

High-throughput generation, optimization and analysis

Nature Biotechnology

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Citation Report

#	ARTICLE	IF	CITATIONS
1	The challenges of integrating multi-omic data sets. <i>Nature Chemical Biology</i> , 2010, 6, 787-789.	3.9	154
2	Structural and operational complexity of the <i>Geobacter sulfurreducens</i> genome. <i>Genome Research</i> , 2010, 20, 1304-1311.	2.4	75
3	Elimination of Thermodynamically Infeasible Loops in Steady-State Metabolic Models. <i>Biophysical Journal</i> , 2011, 100, 544-553.	0.2	203
4	Quantitative prediction of cellular metabolism with constraint-based models: the COBRA Toolbox v2.0. <i>Nature Protocols</i> , 2011, 6, 1290-1307.	5.5	1,408
5	Competitive and cooperative metabolic interactions in bacterial communities. <i>Nature Communications</i> , 2011, 2, 589.	5.8	413
6	Pathogen comparative genomics in the next-generation sequencing era: genome alignments, pangenomics and metagenomics. <i>Briefings in Functional Genomics</i> , 2011, 10, 322-333.	1.3	41
7	A Practical Guide to Genome-Scale Metabolic Models and Their Analysis. <i>Methods in Enzymology</i> , 2011, 500, 509-532.	0.4	45
8	Interrogation of global mutagenesis data with a genome scale model of <i>Neisseria meningitidis</i> to assess gene fitness in vitro and in sera. <i>Genome Biology</i> , 2011, 12, R127.	13.9	30
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11	Flux-Balance Modeling of Plant Metabolism. <i>Frontiers in Plant Science</i> , 2011, 2, 38.	1.7	124
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13	The SuBLiMinaL Toolbox: automating steps in the reconstruction of metabolic networks. <i>Journal of Integrative Bioinformatics</i> , 2011, 8, 187-203.	1.0	67
15	Systems-biology approaches for predicting genomic evolution. <i>Nature Reviews Genetics</i> , 2011, 12, 591-602.	7.7	112
16	In situ to in silico and back: elucidating the physiology and ecology of <i>Geobacter</i> spp. using genome-scale modelling. <i>Nature Reviews Microbiology</i> , 2011, 9, 39-50.	13.6	128
17	Green systems biology " From single genomes, proteomes and metabolomes to ecosystems research and biotechnology. <i>Journal of Proteomics</i> , 2011, 75, 284-305.	1.2	189
18	Prioritizing orphan proteins for further study using phylogenomics and gene expression profiles in <i>Streptomyces coelicolor</i> . <i>BMC Research Notes</i> , 2011, 4, 325.	0.6	2
19	Comparative genome-scale metabolic modeling of actinomycetes: The topology of essential core metabolism. <i>FEBS Letters</i> , 2011, 585, 2389-2394.	1.3	29

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21	Microbial Metagenomics: Beyond the Genome. <i>Annual Review of Marine Science</i> , 2011, 3, 347-371.	5.1	323
22	A survey of metabolic databases emphasizing the MetaCyc family. <i>Archives of Toxicology</i> , 2011, 85, 1015-1033.	1.9	72
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94	Genome-scale metabolic representation of <i>Amycolatopsis balhimycina</i> . <i>Biotechnology and Bioengineering</i> , 2012, 109, 1798-1807.	1.7	19
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