

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	99.9%	x3	▼
Mass Balance	99.6%		▼
Charge Balance	99.7%		▼
Metabolite Connectivity	99.9%		▼
Unbounded Flux In Default Medium	83.2%		▼
Sub Total	97%	x3	▼

Annotation - Metabolites

Presence of Metabolite Annotation 100.0% ▼

Metabolite Annotations Per Database **Info** ▼

pubchem.compound	0.0%	▼
kegg.compound	57.7%	▼
seed.compound	65.8%	▼
inchikey	0.0%	▼
inchi	0.0%	▼
chebi	60.1%	▼
hmdb	0.0%	▼
reactome	30.2%	▼
metanetx.chemical	74.9%	▼
bigg.metabolite	72.2%	▼
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	0.0%	▼
chebi	0.0%	▼
hmdb	0.0%	▼
reactome	0.0%	▼
metanetx.chemical	100.0%	▼
bigg.metabolite	100.0%	▼
biocyc	0.0%	▼

Uniform Metabolite Identifier Namespace 100.0% ▼

Sub Total 67% ▼

Annotation - Reactions

Presence of Reaction Annotation 100.0% ▼

Reaction Annotations Per Database **Info** ▼

rhea	0.0%	▼
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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	iJN1463	▼
Total Metabolites	2,155	▼
Total Reactions	2,940	▼
Total Genes	1,462	▼
Total Compartments	4	▼
Metabolic Coverage	2.01	▼

Metabolite Information

Unique Metabolites	2,155	▼
Duplicate Metabolites in Identical Compartments	0	▼
Metabolites without Charge	0	▼
Metabolites without Formula	0	▼
Medium Components	40	▼

Reaction Information

Purely Metabolic Reactions	1,732	▼
Purely Metabolic Reactions with Constraints	75	▼
Transport Reactions	824	▼
Transport Reactions with Constraints	32	▼
Thermodynamic Reversibility of Purely Metabolic Reactions	0.43	▼
Reactions With Partially Identical Annotations	0.02	▼
Duplicate Reactions	0.00	▼
Reactions With Identical Genes	0.77	▼

Gene-Protein-Reaction (GPR) Associations

Reactions without GPR	451	▼
Fraction of Transport Reactions without GPR	0.39	▼
Enzyme Complexes	312	▼

Biomass

Biomass Reactions Identified	2	▼
Biomass Consistency	Info	▼
BiomassKT2440_Core2	0.98	▼
BiomassKT2440_WT3	0.98	▼
Biomass Production In Default Medium	Info	▼
BiomassKT2440_Core2	0.62	▼
BiomassKT2440_WT3	0.62	▼

metanetx.reaction	20.8%	▼
bigg.reaction	63.6%	▼
reactome	0.0%	▼
ec-code	0.0%	▼
brenda	0.0%	▼
biocyc	0.0%	▼
Reaction Annotation Conformity Per Database	Info	▼
rhea	0.0%	▼
kegg.reaction	0.0%	▼
seed.reaction	0.0%	▼
metanetx.reaction	100.0%	▼
bigg.reaction	100.0%	▼
reactome	0.0%	▼
ec-code	0.0%	▼
brenda	0.0%	▼
biocyc	0.0%	▼
Uniform Reaction Identifier Namespace	100.0%	▼

Sub Total 58% ▼

Annotation - Genes

Presence of Gene Annotation 100.0% ▼

Gene Annotations Per Database **Info** ▼

refseq	98.5%	▼
uniprot	98.5%	▼
ecogene	0.0%	▼
kegg.genes	98.8%	▼
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	99.4%	▼
uniprot	100.0%	▼
ecogene	0.0%	▼
kegg.genes	100.0%	▼
ncbigi	0.0%	▼
ncbigene	0.0%	▼
ncbiprotein	0.0%	▼
ccds	0.0%	▼
hprd	0.0%	▼
asap	0.0%	▼

Sub Total 53% ▼

Annotation - SBO Terms

BiomassKT2440_WT3	false	▼
Biomass Production In Complete Medium	Info	▼
BiomassKT2440_Core2	253.51	▼
BiomassKT2440_WT3	254.91	▼
Blocked Biomass Precursors In Default Medium	Info	▼
BiomassKT2440_Core2	0	▼
BiomassKT2440_WT3	0	▼
Blocked Biomass Precursors In Complete Medium	Info	▼
BiomassKT2440_Core2	0	▼
BiomassKT2440_WT3	0	▼
Ratio of Direct Metabolites in Biomass Reaction	Info	▼
BiomassKT2440_Core2	0.09	▼
BiomassKT2440_WT3	0.09	▼
Number of Missing Essential Biomass Precursors	Info	▼
BiomassKT2440_Core2	2	▼
BiomassKT2440_WT3	1	▼

Energy Metabolism

Non-Growth Associated Maintenance Reaction 1 ▼

Growth-associated Maintenance in Biomass Reaction **Info** ▼

BiomassKT2440_Core2	true	▼
BiomassKT2440_WT3	true	▼

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 247 ▼

Orphan Metabolites 57 ▼

Dead-end Metabolites 85 ▼

Reaction General SBO Presence	100.0%	▼
Metabolic Reaction SBO:0000176 Presence	99.9%	▼
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	100.0%	▼
Gene General SBO Presence	100.0%	▼
Gene SBO:0000243 Presence	100.0%	▼
Biomass Reactions SBO:0000629 Presence	100.0%	▼
Sub Total	100%	x2 ▼

Total Score 91% ^

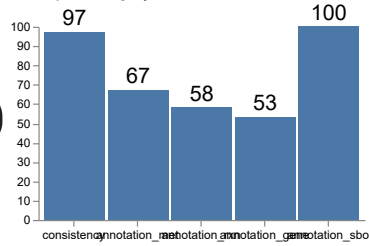
The Total Score is the result of the following calculation. For more information please click on "Readme" in the top left of the report.

$$\frac{(3 \cdot 97.44) + (1 \cdot 67.29) + (1 \cdot 57.90) + (1 \cdot 53.17) + (2 \cdot 99.99)}{(3 \cdot 100) + (1 \cdot 100) + (1 \cdot 100) + (1 \cdot 100) + (2 \cdot 100)} = 90.86$$

Total Score

91%

Score per Category



Metabolite Consumption In Complete Medium 289 ▼

Matrix Conditioning

Ratio Min/Max Non-Zero Coefficients	0.00	▼
Independent Conservation Relations	59	▼
Rank	2096	▼
Degrees Of Freedom	844	▼

Experimental Data Comparison

Growth Prediction	Skipped	▼
Gene Essentiality Prediction	Skipped	▼

Misc. Tests

Environment

Python Version	3.6.8
Platform	Linux
Memote Version	0.9.6