | | pac + o2 + nadh + h -> 2hpa + nad + h2o | pac + o2 + nadh + h -> 2hpa + nad + h2o | pac + o2 + nadh + h -> 2hpa + nad + h2o |
| 2HPAC | Styrene degradation | 2-hydroxy- | 1.14.13 | | | 2hpa + o2 + nadh + h -> homogen + nad + h2o | 2hpa + o2 + nadh + h -> homogen + nad + h2o | 2hpa + o2 + nadh + h -> homogen + nad + h2o |
| SLFR | Sulfur Metabolism | sulfite reductase | | H16_A1639&H16_A299 9&H16_B2500 | cysI2&cysI1&unkno wn | 7 h + 3 nadph + so3 -> 3 h2o + h2s + 3 nadp | 3 h + 3 nadph + so3 -> 3 h2o + h2s + 3 nadp | 3 h + 3 nadph + so3 -> 3 h2o + h2s + 3 nadp |
| PASR1 | Sulfur Metabolism | phosphoadenylyl- sulfate reductase (thioredoxin) | 1.8.4.8 | H16_A2997 | cysH | paps + rthio -> pap + so3 + othio | paps + rthio -> pap + so3 + othio + h | paps + rthio -> pap + so3 + othio + h |
| PASR2 | Sulfur Metabolism | phosphoadenylyl- sulfate reductase (glutaredoxin) | 1.8.4.8 | H16_A2997 | cysH | grxrd + paps -> grxox + pap + so3 | grxrd + paps -> grxox + pap + so3 + h | grxrd + paps -> grxox + pap + so3 + h |
| ADSLFK1 | Sulfur Metabolism | adamılıd-culfata | 2.7.1.25 | H16_B0626 | cysN2 | aps + atp -> adp + paps | aps + atp -> adp + paps + h | aps + atp -> adp + paps + h |
| BPNT | Sulfur Metabolism | 3' 5'-hisphosphate | 3.1.3.7 | | | h2o + pap -> amp + pi | h2o + pap -> amp + pi | h2o + pap -> amp + pi |
| TAUDO | Taurine and Hypotaurine metabolism | | 1.14.11.17 | H16_B1533/H16_B2220/ | unknown/unknown/ unknown/unknown/ unknown/tauD1/tau | akg + o2 + taur -> aacald + co2 + so3 + succ | akg + o2 + taur -> aacald + co2 + so3 + succ | akg + o2 + taur -> aacald + co2 + so3 + succ + h |
| ALADH | Taurine and Hypotaurine | alanine | | H16_B2227/H16_B2521 H16_A2009 | D2/unknown ald | ala + nad + h2o -> pyr + nh4 + nadh + h | ala i nad i b?a - mer i nhđ i nadh i h | ala + nad + h2o -> pyr + nh4 + nadh + h |
| | metabolism Taurine and | culfoacetaldebude | | | diu | | ., | ,, |
| SULALDAC | Hypotaurine metabolism Thiamine | acetyltransferase | 2.3.3.15 | H16_B1870 | xsc | sulald + pi -> actp + so3 + h | sulald + pi -> actp + so3 | sulald + pi -> actp + so3 |
| THMPDP | Metabolism | | | H16_A0239 | thiE | ahmpp + thzp -> ppi + thmp | ahmpp + thzp -> ppi + thmp | ahmpp + thzp -> ppi + thmp |
| НМРМК | Thiamine Metabolism | hydroxymethylpyrimi dine kinase (ATP) | 2.7.1.49 | H16_A0243 | unknown | ahm + atp -> 4ampm + adp | ahm + atp -> 4ampm + adp + h | ahm + atp -> 4ampm + adp + h |
| HETHZK | Thiamine Metabolism | kinase | 2.7.1.50 | | | 4mhetz + atp -> thzp + adp | 4mhetz + atp -> thzp + adp + h | 4mhetz + atp -> thzp + adp + h |
| THMPK | Thiamine Metabolism | kinase | | H16_A3154 | thiL | atp + thmp -> adp + thmpp | atp + thmp + h -> adp + thmpp | atp + thmp -> adp + thmpp |
| PMPMK | Thiamine Metabolism | phosphomethylpyrim idine kinase | | H16_A024 H16_A0520/H16_A0786 | unknown / unknown/unknown/s | 4ampm + atp -> ahmpp + adp | 4ampm + atp + h -> ahmpp + adp | 4ampm + atp -> ahmpp + adp |
| THMPT | Thiamine Metabolism | phosphatase | 3.1.3 | H16_A2434/H16_A2577, H16_B0594/H16_B1063/ H16_B2398 | / ixA/unknown/unkno | thiamin + pi <-> thmp + h2o | thiamin + pi <-> thmp + h2o | thiamin + pi <-> thmp + h2o |
| THMDP | Thiamine Metabolism | thiamin pyrophosphatase | 3.6.1.15 | H16_A0948 | unknown | h2o + thmpp -> pi + thmp | h2o + thmpp -> 2 h + pi + thmp | h2o + thmpp -> h + pi + thmp |
| OXGTDC | Thiamine Metabolism | 2-ovoqlutarate | 4.1.1.71 | | | akg + h + thmpp -> co2 + ssaltpp | akg + h + thmpp -> co2 + ssaltpp | akg + 2 h + thmpp -> co2 + ssaltpp |
| ТНМВ | Thiamine metabolism | thiamine biosynthesis protein | unclear reaction | H16_A0235 | thiC | air -> ahm | air -> ahm | air -> ahm |
| GLYCOX | Thiamine | Inic | | H16_A0236 | thiO | gly -> imgly + h + h2 | gly -> imgly + h + h2 | gly -> imgly + h + h2 |
| P7F0P0:- | metabolism Toluene and | henzovlformate | | _ | unknou- | | | |
| BZFORCL1 | Xylene degradation | carboxy-lyase benzaldehyde | | H16_A1113 | unknown | aobzac + h -> bzald + co2 | aobzac + h -> bzald + co2 | aobzac + h -> bzald + co2 |
| BZALDD1 | Xylene degradation | dehydrogenase (NAD) | 1.2.1.28 | H16_A1772 H16_B0539&H16_B0540 | unknown | bzald + nad + h2o -> benzot + nadh + 2 h | bzald + nad + h2o -> benzot + nadh + 2 h | bzald + nad + h2o -> benzot + nadh + 2 h |
| PHE2MO1 | Toluene and Xylene degradation | phenol 2- monooxygenase | 1.14.15./ | | poxA&poxB&poxC& | tolen + o2 + nadph + 2 h -> ocresol + nadp + h2o | tolen + o2 + nadph + h -> ocresol + nadp + h2o | tolen + o2 + nadph + h -> ocresol + nadp + h2o |

| PHE2MO2 | Toluene and Xylene degradation | phenol 2- n monooxygenase | 1.14.13.7 | 42&H16_B0543&H16_B 0544 | | ocresol + o2 + nadph + 2 h -> dhtolen + nadp + h2o | ocresol + o2 + nadph + h -> dhtolen + nadp + h2o | ocresol + o2 + nadph + h -> dhtolen + nadp + h2o |
|----------|-----------------------------------|--|------------|---|--|---|---|---|
| PHE2MO3 | Toluene and Xylene degradation | phenol 2- n monooxygenase | 1.14.13.7 | H16_B0539&H16_B0540 &H16_B0541&H16_B05 42&H16_B0543&H16_B 0544 | | 3cresol + o2 + nadph + 2 h -> dhtolen + nadp + h2o | 3cresol + o2 + nadph + h -> dhtolen + nadp + h2o | 3cresol + o2 + nadph + h -> dhtolen + nadp + h2o |
| CATCHD1 | Toluene and Xylene degradation | catechol 2,3- n dioxygenase | 1.13.11.2 | H16_B0546 | unknown | dhtolen + o2 -> hkhdn + h | dhtolen + o2 -> hkhdn + h | dhtolen + o2 -> hkhdn + h |
| FBMO6 | Toluene and Xylene degradation | flavin-binding monooxygenase | 1.14.13 | H16_A1145/H16_B0495/ H16_B1480/H16_B2135 | | 3cresol + o2 + nadh + h -> hbzal + nad + h2o | 3cresol + o2 + nadh + h -> hbzal + nad + h2o | 3cresol + o2 + nadh + h -> hbzal + nad + h2o |
| BZALDD2 | Toluene and Xylene degradation | benzaldehyde dehydrogenase (NAD) | 1.2.1.28 | H16_A1772 | unknown | 3hbzald + nad + h2o -> 3hbenzot + nadh + 2 h | 3hbzald + nad + h2o -> 3hbenzot + nadh + 2 h | 3hbzald + nad + h2o -> 3hbenzot + nadh + 2 h |
| BZALDD3 | Toluene and Xylene degradation | benzaldehyde dehydrogenase (NAD) | 1.2.1.28 | H16_A1772 | unknown | mbzald + nadp + h2o -> otolat + nadph + 3 h | mbzald + nadp + h2o -> otolat + nadph + 2 h | mbzald + nadp + h2o -> otolat + nadph + 2 h |
| BZALDD4 | Toluene and Xylene degradation | benzaldehyde dehydrogenase | 1.2.1.28 | H16_A1772 | unknown | mtolald + nadp + h2o -> mtolat + nadph + 3 h | mtolald + nadp + h2o -> mtolat + nadph + 2 h | mtolald + nadp + h2o -> mtolat + nadph + 2 h |
| BZALDD5 | Toluene and Xylene degradation | benzaldehyde | 1.2.1.28 | H16_A1772 | unknown | ptolald + nadp + h2o -> ptolat + nadph + 3 h | ptolald + nadp + h2o -> ptolat + nadph + 2 h | ptolald + nadp + h2o -> ptolat + nadph + 2 h |
| FBMO7 | Toluene and Xylene degradation | flavin-binding | 1.14.13 | H16_A1145/H16_B0495/ H16_B1480/H16_B2135 | | 2 tol4sul + o2 + 2 h2 -> 2 4cresol + 2 so3 | 2 tol4sul + o2 + 2 h2 -> 2 4cresol + 2 so3 | 2 tol4sul + o2 + 2 h2 -> 2 4cresol + 2 so3 |
| CATCHDG1 | Toluene and Xylene degradation | catechol 1,2- n dioxygenase | 1.13.11.1 | H16_A1964/H16_B0968 | catA/pcpA | 4mctch + o2 -> 3mhdd + 2 h | 4mctch + o2 -> 3mhdd + 2 h | 4mctch + o2 -> 3mhdd + 2 h |
| MCCIS1 | Toluene and Xylene degradation | muconate cycloisomerase | 5.5.1.1 | H16_A1966/H16_B0536 | catB3/catB4 | 3mhdd + h -> 4mmclac | 3mhdd + h -> 4mmclac | 3mhdd + h -> 4mmclac |
| CATCHD2 | Toluene and Xylene degradation | catechol 2,3- n dioxygenase | 1.13.11.2 | H16_B0546 | unknown | 4mctch + o2 -> hmcmsald + h | 4mctch + o2 -> hmcmsald + h | 4mctch + o2 -> hmcmsald + h |
| HMSALD2 | Toluene and Xylene degradation | 2-hydroxymuconic semialdehyde | 1.2.1.32 | H16_B0547 | unknown | hmcmsald + nad + h2o -> hmcmct + nadh + 2 h | hmcmsald + nad + h2o -> hmcmct + nadh + 2 h | hmcmsald + nad + h2o -> hmcmct + nadh + 2 h |
| KPENH | Toluene and Xylene degradation | 2-keto-4-pentenoate | 4.2.1.80 | H16_B0548/H16_B0597/ H16_B0884 | mhpD1/bphH/mhpD 3 | hchdn + h2o -> hohx | hchdn + h2o -> hohx | hchdn + h2o -> hohx |
| OXCTD1 | Toluene and Xylene degradation | 4-oxalocrotonate | 4.1.1.77 | H16_B0549 | unknown | omcmc + h -> hchdn + co2 | omcmc + h -> hchdn + co2 | omcmc + h -> hchdn + co2 |
| 4CRESOLD | Toluene and xylene degradation | denydrogenase | 1.17.99.1 | | | 4cresol + fad -> 4hbzald + fadh2 | 4cresol + fad + h -> 4hbzald + fadh2 | 4cresol + fad -> 4hbzald + fadh2 |
| | Trinitrotoluene | (hydroxylating) | _ | | | tnittol + 2 nadh + 2 h -> 4hlmdnit + 2 nad + | tnittol + 2 nadh + 2 h -> 4hlmdnit + 2 nad + | tnittol + 2 nadh + 2 h -> 4hlmdnit + 2 nad + |
| NITRDT1 | degradation Trinitrotoluene | nitroreductase | 1, | H16_A1789 | | h2o tnittol + 2 nadh + 2 h -> 2hlmdnit + 2 nad + | h2o tnittol + 2 nadh + 2 h -> 2hlmdnit + 2 nad + | h2o tnittol + 2 nadh + 2 h -> 2hlmdnit + 2 nad + |
| NITRDT2 | degradation | | 1 | H16_A1789 | | | h2o | h2o |
| AAATT | Trinitrotoluene degradation | arylamine N- acetyltransferase | 2.3.1.5 | H16_B1241 | nhoA | 24danit + accoa -> 4aanit + coa | 24danit + accoa -> 4aanit + coa | 24danit + accoa -> 4aanit + coa |
| NITRDT1p | Trinitrotoluene degradation | nitroreductase | 1,-,-,- | H16_A1789 | | tnittol + 2 nadph + 4 h -> 4hlmdnit + 2 nadp + h2o | tnittol + 2 nadph + 2 h -> 4hlmdnit + 2 nadp + h2o | tnittol + 2 nadph + 2 h -> 4hlmdnit + 2 nadp + h2o |
| TRPPA | Tryptophan | Tryptophanase (L- | 4.1.99.1 | | | h2o + trp <-> indole + nh4 + pyr | h2o + trp <-> indole + nh4 + pyr | h2o + trp <-> indole + nh4 + pyr |
| | metabolism Tryptophan | tryptophan) | | | | | | |
| MNAO10 | metabolism Tryptophan | monoamine oxidase | 1.4.3.4 | H16_A0831 | maoB | 5hknm + o2 -> 46dhqn + nh4 + h2o2 | 5hknm + o2 -> 46dhqn + nh4 + h2o2 | 5hknm + o2 -> 46dhqn + nh4 + h2o2 |
| ACFM2 | metabolism | arylformamidase | 3.5.1.9 | H16_A3005/H16_B1997 | unknown/unknown | 5hnfkn + h2o -> 5hknn + formate + h | Shnfkn + h2o -> Shknn + formate + h | 5hnfkn + h2o -> 5hknn + formate + h |
| LAAO6 | Tryptophan metabolism | L-amino-acid oxidase | 1.4.3.2 | H16_A0845/H16_A0856 | lao1/lao2 | trp + h2o + o2 -> idpyr + nh4 + h2o2 | trp + h2o + o2 -> idpyr + nh4 + h2o2 | trp + h2o + o2 -> idpyr + nh4 + h2o2 |
| IDPD | Tryptophan metabolism | indolepyruvate decarboxylase | 4.1.1.74 | H16_B1399 | ipdC | idpyr + h -> i3aa + co2 | idpyr + h -> i3aa + co2 | idpyr + h -> i3aa + co2 |
| | | ,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,, | | H16_A0232/H16_A0745/ | unknown/unknown/ | | | |
| ALHD8 | Tryptophan metabolism | aldehyde dehydrogenase (NAD+) | 1.2.1.3 | H16_A1114/H16_A1495/ H16_B0212/H16_B0421/ H16_B0737/H16_B0833/ H16_B1534/H16_B1735/ H16_B1751/H16_B1835/ H16_B1960/H16_B2444 | unknown/unknown/ unknown/unknown/ unknown/unknown/ unknown/unknown/ | i3aa + nad + h2o -> i3ac + nadh + 2 h | i3aa + nad + h2o -> i3ac + nadh + 2 h | i3aa + nad + h2o -> i3ac + nadh + 2 h |
| MNAO11 | Tryptophan | monoamine oxidase | 1424 | H16 A0831 | | sertn + h2n + n2 -> 5hiaa + nh4 + h2n2 | sertn + h2o + o2 -> 5hiaa + nh4 + h2o2 | corto i b2o i o2 - Ebios i ob4 i b2o2 |
| | metabolism Tryptophan | | | | | | | |
| MNAO12 | metabolism | monoamine oxidase | 1.4.3.4 | H16_A0831 | maoB | tyrpm + h2o + o2 -> i3aa + nh4 + h2o2 | tyrpm + h2o + o2 -> i3aa + nh4 + h2o2 | tyrpm + h2o + o2 -> i3aa + nh4 + h2o2 |
| ALHD9 | Tryptophan metabolism | aldehyde dehydrogenase (NAD+) | 12.1.3 | H16_A0232/H16_A0745/ H16_A1114/H16_A1495/ H16_B0212/H16_B0421/ H16_B0737/H16_B0833/ H16_B1534/H16_B1735/ H16_B1751/H16_B1835/ H16_B1960/H16_B2444 | unknown/unknown/ unknown/unknown/ unknown/unknown/ unknown/unknown/ unknown/unknown/ | Shiaa + nad + h2o -> Shiac + nadh + 2 h | Shiaa + nad + h2o -> Shiac + nadh + 2 h | Shiaa + nad + h2o -> Shiac + nadh + 2 h |
| FBMO5 | Tryptophan metabolism | flavin-binding monooxygenase | 1.14.13 | H16_A1145/H16_B0495/ H16_B1480/H16_B2135 | | idlac + o2 + nadph + 2 h -> 6hidlac + nadp + h2o | idlac + o2 + nadph + h -> 6hidlac + nadp + h2o | idlac + o2 + nadph + h -> 6hidlac + nadp + h2o |
| TRPD | Tryptophan | tryptophan 2,3- | 1.13.11.11 | H16_A2816/H16_B1418 | | trp + o2 -> forkn | trp + o2 -> forkn | trp + o2 -> forkn |
| KYNRN1 | metabolism Tryptophan | dioxygenase kynureninase | 3.7.1.3 | | | forkn + h2o -> forant + ala + h | forkn + h2o -> forant + ala + h | forkn + h2o -> forant + ala + h |
| | metabolism Tryptophan | | | | | | | |
| ACFM3 | metabolism Tryptophan | arylformamidase | 3.5.1.9 | H16_A3005/H16_B1997 | | forant + h2o -> formate + an + h | forant + h2o -> formate + an + h | forant + h2o -> formate + an + h |
| ACFM4 | metabolism | arylformamidase | 3.5.1.9 | H16_A3005/H16_B1997 | unknown/unknown | forkn + h2o -> formate + kn + h | forkn + h2o -> formate + kn + h | forkn + h2o -> formate + kn + h |
| KYNRN2 | Tryptophan metabolism | kynureninase | 3.7.1.3 | H16_A2815 | kynU | kn + h2o -> an + ala + h | kn + h2o -> an + ala + h | kn + h2o -> an + ala + h |
| AMDS2 | Tryptophan metabolism | amidase | 3.5.1.4 | H16_A1469/H16_B1874/ | unknown/unknown/ aimE | id3act + h2o -> i3ac + nh4 | id3act + h2o -> i3ac + nh4 | id3act + h2o -> i3ac + nh4 |
| NITL1 | Tryptophan | nitrilase | 3.5.5.1 | H16_B2459 H16_A1125 | nit | idactn + 2 h2o -> i3ac + nh4 | idactn + 2 h2o -> i3ac + nh4 | idactn + 2 h2o -> i3ac + nh4 |
| | metabolism Tryptophan | | | H16_A2777/H16_A3109/ | | | | |
| CATL | metabolism Tryptophan | catalase | 1.11.1.6 | H16_B1428 | | | 2 3han + 2 o2 -> cvn + 2 h2o2 + h2 | 2 3han + 2 o2 -> cvn + 2 h2o2 + h2 |
| KYNRN3 | metabolism | kynureninase | 3.7.1.3 | H16_A2815 | kynU | hlk + h2o -> 3han + ala + h | hlk + h2o -> 3han + ala + h | hlk + h2o -> 3han + ala + h |
| PAAD6 | Tryptophan metabolism | phenylacrylic acid decarboxylase | 4.1.1 | H16_B2447 | unknown | hlk + h -> hkn + co2 | hlk + h -> hkn + co2 | hlk + h -> hkn + co2 |
| MNAO14 | Tryptophan metabolism | monoamine oxidase | 1.4.3.4 | H16_A0831 | maoB | hkn + o2 -> 48dhq + nh4 + h2o2 | hkn + o2 -> 48dhq + nh4 + h2o2 | hkn + o2 -> 48dhq + nh4 + h2o2 |
| ACMSD | Tryptophan metabolism | aminocarboxymucon ate-semialdehyde decarboxylase | 4.1.1.45 | H16_B0330 | acmD | 2a3cms + h -> 2amcs + co2 | 2a3cms + 2 h -> 2amcs + co2 | 2a3cms + h -> 2amcs + co2 |
| HMSALD1 | Tryptophan metabolism | 2-hydroxymuconic | 1.2.1.32 | H16_B0547 | unknown | 2amcs + nad + h2o -> 2amc + nadh + 2 h | 2amcs + nad + h2o -> 2amc + nadh + 2 h | 2amcs + nad + h2o -> 2amc + nadh + h |
| OGDH3 | Tryptophan metabolism | 2-oxoglutarate dehydrogenase E1 | 1.2.4.2 | H16_A2325 | odhA | 2oad + coa + nad -> glutcoa + co2 + nadh | 2oad + nad + coa -> glutcoa + co2 + nadh | 2oad + coa + nad -> glutcoa + co2 + nadh |
| BKAR2 | Tryptophan | component beta-ketoacyl-ACP | 1.3.1 | H16_B0731/H16_B0734 | unknown/unknown | 5co46d + nadph + h -> 5co46dp + nadp | 5co46d + nadph + h -> 5co46dp + nadp | 5co46d + nadph + h -> 5co46dp + nadp |
| | metabolism Tryptophan | reductase | a | 10_00/31/П10_00/34 | ananown/driknown | | | |
| KNTAPB | metabolism | | | | | knt + h2o <-> amphebut | knt + h2o <-> amphebut | knt + h2o <-> amphebut |

H16_B0539&H16_B0540

| | Tryptophan | kynurenine- | | | | | | |
|---------|--------------------------------------|--|------------|---|--|--|--|---|
| KNAKGT | metabolism | transaminase | 2.6.1.7 | | | amphebut + glu -> kn + akg | amphebut + glu -> kn + akg | amphebut + glu -> kn + akg |
| 4HPHEA1 | Tyrosine metabolism | 4- hydroxyphenylacetat e-3-hydroxylase | 1.14.13.3 | H16_B0496 | unknown | hpheac + o2 + nadh + h -> 34dhpheac + nad + $h2o$ | hpheac + o2 + nadh + h -> 34dhpheac + nad + h2o | hpheac + o2 + nadh + h -> 34dhpheac + nad + h2o |
| 4HPHEA2 | Tyrosine metabolism | 4- hydroxyphenylacetat e-3-hydroxylase | 1.14.13.3 | H16_B0496 | unknown | $\begin{array}{l} \text{4hpheac + o2 + nadh + h -> 34dhpheac + nad} \\ \text{+ h2o} \end{array}$ | 4hpheac + o2 + nadh + h -> 34dhpheac + nad + h2o | 4hpheac + o2 + nadh + h -> 34dhpheac + nad + $h2o$ |
| MNAO3 | Tyrosine metabolism | monoamine oxidase | 1.4.3.4 | H16_A0831 | maoB | h2o + o2 + tym -> 4hac + h2o2 + nh4 | h2o + o2 + tym -> 4hac + h2o2 + nh4 | h2o + o2 + tym -> 4hac + h2o2 + nh4 |
| FBMO2 | Tyrosine metabolism | flavin-binding monooxygenase | 1.14.13 | H16_A1145/H16_B0495/ H16_B1480/H16_B2135 | | tym + o2 + nadh + h -> dopa + nad + h2o | tym + o2 + nadh + h -> dopa + nad + h2o | tym + o2 + nadh + h -> dopa + nad + h2o |
| FBMO3 | Tyrosine metabolism | flavin-binding monooxygenase | 1.14.13 | | unknown/unknown/ | z4hphea + nadph + 2 h + o2 -> 4hmdn + nadp + 2 h2o | z4hphea + nadph + h + o2 -> 4hmdn + nadp + 2 h2o | z4hphea + nadph + h + o2 -> 4hmdn + nadp + 2 h2o |
| CARHM1 | Tyrosine metabolism | 5-carboxymethyl-2- hydroxymuconate isomerase | 5.3.3.10 | H16_A0624/H16_B1250 | hpaF/unknown | 5cm2hm -> 5c2o3e | 5cm2hm -> 5c2o3e | 5cm2hm -> 5c2o3e |
| ACTF2 | Tyrosine metabolism | acetyltransferase | 2.3.1 | H16_A0039/H16_A0240/ H16_A00269/H16_A0699/ H16_A1315/H16_A1564/ H16_A1315/H16_A1564/ H16_A1639/H16_A3071/ H16_A0039/H16_A3071/ H16_B0018/H16_B0021/ H16_B0018/H16_B0021/ H16_B107/H16_B1623/ H16_B107/H16_B1623/ H16_B189/H16_B1623/ H16_B1899/H16_B16239/ | unknown/unknown/ unknown/unknown/ unknown/unknown/ unknown/unknown/ unknown/unknown/ unknown/pat/unkno wn/unknown/whpD/ unknown/unknown/ unknown/unkno | | 4hpheacoa + gly -> 4hphegly + coa + h | 4hpheacoa + gly -> 4hphegly + coa + h |
| PAAD3 | Tyrosine metabolism | phenylacrylic acid decarboxylase | 4.1.1 | H16_B2447 | unknown | 2 cddh + 2 h + o2 -> 2 dhid + 2 co2 + 2 h2o | 2 cddh + 2 h + o2 -> 2 dhid + 2 co2 + 2 h2o | 2 cddh + 2 h + o2 -> 2 dhid + 2 co2 + 2 h2o |
| PAAD4 | Tyrosine | phenylacrylic acid | 4.1.1 | H16_B2447 | unknown | dpcr + h -> dhid + co2 | dpcr + h -> dhid + co2 | dpcr + h -> dhid + co2 |
| 17010-1 | metabolism | decarboxylase | 7.2.2. | H16_A1069/H16_A1070/ | | aper in a direct con | apa i ii i aiia i coz | apa i ii z diid i coz |
| ACDH2 | Tyrosine metabolism | acyl dehydratase | 4.2.1 | H16_A1289/H16_A2151/ H16_A3307/H16_B0359/ | unknown/unknown/ | 2hhpdd + h2o -> 4h2ohep | 2hhpdd + h2o -> 4h2ohep | 2hhpdd + h2o -> 4h2ohep |
| ACDH3 | Tyrosine metabolism | acyl dehydratase | 42.1 | H16_A1069/H16_A1070/ H16_A1289/H16_A2151/ H16_A3307/H16_B0359/ H16_B0706 | unknown/unknown/ | 203e + h2o -> 4h2ohep | 2o3e + h2o -> 4h2ohep | 203e + h2o -> 4h2ohep |
| DHHED1 | Tyrosine metabolism | 2,4-dihydroxyhept-2- ene-1,7-dioic acid aldolase | 4.1.2 | H16_A0615/H16_B0632/ H16_B1223 | hpal1/unknown/unk nown | 4h2ohep -> sucsal + pyr | 4h2ohep -> sucsal + pyr | 4h2ohep -> sucsal + pyr |
| MALAAC | Tyrosine metabolism | maleylacetoacetate isomerase | 5.2.1.2 | H16_A0362 | unknown | 4maac -> 4faac | 4maac -> 4faac | 4maac -> 4faac |
| FUMAAC | Tyrosine metabolism | fumarylacetoacetase | 3.7.1.2 | H16_B0324/H16_B1670 | unknown/fahA | 4faac + h2o -> acac + fum + h | 4faac + h2o -> acac + fum + h | 4faac + h2o -> acac + fum + h |
| HOMOGD | Tyrosine metabolism | homogentisate 1,2- dioxygenase | 1.13.11.5 | H16_B1671 | hmgA | homogen + o2 -> 4maac + h | homogen + o2 -> 4maac + h | homogen + o2 -> 4maac + h |
| 4HPHED1 | Tyrosine metabolism | 4- hydroxyphenylpyruva te dioxygenase | 1.13.11.27 | H16_B1083 | hpd | 4hpp + o2 -> homogen + co2 | 4hpp + o2 -> homogen + co2 | 4hpp + o2 -> homogen + co2 |
| PAAD5 | Tyrosine metabolism | phenylacpylic acid | 4.1.1 | H16_B2447 | unknown | 2 homogen + 3 o2 + 2 nadph + 6 h -> 2 gtah + 2 co2 + 2 nadp + 4 h2o | 2 homogen + 3 o2 + 2 nadph + 4 h -> 2 gtah + 2 co2 + 2 nadp + 4 h2o | 2 homogen + 3 o2 + 2 nadph + 4 h -> 2 gtah + 2 co2 + 2 nadp + 4 h2o |
| LAAO4 | Tyrosine metabolism | L-amino-acid oxidase | 1.4.3.2 | H16_A0845/H16_A0856 | lao1/lao2 | tyr + h2o + o2 -> 4hpp + nh4 + h2o2 | tyr + h2o + o2 -> 4hpp + nh4 + h2o2 | tyr + h2o + o2 -> 4hpp + nh4 + h2o2 |
| ASPAM5 | Tyrosine | aspartate aminotransferase | 2.6.1.1 | H16_A2857 | unknown | akg + tyr <-> 4hpp + glu | akg + tyr <-> 4hpp + glu | akg + tyr <-> 4hpp + glu |
| MNAO15 | metabolism Tyrosine | monoamine oxidase | | | maoB | dopa + h2o + o2 -> 34dhpac + nh4 + h2o2 | dopa + h2o + o2 -> 34dhpac + nh4 + h2o2 | |
| MNAO4 | metabolism Tyrosine | monoamine oxidase | 1.4.3.4 | H16_A0831 | maoB | motym + h2o + o2 -> 3m4hpa + h2o2 + nh4 | motym + h2o + o2 -> 3m4hpa + h2o2 + | motym + h2o + o2 -> 3m4hpa + h2o2 + nh4 |
| MNAO5 | metabolism Tyrosine | monoamine oxidase | | | maoB | norad + h2o + o2 -> 34dhma + nh4 + h2o2 | nh4 norad + h2o + o2 -> 34dhma + nh4 + h2o2 | |
| MNAO6 | metabolism Tyrosine | monoamine oxidase | | | maoB | adm + h2o + o2 -> 34dhma + methl + h2o2 | adrn + h2o + o2 -> 34dhma + methl + | adrn + h2o + o2 -> 34dhma + methl + h2o2 |
| MNAO7 | metabolism Tyrosine | monoamine oxidase | | _ | | | h2o2 normp + h2o + o2 -> 3m4hpg + nh4 + | |
| MNAO/ | metabolism Tyrosine | monoamine oxidase | | _ | maoB maoB | normp + h2o + o2 -> 3m4hpg + nh4 + h2o2 metp + h2o + o2 -> 3m4hpg + h2o2 + methl | h2o2 metp + h2o + o2 -> 3m4hpg + h2o2 + | normp + h2o + o2 -> 3m4hpg + nh4 + h2o2 metp + h2o + o2 -> 3m4hpq + h2o2 + methl |
| WIIWAOO | metabolism | monoamine oxidase | | U16 A0757/U16 A2220/ | adh/unknown/unkno | | methl | теф + 1120 + 02 -> этнгру + 11202 + теп |
| ALCDd | Tyrosine metabolism | alcohol dehydrogenase | 1.1.1.1 | H16_B0517/H16_B1433/ H16_B1699/H16_B1745/ H16_B1834/H16_B2470 | | 34dhma + nadh + h <-> 34dhpeg + nad | 34dhma + nadh + h <-> 34dhpeg + nad | 34dhma + nadh + h <-> 34dhpeg + nad |
| GENDO | Tyrosine metabolism | gentisate 1,2- dioxygenase | 1.13.11.4 | H16_B0873 | unknown | gensa + o2 -> malpyr + h | gensa + o2 -> malpyr + h | gensa + o2 -> malpyr + h |
| MALPYRI | Tyrosine | maleylpyruvate | 5.2.1.4 | H16_B0875 | unknown | malpyr -> fumpyr | malpyr -> fumpyr | malpyr -> fumpyr |
| ACPYRH | metabolism Tyrosine metabolism | isomerase acylpyruvate hydrolase | 3.7.1.5 | H16_B0428/H16_B0874 | unknown/unknown | fumpyr + h2o -> fum + pyr + h | fumpyr + h2o -> fum + pyr + h | fumpyr + h2o -> fum + pyr + h |
| DHHED2 | Tyrosine | 2,4-dihydroxyhept-2- | 4.1.2 | H16_A0615/H16_B0632/ | hpal1/unknown/unk | dhhedd -> sucsal + pyr | dhhedd -> sucsal + pyr | dhhedd -> sucsal + pyr |
| DITIEDZ | metabolism | aldolase | 4.1.2 | H16_B1223 H16_A0251/H16_A1050/ H16_A1051/H16_A1052/ | nown | diffied -> sucsai + pyi | diffedd -> Sucsai + pyr | uilliedd -> 3dc3ai + pyi |
| NADHDH | Ubiquinone | NADH dehydrogenase | 1.6.5.3 | H16_A1053/H16_A1054/ H16_A1055/H16_A1056/ H16_A1057/H16_A1058/ H16_A1057/H16_A1060/ H16_A1061/H16_A1062/ H16_A1063/ | unknown/nuoA/nuo B/nuoC/nuoD/nuoE/ nuoF/nuoG/nuoH/nu oI/nuoJ/nuoK/nuoL/ nuoM/nuoN/ | uq + 2 h -> uqh2 | uq + 2 h -> uqh2 | uq + 2 h -> uqh2 |
| NAPTS | Ubiquinone Biosynthesis | naphthoate synthase | | H16_B1695 | menB | sbzcoa -> coa + dhn | sbzcoa -> coa + dhn | sbzcoa -> coa + dhn |
| CHMPL | Ubiquinone Biosynthesis | Chorismate pyruvate lyase 3- | 4.1.3.40 | H16_A3165 | unknown | chor -> 4hb + pyr | chor -> 4hb + pyr | chor -> 4hb + pyr |
| DMUQMT | Ubiquinone Biosynthesis | Dimethylubiquinonol 3-methyltransferase | 2.1.1.64 | H16_A0787/H16_A1649 | ubiG/unknown | 2omhmbl + sam -> sah + h + uqh2 | 2omhmbl + sam -> sah + uq | 2omhmbl + sam -> sah + h + uqh2 |
| HBZOCPT | Ubiquinone Biosynthesis | Hydroxybenzoate octaprenyltransferase 2-octaprenyl-6- | 2.5.1 | H16_A3107 | unknown | 4hb + opp -> 3op4hb + ppi | 4hb + opp -> 3op4hb + ppi + h | 4hb + opp -> 3op4hb + ppi + h |
| ОСРНРМ | Ubiquinone Biosynthesis | | 2.1.1.64 | H16_A0787/H16_A1649 | ubiG/unknown | 2op6hp + sam -> 2opmp + sah + h | 2op6hp + sam -> 2opmp + sah + h | 2op6hp + sam -> 2opmp + sah + h |
| OCTMBZM | Ubiquinone Biosynthesis | methoxy- benzoquinol methylase | 2.1.1 | H16_A0445 | ubiE1 | 2ombzl + sam -> 2ommbl + sah + h | 2ombzl + sam -> 2ommbl + sah + h | 2ombzl + sam -> 2ommbl + sah + h |
| ОММВZН | Ubiquinone Biosynthesis | 2-octaprenyl-3- methyl-6-methoxy- 1,4-benzoquinol hydroxylase | 1.14.13 | | | 2ommbl + o2 + nadph + 2 h -> 2omhmbl + nadp + h2o | 2ommbl + o2 + nadph + h -> 2omhmbl + nadp + h2o | 20mmbl + o2 + nadph + h -> 20mhmbl + nadp + h2o |
| OCMPH1 | Ubiquinone Biosynthesis | 2-octaprenyl-6- methoxyphenol hydroxylase | 1.14.13 | H16_A0504 | ubiH | 2opmp + o2 + nadph + 2 h -> 2ombzl + nadp + h2o | 2opmp + o2 + nadph + h -> 2ombzl + nadp + h2o | 2opmp + o2 + nadph + h -> 2ombzl + nadp + h2o |
| OCMPH2 | Ubiquinone Biosynthesis | 2-octaprenyl-6- methoxyphenol hydroxylase | 1.14.13 | H16_A0504 | ubiH | 2 2opmp + o2 -> 2 2ombzl | 2 2opmp + o2 -> 2 2ombzl | 2 2opmp + o2 -> 2 2ombzl |
| ОСМРН3 | Ubiquinone Biosynthesis | 2-octaprenyl-6- methoxyphenol hydroxylase (anaerobic) | 1.14.13 | H16_A0504 | ubiH | 2opmp + 2 atp + 3 h2o + nad -> 2ombzl + 2 adp + h + nadh + 2 pi | 2opmp + 2 atp + 3 h2o + nad -> 2ombzl + 2 adp + 3 h + nadh + 2 pi | 2opmp + 2 atp + 3 h2o + nad -> 2ombzl + 2 adp + 3 h + nadh + 2 pi |
| | | | | | | | | |

| OCHBZDC | Ubiquinone | Octaprenyl- hydroxybenzoate | 4.1.1 | H16_A2859/H16_A3344/ | | 3op4hb + h -> 2opp + co2 | 3op4hb + h -> 2opp + co2 | 3op4hb + h -> 2opp + co2 |
|------------------|---|--|----------|---|--|--|---|--|
| | Biosynthesis Ubiquinone | decarboxylase | | H16_A3366/H16_A3372 | | 2opp + o2 + nadph + 2 h -> 2op6hp + nadp + | 2opp + o2 + nadph + h -> 2op6hp + nadp | 2opp + o2 + nadph + h -> 2op6hp + nadp + |
| OCPPH2 OCPPH1 | Biosynthesis Ubiquinone | hydroxylase 2-Octaprenylphenol | 2.7 | = | ubiB ubiB | h2o | + h2o 2 2opp + o2 -> 2 2op6hp | h2o 2 2opp + o2 -> 2 2op6hp |
| | Biosynthesis Ubiquinone | hydroxylase 2-Octaprenylphenol | | | | | 2opp + 2 atp + 3 h2o + nad -> 2op6hp + 2 | 2opp + 2 atp + 3 h2o + nad -> 2op6hp + 2 adp |
| OCPPH3 | Biosynthesis | hydroxylase (anaerobic) ubiquinone/menaqui | | | ubiB | + h + nadh + 2 pi | adp + 3 h + nadh + 2 pi | + 3 h + nadh + 2 pi |
| UMBM1 | Biosynthesis | none biosynthesis methyltransferase ubiquinone/menaqui | 2.1.1 | H16_A0445 | ubiE1 | 2dmmq8 + sam -> mk + sah | 2dmmq8 + sam -> mk + sah | 2dmmq8 + sam -> mk + sah |
| UMBM2 | Ubiquinone Biosynthesis | | 2.1.1 | H16_A0445 | ubiE1 | pnpq + sam -> pq + sah | pnpq + sam -> pq + sah | pnpq + sam -> pq + sah |
| UBQBM | Ubiquinone Biosynthesis | biosynthesis monooxygenase Coq7 | 1.14.13 | H16_A3283 | unknown | $\begin{array}{l} hpmmbq + o2 + nadph + h \rightarrow hpmhmbq + \\ nadp + h2o \end{array}$ | hpmmbq + o2 + nadph -> hpmhmbq + nadp + h2o | hpmmbq + o2 + nadph -> hpmhmbq + nadp + h2o |
| SPMS3 | Ubiquinone Biosynthesis | spermidine synthase | 2.5.1.16 | H16_A1603/H16_A2204/ H16_A2643/H16_A2647/ | | sama + sprmd -> 5mta + sprm + h | sama + sprmd -> 5mta + sprm + h | sama + sprmd -> 5mta + sprm + h |
| ALHD12 | Ubiquinone Biosynthesis | aldehyde dehydrogenase (NAD+) | 12.1.3 | H16_A0232/H16_A0745/ H16_A1114/H16_A1495/ H16_B0212/H16_B0421/ H16_B0737/H16_B0833/ H16_B1534/H16_B1735/ H16_B1751/H16_B1835/ H16_B1960/H16_B2444 | unknown/unknown/ unknown/unknown/ unknown/unknown/ unknown/unknown/ unknown/unknown/ | bapa + nad + h2o -> bala + nadh + 2 h | bapa + nad + h2o -> bala + nadh + 2 h | bapa + nad + h2o -> bala + nadh + 2 h |
| OMMBZHx | Ubiquinone Biosynthesis | 2-octaprenyl-6- methoxyphenol | 1.14.13 | | | | 2ommbl + 2 atp + 3 h2o + nad -> 2omhmbl + 2 adp + 3 h + nadh + 2 pi | 2ommbl + 2 atp + 3 h2o + nad -> 2omhmbl + 2 adp + 3 h + nadh + 2 pi |
| CAT | Unassigned | hydroxylase catalase | 1.11.1.6 | | | 2 h2o2 -> 2 h2o + o2 | 2 h2o2 -> 2 h2o + o2 | 2 h2o2 -> 2 h2o + o2 |
| MISRXN | unclear reaction Urea Cycle and | unclear reaction N-acetyl-g-glutamyl- | | | | g3p + pyr -> 4mhetz | g3p + pyr -> 4mhetz | g3p + pyr -> 4mhetz |
| ACGPR | Metabolism of amino groups Urea Cycle and | phosphate reductase glutamate-5- | | H16_A0220/H16_B0337 | argC1/argC2 | naglus + nadp + pi <-> acg5p + 3 h + nadph | naglus + nadp + pi <-> acg5p + h + nadph | |
| GLU5SD | Metabolism of amino groups Urea Cycle and | semialdehyde dehydrogenase | 1.2.1.41 | H16_A3136 | proA | glu5p + 3 h + nadph -> glugsal + nadp + pi | glu5p + h + nadph -> glugsal + nadp + pi | gluSp + h + nadph -> glugsal + nadp + pi |
| AGLUS | Metabolism of amino groups Urea Cycle and | N-acetylglutamate synthase | 2.3.1.1 | H16_A2343/H16_A3263 | | accoa + glu -> naglu + coa + h | accoa + glu -> naglu + coa + h | accoa + glu -> naglu + coa + h |
| SPMS1 | Metabolism of amino groups Urea Cycle and | spermidine synthase | 2.5.1.16 | H16_A1603/H16_A2204/ H16_A2643/H16_A2647/ | | sama + ptrc -> 5mta + h + sprmd | sama + ptrc -> 5mta + h + sprmd | sama + ptrc -> 5mta + h + sprmd |
| AORNT | Metabolism of amino groups | acetylornithine transaminase | 2.6.1.11 | H16_A3025 | argD | naom + akg <-> naglus + glu | naorn + akg <-> naglus + glu | naom + akg <-> naglus + glu |
| GLU5K | Urea Cycle and Metabolism of amino groups | glutamate 5-kinase | 2.7.2.11 | H16_A3249 | proB | atp + glu -> adp + glu5p | atp + glu -> adp + glu5p | atp + glu -> adp + glu5p |
| AGLUK | Urea Cycle and Metabolism of amino groups | acetylglutamate kinase | 2.7.2.8 | H16_A0208 | argB | naglu + atp -> acg5p + adp | naglu + atp -> acg5p + adp | naglu + atp -> acg5p + adp |
| ACORND | Urea Cycle and Metabolism of amino groups | acetylornithine deacetylase | 3.5.1.16 | H16_A1454/H16_B0459 | argE1/argE2 | naorn + h2o -> ac + orn | naorn + h2o -> ac + orn | naorn + h2o -> ac + orn |
| AGMT | Urea Cycle and Metabolism of amino groups | agmatinase | 3.5.3.11 | H16_A0044 | speB | agmatine + h2o -> ptrc + urea | agmatine + h2o -> ptrc + urea | agmatine + h2o -> ptrc + urea |
| ARGDC | Urea Cycle and Metabolism of amino groups | arginine decarboxylase | 4.1.1.19 | H16_A2930 | ldcC | arg + h -> agmatine + co2 | arg + h -> agmatine + co2 | arg + h -> agmatine + co2 |
| ACORND | Urea cycle and metabolism of amino groups | acetylornithine deacetylase | 3.5.1.14 | H16_B0491/H16_B1209 | unknown/unknown | naom + h2o -> ac + orn | naorn + h2o -> ac + orn | naorn + h2o -> ac + orn |
| GLUNAC | Urea cycle and metabolism of amino groups | glutamate N- acetyltransferase | 2.3.1.35 | H16_A3263 | argJ | naom + glu <-> orn + naglu | naorn + glu <-> orn + naglu | naom + glu <-> om + naglu |
| ALLPH | Urea cycle and metabolism of amino groups | allophanate hydrolase | 3.5.1.54 | H16_A0125/H16_B1758 | unknown/alpH | u1car + h2o + 3 h -> 2 co2 + 2 nh4 | u1car + h2o + 3 h -> 2 co2 + 2 nh4 | u1car + h2o + 3 h -> 2 co2 + 2 nh4 |
| MNAO13 | Urea cycle and metabolism of amino groups | monoamine oxidase | 1.4.3.4 | H16_A0831 | maoB | acputs + h2o + o2 -> n4aab + nh4 + h2o2 | acputs + h2o + o2 -> n4aab + nh4 + h2o2 | acputs + h2o + o2 -> n4aab + nh4 + h2o2 |
| ALHD10 | Urea cycle and metabolism of amino groups | aldehyde dehydrogenase (NAD+) | 12.1.3 | H16_A0232/H16_A0745/ H16_A1114/H16_A1495/ H16_B0212/H16_B0421/ H16_B0737/H16_B0833/ H16_B1534/H16_B1735/ H16_B1751/H16_B1835/ H16_B1960/H16_B2444 | unknown/unknown/ unknown/unknown/ unknown/unknown/ unknown/unknown/ unknown/unknown/ | n4aab + nad + h2o -> 4aabut + nadh + 2 h | n4aab + nad + h2o -> 4aabut + nadh + 2 h | n4aab + nad + h2o -> 4aabut + nadh + 2 h |
| ALHD11 | Urea cycle and metabolism of amino groups | aldehyde dehydrogenase (NAD+) | 12.1.3 | H16_A0232/H16_A0745/ H16_A1114/H16_A1495/ H16_B0212/H16_B0421/ H16_B0737/H16_B0833/ H16_B1534/H16_B1735/ H16_B1751/H16_B1835/ H16_B1960/H16_B2444 | unknown/unknown/ unknown/unknown/ unknown/unknown/ unknown/unknown/ unknown/unknown/ | 4ab + nadp + h2o -> gaba + nadph + 3 h | 4ab + nadp + h2o -> gaba + nadph + 2 h | 4ab + nadp + h2o -> gaba + nadph + 2 h |
| SPMS2 | Urea cycle and metabolism of amino groups | spermidine synthase | 2.5.1.16 | H16_A1603/H16_A2204/ H16_A2643/H16_A2647/ | | sama + ptrc -> 5mta + sprmd + h | sama + ptrc -> 5mta + sprmd + h | sama + ptrc -> 5mta + sprmd + h |
| AMDS3 | Urea cycle and metabolism of amino groups | amidase | 3.5.1.4 | H16_A1469/H16_B1874/ H16_B2459 | unknown/unknown/ aimE | guadbut + h2o -> guadbutn + nh4 | guadbut + h2o -> guadbutn + nh4 | guadbut + h2o -> guadbutn + nh4 |
| LEUD3 | Valine, Leucine and Isoleucine Biosynthesis | dehydrogenase | 1.4.1.9 | H16_B0449 | unknown | 3mop + nh4 + nadh + h -> ile + nad + h2o | 3mop + nh4 + nadh + h -> ile + nad + h2o | 3mop + nh4 + nadh + h -> ile + nad + h2o |
| LEUD4 | Valine, Leucine and Isoleucine Biosynthesis | leucine dehydrogenase | 1.4.1.9 | ·= · · | unknown | 3mob + nh4 + nadh + h -> val + h2o + nad | 3mob + nh4 + nadh + h -> val + h2o + nad | 3mob + nh4 + nadh + h -> val + h2o + nad |
| 3IPPMD1 | Valine, Leucine and Isoleucine Biosynthesis | 3- isopropylmalate/(R)- 2-methylmalate dehydratase | 4.2.1.33 | (H16_A1236/H16_A1549 /H16_A2621/H16_B0052 /H16_B2275)&(H16_A12 37/H16_A1550/H16_A26 20/H16_B0051/H16_B22 76) | euC4/leu5)&(leuD1/l euD2/leuD3/leuD4/l | r2mm -> 2mm + h2o | r2mm -> 2mm + h2o | r2mm -> 2mm + h2o |
| 3IPPMD2 | Valine, Leucine and Isoleucine Biosynthesis | 2-methylmalate dehydratase | 4.2.1.33 | (H16_A1236/H16_A1549 /H16_A2621/H16_B0052 /H16_B2275)&(H16_A12 37/H16_A1550/H16_A26 20/H16_B0051/H16_B22 76) | euC4/leu5)&(leuD1/l euD2/leuD3/leuD4/l | | 2mm + h2o -> e3mm | 2mm + h2o -> e3mm |
| IPPMD | Valine, Leucine and Isoleucine Biosynthesis | dehydrogenase | 1.1.1.85 | H16_A2133/H16_A2619 | leuB2/leuB3 | e3mm + nad -> obut + co2 + nadh | e3mm + nad -> obut + co2 + nadh | e3mm + nad -> obut + co2 + nadh |
| LEUD1 | Valine, Leucine and Isoleucine degradation | leucine dehydrogenase | 1.4.1.9 | H16_B0449 | unknown | 3rbleu + nad + h2o -> 3o4mp + nh4 + nadh + h | 3rbleu + nad + h2o -> 3o4mp + nh4 + nadh + h | 3rbleu + nad + h2o -> 3o4mp + nh4 + nadh + h |
| | | | | | | | | |

| LEUD2 | Valine, Leucine and Isoleucine degradation | | 1.4.1.9 | H16_B0449 | unknown | leu + h2o + nad <-> 4mop + nh4 + nadh + h | leu + h2o + nad <-> 4mop + nh4 + nadh + h | leu + h2o + nad <-> 4mop + nh4 + nadh + h |
|---------|---|------------------------------------|---------------------|--|--|---|--|---|
| LAAO3 | Valine, Leucine and Isoleucine degradation | L-amino-acid oxidase | 1.4.3.2 | H16_A0845/H16_A0856 | lao1/lao2 | ile + h2o + o2 <-> 3mop + nh4 + h2o2 | ile + h2o + o2 <-> 3mop + nh4 + h2o2 | ile + h2o + o2 <-> 3mop + nh4 + h2o2 |
| DHLLM1 | Valine, Leucine and Isoleucine degradation | | 2.3.1.168 | H16_B2235 | bkdB | coa + s3mbdlipo -> 3mbcoa + dlipo | coa + s3mbdlipo -> 3mbcoa + dlipo | coa + s3mbdlipo -> 3mbcoa + dlipo |
| DHLLM2 | Valine, Leucine and Isoleucine degradation | | 2.3.1.168 | H16_B2235 | bkdB | coa + s2mpdlipo -> 2mppacoa + dlipo | coa + s2mpdlipo -> 2mppacoa + dlipo | coa + s2mpdlipo -> 2mppacoa + dlipo |
| DHLLM3 | Valine, Leucine and Isoleucine degradation | dibudrolinoullucina- | 2.3.1.168 | H16_B2235 | bkdB | coa + s2mbdlipo -> 2mbcoa + dlipo | coa + s2mbdlipo -> 2mbcoa + dlipo | coa + s2mbdlipo -> 2mbcoa + dlipo |
| ISOVC | Valine, Leucine and Isoleucine degradation | isovalend-CoA | 1.3.99.10 | H16_A0167/H16_A1291/ H16_A1972 | ivd1/unknown/ivd2 | 3mbcoa + fad -> 3mccoa + fadh2 | 3mbcoa + fad + h -> 3mccoa + fadh2 | 3mbcoa + fad + h -> 3mccoa + fadh2 |
| ACOADH3 | Valine, Leucine and Isoleucine degradation | | 13.99.3 | H16, A0101,/H16, A0460,/ H16, A0816/H16, A0843,/ H16, A0863/H16, A1067,/ H16, A1068/H16, A1067,/ H16, A1068/H16, A1256/,/ H16, B0014/H16, B0167,/ H16, B0014/H16, B0167,/ H16, B0034/H16, B0167,/ H16, B0034/H16, B0167,/ H16, B0034/H16, B0167,/ H16, B0058/H16, B0167,/ H16, B0058/H16, B0167,/ H16, B0058/H16, B0167,/ H16, B0167,/ H16, B0167,/ H16, B013/H16, B0171,/ H16, B013/H16, B0171,/ H16, B013/H16, B0171,/ H16, B013/H16, B1192/ H16, B013/H16, B1192/ H16, B013/H16, B1192/ H16, B1132/H16, B1192/ H16, B1182/H16, B1192/ H16, B1182/ H16, B1182/ H16, B1182/ H16, B1182/ H16, B1182/ H16, B1182/ H16, | own/unknown/un | 3mbcoa + fad <-> 3mccoa + fadh2 | 3mbcoa + fad + h <-> 3mccoa + fadh2 | 3mbcoa + fad + h <-> 3mccoa + fadh2 |
| ACOADH4 | Valine, Leucine and Isoleucine degradation | | 13.99.3 | H.I. B. 2.158/ H.I. G. A013/H.I. G. A0460/ H.I. G. A0816/H.I. G. A0843/ H.I. G. A0863/H.I. G. A1087/ H.I. G. A1068/H.I. G. A1287/ H.I. G. A1288/H.I. G. A2596/ H.I. G. B0031/H.I. G. B0387/ H.I. G. B0356/H.I. G. B0386/ H.I. G. B0384/H.I. G. B0387/ H.I. G. B0384/H.I. G. B0386/ H.I. G. B0580/H.I. G. B0400/ H.I. G. B0580/H.I. G. B0660/ H.I. G. B0661/H.I. G. B0660/ H.I. G. B0681/H.I. G. B0751/ H.I. G. B0751/H.I. G. B0751/ H.I. G. B1326/H.I. G. B1326/ H.I. G. B1326/H.I. G. B1326/ H.I. G. B1326/H.I. G. B1326/ H.I. G. B1326/H.I. G. B1326/ H.I. G. B1326/H.I. G. B1327/ H.I. G. B1326/H.I. G. B1357/ H.I. G. B1326/H.I. G. B1557/ H.I. G. B1326/H.I. G. B156/H.I. G. B156 | unknown/acaD/unkn own/unknown/unkn own/unknown/unkn own/unknown/unkn own/unknown/unkn own/unknown/unknown/ unknown/unknown/ | .2mppacoa + fad <-> 2mp2ecoa + fadh2 | 2mppacoa + fad + h <-> 2mp2ecoa + fadh2 | 2mppacoa + fad + h <-> 2mp2ecoa + fadh2 |
| ACOADHS | Valine, Leucine and Isoleucine degradation | acyl-CoA dehydrogenase | 13.99.3 | H16. A0101/H16. A0460, H16. A0816/H16. A0843, H16. A0863/H16. A10863, H16. A10863/H16. A10870, H16. A10864/H16. A10870, H16. B1014/H16. B01670, H16. B0301/H16. B01670, H16. B0307/H16. B01670, H16. B0307/H16. B01670, H16. B0307/H16. B01670, H16. B01670, | own/unknown/unkn /unknown/unknown/ /unknown/unknown/ /unknown/unknown/ unknown/unknown/ | 2mbcoa + fad <-> 2m2ecoa + fadh2 | 2mbcoa + fad + h <-> 2m2ecoa + fadh2 | 2mbcoa + fad + h <-> 2m2ecoa + fadh2 |
| BTCOAD1 | Valine, Leucine and Isoleucine degradation Valine, Leucine and | dehydrogenase | 1.3.99.2 | | unknown/unknown/ unknown/unknown | 2 2mppacoa + o2 -> 2 2mp2ecoa + 2 h2o | 2 2mppacoa + o2 -> 2 2mp2ecoa + 2 h2o | 2 2mppacoa + o2 -> 2 2mp2ecoa + 2 h2o |
| BTCOAD2 | Isoleucine degradation Valine, Leucine and | dehydrogenase | 1.3.99.2 | H16_B0752/H16_B0850/ | unknown/unknown/ unknown/unknown | 2 2mbcoa + o2 -> 2 2m2ecoa + 2 h2o | 2 2mbcoa + o2 -> 2 2m2ecoa + 2 h2o | 2 2mbcoa + o2 -> 2 2m2ecoa + 2 h2o |
| HIBD | Isoleucine degradation Valine, Leucine and | dehydrogenase | 1.1.1.31 | H16_B1190/H16_B1657/ | | hibut + nad <-> mmsa + nadh + h | hibut + nad <-> mmsa + nadh + h | hibut + nad <-> mmsa + nadh + h |
| ACCOAA1 | Isoleucine degradation Valine, Leucine and | acetyl-CoA acyltransferase | 2.3.1.16 | H16_A0462/H16_A1290/ H16_B0200 | unknown/unknown/ pcaF | coa + 2maaccoa -> ppcoa + accoa | coa + 2maaccoa -> ppcoa + accoa | coa + 2maaccoa -> ppcoa + accoa |
| BAPT2 | Isoleucine degradation | | 2.6.1.18 | H16_A0272 | aptA | ala + mmsa <-> pyr + l3aibn | ala + mmsa <-> pyr + I3aibn | ala + mmsa <-> pyr + l3aibn |
| ALHD6 | Valine, Leucine and Isoleucine degradation | | 12.1.3 | H16_A0232/H16_A0745/ H16_A1114/H16_A1495/ H16_B0212/H16_B0421/ H16_B0737/H16_B0833/ H16_B1534/H16_B1735/ H16_B1751/H16_B1835/ H16_B1960/H16_B2444 | unknown/unknown/ unknown/unknown/ unknown/unknown/ unknown/unknown/ unknown/unknown/ | mmsa + nad + h2o -> mm + nadh + h | mmsa + nad + h2o -> mm + nadh + 2 h | mmsa + nad + h2o -> mm + nadh + 2 h |
| MMCS | Valine, Leucine and Isoleucine degradation | unclear reaction | unclear reaction | unclear reaction | unclear reaction | mm + coa -> mmcoa-R + h2o | mm + coa + h -> mmcoa-R + h2o | mm + coa + h -> mmcoa-R + h2o |
| MMCE | Valine, Leucine, and Isoleucine Degradation | methylmalonyl-CoA epimerase | 5.1.99.1 | H16_A3551 | unknown | mmcoa-R <-> mmcoa-S | mmcoa-R <-> mmcoa-S | mmcoa-R <-> mmcoa-S |
| ММСМ | Valine, Leucine, and Isoleucine Degradation | Methylmalonyl-CoA mutase | 5.4.99.2 | (H16_A0280/H16_A1949)&H16_B1841&H16_B18 42 | | succoa -> mmcoa-R | succoa -> mmcoa-R | succoa -> mmcoa-R |
| IPMALD | Valine, Leucine, and Isoleucine Metabolism | 3-isopropylmalate dehydrogenase | 1.1.1.85 | | leuB1/leuB2/leuB3/ | 3c2hmp + nad -> oicap + h + nadh | 3c2hmp + nad -> oicap + h + nadh | 3c2hmp + nad -> oicap + h + nadh |

| KARIS1 | Valine, Leucine, and Isoleucine | ketol-acid reductoisomerase | 1.1.1.86 | H16_A1037 | ilvC | dhmva + nadp <-> alac-S + 2 h + nadph | dhmva + nadp <-> alac-S + h + nadph | dhmva + nadp <-> alac-S + h + nadph |
|--------------|--|--|-----------------|---|---|---|---|---|
| KARIS2 | Metabolism Valine, Leucine, and Isoleucine | ketol-acid | 1.1.1.86 | H16_A1037 | ilvC | abut + 2 h + nadph <-> dhmp + nadp | abut + h + nadph <-> dhmp + nadp | abut + h + nadph <-> dhmp + nadp |
| ILETA | Metabolism Valine, Leucine, and Isoleucine | reductoisomerase isoleucine | | H16_A0561 | unknown | akq + ile <-> 3mop + qlu | akq + ile <-> 3mop + qlu | akg + ile <-> 3mop + glu |
| LEUTA | Metabolism Valine, Leucine, and Isoleucine | transaminase leucine transaminase | | H16_A0561 | unknown | 4mop + glu -> akg + leu | 4mop + glu -> akg + leu | 4mop + glu -> akg + leu |
| VALTA | Metabolism Valine, Leucine, and Isoleucine | | | H16 A0561 | unknown | | | |
| | Metabolism Valine, Leucine, | valine transaminase 2-isopropylmalate | | - | | akg + val <-> 3mob + glu | akg + val <-> 3mob + glu | akg + val <-> 3mob + glu |
| IPPMS | and Isoleucine Metabolism Valine, Leucine, | synthase | 2.3.3.13 | H16_A1041/H16_B0081 H16_A1035/ | ilv8/(ilvH&unknown | 3mob + accoa + h2o -> 3c3hmp + coa + h | 3mob + accoa + h2o -> 3c3hmp + coa + h | 3mob + accoa + n2o -> 3c3hmp + coa + n |
| ACLACS | and Isoleucine Metabolism | acetolactate synthase | | (H16_A1036&H16_A223 1&H16_B0313&H16_B0 735&H16_B2452) (H16_A1236&H16_A123 | &unknown&unknow n&unknown) | h + 2 pyr -> alac-S + co2 | h + 2 pyr -> alac-S + co2 | h + 2 pyr -> alac-S + co2 |
| IPMALD1 | Valine, Leucine, and Isoleucine Metabolism | 3-isopropylmalate dehydratase | 4.2.1.33 | 7)/(H16_A1549&H16_A1 550)/(H16_A2620&H16_A2621)/(H16_B0051&H16_B0052)/(H16_B2275&H16_B2276) (H16_A1236&H16_A123 | 2&leuD2)/(leuD3≤ uC3)/(leuD4&leuC4)/ | | 3c2hmp <-> 2ippm + h2o | 3c2hmp <-> 2lppm + h2o |
| IPMALD2 | Valine, Leucine, and Isoleucine Metabolism | 3-isopropylmalate dehydratase | 4.2.1.33 | 7)/(H16_A1549&H16_A1 550)/(H16_A2620&H16_ A2621)/(H16_B0051&H1 6_B0052)/(H16_B2275& H16_B2276) | 2&leuD2)/(leuD3≤ uC3)/(leuD4&leuC4)/ | | 2ippm + h2o <-> 3c3hmp | 2ippm + h2o <-> 3c3hmp |
| DHADT1 | Valine, Leucine, and Isoleucine Metabolism | dihydroxy-acid dehydratase | | H16_A2987/H16_B0280 | unknown/unknown | dhmva -> 3mob + h2o | dhmva -> 3mob + h2o | dhmva -> 3mob + h2o |
| ACHBUTS | Valine, Leucine, and Isoleucine Metabolism | 2-aceto-2- hydroxybutanoate synthase | 2.2.1.6 | H16_A1035/ (H16_A1036&H16_A223 1&H16_B0313&H16_B0 735&H16_B2452) | ilvB/(ilvH&unknown &unknown&unknow n&unknown) | obut + h + pyr -> abut + co2 | obut + h + pyr -> abut + co2 | obut + h + pyr -> abut + co2 |
| DHADT2 | Valine, Leucine, and Isoleucine Metabolism | ihydroxy-acid dehydratase | 4.2.1.9 | H16_A2987/H16_B0280 | unknown/unknown | dhmp -> 3mop + h2o | dhmp -> 3mop + h2o | dhmp -> 3mop + h2o |
| OMCDC | Valine, Leucine, and Isoleucine Metabolism | 2-Oxo-4-methyl-3- carboxypentanoate decarboxylation | spontaneo us | spontaneous | spontaneous | oicap + h -> 4mop + co2 | oicap + h -> 4mop + co2 | oicap + h -> 4mop + co2 |
| PDX5PO | Vitamine B6 metabolism | pyridoxine 5'- phosphate oxidase | 1.4.3.5 | H16_A2802 | pdxH | o2 + pdx5p -> h2o2 + pydx5p | o2 + pdx5p -> h2o2 + pydx5p | o2 + pdx5p -> h2o2 + pydx5p + h |
| PYAM5PO | Vitamine B6 metabolism | pyridoxamine 5'- phosphate oxidase O-Phospho-4- | 1.4.3.5 | H16_A2802 | pdxH | h2o + o2 + pyam5p -> h2o2 + nh4 + pydx5p | h2o + o2 + pyam5p -> h2o2 + nh4 + pydx5p | h2o + o2 + pyam5p -> h2o2 + nh4 + pydx5p + h |
| OHPBAKGT | Vitamine B6 metabolism | hydroxy-L- threonine:2- oxoglutarate aminotransferase | 2.6.1.52 | H16_A0791 | serC | glu + ohpb <-> akg + pht | glu + ohpb <-> akg + pht | glu + ohpb <-> akg + pht |
| HTHRS | Vitamine B6 metabolism | 4-Hydroxy-L- threonine synthase | 4.2.3.1 | H16_A2265 | thrC | h2o + pht -> 4hlt + pi | h2o + pht -> 4hlt + pi | h2o + pht -> 4hlt + pi |
| DALATA | Vitamine B6 | D-alanine | 2.6.1.54 | | | dala + pydx5p -> pyam5p + pyr | dala + pydx5p -> pyam5p + pyr | dala + pydx5p + h -> pyam5p + pyr |
| | metabolism Vitamine B6 | transaminase Erythrose 4- | | | | | | |
| E4PDH | metabolism Vitamine B6 | phosphate dehydrogenase pyridoxal-5'- | 1.2.1.72 | | | e4p + h2o + nad <-> er4p + 2 h + nadh | e4p + h2o + nad <-> er4p + 2 h + nadh | e4p + h2o + nad <-> er4p + 2 h + nadh |
| P5PPR | metabolism | phosphate phosphohydrolase | 3.1.3.74 | | | h2o + pyam5p -> pi + pdla | h2o + pyam5p -> pi + pdla | h2o + pyam5p -> pi + pdla |
| PX5PS | Vitamine B6 metabolism | Pyridoxine 5'- phosphate synthase | 26992 | (H16_A0513/H16_B0216 /H16_B0319)/(H16_A255 2) | | dx5p + nad + pht -> co2 + h + 2 h2o + nadh + pdx5p + pi | dx5p + nad + pht -> co2 + h + 2 h2o + nadh + pdx5p + pi | dx5p + nad + pht -> co2 + h + 2 h2o + nadh + pdx5p + pi |
| ER4PD | Vitamine B6 metabolism | Erythronate 4- phosphate (4per) dehydrogenase | 1.1.1.290 | | | er4p + nad <-> h + nadh + ohpb | er4p + nad <-> h + nadh + ohpb | er4p + nad <-> h + nadh + ohpb |
| PYR5OXM | Vitamine B6 metabolism | pyridoxamine 5'- phosphate oxidase | 1.4.3.5 | H16_A2802 | pdxH | pdla + h2o + o2 <-> pl + nh4 + h2o2 | pdla + h2o + o2 <-> pl + nh4 + h2o2 | pdla + h2o + o2 <-> pl + nh4 + h2o2 + h |
| PYR5OXX | Vitamine B6 metabolism | pyridoxamine 5'- phosphate oxidase | 1.4.3.5 | H16_A2802 | pdxH | pydxn + o2 <-> pl + h2o2 | pydxn + o2 <-> pl + h2o2 | pydxn + o2 <-> pl + h2o2 + h |
| HTHRPD | Vitamine B6 | 4-hydroxythreonine- 4-phosphate | 1.1.1.262 | H16_A0513/H16_B0216/ | pdxA1/pdxA2/pdxA3 | pht + nad -> ao4pob + nadh + h | pht + nad -> ao4pob + nadh + h | pht + nad -> ao4pob + nadh + 2 h |
| SPOTN | metabolism Vitamine B6 | dehydrogenase | | H16_B0319 | | ao4pob + h -> 3a2op + co2 | | |
| 12PPDt | metabolism Transport, | spontaneous S-Propane-1,2-diol | | | | 12ppd-S e <-> 12ppd-S | ao4pob + h -> 3a2op + co2 12ppd-S e <-> 12ppd-S | ao4pob + h -> 3a2op + co2 12ppd-S e <-> 12ppd-S |
| | Extracellular Transport, | facilitated transport NMN transport via | | | | Pro ser | FF- 12-1 | 111111111111111111111111111111111111111 |
| NMNt7 | Extracellular Transport, | NMN glycohydrolase acetaldehyde | | | | h2o + namn_e -> h + nam + r5p | h2o + namn_e -> h + nam + r5p | h2o + namn_e -> h + nam + r5p |
| ACALDt | Extracellular Transport, | reversible transport | | | | acal_e <-> acal | acal_e <-> acal | acal_e <-> acal |
| GUAt1 | Extracellular | Guanine transport | | | | gn_e <-> gn | gn_e <-> gn | gn_e <-> gn |
| HYXNt | Transport, Extracellular | Hypoxanthine transport | | | | hyxn_e <-> hyxn | hyxn_e <-> hyxn | hyxn_e <-> hyxn |
| XANt1 | Transport, Extracellular | xanthine reversible transport | | | | xan_e <-> xan | xan_e <-> xan | xan_e <-> xan |
| NACUP | Transport, Extracellular | Nicotinic acid uptake | | | | nac_e -> nac | nac_e -> nac | nac_e -> nac |
| ASNabc | Transport, Extracellular | L-asparagine transport via ABC system | | | | asn_e + atp + h2o -> adp + asn + pi | asn_e + atp + h2o -> adp + asn + h + pi | asn_e + atp + h2o -> adp + asn + h + pi |
| ASNtr | Transport, Extracellular | L-asparagine reversible transport via proton symport | | | | asn_e + h_e <-> asn + h | asn_e + h_e <-> asn + h | asn_e + h_e <-> asn + h |
| DAPabc | Transport, Extracellular | M-diaminopimelic acid ABC transport | | | | 26dap-M_e + atp + h2o -> 26dap-M + adp + pi | 26dap-M_e + atp + h2o -> 26dap-M + adp + h + pi | 26dap-M_e + atp + h2o -> 26dap-M + adp + h + pi |
| CYSabc | Transport, Extracellular | L-cysteine transport via ABC system | | | | atp + cys_e + h2o -> adp + cys + pi | atp + cys_e + h2o -> adp + cys + h + pi | atp + cys_e + h2o -> adp + cys + h + pi |
| ACtr | Transport, Extracellular | acetate reversible transport via proton | | | | ac_e + h_e <-> ac + h | ac_e + h_e <-> ac + h | ac_e + h_e <-> ac + h |
| ETOHtr | Transport, Extracellular | symport ethanol reversible transport via proton | | | | eth + h -> eth_e + h_e | eth + h -> eth_e + h_e | eth + h -> eth_e + h_e |
| PYRtr | Transport, Extracellular | symport pyruvate reversible transport via proton | | | | h_e + pyr_e <-> h + pyr | h_e + pyr_e <-> h + pyr | h_e + pyr_e <-> h + pyr |
| O2t | Transport, | symport o2 transport | | | | o2_e <-> o2 | o2_e <-> o2 | o2_e <-> o2 |
| CO2t | Extracellular Transport, | (diffusion) CO2 transporter via | | | | co2 e <-> co2 | co2 e <-> co2 | co2 e <-> co2 |
| CO2t H2Ot | Extracellular Transport, | diffusion H2O transport via | | | | _ | _ | _ |
| ⊓∠Ut | Extracellular | diffusion Dihydroxyacetone | | | | h2o_e <-> h2o | h2o_e <-> h2o | h2o_e <-> h2o |
| DHAt | Transport, Extracellular | transport via facilitated diffusion | | | | glyn_e <-> glyn | glyn_e <-> glyn | glyn_e <-> glyn |
| NH3t | Transport, Extracellular | ammonia reversible transport | | | | nh4_e <-> nh4 | nh4_e <-> nh4 | nh4_e <-> nh4 |
| | canacennidi | чанэрогі | | | | | | |

| ARBtr | Transport, Extracellular | L-arabinose transport via proton symport | larabinose_e + h_e <-> larabinose + h | larabinose_e + h_e <-> larabinose + h | larabinose_e + h_e <-> larabinose + h |
|----------|-----------------------------|---|--|---|--|
| ARBabc | Transport, Extracellular | L-arabinose transport via ABC system | larabinose_e + atp + h2o -> adp + larabinose + pi | larabinose_e + atp + h2o -> adp + larabinose + h + pi | larabinose_e + atp + h2o -> adp + larabinose + h + pi |
| HIStr | Transport, Extracellular | L-histidine reversible transport via proton | h_e + his_e <-> h + his | h_e + his_e <-> h + his | h_e + his_e <-> h + his |
| PHEtr | Transport, | symport L-phenylalanine reversible transport | h_e + phe_e <-> h + phe | h e + phe e <-> h + phe | h_e + phe_e <-> h + phe |
| | Extracellular Transport, | via proton symport L-leucine reversible | | | |
| LEUtr | Extracellular | transport via proton symport L-valine reversible | h_e + leu_e <-> h + leu | h_e + leu_e <-> h + leu | h_e + leu_e <-> h + leu |
| VALtr | Transport, Extracellular | transport via proton symport | h_e + val_e <-> h + val | h_e + val_e <-> h + val | h_e + val_e <-> h + val |
| ILEtr | Transport, Extracellular | L-isoleucine reversible transport via proton symport | h_e + ile_e <-> h + ile | h_e + ile_e <-> h + ile | h_e + ile_e <-> h + ile |
| CBL1abc | Transport, Extracellular | Cob(1)alamin transport via ABC system | atp + cbl1_e + h2o -> adp + cbl1 + pi | atp + cbl1_e + h2o -> adp + cbl1 + h + pi | atp + cbl1_e + h2o -> adp + cbl1 + h + pi |
| CADVt | Transport, Extracellular | Lysine/Cadaverine antiporter | 15dap + h_e + lys_e -> 15dap_e + h + lys | 15dap + h_e + lys_e -> 15dap_e + h + lys | 15dap + h_e + lys_e -> 15dap_e + h + lys |
| CRNt7 | Transport, Extracellular | Carnitine/butyrobetai ne antiporter sodium proton | crn_e + gbbtn -> crn + gbbtn_e | crn_e + gbbtn -> cm + gbbtn_e | crn_e + gbbtn -> crn + gbbtn_e |
| NAt_1 | Transport, Extracellular | antiporter (H:NA is 1:1) | h_e + na <-> h + na_e | h_e + na <-> h + na_e | h_e + na <-> h + na_e |
| CITtsuc | Transport, Extracellular | Citrate transport via succinate antiport | cit_e + succ -> cit + succ_e | cit_e + succ -> cit + succ_e | cit_e + succ -> cit + succ_e |
| CSNt2 | Transport, Extracellular | cytosine transport in via proton symport N-Acetyl-D- | ct_e + h_e -> ct + h | ct_e + h_e -> ct + h | ct_e + h_e -> ct + h |
| ACGApts | Transport, Extracellular | glucosamine transport via PEP:Pyr | naga_e + pep -> naga6p + pyr | naga_e + pep -> naga6p + pyr + h | naga_e + pep -> naga6p + pyr + h |
| DALAtr | Transport, | PTS D-alanine transport | dala_e + h_e <-> dala + h | dala_e + h_e <-> dala + h | dala_e + h_e <-> dala + h |
| DSERtr | Extracellular Transport, | via proton symport D-serine transport | h_e + dser_e <-> h + dser | h_e + dser_e <-> h + dser | h_e + dser_e <-> h + dser |
| GLYtr | Extracellular Transport, | via proton symport glycine reversible transport via proton | gly_e + h_e <-> gly + h | gly_e + h_e <-> gly + h | gly_e + h_e <-> gly + h |
| SULabo | Extracellular Transport, | symport sulfate transport via | atp + h2o + so4_e -> adp + pi + so4 | atp + h2o + so4_e -> adp + h + pi + so4 | atp + h2o + so4_e -> adp + h + pi + so4 |
| ASPt_2 | Extracellular Transport, | ABC system Aspartate transport via proton symport | asp_e + 2 h_e -> asp + 2 h | asp_e + 2 h_e -> asp + 2 h | asp_e + 2 h_e -> asp + 2 h |
| | Extracellular Transport, | (2 H) Fumarate transport | | | |
| FUMt_2 | Extracellular | via proton symport (2 H) | fum_e + 2 h_e -> fum + 2 h | fum_e + 2 h_e -> fum + 2 h | fum_e + 2 h_e -> fum + 2 h |
| MALt_2 | Transport, Extracellular | Malate transport via proton symport (2 H) succinate transport | 2 h_e + mal_e -> 2 h + mal | 2 h_e + mal_e -> 2 h + mal | 2 h_e + mal_e -> 2 h + mal |
| SUCCt_2 | Transport, Extracellular | via proton symport (2 H) | 2 h_e + succ_e -> 2 h + succ | 2 h_e + succ_e -> 2 h + succ | 2 h_e + succ_e -> 2 h + succ |
| ASPt_3 | Transport, Extracellular | L-asparate transport via proton symport (3 H) | asp_e + 3 h_e -> asp + 3 h | asp_e + 3 h_e -> asp + 3 h | asp_e + 3 h_e -> asp + 3 h |
| MALt_3 | Transport, Extracellular | Malate transport via proton symport (3 H) | 3 h_e + mal_e -> 3 h + mal | 3 h_e + mal_e -> 3 h + mal | 3 h_e + mal_e -> 3 h + mal |
| SUCCt_3 | Transport, Extracellular | Succintate transport via proton symport (3 H) | 3 h_e + succ_e -> 3 h + succ | 3 h_e + succ_e -> 3 h + succ | 3 h_e + succ_e -> 3 h + succ |
| SUCCet | Transport, Extracellular | Succinate efflux via proton symport | h + succ -> h_e + succ_e | h + succ -> h_e + succ_e | h + succ -> h_e + succ_e |
| FUMt_3 | Transport, Extracellular | Fumarate transport via proton symport (3 H) | fum_e + 3 h_e -> fum + 3 h | fum_e + 3 h_e -> fum + 3 h | fum_e + 3 h_e -> fum + 3 h |
| SUCFUMt | Transport, Extracellular | succinate:fumarate antiporter | fum_e + succ <-> fum + succ_e | fum_e + succ <-> fum + succ_e | fum_e + succ <-> fum + succ_e |
| GALCTNtr | Transport, Extracellular | D-galactonate transport via proton symport, reversible | dgalctn_e + h_e <-> dgalctn + h | dgalctn_e + h_e <-> dgalctn + h | dgalctn_e + h_e <-> dgalctn + h |
| GLCURtr | Transport, Extracellular | D-glucuronate transport via proton symport, reversible | dgluc_e + h_e <-> dgluc + h | dgluc_e + h_e <-> dgluc + h | dgluc_e + h_e <-> dgluc + h |
| OCDCAt | Transport, Extracellular | Octadecanoate transport via proton | h_e + c180_e -> h + c180 | h_e + c180_e -> h + c180 | h_e + c180_e -> h + c180 |
| HDCAt | Transport, Extracellular | symport Hexadecanoate transport via proton | h_e + c160_e -> h + c160 | h_e + c160_e -> h + c160 | h_e + c160_e -> h + c160 |
| TTDCAt | Transport, | symport Tetradecanoate transport via proton | h_e + c140_e -> h + c140 | h_e + c140_e -> h + c140 | h_e + c140_e -> h + c140 |
| FE2abc | Extracellular Transport, | symport iron (II) transport via | | | |
| | Extracellular Transport, | ABC system formate transport via | atp + fe2_e + h2o -> adp + fe2 + pi | atp + fe2_e + h2o -> adp + fe2 + h + pi | atp + fe2_e + h2o -> adp + fe2 + h + pi |
| FORt | Extracellular Transport, | diffusion L-fucose transport | formate_e <-> formate | formate_e <-> formate | formate_e <-> formate |
| FUCt | Extracellular Transport, | via proton symport 4-aminobutyrate | fuc_e + h_e <-> fuc + h | fuc_e + h_e <-> fuc + h | fuc_e + h_e <-> fuc + h |
| ABUTt | Extracellular | transport in via proton symport | gaba_e + h_e -> gaba + h | gaba_e + h_e -> gaba + h | gaba_e + h_e -> gaba + h |
| GALTpts | Transport, Extracellular | Galactitol transport via PEP:Pyr PTS L-glutamine | galt_e + pep -> galt1p + pyr | galt_e + pep -> galt1p + pyr + h | galt_e + pep -> galt1p + pyr + h |
| GLNabc | Transport, Extracellular | transport via ABC system | atp + gln_e + h2o -> adp + gln + pi | $atp + gln_e + h2o -> adp + gln + h + pi$ | atp + gln_e + h2o -> adp + gln + h + pi |
| GLYCt | Transport, Extracellular | glycerol transport via channel | gl <-> gl_e | gl <-> gl_e | gl <-> gl_e |
| GLYALDt | Transport, Extracellular | Glyceraldehyde facilitated diffusion | t3_e <-> t3 | t3_e <-> t3 | t3_e <-> t3 |
| UREAt | Transport, Extracellular | Urea transport via facilitate diffusion | urea_e <-> urea | urea_e <-> urea | urea_e <-> urea |
| GLYC3Pt | Transport, Extracellular | Glycerol-3-phosphate : phosphate antiporter | glyc3p_e + pi -> glyc3p + pi_e | glyc3p_e + pi -> glyc3p + pi_e | glyc3p_e + pi -> glyc3p + pi_e |
| ASPabc | Transport, Extracellular | L-aspartate transport via ABC system | asp_e + atp + h2o -> adp + asp + pi | $asp_e + atp + h2o \rightarrow adp + asp + h + pi$ | $asp_e + atp + h2o \rightarrow adp + asp + h + pi$ |
| GLUabc | Transport, Extracellular | L-glutamate transport via ABC system | atp + glu_e + h2o -> adp + glu + pi | atp + glu_e + h2o -> adp + glu + h + pi | atp + glu_e + h2o -> adp + glu + h + pi |
| ASPt | Transport, Extracellular | L-aspartate transport in via proton | asp_e + h_e -> asp + h | asp_e + h_e -> asp + h | asp_e + h_e -> asp + h |
| GLUtr | Transport, | symport L-glutamate transport via proton | glu_e + h_e <-> glu + h | glu_e + h_e <-> glu + h | glu_e + h_e <-> glu + h |
| | Extracellular | symport, reversible | | | |

| GLUt | Transport, | Na+/glutamate | glu_e + na_e -> glu + na | glu_e + na_e -> glu + na | glu_e + na_e -> glu + na |
|------------|--|--|---|--|---|
| ORNabc | Extracellular Transport, | symport ornithine transport | atp + h2o + orn e -> adp + orn + pi | atp + h2o + om_e -> adp + h + om + pi | atp + h2o + orn_e -> adp + h + orn + pi |
| | Extracellular Transport, | via ABC system L-arginine transport | | | |
| ARGabc | Extracellular Transport, | via ABC system L-histidine transport | arg_e + atp + h2o -> adp + arg + pi | arg_e + atp + h2o -> adp + arg + h + pi | arg_e + atp + h2o -> adp + arg + h + pi |
| HISabc | Extracellular | via ABC system | atp + h2o + his_e -> adp + his + pi | atp + h2o + his_e -> adp + h + his + pi | atp + h2o + his_e -> adp + h + his + pi |
| LYSabc | Transport, Extracellular | L-lysine transport via ABC system | atp + h2o + lys_e -> adp + lys + pi | atp + h2o + lys_e -> adp + h + lys + pi | atp + h2o + lys_e -> adp + h + lys + pi |
| IDONtr | Transport, Extracellular | L-idonate transport via proton symport, reversible | h_e + idon_e <-> h + idon | h_e + idon_e <-> h + idon | h_e + idon_e <-> h + idon |
| GLCNtr | Transport, Extracellular | D-gluconate transport via proton symport, reversible | gluc_e + h_e <-> gluc + h | gluc_e + h_e <-> gluc + h | gluc_e + h_e <-> gluc + h |
| DDGLCNtr | Transport, Extracellular | 2-dehydro-3-deoxy- D-gluconate transport via proton | kdg_e + h_e <-> kdg + h | kdg_e + h_e <-> kdg + h | kdg_e + h_e <-> kdg + h |
| Kabc | Transport, | symport, reversible Potassium ABC | atp + h2o + k_e -> adp + k + pi | atp + h2o + k_e -> adp + h + k + pi | atp + h2o + k e -> adp + h + k + pi |
| | Extracellular Transport, | transporter Lactose transport via | | | |
| LCTSt | Extracellular | proton symport L-isoleucine | h_e + lactose_e <-> h + lactose | h_e + lactose_e <-> h + lactose | h_e + lactose_e <-> h + lactose |
| ILEabc | Transport, Extracellular | transport via ABC system | atp + h2o + ile_e -> adp + ile + pi | atp + h2o + ile_e -> adp + h + ile + pi | atp + h2o + ile_e -> adp + h + ile + pi |
| THRabc | Transport, Extracellular | L-threonine transport via ABC system | atp + h2o + thr_e -> adp + pi + thr | atp + h2o + thr_e -> adp + h + pi + thr | atp + h2o + thr_e -> adp + h + pi + thr |
| ALAabc | Transport, Extracellular | L-alanine transport via ABC system | ala_e + atp + h2o -> adp + ala + pi | ala_e + atp + h2o -> adp + ala + h + pi | ala_e + atp + h2o -> adp + ala + h + pi |
| VALabc | Transport, Extracellular | L-valine transport via ABC system | atp + h2o + val_e -> adp + pi + val | $atp + h2o + val_e \rightarrow adp + h + pi + val$ | $atp + h2o + val_e -> adp + h + pi + val$ |
| LEUabc | Transport, Extracellular | L-leucine transport via ABC system | atp + h2o + leu_e -> adp + leu + pi | atp + h2o + leu_e -> adp + h + leu + pi | atp + h2o + leu_e -> adp + h + leu + pi |
| DLACt | Transport, | D-lactate transport | h_e + lac_e <-> h + lac | h_e + lac_e <-> h + lac | h_e + lac_e <-> h + lac |
| GLYCLTtr | Extracellular Transport, Extracellular | via proton symport glycolate transport via proton symport, | glycolate_e + h_e <-> glycolate + h | glycolate_e + h_e <-> glycolate + h | glycolate_e + h_e <-> glycolate + h |
| | Transport, | reversible L-lactate reversible | | | |
| LLACtr | Extracellular | transport via proton symport L-lysine reversible | h_e + llac_e <-> h + llac | h_e + llac_e <-> h + llac | h_e + llac_e <-> h + llac |
| LYStr | Transport, Extracellular | transport via proton symport maltopentaose | h_e + lys_e <-> h + lys | h_e + lys_e <-> h + lys | h_e + lys_e <-> h + lys |
| MALTPTabc | Transport, Extracellular | transport via ABC system maltotetraose | atp + h2o + maltpt_e -> adp + maltpt + pi | atp + h2o + maltpt_e -> adp + h + maltpt + pi | atp + h2o + maltpt_e -> adp + h + maltpt + pi |
| MALTTTRabc | Transport, Extracellular | transport via ABC system maltohexaose | atp + h2o + mltttr_e -> adp + mltttr + pi | $atp + h2o + mltttr_e -> adp + h + mltttr + pi$ | atp + h2o + mltttr_e -> adp + h + mltttr + pi |
| MALTHXabc | Transport, Extracellular | transport via ABC system | atp + h2o + mlthx_e -> adp + mlthx + pi | $atp + h2o + mlthx_e -> adp + h + mlthx + pi$ | atp + h2o + mlthx_e -> adp + h + mlthx + pi |
| MALTTRabc | Transport, Extracellular | Maltotriose transport via ABC system | atp + h2o + mlttr_e -> adp + mlttr + pi | atp + h2o + mlttr_e -> adp + h + mlttr + pi | atp + h2o + mlttr_e -> adp + h + mlttr + pi |
| FRUpts2 | Transport, Extracellular | Fructose transport via PEP:Pyr PTS (f6p generating) | fru_e + pep -> f6p + pyr | fru_e + pep -> f6p + pyr + h | fru_e + pep -> f6p + pyr + h |
| MANpts | Transport, Extracellular | D-mannose transport via PEP:Pyr PTS | man_e + pep -> man6p + pyr | man_e + pep -> man6p + pyr + h | man_e + pep -> man6p + pyr + h |
| GAMpts | Transport, Extracellular | D-glucosamine transport via PEP.Pyr PTS | gam_e + pep -> ga6p + pyr | gam_e + pep -> ga6p + pyr + h | gam_e + pep -> ga6p + pyr + h |
| MELIBt | Transport, Extracellular Transport, | melibiose transport in via symport L-methionine | h_e + meli_e -> h + meli | h_e + meli_e -> h + meli | h_e + meli_e -> h + meli |
| METabc | Extracellular | transport via ABC system D-methionine | atp + h2o + met_e -> adp + met + pi | atp + h2o + met_e -> adp + h + met + pi | |
| METDabc | Transport, Extracellular | transport via ABC system Indole transport via | atp + h2o + dmet_e -> adp + dmet + pi | atp + h2o + dmet_e -> adp + h + dmet + pi | atp + h2o + dmet_e -> adp + h + dmet + pi |
| INDOLEtr | Transport, Extracellular Transport, | proton symport, reversible N-acetylneuraminate | h_e + indole_e <-> h + indole | h_e + indole_e <-> h + indole | h_e + indole_e <-> h + indole |
| ACNAMt | Extracellular | proton symport | naneu_e + h_e -> naneu + h | naneu_e + h_e -> naneu + h | naneu_e + h_e -> naneu + h |
| NO3t | Transport, Extracellular | nitrate transport in via nitrite antiport | no2 + no3_e -> no2_e + no3 | no2 + no3_e -> no2_e + no3 | no2 + no3_e -> no2_e + no3 |
| NO2tr | Transport, Extracellular | nitrite transport in via proton symport, reversible | h_e + no2_e <-> h + no2 | h_e + no2_e <-> h + no2 | h_e + no2_e <-> h + no2 |
| NAt_2 | Transport, Extracellular | sodium proton antiporter (H:NA is 2) | 2 h_e + na -> 2 h + na_e | 2 h_e + na -> 2 h + na_e | 2 h_e + na -> 2 h + na_e |
| NAt_1.5 | Transport, Extracellular | sodium proton antiporter (H:NA is | 3 h_e + 2 na -> 3 h + 2 na_e | 3 h_e + 2 na -> 3 h + 2 na_e | 3 h_e + 2 na -> 3 h + 2 na_e |
| GSNt | Transport, Extracellular | 1.5) guanosine transport in via proton | gsn_e + h_e -> gsn + h | gsn_e + h_e -> gsn + h | gsn_e + h_e -> gsn + h |
| DGSNt | Transport, Extracellular | symport deoxyguanosine transport in via | dg_e + h_e -> dg + h | dg_e + h_e -> dg + h | dg_e + h_e -> dg + h |
| INSt | Transport, | proton symport inosine transport in | h_e + ins_e -> h + ins | h_e + ins_e -> h + ins | h_e + ins_e -> h + ins |
| DINSt | Extracellular Transport, | via proton symport deoxyinosine transport in via | din e + h e -> din + h | din_e + h_e -> din + h | din e + h e -> din + h |
| ADNt | Extracellular Transport, | proton symport adenosine transport in via proton | adn e + h e -> adn + h | adn e + h e -> adn + h | adn_e + h_e -> adn + h |
| | Extracellular Transport, | symport uridine transport in | | | |
| URIt | Extracellular Transport, | via proton symport | h_e + uri_e -> h + uri | h_e + uri_e -> h + uri | h_e + uri_e -> h + uri |
| CYTDt | Extracellular | cytidine transport in via proton symport | cytd_e + h_e -> cytd + h | cytd_e + h_e -> cytd + h | cytd_e + h_e -> cytd + h |
| DCYTt | Transport, Extracellular | deoxycytidine transport in via proton symport | dc_e + h_e -> dc + h | dc_e + h_e -> dc + h | dc_e + h_e -> dc + h |
| DURIt | Transport, Extracellular | deoxyuridine transport in via proton symport | du_e + h_e -> du + h | du_e + h_e -> du + h | du_e + h_e -> du + h |
| DADNt | Transport, Extracellular | deoxyadenosine transport in via proton symport | da_e + h_e -> da + h | da_e + h_e -> da + h | da_e + h_e -> da + h |
| THMDt | Transport, Extracellular | thymidine transport in via proton symport | h_e + thymd_e -> h + thymd | h_e + thymd_e -> h + thymd | h_e + thymd_e -> h + thymd |
| PNTOt | Transport, Extracellular | Pantothenate sodium symporter | na_e + pnto_e -> na + pnto | na_e + pnto_e -> na + pnto | na_e + pnto_e -> na + pnto |
| | | -yp | | | |

| PItr | Transport, | phosphate reversible transport via | h_e + pi_e <-> h + pi | h_e + pi_e <-> h + pi | h_e + pi_e <-> h + pi |
|--------------|-----------------------------|---|--|---|--|
| | Extracellular | symport | nge v pge v v m v pr | nge v pge v v m v pr | nge i pge va mi pi |
| NMNP | Transport, Extracellular | NMN permease | namn_e -> namn | namn_e -> namn | namn_e -> namn |
| PTRCabc | Transport, Extracellular | putrescine transport via ABC system | atp + h2o + ptrc_e -> adp + pi + ptrc | atp + h2o + ptrc_e -> adp + h + pi + ptrc | atp + h2o + ptrc_e -> adp + h + pi + ptrc |
| SPMDabc | Transport, Extracellular | spermidine transport | atp + h2o + sprmd_e -> adp + pi + sprmd | atp + h2o + sprmd_e -> adp + h + pi + sprmd | atp + h2o + sprmd_e -> adp + h + pi + sprmd |
| PTRCORNt | Transport, | via ABC system putrescine/ornithine | orn + ptrc_e <-> orn_e + ptrc | om + ptrc_e <-> om_e + ptrc | orn + ptrc_e <-> orn_e + ptrc |
| | Extracellular Transport, | antiporter putrescine transport | | | |
| PTRCtr | Extracellular | in via proton symport, reversible | h_e + ptrc_e <-> h + ptrc | h_e + ptrc_e <-> h + ptrc | h_e + ptrc_e <-> h + ptrc |
| PROtr | Transport, | L-proline reversible transport via proton | h_e + pro_e <-> h + pro | h_e + pro_e <-> h + pro | h_e + pro_e <-> h + pro |
| | Extracellular | symport | The state of the s | and a budge of the budge | The state of the s |
| PROabc | Transport, Extracellular | L-proline transport via ABC system | atp + h2o + pro_e -> adp + pi + pro | atp + h2o + pro_e -> adp + h + pi + pro | atp + h2o + pro_e -> adp + h + pi + pro |
| PIabc | Transport, Extracellular | phosphate transport via ABC system | atp + h2o + pi_e -> adp + 2 pi | atp + h2o + pi_e -> adp + h + 2 pi | atp + h2o + pi_e -> adp + h + 2 pi |
| ACMANApts | Transport, Extracellular | N-acetyl-D- mannosamine | nadma_e + pep -> nadma6p + pyr | nadma_e + pep -> nadma6p + pyr + h | nadma_e + pep -> nadma6p + pyr + h |
| | Transport, | transport via PTS mannitol transport | | | |
| MNLpts | Extracellular Transport, | via PEP.Pyr PTS D-fructose transport | mnt_e + pep -> mnt1p + pyr | mnt_e + pep -> mnt1p + pyr + h | mnt_e + pep -> mnt1p + pyr + h |
| FRUpts | Extracellular Transport, | via PEP:Pyr PTS | fru_e + pep -> f1p + pyr | fru_e + pep -> f1p + pyr + h | fru_e + pep -> f1p + pyr + h |
| FRUabc | Extracellular | D-fructose transport via ABC system | atp + h2o + fru_e -> adp + pi + fru | atp + h2o + fru_e -> adp + h + pi + fru | atp + h2o + fru_e -> adp + h + pi + fru |
| PROt | Transport, Extracellular | Na+/Proline-L symporter | na_e + pro_e -> na + pro | na_e + pro_e -> na + pro | na_e + pro_e -> na + pro |
| RMNt | Transport, Extracellular | L-rhamnose transport via proton | h_e + rmn_e -> h + rmn | h_e + rmn_e -> h + rmn | h_e + rmn_e -> h + rmn |
| TCI II - h - | Transport, | symport thiosulfate transport | and the standard and a standard | and the standard and the standard and | ate a 125 a hard a constant to a set a hard |
| TSULabc | Extracellular | via ABC system L-serine reversible | atp + h2o + tsul_e -> adp + pi + tsul | atp + h2o + tsul_e -> adp + h + pi + tsul | atp + h2o + tsul_e -> adp + h + pi + tsul |
| SERtr | Transport, Extracellular | transport via proton symport | h_e + ser_e <-> h + ser | h_e + ser_e> h + ser | h_e + ser_e <-> h + ser |
| THMabc | Transport, Extracellular | thiamine transport via ABC system | atp + h2o + thiamin_e -> adp + pi + thiamin | atp + h2o + thiamin_e -> adp + h + pi + thiamin | atp + h2o + thiamin_e -> adp + h + pi + thiamin |
| SBTpts | Transport, | D-sorbitol transport | pep + sot_e -> pyr + sbt6p | pep + sot_e -> pyr + sbt6p + h | pep + sot_e -> pyr + sbt6p + h |
| SERt | Extracellular Transport, | via PEP:Pyr PTS L-serine via sodium | na_e + ser_e -> na + ser | na_e + ser_e -> na + ser | na_e + ser_e -> na + ser |
| THRt | Extracellular Transport, | symport L-threonine via | na e + thr e -> na + thr | na e + thr e -> na + thr | na_e + thr_e -> na + thr |
| | Extracellular Transport, | sodium symport taurine transport via | | | |
| TAURabc | Extracellular | ABC system L-threonine | atp + h2o + taur_e -> adp + pi + taur | atp + nzo + taur_e -> adp + n + pi + taur | atp + h2o + taur_e -> adp + h + pi + taur |
| THRtr | Transport, Extracellular | reversible transport via proton symport | h_e + thr_e <-> h + thr | h_e + thr_e <-> h + thr | h_e + thr_e <-> h + thr |
| TRPtr | Transport, | L-tryptophan | ha i tra a - h i tra | has traces by tra | hay transport hy tra |
| IRPU | Extracellular | reversible transport via proton symport | h_e + trp_e <-> h + trp | h_e + trp_e <-> h + trp | h_e + trp_e <-> h + trp |
| Ktr | Transport, Extracellular | potassium reversible transport via proton | h_e + k_e <-> h + k | h_e + k_e <-> h + k | h_e + k_e <-> h + k |
| | Transport, | symport L-tyrosine reversible | | | |
| TYRtr | Extracellular | transport via proton symport | h_e + tyr_e <-> h + tyr | h_e + tyr_e <-> h + tyr | h_e + tyr_e <-> h + tyr |
| GLYC3Pabc | Transport, | sn-Glycerol 3- phosphate transport | atp + glyc3p_e + h2o -> adp + glyc3p + pi | atp + glyc3p_e + h2o -> adp + glyc3p + h | atp + $glyc3p_e + h2o -> adp + glyc3p + h +$ |
| | Extracellular | via ABC system Mannose-6- | 37.4- | + pi | pi |
| MAN6Pt_2 | Transport, Extracellular | phosphate transport via phosphate | man6p_e + 2 pi -> man6p + 2 pi_e | man6p_e + 2 pi -> man6p + 2 pi_e | man6p_e + 2 pi -> man6p + 2 pi_e |
| | Extracellalar | antiport | | | |
| G6Pt_2 | Transport, | Glucose-6-phosphate transport via | g6p_e + 2 pi -> g6p + 2 pi_e | g6p_e + 2 pi -> g6p + 2 pi_e | g6p_e + 2 pi -> g6p + 2 pi_e |
| | Extracellular | phosphate antiport | 3,- , 3, ,- | V 1 V- 1- | |
| FUCPt_2 | Transport, Extracellular | Fucose 1-phosphate transport via | fuc1p_e + 2 pi -> fuc1p + 2 pi_e | fuc1p_e + 2 pi -> fuc1p + 2 pi_e | fuc1p_e + 2 pi -> fuc1p + 2 pi_e |
| | Transport, | phosphate antiport uracil transport in via | | | |
| URAt | Extracellular | proton symport | h_e + ura_e -> h + ura | h_e + ura_e -> h + ura | h_e + ura_e -> h + ura |
| XTSNtr | Transport, Extracellular | Xanthosine transport via proton symport | h_e + xtsine_e <-> h + xtsine | h_e + xtsine_e <-> h + xtsine | h_e + xtsine_e <-> h + xtsine |
| INStr | Transport, | inosine transport in via proton symport, | h_e + ins_e <-> h + ins | h_e + ins_e <-> h + ins | h_e + ins_e <-> h + ins |
| IIVSU | Extracellular | reversible | 11_e + 115_e <-> 11 + 115 | 11_e + 115_e <-> 11 + 115 | 11_E + 115_E <-> 11 + 115 |
| ADNtr | Transport, Extracellular | adenosine transport in via proton | adn_e + h_e <-> adn + h | adn_e + h_e <-> adn + h | adn_e + h_e <-> adn + h |
| | Transport, | symport, reversible cytidine transport in | | | |
| CYTDtr | Extracellular | via proton symport, reversible | cytd_e + h_e <-> cytd + h | cytd_e + h_e <-> cytd + h | cytd_e + h_e <-> cytd + h |
| THMDtr | Transport, | thymidine transport in via proton | h_e + thymd_e <-> h + thymd | h_e + thymd_e <-> h + thymd | h_e + thymd_e <-> h + thymd |
| | Extracellular | symport, reversible uridine transport in | * | * | |
| URItr | Transport, Extracellular | via proton symport, reversible | h_e + uri_e <-> h + uri | h_e + uri_e <-> h + uri | h_e + uri_e <-> h + uri |
| en. | Transport, | choline transport via | | | |
| CHLtr | Extracellular | proton symport, reversible | choline_e + h_e <-> choline + h | choline_e + h_e <-> choline + h | choline_e + h_e <-> choline + h |
| ADEtr | Transport, Extracellular | adenine transport via proton symport | ad_e + h_e <-> ad + h | ad_e + h_e <-> ad + h | ad_e + h_e <-> ad + h |
| RIBabc | Transport, | (reversible) D-ribose transport | atp + h2o + rib_e -> adp + pi + rib | atp + h2o + rib_e -> adp + h + pi + rib | atp + h2o + rib_e -> adp + h + pi + rib |
| | Extracellular Transport, | via ABC system | | | |
| FEabc | Extracellular Transport, | | atp + fe3_e + h2o <-> fe3 + adp + pi | | atp + fe3_e + h2o <-> fe3 + adp + h + pi |
| CRNabc | Extracellular Transport, | | atp + h2o + crn_e <-> adp + crn + pi | atp + h2o + crn_e <-> adp + crn + h + pi atp + mobd_e + h2o <-> adp + h + pi + | atp + h2o + crn_e <-> adp + crn + h + pi atp + mobd_e + h2o <-> adp + h + pi + |
| MOBDabc | Extracellular Transport, | | atp + mobd_e + h2o <-> adp + pi + mobd | mobd | mobd atp + h2o + tolen_e <-> tolen + adp + h + |
| TOLabc | Extracellular | | atp + h2o + tolen_e <-> tolen + adp + pi | atp + h2o + tolen_e <-> tolen + adp + n + pi | atp + h2o + tolen_e <-> tolen + adp + h + pi |
| ASO3t1 | Transport, Extracellular | | aso3 <-> aso3_e | aso3 <-> aso3_e | aso3 <-> aso3_e |
| MG2t | Transport, Extracellular | | mg2_e <-> mg2 | mg2_e <-> mg2 | mg2_e <-> mg2 |
| COBTt | Transport, Extracellular | | cobalt2 <-> cobalt2_e | cobalt2 <-> cobalt2_e | cobalt2 <-> cobalt2_e |
| ASPALAt | Transport, Extracellular | | asp_e + ala <-> asp + ala_e | asp_e + ala <-> asp + ala_e | asp_e + ala <-> asp + ala_e |
| ASO3t2 | Transport, Extracellular | | aso3 -> aso3_e | aso3 -> aso3_e | aso3 -> aso3_e |
| BENZOTt | Transport, Extracellular | | benzot_e + h_e -> benzot + h | benzot_e + h_e -> benzot + h | benzot_e + h_e -> benzot + h |
| NA1t | Transport, | | na_e + h <-> na + h_e | na_e + h <-> na + h_e | na_e + h <-> na + h_e |
| | Extracellular | | | | |

| NA1t2 | Transport, Extracellular | | | | na + h_e <-> na_e + h | na + h_e <-> na_e + h | na + h_e <-> na_e + h |
|---------------------------------|---|------------------------------------|----------|---|--|---|---|
| SUCCt | Transport, | | | | succ e + h e -> succ + h | succ e + h e -> succ + h | succ e + h e -> succ + h |
| SUCCtr | Extracellular Transport, | | | | na e + succ e -> na + succ | na e + succ e -> na + succ | na_e + succ_e -> na + succ |
| SO4t | Extracellular Transport, | | | | | | |
| | Extracellular Transport, | | | | so4_e + na_e -> so4 + na | so4_e + na_e -> so4 + na | so4_e + na_e -> so4 + na |
| LYSt | Extracellular Transport, | | | | lys + h_e -> lys_e + h | lys + h_e -> lys_e + h | lys + h_e -> lys_e + h |
| CITt | Extracellular Transport, | | | | cit_e + h_e <-> cit + h | cit_e + h_e <-> cit + h | cit_e + h_e <-> cit + h |
| 4HBZt | Extracellular | | | | 4hb_e + h_e <-> 4hb + h | 4hb_e + h_e <-> 4hb + h | 4hb_e + h_e <-> 4hb + h |
| 3HBZt | Transport, Extracellular | | | | 3hbenzot_e + h_e <-> 3hbenzot + h | 3hbenzot_e + h_e <-> 3hbenzot + h | 3hbenzot_e + h_e <-> 3hbenzot + h |
| BENZt | Transport, Extracellular | | | | benzot_e + h_e <-> benzot + h | benzot_e + h_e <-> benzot + h | benzot_e + h_e <-> benzot + h |
| PHBt | Transport, Extracellular | | | | pbhb + h -> pbhb_e + h_e | pbhb + h -> pbhb_e + h_e | pbhb + h -> pbhb_e + h_e |
| PHENOLt | Transport, Extracellular | | | | phenol_e + h_e -> phenol + h | phenol_e + h_e -> phenol + h | phenol_e + h_e -> phenol + h |
| PPAt | Transport, Extracellular | | | | ppa_e + h_e -> ppa + h | ppa_e + h_e -> ppa + h | ppa_e + h_e -> ppa + h |
| C181t | Transport, Extracellular | | | | c181_e + h_e -> c181 + h | c181_e + h_e -> c181 + h | c181_e + h_e -> c181 + h |
| BUTNt | Transport, Extracellular | | | | butn_e + h_e -> butn + h | butn_e + h_e -> butn + h | butn_e + h_e -> butn + h |
| GENt | Transport, Extracellular | | | | gensa_e + h_e -> gensa + h | gensa_e + h_e -> gensa + h | gensa_e + h_e -> gensa + h |
| 2PGt | Transport, Extracellular | | | | 2pg_e + h_e -> 2pg + h | 2pg_e + h_e -> 2pg + h | 2pg_e + h_e -> 2pg + h |
| 3PGt | Transport, Extracellular | | | | 3pg_e + h_e -> 3pg + h | 3pg_e + h_e -> 3pg + h | 3pg_e + h_e -> 3pg + h |
| 4CRESOLt | Transport, | | | | 4cresol_e + h_e -> 4cresol + h | 4cresol_e + h_e -> 4cresol + h | 4cresol_e + h_e -> 4cresol + h |
| 6CHQt | Extracellular Transport, | | | | 6chq_e + h_e -> 6chq + h | 6chq_e + h_e -> 6chq + h | 6chq_e + h_e -> 6chq + h |
| CATECHt | Extracellular Transport, | | | | catech e + h e -> catech + h | catech_e + h_e -> catech + h | catech_e + h_e -> catech + h |
| CLt | Extracellular Transport, | | | | de <-> d | d e <-> d | cle <-> cl |
| BP23Dt | Extracellular Transport, | | | | _ | _ | _ |
| | Extracellular Transport, | | | | bp23d_e + h_e -> bp23d + h | bp23d_e + h_e -> bp23d + h | bp23d_e + h_e -> bp23d + h |
| GLXt | Extracellular Transport. | | | | glx_e + h_e -> glx + h | glx_e + h_e -> glx + h | glx_e + h_e -> glx + h |
| ICITt | Extracellular Transport, | | | | icit_e + h_e <-> icit + h | icit_e + h_e <-> icit + h | icit_e + h_e <-> icit + h |
| ADIPt | Extracellular Transport, | | | | adip_e + h_e <-> adip + h | adip_e + h_e <-> adip + h | adip_e + h_e <-> adip + h |
| PACt | Extracellular | | | | pac_e + h_e <-> pac + h | pac_e + h_e <-> pac + h | pac_e + h_e <-> pac + h |
| CCMUCt | Transport, Extracellular | | | | ccmuc_e + h_e <-> ccmuc + h | ccmuc_e + h_e <-> ccmuc + h | ccmuc_e + h_e <-> ccmuc + h |
| MCLACTt | Transport, Extracellular | | | | mclact_e + h_e <-> mclact + h | mclact_e + h_e <-> mclact + h | mclact_e + h_e <-> mclact + h |
| 34DHBt | Transport, Extracellular | | | | 34dhb_e + h_e -> 34dhb + h | 34dhb_e + h_e -> 34dhb + h | 34dhb_e + h_e -> 34dhb + h |
| KNTt | Transport, Extracellular | | | | knt_e + h_e <-> knt + h | knt_e + h_e <-> knt + h | knt_e + h_e <-> knt + h |
| ANt | Transport, Extracellular | | | | an_e + h_e <-> an + h | an_e + h_e <-> an + h | an_e + h_e <-> an + h |
| KNt | Transport, Extracellular | | | | kn_e + h_e -> kn + h | kn_e + h_e -> kn + h | kn_e + h_e -> kn + h |
| AOBZACt | Transport, Extracellular | | | | aobzac_e + h_e -> aobzac + h | aobzac_e + h_e -> aobzac + h | aobzac_e + h_e -> aobzac + h |
| ACONCt | Transport, Extracellular | | | | acon-C_e + h_e -> acon-C + h | acon-C_e + h_e -> acon-C + h | acon-C_e + h_e -> acon-C + h |
| UROCANt | Transport, Extracellular | | | | urocan_e + h_e <-> urocan + h | urocan_e + h_e <-> urocan + h | urocan_e + h_e <-> urocan + h |
| 2HBAt | Transport, Extracellular | | | | 2hba_e + h_e -> 2hba + h | 2hba_e + h_e -> 2hba + h | 2hba_e + h_e -> 2hba + h |
| 4HBTt | Transport, | | | | 4hbt_e + h_e -> 4hbt + h | 4hbt_e + h_e -> 4hbt + h | 4hbt_e + h_e -> 4hbt + h |
| 4HPHEACt | Extracellular Transport, | | | | 4hpheac_e + h_e -> 4hpheac + h | 4hpheac_e + h_e -> 4hpheac + h | 4hpheac_e + h_e -> 4hpheac + h |
| 4HPHEAO | Extracellular Transport, | | | | 4hpheac + o2 + nadh + h -> homogen + | 4hpheac + o2 + nadh + h -> homogen + | 4hpheac + o2 + nadh + h -> homogen + |
| OBUTt | Extracellular Transport, | | | | nad + h2o obut_e + h_e -> obut + h | nad + h2o obut_e + h_e -> obut + h | nad + h2o obut_e + h_e -> obut + h |
| R3HBNt | Extracellular Transport, | | | | r3hbn e + h e -> r3hbn + h | r3hbn_e + h_e -> r3hbn + h | r3hbn_e + h_e -> r3hbn + h |
| BZALDt | Extracellular Transport, | | | | | | bzald e + h e -> bzald + h |
| | Extracellular Transport, | | | | bzald_e + h_e -> bzald + h | bzald_e + h_e -> bzald + h | |
| 4FLRBZt | Extracellular Transport, | | | | 4firbz_e + h_e -> 4firbz + h | 4firbz_e + h_e -> 4firbz + h | 4flrbz_e + h_e -> 4flrbz + h |
| 4FLTHRt | Extracellular | L-ascorbate transport | t | | 4flthr + h -> 4flthr_e + h_e | 4flthr + h -> 4flthr_e + h_e | 4fithr + h -> 4fithr_e + h_e |
| ASCBpts | Transport, Inner Membrane | via PEP:Pyr PTS (periplasm) | 2.7.1.69 | H16_A0324 fruA | ascb_e + pep -> ascb6p + pyr | ascb_e + pep -> ascb6p + pyr + h | ascb_e + pep -> ascb6p + pyr + h |
| IMLTAP | Transport, Outer Membrane | ATPase (isomaltose) | 3.6.1 | H16_A2683/H16_A3646/ unknown/parA2/pox H16_B0538/H16_B1613 R/unknown | imal_e + atp + h2o -> imal + pi + adp | atp + h2o + imal_e -> imal + pi + adp + h | imal_e + atp + h2o -> imal + pi + adp + h |
| Maintenance | | | | 1110_B033B/1110_B1013 IVGIIKIIOWII | atp + h2o -> adp + pi | atp + h2o -> adp + pi + h | atp + h2o -> adp + pi + h |
| LPS | Lipopolysaccharide Biosynthesis / Recycling | Lipopolysaccharide biosynthesis | | | cdpetn + 0.42 ckdo -> 0.42 adp + 0.28 udp + 0.42 cmp + 0.28 cdp + LPS | 0.14 lipa + 0.42 adphep + 0.28 udpg + 0.28 cdpetn + 0.42 ckdo -> 0.42 adp + 0.28 udp + 0.42 cmp + 0.28 cdp + LPS 1.211 ala + 0.456 arg + 0.369 asn + 0.369 asp + | 0.14 lipa + 0.42 adphep + 0.28 udpg + 0.28 cdpetn + 0.42 ckdo -> 0.42 adp + 0.28 udp + 0.42 cmp + 0.28 cdp + LPS 1.211 ala + 0.456 arg + 0.369 asn + 0.369 asp + |
| Protein | | | | | 0.115 cys + 0.512 gln + 0.512 glu + 1.135 gly + 0.223 his + 0.306 ile + 0.522 leu + 0.189 lys + 0.159 met + 0.43 phe + 0.997 pro + 0.421 ser + | 0.115 cys + 0.512 gln + 0.512 glu + 1.135 gly + 0.223 his + 0.306 ile + 0.522 leu + 0.189 lys + 0.159 met + 0.43 phe + 0.997 pro + 0.421 ser + | 0.115 cys + 0.512 gln + 0.512 glu + 1.135 gly + 0.223 his + 0.306 ile + 0.522 leu + 0.189 lys + |
| | | | | | atp -> 40 adp + PROTEIN | atp -> 40 adp + PROTEIN | atp -> 40 adp + PROTEIN 0.564 datp + 1.054 dctp + 0.564 dttp + 1.054 |
| DNA | | | 2.7.7.7 | | dgtp + 4.4 atp -> 4.4 adp + 4.4 pi + DNA | dgtp + 4.4 atp -> 4.4 adp + 4.4 pi + DNA | dgtp + 4.4 atp -> 4.4 adp + 4.4 pi + DNA 0.631 atp + 0.75 gtp + 0.998 ctp + 0.747 utp -> |
| RNA | | | 2.7.7.6 | | 1.25 adp + 1.25 pi + RNA | 1.25 adp + 1.25 pi + RNA | 1.25 adp + 1.25 pi + RNA |
| Phospholipid | | | | | PHOSPHOLIPID | 0.927 pe + 0.283 pg + 0.093 clpn -> PHOSPHOLIPID 0.656 pydyn + 0.145 coa + 0.141 fad + 0.243 fmp | 0.927 pe + 0.283 pg + 0.093 clpn -> PHOSPHOLIPID |
| Cofactors and vitamins (CAV) | | | | | + 0.14 uq + 0.167 nad + 0.149 nadp + 0.249 thf | + 0.14 uq + 0.167 nad + 0.149 nadp + 0.249 thf | |
| Carbohydrate | | | | | | + 0.418 thiamin -> CAV 3.937 udpnag + 0.984 udpacgal -> 4.921 udp + | |
| (CARBO) | | | | | 0.68 PROTEIN + 0.031 DNA + 0.06 RNA + 0.06 | | CARBO 0.68 PROTEIN + 0.031 DNA + 0.06 RNA + 0.06 |
| Biomass | | | | | | | PEPTIDO + 0.055 CARBO + 0.03 CAV + 0.034 LPS + 0.0495 PHOSPHOLIPID + 15.3 atp -> BIOMASS + 15.3 adp + 15.3 pi |