

Table 1. Genome-scale metabolic models of human-related microorganisms and human tissues

Model	Species	Gram stain	ORFs	Metabolites	Reactions	Body site	Refs.
Bacteria							
iGB555 ^a	<i>Neisseria meningitidis</i>	G–	555	471	496	Various, meninges	[55]
iVM679	<i>Porphyromonas gingivalis</i>	G–	679	564	679	Oral microflora	[56]
iMO1056	<i>Pseudomonas aeruginosa</i>	G–	1056	760	883	Lung	[57]
iNJ661	<i>M. tuberculosis</i>	G+	661	828	939	Lung, alveolar macrophage	[36]
iAN818 ^a	<i>Yersinia pestis</i>	G–	818	825	1020	Systemic, various	[58]
iSB619	<i>Staphylococcus aureus</i>	G+	619	571	640	Oral microflora, various	[59]
iIT341	<i>Helicobacter pylori</i>	G–	341	485	476	Pylorus, various	[60]
iPS189	<i>Mycoplasma genitalium</i>	G+	189	274	262	Genital tract	[61]
iBT721 ^a	<i>Lactobacillus plantarum</i>	G+	721	531	643	Probiotic	[62]
iMA945	<i>Salmonella typhimurium</i>	G–	945	1036	1964	Gastrointestinal tract	[63]
Protist							
iCH366 ^a	<i>Plasmodium falciparum</i>	NA	366	616	1001	Liver, erythrocyte	[64]
Human							
Recon 1	<i>Homo sapiens</i>	NA	1496	2712	3311	Global	[37]
EHMN	<i>H. sapiens</i>	NA	2322	2671	2823	Global	[38]
	<i>H. sapiens</i>	NA	NR	1360	1827	Hepatocyte	[39]
HepatoNet1	<i>H. sapiens</i>	NA	NR	777	2539	Hepatocyte	[65]
iAB-AMØ-1410-Mt-661	<i>H. sapiens/M. tuberculosis</i>	NA	1410/661	2583/828	3394/939	Alveolar macrophage	[40]

^aModel name according to the conventional naming standard.
Abbreviations: NA, not applicable; NR, not reported.