



## 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 required. See readme for more details.

### Consistency

Stoichiometric Consistency	100.0%	↕
Mass Balance	98.8%	↕
Charge Balance	99.0%	↕
Metabolite Connectivity	100.0%	↕
Unbounded Flux In Default Medium	99.8%	↕
Sub Total	100%	↕

### Annotation - Metabolites

Presence of Metabolite Annotation	100.0%	↕
Metabolite Annotations Per Database	Info	↕
pubchem.compound	0.0%	↕
kegg.compound	83.1%	↕
seed.compound	85.6%	↕
inchikey	0.0%	↕
inchi	52.6%	↕
chebi	0.0%	↕
hmdb	0.0%	↕
reactome	0.0%	↕
metanetx.chemical	0.0%	↕
bigg.metabolite	77.9%	↕
biocyc	0.0%	↕
Metabolite Annotation Conformity Per Database	Info	↕
pubchem.compound	0.0%	↕
kegg.compound	100.0%	↕
seed.compound	100.0%	↕
inchikey	0.0%	↕
inchi	100.0%	↕
chebi	0.0%	↕
hmdb	0.0%	↕
reactome	0.0%	↕
metanetx.chemical	0.0%	↕
bigg.metabolite	100.0%	↕
biocyc	0.0%	↕
Uniform Metabolite Identifier Namespace	0.0%	↕
Sub Total	41%	↕

### Annotation - Reactions

Presence of Reaction Annotation	99.1%	↕
Reaction Annotations Per Database	Info	↕
rhea	0.0%	↕
kegg.reaction	0.0%	↕
seed.reaction	63.6%	↕
metanetx.reaction	0.0%	↕
bigg.reaction	0.0%	↕
reactome	0.0%	↕
ec-code	64.8%	↕
brenda	0.0%	↕
biocyc	0.0%	↕
Reaction Annotation Conformity Per Database	Info	↕
rhea	0.0%	↕
kegg.reaction	0.0%	↕
seed.reaction	100.0%	↕
metanetx.reaction	0.0%	↕
bigg.reaction	0.0%	↕
reactome	0.0%	↕
ec-code	99.8%	↕
brenda	0.0%	↕
biocyc	0.0%	↕
Uniform Reaction Identifier Namespace	100.0%	↕
Sub Total	59%	↕

### Annotation - Genes

Presence of Gene Annotation	100.0%	↕
Gene Annotations 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%	↕
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%	↕
Sub Total	33%	↕

### Annotation - SBO Terms

Metabolite General SBO Presence	100.0%	↕
Metabolite SBO:0000247 Presence	100.0%	↕
Reaction General SBO Presence	99.1%	↕
Metabolic Reaction SBO:0000176 Presence	98.8%	↕
Transport Reaction SBO:0000185 Presence	98.2%	↕
Exchange Reaction SBO:0000627 Presence	100.0%	↕
Demand Reaction SBO:0000628 Presence	100.0%	↕
Sink Reactions SBO:0000632 Presence	100.0%	↕
Gene General SBO Presence	100.0%	↕
Gene SBO:0000243 Presence	100.0%	↕
Biomass Reactions SBO:0000629 Presence	100.0%	↕

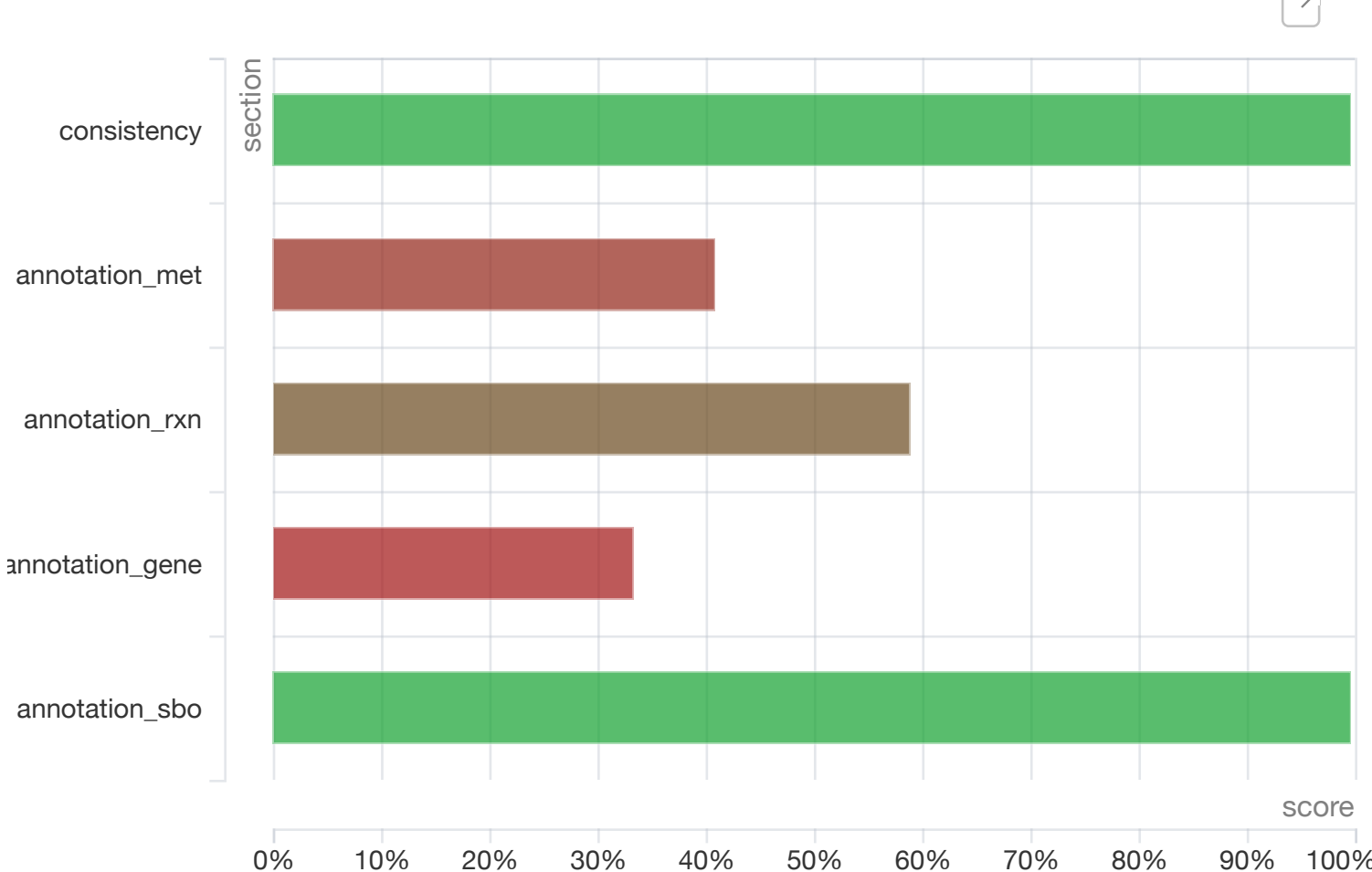
Sub Total	100%	↕
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Total Score	89%	↕
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Total Score

# 89%

Score per Category



## 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_ICS1224	↕
Total Metabolites	984	↕
Total Reactions	1,256	↕
Total Genes	1,226	↕
Total Compartments	2	↕
Metabolic Coverage	1.02	↕
Uncoserved Metabolites	0	↕
Minimal Inconsistent Net Stoichiometries	0	↕

### Metabolite Information

Unique Metabolites	984	↕
Duplicate Metabolites in Identical Compartments	4	↕
Metabolites without Charge	0	↕
Metabolites without Formula	0	↕
Medium Components	20	↕

### Reaction Information

Purely Metabolic Reactions	917	↕
Purely Metabolic Reactions with Constraints	0	↕
Transport Reactions	168	↕
Transport Reactions with Constraints	0	↕
Reactions With Partially Identical Annotations	0.00	↕
Duplicate Reactions	0.00	↕
Reactions With Identical Genes	0.43	↕

### Gene-Protein-Reaction (GPR) Associations

Reactions without GPR	14	↕
Fraction of Transport Reactions without GPR	0.04	↕
Enzyme Complexes	241	↕

### Biomass

Biomass Reactions Identified	1	↕
Biomass Consistency	Errored	↕
Biomass Production In Default Medium	0.15	↕
Unrealistic Growth Rate In Default Medium	false	↕
Biomass Production In Complete Medium	63.97	↕
Blocked Biomass Precursors In Default Medium	1	↕
Blocked Biomass Precursors In Complete Medium	1	↕
Ratio of Direct Metabolites in Biomass Reaction	0.20	↕
Number of Missing Essential Biomass Precursors	29	↕

### Energy Metabolism

Non-Growth Associated Maintenance Reaction	Errored	↕
Growth-associated Maintenance in Biomass Reaction	false	↕
Number of Reversible Oxygen-Containing Reactions	5	↕
Erroneous Energy-generating Cycles	Info	↕
MNXM3	Skipped	↕
MNXM63	Skipped	↕
MNXM51	Skipped	↕
MNXM121	Skipped	↕
MNXM423	Skipped	↕
MNXM6	Skipped	↕
MNXM10	Skipped	↕
MNXM38	Skipped	↕
MNXM208	Skipped	↕
MNXM191	Skipped	↕
MNXM223	Skipped	↕
MNXM7517	Skipped	↕
MNXM12233	Skipped	↕
MNXM558	Skipped	↕
MNXM21	Skipped	↕
MNXM89557	Skipped	↕

### Network Topology

Universally Blocked Reactions	10	↕
Orphan Metabolites	0	↕
Dead-end Metabolites	3	↕
Stoichiometrically Balanced Cycles	3	↕
Metabolite Production In Complete Medium	135	↕
Metabolite Consumption In Complete Medium	144	↕

### Matrix Conditioning

Ratio Min/Max Non-Zero Coefficients	0.00	↕
Independent Conservation Relations	8	↕
Rank	976	↕
Degrees Of Freedom	280	↕

### Experimental Data Comparison

Growth Prediction	Skipped	↕
Gene Essentiality Prediction	Skipped	↕

### Misc. Tests

### Environment

Python Version	3.8.5
Platform	Darwin
Memote Version	0.12.0