

Method	Organisms	Input data	Validation	Methods compared
Akesson-04	<i>S.cerevisiae</i>	Piper et al, 2002	Secretion rates (same study) and ¹³ C fluxes (Gombert et al, 2001)	
GIMME	E.coli, Human	Fong and Palsson 2004; Park et al, 2006; Parikh et al 2007	Consistency between original and readjusted expression levels	
iMAT	<i>S.cerevisiae</i> , Human	Lapujade et al, 2004; Shmueli et al, 2003; Mishra et al, 2006	Consistency of human tissue-specific gene activity with known evidence (multiple databases); <i>S.cerevisiae</i> MFA data (Lapujade et al, 2004)	
Moxley-09	<i>S.cerevisiae</i>	Same study	¹³ C fluxes (same study)	
E-Flux	<i>M.tuberculosis</i>	Boshoff et al, 2004	Qualitative agreement with known inhibitory drugs (Boshoff et al, 2004)	
PROM	E.coli, <i>M.tuberculosis</i>	Covert et al 2004; Boshoff et al, 2004	Growth rate of multiple mutants for E.coli (Covert et al, 2004) and <i>M.tuberculosis</i> (Sassetti et al, 2003; Gao et al, 2005; Lamichhane et al, 2003)	rFBA
MADE	<i>S.cerevisiae</i>	Roberts and Hudson, 2006	Consistency between original and adjusted gene expression patterns	
tFBA	<i>S.cerevisiae</i>	Knijnenburg et al, 2009	Qualitative agreement between gene expression and flux changes (Boer et al, 2003; Tai et al, 2005)	FBA, rFBA
INIT	Human	Human Proteome Atlas database	Comparison of generated hepatocyte model with manually curated model, qualitative agreement of predicted drug targets in cancer cell lines	
Lee-12	<i>S.cerevisiae</i>	Same study	Secretion rates (same study)	FBA, GIMME, iMAT
Fang-12	<i>S.cerevisiae</i> , <i>M.tuberculosis</i>	Park et al, 2003	MFA data for <i>S. cerevisiae</i> (Lapujade et al, 2004). Qualitative agreement with known metabolic adaptation responses of <i>M. tuberculosis</i>	
RELATCH	E.coli, <i>S.cerevisiae</i> , <i>B.subtilis</i>	Covert et al 2004; Canelas et al, 2010; Tannler et al, 2008	¹³ C fluxes for E.coli (Fong et al, 2006; Ishii et al, 2004), <i>S. cerevisiae</i> (Blank et al, 2005) and <i>B.subtilis</i> (Fischer and Sauer, 2005)	FBA, MOMA, ROOM
TEAM	<i>S.oneidensis</i>	Beg et al, 2012	Qualitative agreement with temporal exometabolome profiles (Beg et al, 2012)	dFBA
AdaM	E.coli	Jozefczuk et al, 2010	No validation with independent experimental data	MADE
GX-FBA	<i>S.cerevisiae</i> , <i>Y pestis</i>	Lapujade et al, 2004; Han et al, 2004; Motin et al, 2004; Qiu et al 2005; Qiu et al 2006	MFA data for <i>S.cerevisiae</i> (Lapujade et al, 2004), qualitative agreement with known metabolic responses of <i>Y pestis</i>	
mCADRE	Human	McCall et al, 2011	Qualitative agreement of generated models for liver and other tissues with literature based evidence	MBA
FCGs	E.coli	Ishii et al, 2007	¹³ C fluxes (Ishii et al, 2007)	FBA, MOMA
EXAMO	<i>S.cerevisiae</i>	Gasch et al, 2000	Gene essentiality data (Giaever et al, 2002; Snitkin et al 2008); Predicted fluxes in qualitative agreement with known yeast physiology	MBA, iMAT