Table S1. Resources for Further Reading

	Title	Description	PMID
1. Network Reconstruction	A protocol for generating a high-quality genome-scale metabolic reconstruction	96 step standard operating procedure for construction and curation of metabolic network reconstructions	PMC3125167
	The Biomass Objective Function	Guide to accurately formulating the biomass objective function for calculation of cellular growth using FBA	PMC2912156
	Towards multidimensional genome annotation	Procedure for going from a genome annotation to a functional model using constraints based methods	16418748
	Reconstruction of biochemical networks in microorganisms	Comprehensive review of process used to build and validate a metabolic network reconstruction	19116616
	Reconstructing the metabolic network of a bacterium from its genome	How to improve a metabolic network reconstruction using high-throughput data, gene-context and phylogeny	16169729
	Software platforms to facilitate reconstructing genome-scale metabolic networks	Review of software tools used for building a metabolic network reconstruction	24148076
2. Prediction using GEMs	What is flux balance analysis?	Primer on the theoretical basis and practical application of flux balance analysis	PMC3108565
	Quantitative prediction of cellular metabolism with constraint-based models: the COBRA Toolbox (1.0, 2.0)	Two step-by-step guides to using the COBRA toolbox for quantitative prediction of cellular metabolism	17406635, 21886097
	Applications of genome-scale metabolic reconstructions	A review of the uses of metabolic network reconstructions	19888215
	BiGG: a Biochemical Genetic and Genomic knowledgebase of large scale metabolic reconstructions	Database of available metabolic network reconstructions	20426874
	Automated genome annotation and metabolic model reconstruction in the SEED and Model SEED	Database of automatically generated metabolic network reconstructions	20802497
3. Model improvement	Systematizing the generation of missing metabolic knowledge	Review of gap-filling procedure and source of algorithms and software tools used for gap-filling analyses	20589842
	Systems approach to refining genome annotation	Example of in-scilico gap-filling approach combine with experimental validation for biological discovery	17088549

	GrowMatch: an automated method for reconciling in silico/in vivo growth predictions	Automated approach for comparing and resolving model vs experimental inconsistencies	19282964
4. Quantitative phenotype prediction	In silico predictions of Escherichia coli metabolic capabilities are consistent with experimental data	Carbon source and oxygen uptake rates match predicted optimal ratios by FBA	11175725
	Escherichia coli K-12 undergoes adaptive evolution to achieve in silico predicted optimal growth.	Carbon source and oxygen uptake rates evolve to predicted optimal ratios for cases when the wild-type strain does not match predicted values	12432395
	Multidimensional optimality of microbial metabolism	Metabolic fluxes from multiple bacteria operate close to Pareto-optimal surface of three competing objectives	22556256
	Optknock: a bi-level programming framework for identifying gene knockout strategies for microbial strain optimization	One of the first algorithms for strain design in metabolic engineering using genome-scale metabolic models	14595777
5. Multi-omic data integration	Constraining the metabolic genotype-phenotype relationship using a phylogeny of in silico methods	A recent review on constraint-based computational methods, including omics analysis methods	22367118
	A community-driven global reconstruction of human metabolism	The most recent metabolic reconstruction of human metabolism	23455439
	Using the reconstructed genome-scale human metabolic network to study physiology and pathology	A review on the use of the human metabolic reconstruction to study physiology and pathology	22142339
6. Beyond metabolism to molecular biology	In silico method for modeling metabolism and gene product expression at genome scale.	Integrated model of metabolism and gene expression for T. maritima	22760628
	Genome-scale models of metabolism and gene expression extend and refine growth phenotype prediction.	Integrated model of metabolism and gene expression for E. coli	24084808
	Computing the functional proteome: recent progress and future prospects for genome-scale model	A perspective on the predictions possible with ME-Models and how the models will be expanded and refined	25576845

	Three-dimensional structural view of the central metabolic network of Thermotoga maritima.	GEM-PRO for T. maritima	19762644
	Structural systems biology evaluation of metabolic thermotolerance in Escherichia coli.	GEM-PRO for E. coli	23744946