Pathos

A metabolomics tool from Glasgow Polyomics

Upload File | Analyse | Feedback | Instructions

Organism: All Organisms Run

Base Condition: Mean: Time0 Experimental Condition: Mean: Time81

Cut-offs for colour-flagging: 10.0× 5.0× 2.0× 0.5× 0.2× 0.1×

File: 'pathos_KEGGlist.txt'
Kegg Maps for All Organisms with compounds from input list

KEY hide **All maps** v

v : View metabolites found for a particular map (or all maps) — toggles list on and off.
G : Link to a graph of results for a particular metabolite. Change indication scale — [increase G G G G G G G decrease]

Arginine and proline metabolism: 17 metabolites out of 67 (15 changed) v

- G (S)-1-Pyrroline-5-carboxylate C5H7NO2
- G 1-Pyrroline-4-hydroxy-2-carboxylate C5H7NO3
- G 2,5-Dioxopentanoate C5H6O4
- G 4-Aminobutyraldehyde C4H9NO
- G Creatine C4H9N3O2
- G Creatinine C4H7N3O
- G D-Proline C5H9NO2
- G L-1-Pyrroline-3-hydroxy-5-carboxylate C5H7NO3
- G L-Arginine C6H14N4O2
- G L-Glutamate C5H9NO4
- G L-Glutamate 5-semialdehyde C5H9NO3
- G L-Ornithine C5H12N2O2
- G L-Proline C5H9NO2
- G N-Acetylputrescine C6H14N2O
- G N-Carbamoylsarcosine C4H8N2O3
- G N2-Succinyl-L-ornithine C9H16N2O5
- G Phosphocreatine C4H10N3O5P

Generate map of **Arginine and proline metabolism** highlighting potential metabolites.

Aminoacyl-tRNA biosynthesis: 12 metabolites out of 24 (11 changed) v

- G L-Alanine C3H7NO2
- G L-Arginine C6H14N4O2
- G L-Asparagine C4H8N2O3
- G L-Glutamate C5H9NO4
- G L-Glutamine C5H10N2O3
- G L-Histidine C6H9N3O2
- G L-Leucine C6H13NO2
- G L-Lysine C6H14N2O2
- G L-Methionine C5H11NO2S
- G L-Phenylalanine C9H11NO2
- G L-Proline C5H9NO2
- G L-Tryptophan C11H12N2O2

Generate map of **Aminoacyl-tRNA biosynthesis** highlighting potential metabolites.

Glycine, serine and threonine metabolism: 12 metabolites out of 45 (11 changed) v

- G (R)-1-Aminopropan-2-ol C3H9NO
- G 2-Oxobutanoate C4H6O3

G Aminoacetone C3H7NO
G Betaine C5H11NO2
G Betaine aldehyde C5H12NO
G Choline C5H14NO
G Creatine C4H9N3O2
G D-Glycerate C3H6O4
G L-2-Amino-3-oxobutanoic acid C4H7NO3
G L-Homoserine C4H9NO3
G L-Tryptophan C11H12N2O2
G N,N-Dimethylglycine C4H9NO2
Generate map of **Glycine, serine and threonine metabolism** highlighting potential metabolites.

Pyrimidine metabolism: 17 metabolites out of 55 (11 changed) v
G (S)-Dihydroorotate C5H6N2O4
G 3-Oxopropanoate C3H4O3
G 5-Methylcytosine C5H7N3O
G Carbamoyl phosphate CH4NO5P
G Cytidine C9H13N3O5
G Cytosine C4H5N3O
G Deoxycytidine C9H13N3O4
G Deoxyuridine C9H12N2O5
G FucoseMalonate C3H4O4
G L-Glutamine C5H10N2O3
G Orotate C5H4N2O4
G Pseudouridine C9H12N2O6
G Thymidine C10H14N2O5
G Thymine C5H6N2O2
G TrypsinUridine C9H12N2O6
G beta-Alanine C3H7NO2
G dTTP C10H17N2O14P3
Generate map of **Pyrimidine metabolism** highlighting potential metabolites.

Biosynthesis of unsaturated fatty acids: 12 metabolites out of 49 (10 changed) v
G (13Z)-Docosenoic acid C22H42O2
G (15Z)-Tetracosenoic acid C24H46O2
G (5Z,8Z,11Z,14Z)-Icosatetraenoic acid C20H32O2
G (9Z)-Octadecenoic acid C18H34O2
G Docosanoic acid C22H44O2
G Hexadecanoic acid C16H32O2
G Icosadienoic acid C20H36O2
G Icosanoic acid C20H40O2
G Icosenoic acid C20H38O2
G Linoleate C18H32O2
G Octadecanoic acid C18H36O2
G Tetracosanoic acid C24H48O2
Generate map of **Biosynthesis of unsaturated fatty acids** highlighting potential metabolites.

Tryptophan metabolism: 11 metabolites out of 80 (10 changed) v
G 2-Aminomuconate semialdehyde C6H7NO3
G 2-Aminophenol C6H7NO
G 2-Oxoadipate C6H8O5
G 3-Hydroxyanthranilate C7H7NO3
G 3-Indoleacetonitrile C10H8N2
G 4,6-Dihydroxyquinoline C9H7NO2
G 5-Hydroxy-L-tryptophan C11H12N2O3
G 5-Methoxyindoleacetate C11H11NO3
G Indole C8H7N
G Indolelactate C11H11NO3
G L-Tryptophan C11H12N2O2
Generate map of **Tryptophan metabolism** highlighting potential metabolites.

Lysine degradation: 11 metabolites out of 42 (9 changed) v
G (S)-5-Amino-3-oxohexanoic acid C6H11NO3

G 2-Oxoadipate C6H8O5
G 5-Aminopentanamide C5H12N2O
G 5-Oxopentanoate C5H8O3
G Carnitine C7H16NO3
G L-2-Aminoadipate C6H11NO4
G L-Lysine C6H14N2O2
G N2-(D-1-Carboxyethyl)-L-lysine C9H18N2O4
G N6-Acetyl-N6-hydroxy-L-lysine C8H16N2O4
G N6-Hydroxy-L-lysine C6H14N2O3
G Piperideine C5H9N
Generate map of **Lysine degradation** highlighting potential metabolites.

Cysteine and methionine metabolism: 10 metabolites out of 54 (8 changed) v
G 2-Aminoacrylate C3H5NO2
G 2-Oxobutanoate C4H6O3
G L-Alanine C3H7NO2
G L-Homoserine C4H9NO3
G L-Methionine C5H11NO2S
G L-Methionine S-oxide C5H11NO3S
G Mercaptopyruvate C3H4O3S
G O-Acetyl-L-homoserine C6H11NO4
G O-Succinyl-L-homoserine C8H13NO6
G Sulfate H2SO4
Generate map of **Cysteine and methionine metabolism** highlighting potential metabolites.

Glyoxylate and dicarboxylate metabolism: 9 metabolites out of 55 (8 changed) v
G (S)-Malate C4H6O5
G 2-Hydroxy-3-oxoadipate C6H8O6
G 4-Hydroxy-2-oxoglutarate C5H6O6
G D-Glycerate C3H6O4
G Isocitrate C6H8O7
G L-Glutamate C5H9NO4
G L-Glutamine C5H10N2O3
G Succinate C4H6O4
G cis-Aconitate C6H6O6
Generate map of **Glyoxylate and dicarboxylate metabolism** highlighting potential metabolites.

Phenylalanine metabolism: 10 metabolites out of 64 (8 changed) v
G 2-Hydroxy-2,4-pentadienoate C5H6O3
G 2-Phenylacetamide C8H9NO
G 3-(3-Hydroxy-phenyl)-propanoic acid C9H10O3
G 4-Hydroxybenzoate C7H6O3
G Hippurate C9H9NO3
G L-Phenylalanine C9H11NO2
G Phenylacetylglycine C10H11NO3
G Phenylpropanoate C9H10O2
G Succinate C4H6O4
G enol-Phenylpyruvate C9H8O3
Generate map of **Phenylalanine metabolism** highlighting potential metabolites.

Purine metabolism: 11 metabolites out of 90 (8 changed) v
G 3',5'-Cyclic AMP C10H12N5O6P
G Adenine C5H5N5
G Carbamoyl phosphate CH4NO5P
G Guanine C5H5N5O
G Guanosine C10H13N5O5
G Hypoxanthine C5H4N4O
G Inosine C10H12N4O5
G L-Glutamine C5H10N2O3
G Sulfate H2SO4
G Urate C5H4N4O3
G Urate-3-ribonucleoside C10H12N4O7
Generate map of **Purine metabolism** highlighting potential metabolites.

beta-Alanine metabolism: 10 metabolites out of 32 (8 changed)

G 3-Aminopropanal C3H7NO
G 3-Oxopropanoate C3H4O3
G 4-Aminobutyraldehyde C4H9NO
G Carnosine C9H14N4O3
G FucoseMalonate C3H4O4
G L-Histidine C6H9N3O2
G Pantothenate C9H17NO5
G Propynoate C3H2O2
G beta-Alanine C3H7NO2
G beta-Aminopropionitrile C3H6N2

Generate map of **beta-Alanine metabolism** highlighting potential metabolites.

Alanine, aspartate and glutamate metabolism: 11 metabolites out of 25 (7 changed)

G (S)-1-Pyrroline-5-carboxylate C5H7NO2
G 2-Oxoglutaramate C5H7NO4
G Carbamoyl phosphate CH4NO5P
G D-Aspartate C4H7NO4
G D-Glucosamine 6-phosphate C6H14NO8P
G L-Alanine C3H7NO2
G L-Asparagine C4H8N2O3
G L-Glutamate C5H9NO4
G L-Glutamine C5H10N2O3
G N-Acetyl-L-aspartate C6H9NO5
G Succinate C4H6O4

Generate map of **Alanine, aspartate and glutamate metabolism** highlighting potential metabolites.

C5-Branched dibasic acid metabolism: 7 metabolites out of 32 (7 changed)

G 2-Methylmaleate C5H6O4
G 2-Oxobutanoate C4H6O3
G 4-Hydroxy-4-methylglutamate C6H11NO5
G L-Glutamate C5H9NO4
G Methyloxaloacetate C5H6O5
G Propanoyl phosphate C3H7O5P
G cis-Aconitate C6H6O6

Generate map of **C5-Branched dibasic acid metabolism** highlighting potential metabolites.

Lysine biosynthesis: 7 metabolites out of 26 (7 changed)

G (R)-2-Hydroxybutane-1,2,4-tricarboxylate C7H10O7
G 2,3,4,5-Tetrahydrodipicolinate C7H9NO4
G 2-Oxoadipate C6H8O5
G L-2-Aminoadipate C6H11NO4
G L-Homoserine C4H9NO3
G L-Lysine C6H14N2O2
G meso-2,6-Diaminoheptanedioate C7H14N2O4

Generate map of **Lysine biosynthesis** highlighting potential metabolites.

Primary bile acid biosynthesis: 7 metabolites out of 47 (7 changed)

G 3alpha,7alpha,12alpha,26-Tetrahydroxy-5beta-cholestane C27H48O4
G 3alpha,7alpha,12alpha-Trihydroxy-5beta-cholanate C24H40O5
G Chenodeoxycholate C24H40O4
G Glycocholate C26H43NO6
G Taurine C2H7NO3S
G Taurochenodeoxycholate C26H45NO6S
G Taurocholate C26H45NO7S

Generate map of **Primary bile acid biosynthesis** highlighting potential metabolites.

Propanoate metabolism: 8 metabolites out of 41 (7 changed)

G (S)-Methylmalonate semialdehyde C4H6O3
G 2-Methylcitrate C7H10O7
G 2-Oxobutanoate C4H6O3
G 3-Oxopropanoate C3H4O3

G Propanoyl phosphate C3H7O5P
G Propynoate C3H2O2
G Succinate C4H6O4
G beta-Alanine C3H7NO2
Generate map of **Propanoate metabolism** highlighting potential metabolites.

Tyrosine metabolism: 14 metabolites out of 75 (7 changed) v
G 2-Carboxy-2,3-dihydro-5,6-dihydroxyindole C9H9NO4
G 2-Hydroxy-3-(4-hydroxyphenyl)propenoate C9H8O4
G 3-(4-Hydroxyphenyl)lactate C9H10O4
G 3-(4-Hydroxyphenyl)pyruvate C9H8O4
G 3-Amino-3-(4-hydroxyphenyl)propanoate C9H11NO3
G 4-Hydroxyphenylacetaldehyde C8H8O2
G 4-Hydroxyphenylethanol C8H10O2
G 5,6-Dihydroxyindole C8H7NO2
G Dopaquinone C9H9NO4
G Indole-5,6-quinone C8H5NO2
G L-Adrenaline C9H13NO3
G Succinate C4H6O4
G p-Benzenediol C6H6O2
G p-Hydroxyphenylacetylglycine C10H11NO4
Generate map of **Tyrosine metabolism** highlighting potential metabolites.

Amino sugar and nucleotide sugar metabolism: 7 metabolites out of 77 (6 changed) v
G D-Glucosamine C6H13NO5
G D-Glucosamine 6-phosphate C6H14NO8P
G D-Glucuronate C6H10O7
G L-Arabinose C5H10O5
G N-Acetyl-D-glucosamine 6-phosphate C8H16NO9P
G N-Acetylneuraminate C11H19NO9
G UDP-N-acetyl-D-galactosamine C17H27N3O17P2
Generate map of **Amino sugar and nucleotide sugar metabolism** highlighting potential metabolites.

Glucosinolate biosynthesis: 6 metabolites out of 72 (6 changed) v
G (S)-3-Methyl-2-oxopentanoic acid C6H10O3
G 3-Methyl-2-oxobutanoic acid C5H8O3
G L-Leucine C6H13NO2
G L-Methionine C5H11NO2S
G L-Phenylalanine C9H11NO2
G L-Tryptophan C11H12N2O2
Generate map of **Glucosinolate biosynthesis** highlighting potential metabolites.

Glycerophospholipid metabolism: 6 metabolites out of 18 (6 changed) v
G Choline C5H14NO
G Choline phosphate C5H15NO4P
G Ethanolamine phosphate C2H8NO4P
G sn-Glycerol 3-phosphate C3H9O6P
G sn-glycero-3-Phosphocholine C8H21NO6P
G sn-glycero-3-Phosphoethanolamine C5H14NO6P
Generate map of **Glycerophospholipid metabolism** highlighting potential metabolites.

Histidine metabolism: 9 metabolites out of 44 (6 changed) v
G 1H-Imidazole-4-ethanamine C5H9N3
G Carnosine C9H14N4O3
G Imidazol-5-yl-pyruvate C6H6N2O3
G L-Glutamate C5H9NO4
G L-Histidine C6H9N3O2
G Methylimidazoleacetic acid C6H8N2O2
G N(pi)-Methyl-L-histidine C7H11N3O2
G N-Formimino-L-glutamate C6H10N2O4
G Urocanate C6H6N2O2
Generate map of **Histidine metabolism** highlighting potential metabolites.

1,4-Dichlorobenzene degradation: 6 metabolites out of 74 (5 changed) v
G 2-Aminomuconate semialdehyde C6H7NO3

G 2-Aminophenol C6H7NO
G 3-Hydroxyanthranilate C7H7NO3
G 4-Hydroxyaniline C6H7NO
G 4-Hydroxybenzoate C7H6O3
G p-Benzenediol C6H6O2
Generate map of **1,4-Dichlorobenzene degradation** highlighting potential metabolites.

Butanoate metabolism: 7 metabolites out of 38 (5 changed) v
G (R)-3-Hydroxybutanoate C4H8O3
G 3-Butyn-1-ol C4H6O
G 3-Butynoate C4H4O2
G 4-Hydroxybutanoic acid C4H8O3
G Butanal C4H8O
G L-Glutamate C5H9NO4
G Succinate C4H6O4
Generate map of **Butanoate metabolism** highlighting potential metabolites.

Cyanoamino acid metabolism: 6 metabolites out of 24 (5 changed) v
G (Z)-4-Hydroxyphenylacetaldehyde-oxime C8H9NO2
G (Z)-Phenylacetaldehyde oxime C8H9NO
G L-Asparagine C4H8N2O3
G L-Phenylalanine C9H11NO2
G Phenylacetonitrile C8H7N
G beta-Aminopropionitrile C3H6N2
Generate map of **Cyanoamino acid metabolism** highlighting potential metabolites.

Fatty acid biosynthesis: 8 metabolites out of 11 (5 changed) v
G (9Z)-Hexadecenoic acid C16H30O2
G (9Z)-Octadecenoic acid C18H34O2
G Decanoic acid C10H20O2
G Dodecanoic acid C12H24O2
G Hexadecanoic acid C16H32O2
G Octadecanoic acid C18H36O2
G Octanoic acid C8H16O2
G Tetradecanoic acid C14H28O2
Generate map of **Fatty acid biosynthesis** highlighting potential metabolites.

Galactose metabolism: 5 metabolites out of 41 (5 changed) v
G 3-beta-D-Galactosyl-sn-glycerol C9H18O8
G D-Sorbitol C6H14O6
G Glycerol C3H8O3
G Lactose C12H22O11
G myo-Inositol C6H12O6
Generate map of **Galactose metabolism** highlighting potential metabolites.

Reductive carboxylate cycle (CO2 fixation): 6 metabolites out of 40 (5 changed) v
G (S)-Malate C4H6O5
G 3-Oxopropanoate C3H4O3
G 4-Hydroxybutanoic acid C4H8O3
G Isocitrate C6H8O7
G Succinate C4H6O4
G cis-Aconitate C6H6O6
Generate map of **Reductive carboxylate cycle (CO2 fixation)** highlighting potential metabolites.

Secondary bile acid biosynthesis: 5 metabolites out of 11 (5 changed) v
G 3alpha,7alpha,12alpha-Trihydroxy-5beta-cholanate
C24H40O5
G Chenodeoxycholate C24H40O4
G Glycocholate C26H43NO6
G Taurochenodeoxycholate C26H45NO6S
G Taurocholate C26H45NO7S
Generate map of **Secondary bile acid biosynthesis** highlighting potential metabolites.

Tropane, piperidine and pyridine alkaloid biosynthesis: 7 metabolites out of 61 (5 changed) v
G 1-Methylpyrrolinium C5H10N

G L-Lysine C6H14N2O2
G L-Phenylalanine C9H11NO2
G Nicotinate C6H5NO2
G Nicotine C10H14N2
G Piperideine C5H9N
G Retronecine C8H13NO2
Generate map of **Tropane, piperidine and pyridine alkaloid biosynthesis** highlighting potential metabolites.

Valine, leucine and isoleucine biosynthesis: 6 metabolites out of 23 (5 changed) v
G (2S)-2-Isopropylmalate C7H12O5
G (S)-3-Methyl-2-oxopentanoic acid C6H10O3
G 2-Methylmaleate C5H6O4
G 2-Oxobutanoate C4H6O3
G 3-Methyl-2-oxobutanoic acid C5H8O3
G L-Leucine C6H13NO2
Generate map of **Valine, leucine and isoleucine biosynthesis** highlighting potential metabolites.

D-Glutamine and D-glutamate metabolism: 4 metabolites out of 9 (4 changed) v
G D-Glutamate C5H9NO4
G D-Glutamine C5H10N2O3
G L-Glutamate C5H9NO4
G L-Glutamine C5H10N2O3
Generate map of **D-Glutamine and D-glutamate metabolism** highlighting potential metabolites.

Glycerolipid metabolism: 4 metabolites out of 12 (4 changed) v
G 3-beta-D-Galactosyl-sn-glycerol C9H18O8
G D-Glycerate C3H6O4
G Glycerol C3H8O3
G sn-Glycerol 3-phosphate C3H9O6P
Generate map of **Glycerolipid metabolism** highlighting potential metabolites.

Pentose and glucuronate interconversions: 6 metabolites out of 50 (4 changed) v
G 2,5-Dioxopentanoate C5H6O4
G D-Glucuronate C6H10O7
G D-Xylulose C5H10O5
G Glycerol C3H8O3
G L-Arabinose C5H10O5
G Xylitol C5H12O5
Generate map of **Pentose and glucuronate interconversions** highlighting potential metabolites.

Pentose phosphate pathway: 5 metabolites out of 34 (4 changed) v
G 2-Deoxy-D-ribose 5-phosphate C5H11O7P
G D-Gluconic acid C6H12O7
G D-Glucono-1,5-lactone C6H10O6
G D-Glycerate C3H6O4
G beta-D-Glucose C6H12O6
Generate map of **Pentose phosphate pathway** highlighting potential metabolites.

Porphyrin and chlorophyll metabolism: 4 metabolites out of 93 (4 changed) v
G (R)-1-Aminopropan-2-ol C3H9NO
G L-Glutamate C5H9NO4
G Porphobilinogen C10H14N2O4
G Precorrin 3B C43H50N4O17
Generate map of **Porphyrin and chlorophyll metabolism** highlighting potential metabolites.

Valine, leucine and isoleucine degradation: 4 metabolites out of 32 (4 changed) v
G (S)-3-Methyl-2-oxopentanoic acid C6H10O3
G 3-Methyl-2-oxobutanoic acid C5H8O3
G L-3-Amino-isobutanoate C4H9NO2
G L-Leucine C6H13NO2
Generate map of **Valine, leucine and isoleucine degradation** highlighting potential metabolites.

Ascorbate and aldarate metabolism: 7 metabolites out of 45 (3 changed) v
G 2,5-Dioxopentanoate C5H6O4
G D-Glucuronate C6H10O7
G L-Arabinonate C5H10O6

G L-Arabinose C5H10O5
G Monodehydroascorbate C6H7O6
G Threonate C4H8O5
G myo-Inositol C6H12O6
Generate map of **Ascorbate and aldarate metabolism** highlighting potential metabolites.

Biotin metabolism: 3 metabolites out of 11 (3 changed) v
G 6-Carboxyhexanoate C7H12O4
G Dethiobiotin C10H18N2O3
G L-Lysine C6H14N2O2
Generate map of **Biotin metabolism** highlighting potential metabolites.

Caffeine metabolism: 3 metabolites out of 21 (3 changed) v
G 1-Methyluric acid C6H6N4O3
G 5-Acetylamino-6-amino-3-methyluracil C7H10N4O3
G 7-Methylxanthine C6H6N4O2
Generate map of **Caffeine metabolism** highlighting potential metabolites.

Citrate cycle (TCA cycle): 4 metabolites out of 16 (3 changed) v
G (S)-Malate C4H6O5
G Isocitrate C6H8O7
G Succinate C4H6O4
G cis-Aconitate C6H6O6
Generate map of **Citrate cycle (TCA cycle)** highlighting potential metabolites.

Fructose and mannose metabolism: 3 metabolites out of 41 (3 changed) v
G 2(alpha-D-Mannosyl)-D-glycerate C9H16O9
G 2-Dehydro-3-deoxy-L-rhamnonate C6H10O5
G D-Sorbitol C6H14O6
Generate map of **Fructose and mannose metabolism** highlighting potential metabolites.

Inositol phosphate metabolism: 4 metabolites out of 30 (3 changed) v
G 3-Oxopropanoate C3H4O3
G D-Glucose 6-phosphate C6H13O9P
G D-Glucuronate C6H10O7
G myo-Inositol C6H12O6
Generate map of **Inositol phosphate metabolism** highlighting potential metabolites.

Linoleic acid metabolism: 6 metabolites out of 25 (3 changed) v
G (5Z,8Z,11Z,14Z)-Icosatetraenoic acid C20H32O2
G 9(S)-HODE C18H32O3
G 9(S)-HPODE C18H32O4
G 9,10-DHOME C18H34O4
G 9,12,13-TriHOME C18H34O5
G Linoleate C18H32O2
Generate map of **Linoleic acid metabolism** highlighting potential metabolites.

Methane metabolism: 4 metabolites out of 60 (3 changed) v
G (S)-Malate C4H6O5
G 2-Oxoadipate C6H8O5
G 3-(4-Hydroxyphenyl)pyruvate C9H8O4
G D-Glycerate C3H6O4
Generate map of **Methane metabolism** highlighting potential metabolites.

Nicotinate and nicotinamide metabolism: 5 metabolites out of 46 (3 changed) v
G 1-Methylpyrrolinium C5H10N
G 2,3-Dimethylmaleate C6H8O4
G Maleamate C4H5NO3
G Nicotinamide C6H6N2O
G Nicotinate C6H5NO2
Generate map of **Nicotinate and nicotinamide metabolism** highlighting potential metabolites.

Pantothenate and CoA biosynthesis: 4 metabolites out of 25 (3 changed) v
G 2-Acetolactate C5H8O4
G 3-Methyl-2-oxobutanoic acid C5H8O3
G Pantothenate C9H17NO5

G beta-Alanine C3H7NO2

Generate map of **Pantothenate and CoA biosynthesis** highlighting potential metabolites.

Peptidoglycan biosynthesis: 3 metabolites out of 26 (3 changed)

G D-Alanine C3H7NO2

G D-Alanyl-D-alanine C6H12N2O3

G Orthophosphate H3PO4

Generate map of **Peptidoglycan biosynthesis** highlighting potential metabolites.

Phenylalanine, tyrosine and tryptophan biosynthesis: 4 metabolites out of 31 (3 changed)

G 3-(4-Hydroxyphenyl)pyruvate C9H8O4

G Indole C8H7N

G L-Phenylalanine C9H11NO2

G L-Tryptophan C11H12N2O2

Generate map of **Phenylalanine, tyrosine and tryptophan biosynthesis** highlighting potential metabolites.

Pyruvate metabolism: 5 metabolites out of 28 (3 changed)

G (2S)-2-Isopropylmalate C7H12O5

G (R)-2-Hydroxybutane-1,2,4-tricarboxylate C7H10O7

G (R)-Lactate C3H6O3

G (S)-Malate C4H6O5

G Succinate C4H6O4

Generate map of **Pyruvate metabolism** highlighting potential metabolites.

Starch and sucrose metabolism: 4 metabolites out of 37 (3 changed)

G D-Glucose 6-phosphate C6H13O9P

G D-Glucuronate C6H10O7

G alpha,alpha'-Trehalose 6-phosphate C12H23O14P

G beta-D-Glucose C6H12O6

Generate map of **Starch and sucrose metabolism** highlighting potential metabolites.

Styrene degradation: 4 metabolites out of 23 (3 changed)

G (Z)-Phenylacetaldehyde oxime C8H9NO

G 2-Hydroxy-2,4-pentadienoate C5H6O3

G 2-Phenylacetamide C8H9NO

G Phenylacetonitrile C8H7N

Generate map of **Styrene degradation** highlighting potential metabolites.

Sulfur metabolism: 5 metabolites out of 21 (3 changed)

G L-Homoserine C4H9NO3

G O-Succinyl-L-homoserine C8H13NO6

G Succinate C4H6O4

G Sulfate H2SO4

G Taurine C2H7NO3S

Generate map of **Sulfur metabolism** highlighting potential metabolites.

Taurine and hypotaurine metabolism: 5 metabolites out of 22 (3 changed)

G 2-Hydroxyethanesulfonate C2H6O4S

G L-Alanine C3H7NO2

G L-Glutamate C5H9NO4

G Taurine C2H7NO3S

G Taurocholate C26H45NO7S

Generate map of **Taurine and hypotaurine metabolism** highlighting potential metabolites.

Arachidonic acid metabolism: 2 metabolites out of 74 (2 changed)

G (5Z,8Z,11Z,14Z)-Icosatetraenoic acid C20H32O2

G 2,3-Dinor-8-iso prostaglandin F2alpha C18H30O5

Generate map of **Arachidonic acid metabolism** highlighting potential metabolites.

Benzoate degradation via hydroxylation: 3 metabolites out of 66 (2 changed)

G 2-Hydroxy-2,4-pentadienoate C5H6O3

G 4-Hydroxybenzoate C7H6O3

G p-Benzenediol C6H6O2

Generate map of **Benzoate degradation via hydroxylation** highlighting potential metabolites.

Carbazole degradation: 2 metabolites out of 18 (2 changed)

G 2-Hydroxy-2,4-pentadienoate C5H6O3

G 3-Hydroxyanthranilate C7H7NO3

Generate map of **Carbazole degradation** highlighting potential metabolites.

Clavulanic acid biosynthesis: 2 metabolites out of 10 (2 changed) v

G Dihydroclavaminic acid C8H12N2O4

G L-Arginine C6H14N4O2

Generate map of **Clavulanic acid biosynthesis** highlighting potential metabolites.

D-Alanine metabolism: 3 metabolites out of 4 (2 changed) v

G D-Alanine C3H7NO2

G D-Alanyl-D-alanine C6H12N2O3

G L-Alanine C3H7NO2

Generate map of **D-Alanine metabolism** highlighting potential metabolites.

Ether lipid metabolism: 2 metabolites out of 2 (2 changed) v

G sn-glycero-3-Phosphocholine C8H21NO6P

G sn-glycero-3-Phosphoethanolamine C5H14NO6P

Generate map of **Ether lipid metabolism** highlighting potential metabolites.

Fluorene degradation: 2 metabolites out of 36 (2 changed) v

G 2-Hydroxy-2,4-pentadienoate C5H6O3

G Phthalate C8H6O4

Generate map of **Fluorene degradation** highlighting potential metabolites.

Nitrogen metabolism: 3 metabolites out of 16 (2 changed) v

G Carbamoyl phosphate CH4NO5P

G L-Glutamate C5H9NO4

G L-Glutamine C5H10N2O3

Generate map of **Nitrogen metabolism** highlighting potential metabolites.

Phenylpropanoid biosynthesis: 2 metabolites out of 51 (2 changed) v

G L-Phenylalanine C9H11NO2

G Sinapyl alcohol C11H14O4

Generate map of **Phenylpropanoid biosynthesis** highlighting potential metabolites.

Streptomycin biosynthesis: 2 metabolites out of 23 (2 changed) v

G D-Glucose 6-phosphate C6H13O9P

G myo-Inositol C6H12O6

Generate map of **Streptomycin biosynthesis** highlighting potential metabolites.

Terpenoid backbone biosynthesis: 2 metabolites out of 30 (2 changed) v

G (R)-Mevalonate C6H12O4

G 2-C-Methyl-D-erythritol 4-phosphate C5H13O7P

Generate map of **Terpenoid backbone biosynthesis** highlighting potential metabolites.

Thiamine metabolism: 2 metabolites out of 22 (2 changed) v

G Iminoglycine C2H3NO2

G Thiamine C12H17N4OS

Generate map of **Thiamine metabolism** highlighting potential metabolites.

Ubiquinone and other terpenoid-quinone biosynthesis: 3 metabolites out of 36 (2 changed) v

G 3-(4-Hydroxyphenyl)lactate C9H10O4

G 3-(4-Hydroxyphenyl)pyruvate C9H8O4

G 4-Hydroxybenzoate C7H6O3

Generate map of **Ubiquinone and other terpenoid-quinone biosynthesis** highlighting potential metabolites.

Zeatin biosynthesis: 2 metabolites out of 36 (2 changed) v

G 3-Methylbut-2-enal C5H8O

G Adenine C5H5N5

Generate map of **Zeatin biosynthesis** highlighting potential metabolites.

1- and 2-Methylnaphthalene degradation: 1 metabolite out of 64 (1 changed) v

G Phthalate C8H6O4

Generate map of **1- and 2-Methylnaphthalene degradation** highlighting potential metabolites.

2,4-Dichlorobenzoate degradation: 1 metabolite out of 29 (1 changed) v

G 4-Hydroxybenzoate C7H6O3

Generate map of **2,4-Dichlorobenzoate degradation** highlighting potential metabolites.

3-Chloroacrylic acid degradation: 1 metabolite out of 10 (1 changed)

G 3-Oxopropanoate C3H4O3

Generate map of **3-Chloroacrylic acid degradation** highlighting potential metabolites.

Benzoate degradation via CoA ligation: 2 metabolites out of 57 (1 changed)

G 4-Hydroxybenzoate C7H6O3

G Succinate C4H6O4

Generate map of **Benzoate degradation via CoA ligation** highlighting potential metabolites.

Benzoxazinoid biosynthesis: 1 metabolite out of 9 (1 changed)

G Indole C8H7N

Generate map of **Benzoxazinoid biosynthesis** highlighting potential metabolites.

Biphenyl degradation: 1 metabolite out of 29 (1 changed)

G 2-Hydroxy-2,4-pentadienoate C5H6O3

Generate map of **Biphenyl degradation** highlighting potential metabolites.

Bisphenol A degradation: 2 metabolites out of 21 (1 changed)

G 4-Hydroxybenzoate C7H6O3

G p-Benzenediol C6H6O2

Generate map of **Bisphenol A degradation** highlighting potential metabolites.

Carbon fixation in photosynthetic organisms: 2 metabolites out of 22 (1 changed)

G (S)-Malate C4H6O5

G L-Alanine C3H7NO2

Generate map of **Carbon fixation in photosynthetic organisms** highlighting potential metabolites.

D-Arginine and D-ornithine metabolism: 2 metabolites out of 9 (1 changed)

G L-Arginine C6H14N4O2

G L-Ornithine C5H12N2O2

Generate map of **D-Arginine and D-ornithine metabolism** highlighting potential metabolites.

Diterpenoid biosynthesis: 1 metabolite out of 69 (1 changed)

G Taxa-4(20),11(12)-dien-5alpha-yl acetate C22H34O2

Generate map of **Diterpenoid biosynthesis** highlighting potential metabolites.

Ethylbenzene degradation: 1 metabolite out of 14 (1 changed)

G 2-Hydroxy-2,4-pentadienoate C5H6O3

Generate map of **Ethylbenzene degradation** highlighting potential metabolites.

Glutathione metabolism: 2 metabolites out of 29 (1 changed)

G L-Glutamate C5H9NO4

G L-Ornithine C5H12N2O2

Generate map of **Glutathione metabolism** highlighting potential metabolites.

Glycolysis / Gluconeogenesis: 1 metabolite out of 28 (1 changed)

G beta-D-Glucose C6H12O6

Generate map of **Glycolysis / Gluconeogenesis** highlighting potential metabolites.

Indole alkaloid biosynthesis: 1 metabolite out of 47 (1 changed)

G L-Tryptophan C11H12N2O2

Generate map of **Indole alkaloid biosynthesis** highlighting potential metabolites.

Isoquinoline alkaloid biosynthesis: 2 metabolites out of 93 (1 changed)

G 3-(4-Hydroxyphenyl)pyruvate C9H8O4

G 4-Hydroxyphenylacetaldehyde C8H8O2

Generate map of **Isoquinoline alkaloid biosynthesis** highlighting potential metabolites.

Novobiocin biosynthesis: 2 metabolites out of 23 (1 changed)

G 3-(4-Hydroxyphenyl)pyruvate C9H8O4

G L-Proline C5H9NO2

Generate map of **Novobiocin biosynthesis** highlighting potential metabolites.

Oxidative phosphorylation: 2 metabolites out of 13 (1 changed)

G Orthophosphate H3PO4

G Succinate C4H6O4

Generate map of **Oxidative phosphorylation** highlighting potential metabolites.

Penicillin and cephalosporin biosynthesis: 1 metabolite out of 16 (1 changed)

G L-2-Aminoadipate C6H11NO4

Generate map of **Penicillin and cephalosporin biosynthesis** highlighting potential metabolites.

Phosphatidylinositol signaling system: 1 metabolite out of 16 (1 changed)

G myo-Inositol C6H12O6

Generate map of **Phosphatidylinositol signaling system** highlighting potential metabolites.

Phosphonate and phosphinate metabolism: 1 metabolite out of 39 (1 changed)

G Phosphonoacetaldehyde C2H5O4P

Generate map of **Phosphonate and phosphinate metabolism** highlighting potential metabolites.

Photosynthesis: 1 metabolite out of 10 (1 changed)

G Orthophosphate H3PO4

Generate map of **Photosynthesis** highlighting potential metabolites.

Puromycin biosynthesis: 1 metabolite out of 12 (1 changed)

G Puromycin C22H29N7O5

Generate map of **Puromycin biosynthesis** highlighting potential metabolites.

Riboflavin metabolism: 3 metabolites out of 19 (1 changed)

G Lumichrome C12H10N4O2

G Riboflavin C17H20N4O6

G p-Benzenediol C6H6O2

Generate map of **Riboflavin metabolism** highlighting potential metabolites.

Sphingolipid metabolism: 1 metabolite out of 11 (1 changed)

G Ethanolamine phosphate C2H8NO4P

Generate map of **Sphingolipid metabolism** highlighting potential metabolites.

Synthesis and degradation of ketone bodies: 1 metabolite out of 6 (1 changed)

G (R)-3-Hydroxybutanoate C4H8O3

Generate map of **Synthesis and degradation of ketone bodies** highlighting potential metabolites.

Tetrachloroethene degradation: 1 metabolite out of 36 (1 changed)

G 3-Oxopropanoate C3H4O3

Generate map of **Tetrachloroethene degradation** highlighting potential metabolites.

Toluene and xylene degradation: 1 metabolite out of 38 (1 changed)

G 2-Hydroxy-2,4-pentadienoate C5H6O3

Generate map of **Toluene and xylene degradation** highlighting potential metabolites.

Trinitrotoluene degradation: 1 metabolite out of 20 (1 changed)

G (S)-Methylmalonate semialdehyde C4H6O3

Generate map of **Trinitrotoluene degradation** highlighting potential metabolites.

Vitamin B6 metabolism: 1 metabolite out of 28 (1 changed)

G 4-Pyridoxolactone C8H7NO3

Generate map of **Vitamin B6 metabolism** highlighting potential metabolites.

alpha-Linolenic acid metabolism: 1 metabolite out of 39 (1 changed)

G 3-Hexenal C6H10O

Generate map of **alpha-Linolenic acid metabolism** highlighting potential metabolites.

Betalain biosynthesis: 2 metabolites out of 24

G 2-Carboxy-2,3-dihydro-5,6-dihydroxyindole C9H9NO4

G Dopaquinone C9H9NO4

Generate map of **Betalain biosynthesis** highlighting potential metabolites.

Limonene and pinene degradation: 2 metabolites out of 59

G (-)-Limonene C10H16

G (1S,4R)-1-Hydroxy-2-oxolimonene C10H16O2

Generate map of **Limonene and pinene degradation** highlighting potential metabolites.

gamma-Hexachlorocyclohexane degradation: 2 metabolites out of 72

G Succinate C4H6O4

G p-Benzenediol C6H6O2

Generate map of **gamma-Hexachlorocyclohexane degradation** highlighting potential metabolites.

Atrazine degradation: 1 metabolite out of 21

G Urea-1-carboxylate C2H4N2O3

Generate map of **Atrazine degradation** highlighting potential metabolites.

Biosynthesis of vancomycin group antibiotics: 1 metabolite out of 18 v

G 3-(4-Hydroxyphenyl)pyruvate C9H8O4

Generate map of **Biosynthesis of vancomycin group antibiotics** highlighting potential metabolites.

Fatty acid elongation in mitochondria: 1 metabolite out of 28 v

G Hexadecanoic acid C16H32O2

Generate map of **Fatty acid elongation in mitochondria** highlighting potential metabolites.

Fatty acid metabolism: 1 metabolite out of 39 v

G Hexadecanoic acid C16H32O2

Generate map of **Fatty acid metabolism** highlighting potential metabolites.

Metabolism of xenobiotics by cytochrome P450: 1 metabolite out of 82 v

G Nicotine C10H14N2

Generate map of **Metabolism of xenobiotics by cytochrome P450** highlighting potential metabolites.

Monoterpenoid biosynthesis: 1 metabolite out of 44 v

G (-)-Limonene C10H16

Generate map of **Monoterpenoid biosynthesis** highlighting potential metabolites.

Selenoamino acid metabolism: 1 metabolite out of 14 v

G L-Alanine C3H7NO2

Generate map of **Selenoamino acid metabolism** highlighting potential metabolites.

Stilbenoid, diarylheptanoid and gingerol biosynthesis: 1 metabolite out of 24 v

G [6]-Gingerol C17H26O4

Generate map of **Stilbenoid, diarylheptanoid and gingerol biosynthesis** highlighting potential metabolites.

Maps containing No Compounds from Data Set: show

David Leader fecit