## Independent Section

Contains tests that are independent of the class of modeled organism, a model's complexity or types of identifiers that are used to describe its ~~components. Parameterization or initialization of the network is not~~

### Consistency

| | | |
|---|---|---|
| Stoichiometric Consistency | 100.0% | X3 ⌄ |
| Mass Balance | 99.7% | ⌄ |
| Charge Balance | 96.6% | ⌄ |
| Metabolite Connectivity | 100.0% | ⌄ |
| Unbounded Flux In Default Medium | 96.0% | ⌄ |
| Sub Total | 99% | X3 ⌄ |

### Annotation - Metabolites

| | | |
|---|---|---|
| Presence of Metabolite Annotation | 97.0% | ⌄ |
| Metabolite Annotations Per Database | Info | ⌄ |
| pubchem.compound | 0.0% | ⌄ |
| kegg.compound | 35.8% | ⌄ |
| seed.compound | 0.0% | ⌄ |
| inchikey | 0.0% | ⌄ |
| inchi | 0.0% | ⌄ |
| chebi | 0.0% | ⌄ |

## Specific Section

Covers general statistics and specific aspects of a metabolic network that are not universally applicable. See readme for more details.

### SBML

| | | |
|---|---|---|
| SBML Level and Version | SBML Level 3 Version 1 | ⌄ |
| FBC enabled | true | ⌄ |

### Basic Information

| | | |
|---|---|---|
| Model Identifier | M_model Gapfilled | ⌄ |
| Total Metabolites | 1,269 | ⌄ |
| Total Reactions | 1,526 | ⌄ |
| Total Genes | 888 | ⌄ |
| Total Compartments | 1 | ⌄ |
| Metabolic Coverage | 1.72 | ⌄ |
| Uncoserved Metabolites | 0 | ⌄ |
| Minimal Inconsistent Net Stoichiometries | 0 | ⌄ |

### Metabolite Information

| | | |
|---|---|---|
| Unique Metabolites | 1,269 | ⌄ |
| Duplicate Metabolites in Identical Compartments | 0 | ⌄ |

| | | |
|---|---|---|
| metanetx.chemical | 93.9% | ⌄ |
| bigg.metabolite | 0.0% | ⌄ |
| biocyc | 0.0% | ⌄ |
| Metabolite Annotation Conformity Per Database | Info | ⌄ |
| pubchem.compound | 0.0% | ⌄ |
| kegg.compound | 100.0% | ⌄ |
| seed.compound | 0.0% | ⌄ |
| inchikey | 0.0% | ⌄ |
| inchi | 0.0% | ⌄ |
| chebi | 0.0% | ⌄ |
| hmdb | 100.0% | ⌄ |
| reactome | 0.0% | ⌄ |
| metanetx.chemical | 100.0% | ⌄ |
| bigg.metabolite | 0.0% | ⌄ |
| biocyc | 0.0% | ⌄ |
| Uniform Metabolite Identifier Namespace | 100.0% | ⌄ |
| Sub Total | 59% | ⌄ |

## Annotation - Reactions

| | | |
|---|---|---|
| Presence of Reaction Annotation | 96.1% | ⌄ |
| Reaction Annotations Per Database | Info | ⌄ |

| | | |
|---|---|---|
| Medium Components | 36 | ⌄ |

## Reaction Information

| | | |
|---|---|---|
| Purely Metabolic Reactions | 1,366 | ⌄ |
| Purely Metabolic Reactions with Constraints | 11 | ⌄ |
| Transport Reactions | 0 | ⌄ |
| Transport Reactions with Constraints | 0 | ⌄ |
| Reactions With Partially Identical Annotations | 0.04 | ⌄ |
| Duplicate Reactions | 0.00 | ⌄ |
| Reactions With Identical Genes | 0.51 | ⌄ |

## Gene-Protein-Reaction (GPR) Associations

| | | |
|---|---|---|
| Reactions without GPR | 112 | ⌄ |
| Fraction of Transport Reactions without GPR | 1.00 | ⌄ |
| Enzyme Complexes | 151 | ⌄ |

## Biomass

| | | |
|---|---|---|
| Biomass Reactions Identified | 3 | ⌄ |
| Biomass Consistency | Info | ⌄ |
| BIOMASS_high_salinity | 1.17 | ⌄ |
| BIOMASS_low_salinity | 1.11 | ⌄ |

| | | |
|---|---|---|
| seed.reaction | 0.0% | ⌄ |
| metanetx.reaction | 94.6% | ⌄ |
| bigg.reaction | 0.0% | ⌄ |
| reactome | 0.0% | ⌄ |
| ec-code | 45.2% | ⌄ |
| brenda | 0.0% | ⌄ |
| biocyc | 0.0% | ⌄ |
| Reaction Annotation Conformity Per Database | Info | ⌄ |
| rhea | 0.0% | ⌄ |
| kegg.reaction | 100.0% | ⌄ |
| seed.reaction | 0.0% | ⌄ |
| metanetx.reaction | 100.0% | ⌄ |
| bigg.reaction | 0.0% | ⌄ |
| reactome | 0.0% | ⌄ |
| ec-code | 100.0% | ⌄ |
| brenda | 0.0% | ⌄ |
| biocyc | 0.0% | ⌄ |
| Uniform Reaction Identifier Namespace | 99.8% | ⌄ |
| Sub Total | 61% | ⌄ |

## Annotation - Genes

| | | |
|---|---|---|
| BIOMASS_high_salinity | 0.64 | ⌄ |
| BIOMASS_low_salinity | 0.72 | ⌄ |
| BIOMASS_medium_salinity | 0.70 | ⌄ |
| Unrealistic Growth Rate In Default Medium | Info | ⌄ |
| BIOMASS_high_salinity | false | ⌄ |
| BIOMASS_low_salinity | false | ⌄ |
| BIOMASS_medium_salinity | false | ⌄ |
| Biomass Production In Complete Medium | Info | ⌄ |
| BIOMASS_high_salinity | 100.22 | ⌄ |
| BIOMASS_low_salinity | 79.55 | ⌄ |
| BIOMASS_medium_salinity | 83.18 | ⌄ |
| Blocked Biomass Precursors In Default Medium | Info | ⌄ |
| BIOMASS_high_salinity | 0 | ⌄ |
| BIOMASS_low_salinity | 0 | ⌄ |
| BIOMASS_medium_salinity | 0 | ⌄ |
| Blocked Biomass Precursors In Complete Medium | Info | ⌄ |
| BIOMASS_high_salinity | 0 | ⌄ |
| BIOMASS_low_salinity | 0 | ⌄ |
| BIOMASS_medium_salinity | 0 | ⌄ |
| Ratio of Direct Metabolites in Biomass Reaction | Info | ⌄ |

| | | |
|---|---|---|
| refseq | 0.0% | ⌄ |
| uniprot | 0.0% | ⌄ |
| ecogene | 0.0% | ⌄ |
| kegg.genes | 0.0% | ⌄ |
| ncbigi | 0.0% | ⌄ |
| ncbigene | 0.0% | ⌄ |
| ncbiprotein | 0.0% | ⌄ |
| ccds | 0.0% | ⌄ |
| hprd | 0.0% | ⌄ |
| asap | 0.0% | ⌄ |
| Gene Annotation Conformity Per Database | Info | ⌄ |
| refseq | 0.0% | ⌄ |
| uniprot | 0.0% | ⌄ |
| ecogene | 0.0% | ⌄ |
| kegg.genes | 0.0% | ⌄ |
| ncbigi | 0.0% | ⌄ |
| ncbigene | 0.0% | ⌄ |
| ncbiprotein | 0.0% | ⌄ |
| ccds | 0.0% | ⌄ |
| hprd | 0.0% | ⌄ |
| asap | 0.0% | ⌄ |

| | | |
|---|---|---|
| BIOMASS_medium_salinity | 0.00 | ⌄ |
| Number of Missing Essential Biomass Precursors | Info | ⌄ |
| BIOMASS_high_salinity | 24 | ⌄ |
| BIOMASS_low_salinity | 24 | ⌄ |
| BIOMASS_medium_salinity | 24 | ⌄ |

## Energy Metabolism

| | | |
|---|---|---|
| Non-Growth Associated Maintenance Reaction | Errored | ⌄ |
| Growth-associated Maintenance in Biomass Reaction | Info | ⌄ |
| BIOMASS_high_salinity | false | ⌄ |
| BIOMASS_low_salinity | false | ⌄ |
| BIOMASS_medium_salinity | false | ⌄ |
| Number of Reversible Oxygen-Containing Reactions | 9 | ⌄ |
| Erroneous Energy-generating Cycles | Info | ⌄ |
| MNXM3 | Skipped | ⌄ |
| MNXM63 | Skipped | ⌄ |
| MNXM51 | Skipped | ⌄ |
| MNXM121 | Skipped | ⌄ |
| MNXM423 | Skipped | ⌄ |
| MNXM6 | Skipped | ⌄ |
| MNXM10 | Skipped | ⌄ |

## Annotation - SBO Terms

| | | |
|---|---|---|
| Metabolite General SBO Presence | 0.0% | ⌄ |
| Metabolite SBO:0000247 Presence | 0.0% | ⌄ |
| Reaction General SBO Presence | 0.0% | ⌄ |
| Metabolic Reaction SBO:0000176 Presence | 0.0% | ⌄ |
| Transport Reaction SBO:0000185 Presence | Skipped | ⌄ |
| Exchange Reaction SBO:0000627 Presence | 0.0% | ⌄ |
| Demand Reaction SBO:0000628 Presence | Skipped | ⌄ |
| Sink Reactions SBO:0000632 Presence | Skipped | ⌄ |
| Gene General SBO Presence | 0.0% | ⌄ |
| Gene SBO:0000243 Presence | 0.0% | ⌄ |
| Biomass Reactions SBO:0000629 Presence | 0.0% | ⌄ |
| Sub Total | 0% | X2 ⌄ |
| Total Score | 47% | ⌄ |

Total Score

# 47%

Score per Category

| | | |
|---|---|---|
| MNXM191 | Skipped | ⌄ |
| MNXM223 | Skipped | ⌄ |
| MNXM7517 | Skipped | ⌄ |
| MNXM12233 | Skipped | ⌄ |
| MNXM558 | Skipped | ⌄ |
| MNXM21 | Skipped | ⌄ |
| MNXM89557 | Skipped | ⌄ |

## Network Topology

| | | |
|---|---|---|
| Universally Blocked Reactions | 433 | ⌄ |
| Orphan Metabolites | 55 | ⌄ |
| Dead-end Metabolites | 75 | ⌄ |
| Stoichiometrically Balanced Cycles | 37 | ⌄ |
| Metabolite Production In Complete Medium | 307 | ⌄ |
| Metabolite Consumption In Complete Medium | 393 | ⌄ |

## Matrix Conditioning

| | | |
|---|---|---|
| Ratio Min/Max Non-Zero Coefficients | 0.00 | ⌄ |
| Independent Conservation Relations | 68 | ⌄ |
| Rank | 1201 | ⌄ |
| Degrees Of Freedom | 325 | ⌄ |

annotation_met

annotation_rxn

annotation_gene

annotation_sbo

| Growth Prediction | Skipped ∨ |
| Gene Essentiality Prediction | Skipped ∨ |

## Misc. Tests

## Environment

| Python Version | 3.8.5 |
| Platform | Windows |
| Memote Version | 0.13.0 |