

Table 9.2 Available predictive genome-scale metabolic network reconstructions

Name	Strain	Organism properties	Reconstruction properties				References
		Genes	Genes	Metabolites	Reactions	Compartments	
BACTERIA							
<i>Bacillus subtilis</i>		4,225	844	988	1020	2 (c,e)	(Oh et al. 2007)
<i>Clostridium acetobutylicum</i>	ATCC 824	3,848	474	422	552	2 (c,e)	(Senger and Papoutsakis 2008)
<i>Clostridium acetobutylicum</i>	ATCC 824	3,848	432	479	502	2 (c,e)	(Lee et al. 2008)
<i>Escherichia coli</i>	K12 MG1655	4,405	660	438	627	2 (c,e)	(Edwards and Palsson 2000)
<i>Escherichia coli</i>	K12 MG1655	4,405	904	625	931	2 (c,e)	(Reed et al. 2003)
<i>Escherichia coli</i>	K12 MG1655	4,405	1260	1039	2077	3 (c,e,p)	(Feist et al. 2007)
<i>Geobacter sulfurreducens</i>		3,530	588	541	523	2 (c,e)	(Mahadevan et al. 2006)
<i>Haemophilus influenzae</i>	Rd	1,775	296	343	488	2 (c,e)	(Edwards and Palsson 1999)
<i>Haemophilus influenzae</i>	Rd	1,775	400	451	461	2 (c,e)	(Schilling and Palsson 2000)
<i>Helicobacter pylori</i>	26695	1,632	341	485	476	2 (c,e)	(Thiele et al. 2005b)
<i>Helicobacter pylori</i>	26695	1,632	291	340	388	2 (c,e)	(Schilling et al. 2002)
<i>Lactobacillus plantarum</i>	WCFS1	3,009	721	531	643	2 (c,e)	(Teusink et al. 2006)
<i>Lactococcus lactis</i>	ssp. lactis IL1403	2,310	358	422	621	2 (c,e)	(Oliveira et al. 2005)
<i>Mannheimia succiniciproducens</i>	MBEL55E	2,384	425	519	686	2 (c,e)	(Kim et al. 2007)
<i>Mycobacterium tuberculosis</i>	H37Rv	4,402	726	739	849	2 (c,e)	(Beste et al. 2007)
<i>Mycobacterium tuberculosis</i>	H37Rv	4,402	661	828	939	2 (c,e)	(Jamshidi and Palsson 2007)
<i>Mycoplasma genitalium</i>	G-37	521	189	276	264	2 (c,e)	Personal Comm.: Patrick F. Suthers
<i>Neisseria meningitidis</i>	serogroup B	2,226	555	471	496	2 (c,e)	(Baart et al. 2007)
<i>Pseudomonas aeruginosa</i>	PA01	5,640	1056		883	2 (c,e)	(Oberhardt et al. 2008)
<i>Pseudomonas putida</i>	KT2440	5,350	746	911	950	3 (c,e,p)	(Nogales 2008)
<i>Rhizobium etli</i>	CFN42	3,168	363	371	387	2 (c,e)	(Resendis-Antonio et al. 2007)

Table 9.2 (continued)

Name	Strain	Organism properties	Reconstruction properties				References
		Genes	Genes	Metabolites	Reactions	Compartments	
<i>Staphylococcus aureus</i>	N315	2,588	619	571	641	2 (c,e)	(Becker and Palsson 2005)
<i>Staphylococcus aureus</i>	N315	2,588	551	604	712	2 (c,e)	(Heinemann et al. 2005)
<i>Streptomyces coelicolor</i>	A3(2)	8,042	700	500	700	2 (c,e)	(Borodina et al. 2005)
ARCHAEA							
<i>Methanosarcina barkeri</i>	Fusaro	5,072	692	558	619	2 (c,e)	(Feist et al. 2006)
<i>Halobacterium salinarum</i>	R-1	2,867	490	557	711	2 (c,e)	(Gonzalez et al. 2008)
EUKARYOTES							
<i>Aspergillus nidulans</i>		9,451	666	732	794	4	(David et al. 2008)
<i>Homo sapiens</i>		28,783	1,496	2,766	3,311	8	(Duarte et al. 2007)
<i>Leishmania major</i>	Friedlin	8,370	560	1,101	1,112	8	(Chavali et al. 2008)
<i>Mus musculus</i>		28,287	473	872	1,220	3 (c,e,m)	(Sheikh et al. 2005)
<i>Saccharomyces cerevisiae</i>	Sc288	6,183	708	584	1,175	3 (c,e,m)	(Forster et al. 2003)
<i>Saccharomyces cerevisiae</i>	Sc288	6,183	750	646	1,149	8	(Duarte et al. 2004)
<i>Saccharomyces cerevisiae</i>	Sc288	6,183	672	636	1,038	3 (c,e,m)	(Kuepfer et al. 2005)

This list includes genome-scale metabolic network reconstructions that have been converted into predictive genome-scale models and whose predictive power has been validated against experimental data. Compartments: c – cytosol, e – extraorganism, p – periplasm, m – mitochondrion.