

Metabolic Map: *Mus musculus*

Species code: mmu

Enzyme coverage threshold: 66%

Rescued modules: 5

Summary Statistics

Input Data

| Metric | Count |
|-------------------------------------|--------|
| Total KEGG reactions | 12,384 |
| Species enzyme-backed reactions | 2,153 |
| Modules selected | 125 |
| Reactions before graph construction | 3,040 |

Final Graph

| Node Type | Count |
|-----------|-------|
| Reactions | 1,610 |
| Compounds | 1,014 |
| Genes | 1,312 |
| Modules | 106 |
| Pathways | 120 |

Total edges: 15,241

Graph Schema

Node Types

Each node has a `group` attribute: `Compound`, `Reaction`, `Gene`, `Module`, or `Pathway`.

Node Identifiers

| Group | ID Format | Example |
|----------|----------------------------------|---------------------------------|
| Compound | <code>kegg:CXXXXXX</code> | <code>kegg:C00001</code> |
| Reaction | <code>kegg:RXXXXXX</code> | <code>kegg:R00286</code> |
| Module | <code>kegg:MXXXXXX</code> | <code>kegg:M00001</code> |
| Pathway | <code>kegg:mapXXXXXX</code> | <code>kegg:map00010</code> |
| Gene | <code>kegg:mmu:XXXXXXXXXX</code> | <code>kegg:mmu:100037283</code> |

Additional Node Attributes

| Group | Attributes |
|----------|--|
| Compound | <code>compound_name</code> |
| Gene | <code>gene_symbol</code> , <code>ensembl_id</code> , <code>ncbi_gene_id</code> |
| Module | <code>module_name</code> |
| Pathway | <code>pathway_name</code> |

Edge Attributes

- **Compound ↔ Reaction:** `coef` (stoichiometric coefficient), `compartment`
- **Gene/Module/Pathway → Reaction:** no additional attributes

Rescued Modules

The following modules were manually included despite lacking species-specific KEGG submaps:

- M00104
- M00088
- M00978
- M00843
- M00367

Dropped Modules

The following 28 modules met the coverage threshold but were not included:

| Module | Coverage | Reactions | Reason | Name |
|--------|----------|-----------|---------------------------------|--|
| M00013 | 86% | 7 | no species-specific KEGG submap | Malonate semialdehyde pathway, propan... |
| M00074 | 80% | 5 | no species-specific KEGG submap | N-glycan biosynthesis, high-mannose type |
| M00093 | 67% | 3 | no species-specific KEGG submap | Phosphatidylethanolamine (PE) biosynt... |
| M00102 | 76% | 18 | no species-specific KEGG submap | Ergocalciferol biosynthesis, FPP => e... |
| M00133 | 75% | 4 | no species- | |

| Module | Coverage | Reactions | Reason | Name |
|---------------|-----------------|------------------|---------------------------------|--|
| | | | specific KEGG submap | Polyamine biosynthesis, arginine => a... |
| M00140 | 100% | 4 | no species-specific KEGG submap | C1-unit interconversion, prokaryotes |
| M00144 | 100% | 1 | no species-specific KEGG submap | NADH:quinone oxidoreductase, prokaryotes |
| M00145 | 100% | 1 | no species-specific KEGG submap | NAD(P)H:quinone oxidoreductase, chlor... |
| M00149 | 100% | 1 | no species-specific KEGG submap | Succinate dehydrogenase, prokaryotes |
| M00150 | 100% | 1 | no species-specific KEGG submap | Fumarate reductase, prokaryotes |
| M00157 | 100% | 1 | no species-specific KEGG submap | F-type ATPase, prokaryotes and chloro... |
| M00159 | 100% | 1 | no species-specific | V/A-type ATPase, prokaryotes |

| Module | Coverage | Reactions | Reason | Name |
|---------------|-----------------|------------------|---------------------------------|---|
| | | | KEGG submap | |
| M00165 | 71% | 14 | no species-specific KEGG submap | Reductive pentose phosphate cycle (Ca...) |
| M00171 | 75% | 6 | no species-specific KEGG submap | C4-dicarboxylic acid cycle, NAD - mal... |
| M00344 | 75% | 4 | no species-specific KEGG submap | Formaldehyde assimilation, xylulose m... |
| M00346 | 70% | 9 | no species-specific KEGG submap | Formaldehyde assimilation, serine pat... |
| M00364 | 100% | 4 | no species-specific KEGG submap | C10-C20 isoprenoid biosynthesis, bact... |
| M00365 | 100% | 4 | no species-specific KEGG submap | C10-C20 isoprenoid biosynthesis, archaea |
| M00366 | 100% | 4 | no species-specific | C10-C20 isoprenoid biosynthesis, plants |

| Module | Coverage | Reactions | Reason | Name |
|---------------|-----------------|------------------|---------------------------------|--|
| | | | KEGG submap | |
| M00532 | 83% | 12 | no species-specific KEGG submap | Photorespiration |
| M00546 | 75% | 8 | no species-specific KEGG submap | Purine degradation, xanthine => urea |
| M00881 | 100% | 4 | no species-specific KEGG submap | Lipoic acid biosynthesis, plants and ... |
| M00922 | 67% | 3 | no species-specific KEGG submap | CMP-Neu5Ac biosynthesis, bacteria, UD... |
| M00926 | 67% | 9 | no species-specific KEGG submap | Heme biosynthesis, bacteria, glutamyl... |
| M00936 | 75% | 4 | no species-specific KEGG submap | Melatonin biosynthesis, plants, trypt... |
| M00954 | 67% | 3 | no species-specific | CMP-KDN biosynthesis, Man-6P => CMP-KDN |

| Module | Coverage | Reactions | Reason | Name |
|---------------|-----------------|------------------|---------------------------------|---|
| | | | KEGG submap | |
| M00997 | 67% | 3 | no species-specific KEGG submap | UDP-Xyl/L-Ara biosynthesis, UDP-Glc => G... |
| M01006 | 80% | 5 | no species-specific KEGG submap | GDP-D-Rha4N biosynthesis, Fru-6P => G... |