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	99.2%
Charge Balance	99.2%
Metabolite Connectivity	100.0%
Unbounded Flux In Default Medium	96.0%
Sub Total	99%

Annotation - Metabolites

Presence of Metabolite Annotation	100.0%
Metabolite Annotations Per Database	Info
pubchem.compound	0.0%
kegg.compound	78.5%
seed.compound	87.9%
inchikey	78.4%
inchi	0.0%
chebi	81.2%
hmdb	61.7%
reactome	47.4%
metanetx.chemical	97.0%
bigg.metabolite	99.6%
biocyc	80.3%
Metabolite Annotation Conformity Per Database	Info
pubchem.compound	0.0%
kegg.compound	100.0%
seed.compound	100.0%
inchikey	100.0%
inchi	0.0%
chebi	100.0%
hmdb	100.0%
reactome	100.0%
metanetx.chemical	100.0%
bigg.metabolite	100.0%
biocyc	100.0%
Uniform Metabolite Identifier Namespace	100.0%
Sub Total	87%

Annotation - Reactions

Presence of Reaction Annotation	100.0%
Reaction Annotations Per Database	Info
rhea	42.9%
kegg.reaction	32.9%
seed.reaction	64.1%
metanetx.reaction	80.5%
bigg.reaction	84.6%
reactome	12.6%
ec-code	44.7%
brenda	0.0%
biocyc	42.2%
Reaction Annotation Conformity Per Database	Info
rhea	98.2%
kegg.reaction	100.0%
seed.reaction	100.0%
metanetx.reaction	100.0%
bigg.reaction	99.9%
reactome	100.0%
ec-code	99.0%
brenda	0.0%
biocyc	100.0%
Uniform Reaction Identifier Namespace	99.9%
Sub Total	83%

Annotation - Genes

Presence of Gene Annotation	100.0%
Gene Annotations Per Database	Info
refseq	0.0%
uniprot	96.7%
ecogene	0.0%
kegg.genes	94.2%
ncbigi	0.0%
ncbigene	98.0%
ncbiprotein	97.8%
ccds	0.0%
hprd	0.0%
asap	0.0%
Gene Annotation Conformity Per Database	Info
refseq	0.0%
uniprot	100.0%
ecogene	0.0%
kegg.genes	5.8%
ncbigi	0.0%
ncbigene	100.0%
ncbiprotein	100.0%
ccds	0.0%
hprd	0.0%
asap	0.0%
Sub Total	56%

Annotation - SBO Terms

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	Errored
FBC enabled	Errored

Basic Information

Model Identifier	default_model
Total Metabolites	1,161
Total Reactions	1,385
Total Genes	638
Total Compartments	3
Metabolic Coverage	2.17
Uncoserved Metabolites	0
Minimal Inconsistent Net Stoichiometries	Skipped

Metabolite Information

Unique Metabolites	747
Duplicate Metabolites in Identical Compartments	0
Metabolites without Charge	0
Metabolites without Formula	0
Medium Components	55

Reaction Information

Purely Metabolic Reactions	757
Purely Metabolic Reactions with Constraints	1
Transport Reactions	420
Transport Reactions with Constraints	3
Reactions With Partially Identical Annotations	0.08
Duplicate Reactions	0.00
Reactions With Identical Genes	0.37

Gene-Protein-Reaction (GPR) Associations

Reactions without GPR	303
Fraction of Transport Reactions without GPR	0.62
Enzyme Complexes	135

Biomass

Biomass Reactions Identified	1
Biomass Consistency	1.00
Biomass Production In Default Medium	1.04
Unrealistic Growth Rate In Default Medium	false
Biomass Production In Complete Medium	80.94
Blocked Biomass Precursors In Default Medium	1
Blocked Biomass Precursors In Complete Medium	1
Ratio of Direct Metabolites in Biomass Reaction	0.15
Number of Missing Essential Biomass Precursors	1

Energy Metabolism

Non-Growth Associated Maintenance Reaction	1
Growth-associated Maintenance in Biomass Reaction	true
Number of Reversible Oxygen-Containing Reactions	3
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	234
Orphan Metabolites	68
Dead-end Metabolites	65
Stoichiometrically Balanced Cycles	30
Metabolite Production In Complete Medium	228
Metabolite Consumption In Complete Medium	252

Matrix Conditioning

Ratio Min/Max Non-Zero Coefficients	0.00
Independent Conservation Relations	51
Rank	1110
Degrees Of Freedom	275

Experimental Data Comparison

Growth Prediction	Skipped
Gene Essentiality Prediction	Skipped

Misc. Tests

Environment

Reaction General SBO Presence	100.0%
Metabolic Reaction SBO:0000176 Presence	90.6%
Transport Reaction SBO:0000185 Presence	100.0%
Exchange Reaction SBO:0000627 Presence	100.0%
Demand Reaction SBO:0000628 Presence	100.0%
Sink Reactions SBO:0000632 Presence	Skipped
Gene General SBO Presence	100.0%
Gene SBO:0000243 Presence	100.0%
Biomass Reactions SBO:0000629 Presence	100.0%
Sub Total	90%
Total Score	91%

Total Score

91%

Score per Category