

A consensus yeast metabolic network reconstruction of approach to systems biology

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Citation Report

#	ARTICLE	IF	CITATIONS
2	Reconstruction of an in silico metabolic model of Arabidopsis thaliana through database integration. Nature Precedings, 2009, , .	0.1	1
3	Metabolite and reaction inference based on enzyme specificities. Bioinformatics, 2009, 25, 2975-2982.	1.8	18
4	libAnnotationSBML: a library for exploiting SBML annotations. Bioinformatics, 2009, 25, 2292-2293.	1.8	28
5	KiPar, a tool for systematic information retrieval regarding parameters for kinetic modelling of yeast metabolic pathways. Bioinformatics, 2009, 25, 1404-1411.	1.8	16
6	Pathway identification by network pruning in the metabolic network of <i>Escherichia coli</i> . Bioinformatics, 2009, 25, 3282-3288.	1.8	33
7	Understanding human metabolic physiology: a genome-to-systems approach. Trends in Biotechnology, 2009, 27, 37-44.	4.9	44
8	Metabolite signal identification in accurate mass metabolomics data with MZedDB, an interactive m/z annotation tool utilising predicted ionisation behaviour 'rules'. BMC Bioinformatics, 2009, 10, 227.	1.2	142
9	Connecting extracellular metabolomic measurements to intracellular flux states in yeast. BMC Systems Biology, 2009, 3, 37.	3.0	391
10	Deterministic mathematical models of the cAMP pathway in <i>Saccharomyces cerevisiae</i> . BMC Systems Biology, 2009, 3, 70.	3.0	22
11	â€Metabolite-likenessâ€™™ as a criterion in the design and selection of pharmaceutical drug libraries. Drug Discovery Today, 2009, 14, 31-40.	3.2	117
12	Systems biology of lipid metabolism: From yeast to human. FEBS Letters, 2009, 583, 3905-3913.	1.3	97
13	Systems Biology: The elements and principles of Life. FEBS Letters, 2009, 583, 3882-3890.	1.3	77
14	Timing matters. FEBS Letters, 2009, 583, 4013-4018.	1.3	10
15	Nested uncertainties in biochemical models. IET Systems Biology, 2009, 3, 1-9.	0.8	35
16	Flux balance analysis: A geometric perspective. Journal of Theoretical Biology, 2009, 258, 311-315.	0.8	66
17	Potential natural product discovery from microbes through a diversity-guided computational framework. Applied Microbiology and Biotechnology, 2009, 82, 579-586.	1.7	11
18	Genomeâ€scale metabolic networks. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2009, 1, 285-297.	6.6	115
20	Iron behaving badly: inappropriate iron chelation as a major contributor to the aetiology of vascular and other progressive inflammatory and degenerative diseases. BMC Medical Genomics, 2009, 2, 2.	0.7	421

#	ARTICLE	IF	CITATIONS
21	Assessing the impact of transcriptomics, proteomics and metabolomics on fungal phytopathology. <i>Molecular Plant Pathology</i> , 2009, 10, 703-715.	2.0	121
22	¹³ C-based metabolic flux analysis. <i>Nature Protocols</i> , 2009, 4, 878-892.	5.5	520
23	Evolution of biomolecular networks – lessons from metabolic and protein interactions. <i>Nature Reviews Molecular Cell Biology</i> , 2009, 10, 791-803.	16.1	257
24	Yeast systems biotechnology for the production of heterologous proteins. <i>FEMS Yeast Research</i> , 2009, 9, 335-348.	1.1	69
25	Impact of yeast systems biology on industrial biotechnology. <i>Journal of Biotechnology</i> , 2009, 144, 204-211.	1.9	24
26	Biotechnology in Turkey: An overview. <i>Biotechnology Journal</i> , 2009, 4, 981-991.	1.8	2
27	Accomplishments in genome-scale <i>in silico</i> modeling for industrial and medical biotechnology. <i>Biotechnology Journal</i> , 2009, 4, 1653-1670.	1.8	77
28	Mass spectrometry tools and metabolite-specific databases for molecular identification in metabolomics. <i>Analyst</i> , 2009, 134, 1322.	1.7	240
29	The Automation of Science. <i>Science</i> , 2009, 324, 85-89.	6.0	458
30	An integrative approach towards completing genome-scale metabolic networks. <i>Molecular BioSystems</i> , 2009, 5, 1889.	2.9	67
31	Applications of genome-scale metabolic reconstructions. <i>Molecular Systems Biology</i> , 2009, 5, 320.	3.2	759
32	Chapter 22 Enzyme Kinetics and Computational Modeling for Systems Biology. <i>Methods in Enzymology</i> , 2009, 467, 583-599.	0.4	23
33	Pathway databases and tools for their exploitation: benefits, current limitations and challenges. <i>Molecular Systems Biology</i> , 2009, 5, 290.	3.2	173
34	Calling International Rescue: knowledge lost in literature and data landslide!. <i>Biochemical Journal</i> , 2009, 424, 317-333.	1.7	56
35	Implications of the Dominant Role of Transporters in Drug Uptake by Cells (Supplementary Material). <i>Current Topics in Medicinal Chemistry</i> , 2009, 9, 163-181.	1.0	81
36	A Combined ¹ H Nuclear Magnetic Resonance and Electrospray Ionization–Mass Spectrometry Analysis to Understand the Basal Metabolism of Plant-Pathogenic <i>Fusarium</i> spp.. <i>Molecular Plant-Microbe Interactions</i> , 2010, 23, 1605-1618.	1.4	26
37	Towards whole-body systems physiology. <i>Molecular Systems Biology</i> , 2010, 6, 409.	3.2	26
38	Predicting novel pathways in genome-scale metabolic networks. <i>Biochemical Society Transactions</i> , 2010, 38, 1202-1205.	1.6	6

#	ARTICLE	IF	CITATIONS
39	Why does yeast ferment? A flux balance analysis study. <i>Biochemical Society Transactions</i> , 2010, 38, 1225-1229.	1.6	26
40	Systems metabolic engineering: Genome-scale models and beyond. <i>Biotechnology Journal</i> , 2010, 5, 647-659.	1.8	122
41	Systems biology and modeling in neuroblastoma: practicalities and perspectives. <i>Expert Review of Molecular Diagnostics</i> , 2010, 10, 131-145.	1.5	11
42	Towards a unifying, systems biology understanding of large-scale cellular death and destruction caused by poorly liganded iron: Parkinson's, Huntington's, Alzheimer's, prions, bactericides, chemical toxicology and others as examples. <i>Archives of Toxicology</i> , 2010, 84, 825-889.	1.9	330
43	Event extraction for systems biology by text mining the literature. <i>Trends in Biotechnology</i> , 2010, 28, 381-390.	4.9	160
44	BiGG: a Biochemical Genetic and Genomic knowledgebase of large scale metabolic reconstructions. <i>BMC Bioinformatics</i> , 2010, 11, 213.	1.2	486
45	Investigating the validity of current network analysis on static conglomerate networks by protein network stratification. <i>BMC Bioinformatics</i> , 2010, 11, 466.	1.2	8
46	Systematic integration of experimental data and models in systems biology. <i>BMC Bioinformatics</i> , 2010, 11, 582.	1.2	28
47	Whole genome sequencing of <i>Saccharomyces cerevisiae</i> : from genotype to phenotype for improved metabolic engineering applications. <i>BMC Genomics</i> , 2010, 11, 723.	1.2	64
48	A detailed genome-wide reconstruction of mouse metabolism based on human Recon 1. <i>BMC Systems Biology</i> , 2010, 4, 140.	3.0	147
49	Improving the iMM904 <i>S. cerevisiae</i> metabolic model using essentiality and synthetic lethality data. <i>BMC Systems Biology</i> , 2010, 4, 178.	3.0	88
50	Towards a genome-scale kinetic model of cellular metabolism. <i>BMC Systems Biology</i> , 2010, 4, 6.	3.0	132
51	Industrial systems biology. <i>Biotechnology and Bioengineering</i> , 2010, 105, 439-460.	1.7	130
52	Computational analysis of phenotypic space in heterologous polyketide biosynthesis—Applications to <i>Escherichia coli</i> , <i>Bacillus subtilis</i> , and <i>Saccharomyces cerevisiae</i> . <i>Journal of Theoretical Biology</i> , 2010, 262, 197-207.	0.8	16
53	Organising metabolic networks: Cycles in flux distributions. <i>Journal of Theoretical Biology</i> , 2010, 265, 250-260.	0.8	9
54	Metabolic flux analysis and pharmaceutical production. <i>Metabolic Engineering</i> , 2010, 12, 81-95.	3.6	101
55	MI-Pack: Increased confidence of metabolite identification in mass spectra by integrating accurate masses and metabolic pathways. <i>Chemometrics and Intelligent Laboratory Systems</i> , 2010, 104, 75-82.	1.8	78
56	Data integration and analysis of biological networks. <i>Current Opinion in Biotechnology</i> , 2010, 21, 78-84.	3.3	44

#	ARTICLE	IF	CITATIONS
57	Computational methods for metabolic reconstruction. <i>Current Opinion in Biotechnology</i> , 2010, 21, 70-77.	3.3	46
58	Software that goes with the flow in systems biology. <i>BMC Biology</i> , 2010, 8, 140.	1.7	5
59	Nutrient control of eukaryote cell growth: a systems biology study in yeast. <i>BMC Biology</i> , 2010, 8, 68.	1.7	89
60	Integration of metabolic databases for the reconstruction of genome-scale metabolic networks. <i>BMC Systems Biology</i> , 2010, 4, 114.	3.0	79
61	Reconstruction of the yeast protein-protein interaction network involved in nutrient sensing and global metabolic regulation. <i>BMC Systems Biology</i> , 2010, 4, 68.	3.0	9
62	The application of flux balance analysis in systems biology. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2010, 2, 372-382.	6.6	116
63	Comparative systems biology: from bacteria to man. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2010, 2, 518-532.	6.6	15
64	<i>In silico</i> models of cancer. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2010, 2, 438-459.	6.6	103
65	Enzyme kinetics informatics: from instrument to browser. <i>FEBS Journal</i> , 2010, 277, 3769-3779.	2.2	20
66	Towards genome-scale signalling-network reconstructions. <i>Nature Reviews Genetics</i> , 2010, 11, 297-307.	7.7	111
67	Reconstruction and Validation of RefRec: A Global Model for the Yeast Molecular Interaction Network. <i>PLoS ONE</i> , 2010, 5, e10662.	1.1	12
68	Modelling the Response of FOXO Transcription Factors to Multiple Post-Translational Modifications Made by Ageing-Related Signalling Pathways. <i>PLoS ONE</i> , 2010, 5, e11092.	1.1	32
69	A Compartmental Model Analysis of Integrative and Self-Regulatory Ion Dynamics in Pollen Tube Growth. <i>PLoS ONE</i> , 2010, 5, e13157.	1.1	31
70	Growth-limiting Intracellular Metabolites in Yeast Growing under Diverse Nutrient Limitations. <i>Molecular Biology of the Cell</i> , 2010, 21, 198-211.	0.9	217
71	The Metabolic Network of <i>Synechocystis</i> sp. PCC 6803: Systemic Properties of Autotrophic Growth. <i>Plant Physiology</i> , 2010, 154, 410-422.	2.3	173
72	PathText: a text mining integrator for biological pathway visualizations. <i>Bioinformatics</i> , 2010, 26, i374-i381.	1.8	47
73	How to Understand the Cell by Breaking It: Network Analysis of Gene Perturbation Screens. <i>PLoS Computational Biology</i> , 2010, 6, e1000655.	1.5	51
74	Quantitative Analysis of Cellular Metabolic Dissipative, Self-Organized Structures. <i>International Journal of Molecular Sciences</i> , 2010, 11, 3540-3599.	1.8	25

#	ARTICLE	IF	CITATIONS
75	SBRML: a markup language for associating systems biology data with models. <i>Bioinformatics</i> , 2010, 26, 932-938.	1.8	54
76	BioMet Toolbox: genome-wide analysis of metabolism. <i>Nucleic Acids Research</i> , 2010, 38, W144-W149.	6.5	91
77	Environments that Induce Synthetic Microbial Ecosystems. <i>PLoS Computational Biology</i> , 2010, 6, e1001002.	1.5	280
78	Systems Biology of Industrial Microorganisms. , 2010, 120, 51-99.		14
79	IGERS: Inferring Gibbs Energy Changes of Biochemical Reactions from Reaction Similarities. <i>Biophysical Journal</i> , 2010, 98, 2478-2486.	0.2	14
80	Further developments towards a genome-scale metabolic model of yeast. <i>BMC Systems Biology</i> , 2010, 4, 145.	3.0	95
81	Parameter Balancing in Kinetic Models of Cell Metabolism. <i>Journal of Physical Chemistry B</i> , 2010, 114, 16298-16303.	1.2	43
82	Metabolic control analysis indicates a change of strategy in the treatment of cancer. <i>Mitochondrion</i> , 2010, 10, 626-639.	1.6	77
83	Extensive In Vivo Metabolite-Protein Interactions Revealed by Large-Scale Systematic Analyses. <i>Cell</i> , 2010, 143, 639-650.	13.5	200
84	Reconstruction annotation jamborees: a community approach to systems biology. <i>Molecular Systems Biology</i> , 2010, 6, 361.	3.2	54
85	THE IMPORTANCE OF COMPARTMENTALIZATION IN METABOLIC FLUX MODELS: YEAST AS AN ECOSYSTEM OF ORGANELLES. , 2010, , .		25
87	Dynamic Transcriptional and Metabolic Responses in Yeast Adapting to Temperature Stress. <i>OMICS A Journal of Integrative Biology</i> , 2010, 14, 249-259.	1.0	53
88	Systems level studies of mammalian metabolomes: the roles of mass spectrometry and nuclear magnetic resonance spectroscopy. <i>Chemical Society Reviews</i> , 2011, 40, 387-426.	18.7	689
90	Advances in plant disease and pest management. <i>Journal of Agricultural Science</i> , 2011, 149, 91-114.	0.6	78
91	Comprehensive quantitative analysis of central carbon and amino acid metabolism in <i>Saccharomyces cerevisiae</i> under multiple conditions by targeted proteomics. <i>Molecular Systems Biology</i> , 2011, 7, 464.	3.2	105
92	A Survey on Methods for Modeling and Analyzing Integrated Biological Networks. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2011, 8, 943-958.	1.9	50
93	Search Computing. <i>Lecture Notes in Computer Science</i> , 2011, , .	1.0	7
94	Enzyme Kinetics for Systems Biology. <i>Methods in Enzymology</i> , 2011, 500, 233-257.	0.4	16

#	ARTICLE	IF	CITATIONS
95	Yeast Systems Biology. <i>Methods in Molecular Biology</i> , 2011, , .	0.4	7
96	Whole-Genome Metabolic Network Reconstruction and Constraint-Based Modeling. <i>Methods in Enzymology</i> , 2011, 500, 411-433.	0.4	33
97	Genome-Scale Metabolic Models of <i>Saccharomyces cerevisiae</i> . <i>Methods in Molecular Biology</i> , 2011, 759, 445-463.	0.4	18
99	Sample Preparation Related to the Intracellular Metabolome of Yeast. <i>Methods in Enzymology</i> , 2011, 500, 277-297.	0.4	15
100	Synergies between synthetic biology and metabolic engineering. <i>Nature Biotechnology</i> , 2011, 29, 693-695.	9.4	128
101	The SuBliMinal Toolbox: automating steps in the reconstruction of metabolic networks. <i>Journal of Integrative Bioinformatics</i> , 2011, 8, 187-203.	1.0	67
102	An introduction to biological nuclear magnetic resonance spectroscopy. <i>Biological Reviews</i> , 2011, 86, 493-510.	4.7	111
103	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
104	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
105	Post-genomics resources and tools for studying apicomplexan metabolism. <i>Trends in Parasitology</i> , 2011, 27, 131-140.	1.5	14
106	Computational Tools for Systems Biology. , 2011, , 213-243.		0
107	Software for systems biology: from tools to integrated platforms. <i>Nature Reviews Genetics</i> , 2011, 12, 821-832.	7.7	228
108	Eukaryotic metabolism: Measuring compartment fluxes. <i>Biotechnology Journal</i> , 2011, 6, 1071-1085.	1.8	49
109	Metabolic Profiling Uncovers a Phenotypic Signature of Small for Gestational Age in Early Pregnancy. <i>Journal of Proteome Research</i> , 2011, 10, 3660-3673.	1.8	99
110	The yin and yang of yeast: biodiversity research and systems biology as complementary forces driving innovation in biotechnology. <i>Biotechnology Letters</i> , 2011, 33, 477-487.	1.1	5
111	Modeling dynamics of disaster spreading in community networks. <i>Nonlinear Dynamics</i> , 2011, 64, 157-165.	2.7	10
112	Mining metabolites: extracting the yeast metabolome from the literature. <i>Metabolomics</i> , 2011, 7, 94-101.	1.4	37
113	Unpredictability of metabolism – the key role of metabolomics science in combination with next-generation genome sequencing. <i>Analytical and Bioanalytical Chemistry</i> , 2011, 400, 1967-1978.	1.9	87

#	ARTICLE	IF	CITATIONS
114	In silico improvement of heterologous biosynthesis of erythromycin precursor 6-deoxyerythronolide B in Escherichia coli. <i>Biotechnology and Bioprocess Engineering</i> , 2011, 16, 445-456.	1.4	15
115	In silico analysis and experimental improvement of taxadiene heterologous biosynthesis in Escherichia coli. <i>Biotechnology and Bioprocess Engineering</i> , 2011, 16, 205-215.	1.4	34
116	Engineering strategy of yeast metabolism for higher alcohol production. <i>Microbial Cell Factories</i> , 2011, 10, 70.	1.9	42
117	Genome-scale reconstruction of metabolic network for a halophilic extremophile, <i>Chromohalobacter salexigens</i> DSM 3043. <i>BMC Systems Biology</i> , 2011, 5, 12.	3.0	58
118	Integrating systems biology models and biomedical ontologies. <i>BMC Systems Biology</i> , 2011, 5, 124.	3.0	44
119	Critical assessment of human metabolic pathway databases: a stepping stone for future integration. <i>BMC Systems Biology</i> , 2011, 5, 165.	3.0	59
120	MEMOSys: Bioinformatics platform for genome-scale metabolic models. <i>BMC Systems Biology</i> , 2011, 5, 20.	3.0	29
121	A community effort towards a knowledge-base and mathematical model of the human pathogen <i>Salmonella Typhimurium</i> LT2. <i>BMC Systems Biology</i> , 2011, 5, 8.	3.0	128
122	Metabolites as global regulators: A new view of protein regulation. <i>BioEssays</i> , 2011, 33, 485-489.	1.2	36
123	Algorithms and tools for the preprocessing of LC-MS metabolomics data. <i>Chemometrics and Intelligent Laboratory Systems</i> , 2011, 108, 23-32.	1.8	138
124	Enzyme maintenance effort as criterion for the characterization of alternative pathways and length distribution of isofunctional enzymes. <i>BioSystems</i> , 2011, 105, 122-129.	0.9	2
125	The strength of chemical linkage as a criterion for pruning metabolic graphs. <i>Bioinformatics</i> , 2011, 27, 1957-1963.	1.8	3
126	Sustainable Model Building. <i>Methods in Enzymology</i> , 2011, 500, 371-395.	0.4	11
127	A Profile of Today's SBML-Compatible Software. , 2011, , .		9
128	Network Reconstruction from Random Phase Resetting. <i>Physical Review Letters</i> , 2011, 107, 034101.	2.9	98
129	Automated analysis of information processing, kinetic independence and modular architecture in biochemical networks using MIDIA. <i>Bioinformatics</i> , 2011, 27, 584-586.	1.8	5
130	Mass-balanced randomization of metabolic networks. <i>Bioinformatics</i> , 2011, 27, 1397-1403.	1.8	25
131	Customizable views on semantically integrated networks for systems biology. <i>Bioinformatics</i> , 2011, 27, 1299-1306.	1.8	9

#	ARTICLE	IF	CITATIONS
132	Extending Biochemical Databases by Metabolomic Surveys. <i>Journal of Biological Chemistry</i> , 2011, 286, 23637-23643.	1.6	67
133	Retrieval, alignment, and clustering of computational models based on semantic annotations. <i>Molecular Systems Biology</i> , 2011, 7, 512.	3.2	32
134	Social engineering for virtual 'big science' in systems biology. <i>Nature Chemical Biology</i> , 2011, 7, 323-326.	3.9	35
135	Reconciliation of Genome-Scale Metabolic Reconstructions for Comparative Systems Analysis. <i>PLoS Computational Biology</i> , 2011, 7, e1001116.	1.5	111
136	Chemical Basis of Metabolic Network Organization. <i>PLoS Computational Biology</i> , 2011, 7, e1002214.	1.5	12
137	Kinetic modelling of large-scale metabolic networks. , 2011, , .		2
138	Understanding complexity in neurodegenerative diseases: in silico reconstruction of emergence. <i>Frontiers in Physiology</i> , 2012, 3, 291.	1.3	16
139	Evolutionary significance of metabolic network properties. <i>Journal of the Royal Society Interface</i> , 2012, 9, 1168-1176.	1.5	19
140	Large-scale sequestration of atmospheric carbon via plant roots in natural and agricultural ecosystems: why and how. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2012, 367, 1589-1597.	1.8	217
141	Expanding the chemical palate of cells by combining systems biology and metabolic engineering. <i>Metabolic Engineering</i> , 2012, 14, 289-297.	3.6	131
142	Production of recombinant proteins by yeast cells. <i>Biotechnology Advances</i> , 2012, 30, 1108-1118.	6.0	272
143	Improving the description of metabolic networks: the TCA cycle as example. <i>FASEB Journal</i> , 2012, 26, 3625-3636.	0.2	22
144	YMDB: the Yeast Metabolome Database. <i>Nucleic Acids Research</i> , 2012, 40, D815-D820.	6.5	162
145	Analytical Challenges of Microbial Biofilms on Medical Devices. <i>Analytical Chemistry</i> , 2012, 84, 3858-3866.	3.2	113
146	IMPORTANCE OF UNDERSTANDING THE MAIN METABOLIC REGULATION IN RESPONSE TO THE SPECIFIC PATHWAY MUTATION FOR METABOLIC ENGINEERING OF ESCHERICHIA COLI. <i>Computational and Structural Biotechnology Journal</i> , 2012, 3, e201210018.	1.9	12
147	Modelling cyanobacteria: from metabolism to integrative models of phototrophic growth. <i>Journal of Experimental Botany</i> , 2012, 63, 2259-2274.	2.4	45
148	Synthetic Biology Triggers New Era of Antibiotics Development. <i>Sub-Cellular Biochemistry</i> , 2012, 64, 95-114.	1.0	9
149	Evaluating Sphingolipid Biochemistry in the Consensus Reconstruction of Yeast Metabolism. <i>Industrial Biotechnology</i> , 2012, 8, 72-78.	0.5	2

#	ARTICLE	IF	CITATIONS
150	MetRxn: a knowledgebase of metabolites and reactions spanning metabolic models and databases. BMC Bioinformatics, 2012, 13, 6.	1.2	120
151	Production of 2,3-butanediol in <i>Saccharomyces cerevisiae</i> by in silico aided metabolic engineering. Microbial Cell Factories, 2012, 11, 68.	1.9	132
152	Genome-scale metabolic reconstructions of <i>Pichia stipitis</i> and <i>Pichia pastoris</i> and in silico evaluation of their potentials. BMC Systems Biology, 2012, 6, 24.	3.0	101
153	A genome-scale metabolic model of the lipid-accumulating yeast <i>Yarrowia lipolytica</i> . BMC Systems Biology, 2012, 6, 35.	3.0	105
154	Yeast 5 â€“ an expanded reconstruction of the <i>Saccharomyces cerevisiae</i> metabolic network. BMC Systems Biology, 2012, 6, 55.	3.0	118
155	Improving metabolic flux predictions using absolute gene expression data. BMC Systems Biology, 2012, 6, 73.	3.0	126
156	MicrobesFlux: a web platform for drafting metabolic models from the KEGG database. BMC Systems Biology, 2012, 6, 94.	3.0	50
157	Fungal Hsp90: a biological transistor that tunes cellular outputs to thermal inputs. Nature Reviews Microbiology, 2012, 10, 693-704.	13.6	84
158	Understanding the immune response to seasonal influenza vaccination in older adults: a systems biology approach. Expert Review of Vaccines, 2012, 11, 985-994.	2.0	128
159	Design of Pathway-Level Bioprocess Monitoring and Control Strategies Supported by Metabolic Networks. Advances in Biochemical Engineering/Biotechnology, 2012, 132, 193-215.	0.6	0
160	Organization Principles in Genetic Interaction Networks. Advances in Experimental Medicine and Biology, 2012, 751, 53-78.	0.8	2
161	Fifteen years of large scale metabolic modeling of yeast: Developments and impacts. Biotechnology Advances, 2012, 30, 979-988.	6.0	106
162	Opportunities in systems biology to discover mechanisms and repurpose drugs for CNS diseases. Drug Discovery Today, 2012, 17, 1208-1216.	3.2	23
163	Urinary Metabolomics in Newborns and Infants. Advances in Clinical Chemistry, 2012, 58, 193-223.	1.8	31
164	Evolutionary Systems Biology. Advances in Experimental Medicine and Biology, 2012, , .	0.8	31
165	Identification of Functional Differences in Metabolic Networks Using Comparative Genomics and Constraint-Based Models. PLoS ONE, 2012, 7, e34670.	1.1	41
166	Multiscale Modeling of Metabolism and Macromolecular Synthesis in <i>E. coli</i> and Its Application to the Evolution of Codon Usage. PLoS ONE, 2012, 7, e45635.	1.1	100
167	Reconstruction and In Silico Analysis of Metabolic Network for an Oleaginous Yeast, <i>Yarrowia lipolytica</i> . PLoS ONE, 2012, 7, e51535.	1.1	79

#	ARTICLE	IF	CITATIONS
168	Protein Phylogenetic Analysis of Ca ²⁺ /cation Antiporters and Insights into their Evolution in Plants. <i>Frontiers in Plant Science</i> , 2012, 3, 1.	1.7	490
169	Literature Retrieval and Mining in Bioinformatics: State of the Art and Challenges. <i>Advances in Bioinformatics</i> , 2012, 2012, 1-10.	5.7	16
170	Human Metabolic Network: Reconstruction, Simulation, and Applications in Systems Biology. <i>Metabolites</i> , 2012, 2, 242-253.	1.3	9
171	Analyzing LC/MS Metabolic Profiling Data in the Context of Existing Metabolic Networks. <i>Current Metabolomics</i> , 2012, 1, 84-91.	0.5	7
172	Functional Proteomics: Mapping Lipid-Protein Interactomes. , 0, , .		0
173	Tutorial on biological networks. <i>Wiley Interdisciplinary Reviews: Data Mining and Knowledge Discovery</i> , 2012, 2, 298-325.	4.6	11
174	Time-Structure of the Yeast Metabolism In vivo. <i>Advances in Experimental Medicine and Biology</i> , 2012, 736, 359-379.	0.8	21
175	Metagenomic systems biology of the human gut microbiome reveals topological shifts associated with obesity and inflammatory bowel disease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 594-599.	3.3	699
176	Genome-Scale Network Modeling. , 2012, , 1-23.		2
177	Using Flux Balance Analysis to Guide Microbial Metabolic Engineering. <i>Methods in Molecular Biology</i> , 2012, 834, 197-216.	0.4	25
178	A vision for a biomedical cloud. <i>Journal of Internal Medicine</i> , 2012, 271, 122-130.	2.7	38
179	Using the reconstructed genome-scale human metabolic network to study physiology and pathology. <i>Journal of Internal Medicine</i> , 2012, 271, 131-141.	2.7	98
180	The importance of post-translational modifications in regulating <i>Saccharomyces cerevisiae</i> metabolism. <i>FEMS Yeast Research</i> , 2012, 12, 104-117.	1.1	78
181	From network models to network responses: integration of thermodynamic and kinetic properties of yeast genome-scale metabolic networks. <i>FEMS Yeast Research</i> , 2012, 12, 129-143.	1.1	70
182	Cell growth and cell cycle in <i>Saccharomyces cerevisiae</i> : Basic regulatory design and protein-protein interaction network. <i>Biotechnology Advances</i> , 2012, 30, 52-72.	6.0	48
183	Dynamic flux balance analysis of the metabolism of <i>Saccharomyces cerevisiae</i> during the shift from fully respirative or respirofermentative metabolic states to anaerobiosis. <i>FEBS Journal</i> , 2012, 279, 3338-3354.	2.2	29
184	Scientific discovery as a combinatorial optimisation problem: How best to navigate the landscape of possible experiments?. <i>BioEssays</i> , 2012, 34, 236-244.	1.2	44
185	Comprehensive two-dimensional gas chromatography in metabolomics. <i>Analytical and Bioanalytical Chemistry</i> , 2012, 402, 1993-2013.	1.9	104

#	ARTICLE	IF	CITATIONS
186	Next-generation sequencing and its potential impact on food microbial genomics. <i>Annals of Microbiology</i> , 2013, 63, 21-37.	1.1	62
187	Parameter identification of in vivo kinetic models: Limitations and challenges. <i>Biotechnology Journal</i> , 2013, 8, 768-775.	1.8	29
188	Computational approaches for understanding energy metabolism. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2013, 5, 733-750.	6.6	12
189	Application of targeted proteomics and biological parts assembly in <i>E. coli</i> to optimize the biosynthesis of an anti-malarial drug precursor, amorpho-4,11-diene. <i>Chemical Engineering Science</i> , 2013, 103, 21-28.	1.9	14
190	Measurement, Monitoring, Modelling and Control of Bioprocesses. <i>Advances in Biochemical Engineering/Biotechnology</i> , 2013, 132, v-viii.	0.6	18
191	Consensus and conflict cards for metabolic pathway databases. <i>BMC Systems Biology</i> , 2013, 7, 50.	3.0	10
192	Mapping condition-dependent regulation of metabolism in yeast through genome-scale modeling. <i>BMC Systems Biology</i> , 2013, 7, 36.	3.0	101
193	AMBIENT: Active Modules for Bipartite Networks - using high-throughput transcriptomic data to dissect metabolic response. <i>BMC Systems Biology</i> , 2013, 7, 26.	3.0	9
194	<i>Systems Biology</i> , 2013, , .		9
195	An analysis of a "community-driven" reconstruction of the human metabolic network. <i>Metabolomics</i> , 2013, 9, 757-764.	1.4	30
196	Mass appeal: metabolite identification in mass spectrometry-focused untargeted metabolomics. <i>Metabolomics</i> , 2013, 9, 44-66.	1.4	452
197	Qualitative Modelling of Metabolic Networks. <i>Advances in Botanical Research</i> , 2013, 67, 557-591.	0.5	0
198	A new regulatory principle for in vivo biochemistry: Pleiotropic low affinity regulation by the adenine nucleotides " Illustrated for the glycolytic enzymes of <i>Saccharomyces cerevisiae</i> . <i>FEBS Letters</i> , 2013, 587, 2860-2867.	1.3	14
199	Single-Cell Metabolomics: Analytical and Biological Perspectives. <i>Science</i> , 2013, 342, 1243259.	6.0	540
200	In silico profiling of <i>Escherichia coli</i> and <i>Saccharomyces cerevisiae</i> as terpenoid factories. <i>Microbial Cell Factories</i> , 2013, 12, 84.	1.9	78
201	Increased isobutanol production in <i>Saccharomyces cerevisiae</i> by eliminating competing pathways and resolving cofactor imbalance. <i>Microbial Cell Factories</i> , 2013, 12, 119.	1.9	126
202	Path2Models: large-scale generation of computational models from biochemical pathway maps. <i>BMC Systems Biology</i> , 2013, 7, 116.	3.0	145
203	A novel untargeted metabolomics correlation-based network analysis incorporating human metabolic reconstructions. <i>BMC Systems Biology</i> , 2013, 7, 107.	3.0	64

#	ARTICLE	IF	CITATIONS
204	Economic and environmental impacts of microbial biodiesel. <i>Nature Biotechnology</i> , 2013, 31, 789-793.	9.4	77
205	The stimulatory effect of mannitol on levan biosynthesis: Lessons from metabolic systems analysis of <i>Halomonas smyrnensis</i> AAD6 ^T . <i>Biotechnology Progress</i> , 2013, 29, 1386-1397.	1.3	38
206	Nucleotide degradation and ribose salvage in yeast. <i>Molecular Systems Biology</i> , 2013, 9, 665.	3.2	58
207	The promiscuous binding of pharmaceutical drugs and their transporter-mediated uptake into cells: what we (need to) know and how we can do so. <i>Drug Discovery Today</i> , 2013, 18, 218-239.	3.2	130
208	A model of yeast glycolysis based on a consistent kinetic characterisation of all its enzymes. <i>FEBS Letters</i> , 2013, 587, 2832-2841.	1.3	113
209	Improving the reuse of computational models through version control. <i>Bioinformatics</i> , 2013, 29, 742-748.	1.8	21
210	Sequencing and annotation of the <i>Ophiostoma ulmigenome</i> . <i>BMC Genomics</i> , 2013, 14, 162.	1.2	40
211	Computing life: Add logos to biology and bios to physics. <i>Progress in Biophysics and Molecular Biology</i> , 2013, 111, 69-74.	1.4	10
212	Metabolic Differences in Microbial Cell Populations Revealed by Nanophotonic Ionization. <i>Angewandte Chemie - International Edition</i> , 2013, 52, 3650-3653.	7.2	57
213	Structure and dynamics of molecular networks: A novel paradigm of drug discovery. , 2013, 138, 333-408.		779
214	Finding novel pharmaceuticals in the systems biology era using multiple effective drug targets, phenotypic screening and knowledge of transporters: where drug discovery went wrong and how to fix it. <i>FEBS Journal</i> , 2013, 280, 5957-5980.	2.2	95
216	Development of microbial cell factories for bio-refinery through synthetic bioengineering. <i>Journal of Biotechnology</i> , 2013, 163, 204-216.	1.9	55
217	Genome-Scale Model Management and Comparison. <i>Methods in Molecular Biology</i> , 2013, 985, 3-16.	0.4	1
218	A community-driven global reconstruction of human metabolism. <i>Nature Biotechnology</i> , 2013, 31, 419-425.	9.4	920
219	Genetics and iron in the systems biology of Parkinson's disease and some related disorders. <i>Neurochemistry International</i> , 2013, 62, 637-652.	1.9	56
220	Multi-scale modeling for sustainable chemical production. <i>Biotechnology Journal</i> , 2013, 8, 973-984.	1.8	14
221	Genome-scale modeling enables metabolic engineering of <i>Saccharomyces cerevisiae</i> for succinic acid production. <i>Journal of Industrial Microbiology and Biotechnology</i> , 2013, 40, 735-747.	1.4	64
222	PathNER: a tool for systematic identification of biological pathway mentions in the literature. <i>BMC Systems Biology</i> , 2013, 7, S2.	3.0	18

#	ARTICLE	IF	CITATIONS
223	MetaNetX.org: a website and repository for accessing, analysing and manipulating metabolic networks. <i>Bioinformatics</i> , 2013, 29, 815-816.	1.8	120
224	Revising the Representation of Fatty Acid, Glycerolipid, and Glycerophospholipid Metabolism in the Consensus Model of Yeast Metabolism. <i>Industrial Biotechnology</i> , 2013, 9, 215-228.	0.5	148
225	A method for integrating and ranking the evidence for biochemical pathways by mining reactions from text. <i>Bioinformatics</i> , 2013, 29, i44-i52.	1.8	34
226	The RAVEN Toolbox and Its Use for Generating a Genome-scale Metabolic Model for <i>Penicillium chrysogenum</i> . <i>PLoS Computational Biology</i> , 2013, 9, e1002980.	1.5	364
227	Kozak Consensus Sequence. , 2013, , 1087-1087.		0
228	Industrial Systems Biology of <i>Saccharomyces cerevisiae</i> Enables Novel Succinic Acid Cell Factory. <i>PLoS ONE</i> , 2013, 8, e54144.	1.1	142
229	Simple topological properties predict functional misannotations in a metabolic network. <i>Bioinformatics</i> , 2013, 29, i154-i161.	1.8	15
230	Version 6 of the consensus yeast metabolic network refines biochemical coverage and improves model performance. <i>Database: the Journal of Biological Databases and Curation</i> , 2013, 2013, bat059.	1.4	89
231	Large-Scale Metabolic Models: From Reconstruction to Differential Equations. <i>Industrial Biotechnology</i> , 2013, 9, 179-184.	0.5	58
232	Concise Review: New Paradigms for Down Syndrome Research Using Induced Pluripotent Stem Cells: Tackling Complex Human Genetic Disease. <i>Stem Cells Translational Medicine</i> , 2013, 2, 175-184.	1.6	13
233	Systems biology methods and developments for <i>Saccharomyces cerevisiae</i> and other industrial yeasts in relation to the production of fermented food and food ingredients. , 2013, , 42-80.		0
234	"Mining events from the literature for bioinformatics applications" by S. Ananiadou, P. Thompson, and R. Nawaz; with Martin Vesely as coordinator. <i>SIGWEB Newsletter: the Newsletter of ACM's Special Interest Group on Hypertext and Hypermedia</i> , 2013, , 1-12.	0.5	1
236	CASMI—The Small Molecule Identification Process from a Birmingham Perspective. <i>Metabolites</i> , 2013, 3, 397-411.	1.3	13
237	Systematic Construction of Kinetic Models from Genome-Scale Metabolic Networks. <i>PLoS ONE</i> , 2013, 8, e79195.	1.1	102
238	Identification of Novel Knockout Targets for Improving Terpenoids Biosynthesis in <i>Saccharomyces cerevisiae</i> . <i>PLoS ONE</i> , 2014, 9, e112615.	1.1	34
239	Improving Collaboration by Standardization Efforts in Systems Biology. <i>Frontiers in Bioengineering and Biotechnology</i> , 2014, 2, 61.	2.0	52
240	Systems biology solutions to challenges in marine biotechnology. <i>Frontiers in Marine Science</i> , 2014, 1, .	1.2	4
241	Death by a thousand cuts: the challenges and diverse landscape of lignocellulosic hydrolysate inhibitors. <i>Frontiers in Microbiology</i> , 2014, 5, 90.	1.5	80

#	ARTICLE	IF	CITATIONS
242	Linking metabolomics data to underlying metabolic regulation. <i>Frontiers in Molecular Biosciences</i> , 2014, 1, 22.	1.6	36
243	Multi-Capillary Column-Ion Mobility Spectrometry of Volatile Metabolites Emitted by <i>Saccharomyces Cerevisiae</i> . <i>Metabolites</i> , 2014, 4, 751-774.	1.3	13
244	Computational Strategies for a System-Level Understanding of Metabolism. <i>Metabolites</i> , 2014, 4, 1034-1087.	1.3	54
245	Understanding Principles of the Dynamic Biochemical Networks of Life Through Systems Biology. , 2014, , 21-44.		7
246	Predicting Phenotype from Genotype Through Reconstruction and Integrative Modeling of Metabolic and Regulatory Networks. , 2014, , 307-325.		2
247	Toward genome-scale models of the Chinese hamster ovary cells: incentives, status and perspectives. <i>Pharmaceutical Bioprocessing</i> , 2014, 2, 437-448.	0.8	13
248	Reconstruction of metabolic pathways by combining probabilistic graphical model-based and knowledge-based methods. <i>BMC Proceedings</i> , 2014, 8, S5.	1.8	12
249	Comparative Genome-Scale Reconstruction of Gapless Metabolic Networks for Present and Ancestral Species. <i>PLoS Computational Biology</i> , 2014, 10, e1003465.	1.5	84
250	How drugs get into cells: tested and testable predictions to help discriminate between transporter-mediated uptake and lipoidal bilayer diffusion. <i>Frontiers in Pharmacology</i> , 2014, 5, 231.	1.6	136
251	Sequence divergence and diversity suggests ongoing functional diversification of vertebrate NAD metabolism. <i>DNA Repair</i> , 2014, 23, 39-48.	1.3	15
252	Untangling complex dynamical systems via derivative-variable correlations. <i>Scientific Reports</i> , 2014, 4, 5030.	1.6	27
253	MEMOSys 2.0: an update of the bioinformatics database for genome-scale models and genomic data. <i>Database: the Journal of Biological Databases and Curation</i> , 2014, 2014, bau004.	1.4	16
254	Metabolic engineering of <i>Saccharomyces cerevisiae</i> for itaconic acid production. <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 8155-8164.	1.7	87
255	Metabolomics applied in bioenergy. <i>Chemical and Biological Technologies in Agriculture</i> , 2014, 1, .	1.9	15
256	A future of the model organism model. <i>Molecular Biology of the Cell</i> , 2014, 25, 549-553.	0.9	23
257	Processing biological literature with customizable Web services supporting interoperable formats. <i>Database: the Journal of Biological Databases and Curation</i> , 2014, 2014, bau064-bau064.	1.4	12
258	Metabolomics and systems pharmacology: why and how to model the human metabolic network for drug discovery. <i>Drug Discovery Today</i> , 2014, 19, 171-182.	3.2	140
259	Integration of transcription and flux data reveals molecular paths associated with differences in oxygen-dependent phenotypes of <i>Saccharomyces cerevisiae</i> . <i>BMC Systems Biology</i> , 2014, 8, 16.	3.0	2

#	ARTICLE	IF	CITATIONS
260	Age-correlated stress resistance improves fitness of yeast: support from agent-based simulations. <i>BMC Systems Biology</i> , 2014, 8, 18.	3.0	12
261	Software platforms to facilitate reconstructing genome-scale metabolic networks. <i>Environmental Microbiology</i> , 2014, 16, 49-59.	1.8	69
262	Recent developments and applications of metabolomics in microbiological investigations. <i>TrAC - Trends in Analytical Chemistry</i> , 2014, 56, 37-48.	5.8	68
263	Kinetic models in industrial biotechnology – Improving cell factory performance. <i>Metabolic Engineering</i> , 2014, 24, 38-60.	3.6	238
264	Knowledge representation in metabolic pathway databases. <i>Briefings in Bioinformatics</i> , 2014, 15, 455-470.	3.2	16
265	Optimizing genome-scale network reconstructions. <i>Nature Biotechnology</i> , 2014, 32, 447-452.	9.4	185
266	Molecular Mechanisms in Yeast Carbon Metabolism. , 2014, , .		7
267	An integrative, multi-scale, genome-wide model reveals the phenotypic landscape of <i>Escherichia coli</i> . <i>Molecular Systems Biology</i> , 2014, 10, 735.	3.2	73
268	Developmental strategies and regulation of cell-free enzyme system for ethanol production: a molecular prospective. <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 9561-9578.	1.7	34
269	NExT: Integration of Thermodynamic Constraints and Metabolomics Data into a Metabolic Network. <i>Methods in Molecular Biology</i> , 2014, 1191, 65-78.	0.4	8
270	Network Thermodynamic Curation of Human and Yeast Genome-Scale Metabolic Models. <i>Biophysical Journal</i> , 2014, 107, 493-503.	0.2	32
271	Applications of computational modeling in metabolic engineering of yeast. <i>FEMS Yeast Research</i> , 2014, 15, n/a-n/a.	1.1	28
272	Regulation of amino acid metabolic enzymes and transporters in plants. <i>Journal of Experimental Botany</i> , 2014, 65, 5535-5556.	2.4	297
273	Construction of robust dynamic genome-scale metabolic model structures of <i>Saccharomyces cerevisiae</i> through iterative re-parameterization. <i>Metabolic Engineering</i> , 2014, 25, 159-173.	3.6	29
274	The future of genome-scale modeling of yeast through integration of a transcriptional regulatory network. <i>Quantitative Biology</i> , 2014, 2, 30-46.	0.3	8
276	Environmental systems biology of cold-tolerant phenotype in <i>Saccharomyces</i> species adapted to grow at different temperatures. <i>Molecular Ecology</i> , 2014, 23, 5241-5257.	2.0	79
277	iOD907, the first genome-scale metabolic model for the milk yeast <i>Kluyveromyces lactis</i> . <i>Biotechnology Journal</i> , 2014, 9, 776-790.	1.8	52
278	- DESIGN AND TAILORING OF POLYHYDROXYALKANOATE-BASED BIOMATERIALS CONTAINING 4-HYDROXYBUTYRATE MONOMER. , 2014, , 304-323.		0

#	ARTICLE	IF	CITATIONS
280	A multi-scale, multi-disciplinary approach for assessing the technological, economic and environmental performance of bio-based chemicals. <i>Biochemical Society Transactions</i> , 2015, 43, 1151-1156.	1.6	3
281	Genome-scale modelling of microbial metabolism with temporal and spatial resolution. <i>Biochemical Society Transactions</i> , 2015, 43, 1164-1171.	1.6	23
282	Modeling cancer metabolism on a genome scale. <i>Molecular Systems Biology</i> , 2015, 11, 817.	3.2	152
284	Network reconstruction and validation of the Snf1/AMPK pathway in baker's yeast based on a comprehensive literature review. <i>Npj Systems Biology and Applications</i> , 2015, 1, 15007.	1.4	20
285	The transporter-mediated cellular uptake of pharmaceutical drugs is based on their metabolite-likeness and not on their bulk biophysical properties: Towards a systems pharmacology. <i>Perspectives in Science</i> , 2015, 6, 66-83.	0.6	18
286	Characterization of intrinsic variability in time-series metabolomic data of cultured mammalian cells. <i>Biotechnology and Bioengineering</i> , 2015, 112, 2276-2283.	1.7	4
287	Constructing kinetic models of metabolism at genome-scales: A review. <i>Biotechnology Journal</i> , 2015, 10, 1345-1359.	1.8	72
288	Optimizing eukaryotic cell hosts for protein production through systems biotechnology and genome-scale modeling. <i>Biotechnology Journal</i> , 2015, 10, 939-949.	1.8	46
289	Cell scale host-pathogen modeling: another branch in the evolution of constraint-based methods. <i>Frontiers in Microbiology</i> , 2015, 6, 1032.	1.5	12
290	Comparative Analysis of Yeast Metabolic Network Models Highlights Progress, Opportunities for Metabolic Reconstruction. <i>PLoS Computational Biology</i> , 2015, 11, e1004530.	1.5	70
291	Genome scale models of yeast: towards standardized evaluation and consistent omic integration. <i>Integrative Biology (United Kingdom)</i> , 2015, 7, 846-858.	0.6	66
292	Flux balance analysis of genome-scale metabolic model of rice (<i>Oryza sativa</i>): Aiming to increase biomass. <i>Journal of Biosciences</i> , 2015, 40, 819-828.	0.5	6
293	Towards improved genome-scale metabolic network reconstructions: unification, transcript specificity and beyond. <i>Briefings in Bioinformatics</i> , 2015, 17, bbv100.	3.2	19
294	Growth and metabolism of <i>Beauveria bassiana</i> spores and mycelia. <i>BMC Microbiology</i> , 2015, 15, 267.	1.3	33
295	The virtue of innovation: innovation through the lenses of biological evolution. <i>Journal of the Royal Society Interface</i> , 2015, 12, 20141183.	1.5	17
296	Pantograph: A template-based method for genome-scale metabolic model reconstruction. <i>Journal of Bioinformatics and Computational Biology</i> , 2015, 13, 1550006.	0.3	29
297	A "rule of 0.5" for the metabolite-likeness of approved pharmaceutical drugs. <i>Metabolomics</i> , 2015, 11, 323-339.	1.4	84
298	Synthetic Biology for Specialty Chemicals. <i>Annual Review of Chemical and Biomolecular Engineering</i> , 2015, 6, 35-52.	3.3	24

#	ARTICLE	IF	CITATIONS
299	What would be the observable consequences if phospholipid bilayer diffusion of drugs into cells is negligible?. Trends in Pharmacological Sciences, 2015, 36, 15-21.	4.0	46
300	Synthetic biology for the directed evolution of protein biocatalysts: navigating sequence space intelligently. Chemical Society Reviews, 2015, 44, 1172-1239.	18.7	316
301	Genome-scale modeling for metabolic engineering. Journal of Industrial Microbiology and Biotechnology, 2015, 42, 327-338.	1.4	82
302	Event-based text mining for biology and functional genomics. Briefings in Functional Genomics, 2015, 14, 213-230.	1.3	58
303	Inferring causal metabolic signals that regulate the dynamic TORC1-dependent transcriptome. Molecular Systems Biology, 2015, 11, 802.	3.2	49
304	Multi-scale exploration of the technical, economic, and environmental dimensions of bio-based chemical production. Metabolic Engineering, 2015, 31, 1-12.	3.6	32
305	Systems modeling approaches for microbial community studies: from metagenomics to inference of the community structure. Frontiers in Microbiology, 2015, 6, 213.	1.5	60
306	Many InChIs and quite some feat. Journal of Computer-Aided Molecular Design, 2015, 29, 681-694.	1.3	19
307	Metabolic Needs and Capabilities of Toxoplasma gondii through Combined Computational and Experimental Analysis. PLoS Computational Biology, 2015, 11, e1004261.	1.5	92
308	Mimoz: web-based semantic zooming and navigation in metabolic networks. BMC Systems Biology, 2015, 9, 10.	3.0	5
309	Dynamic phosphoproteomics reveals TORC1-dependent regulation of yeast nucleotide and amino acid biosynthesis. Science Signaling, 2015, 8, rs4.	1.6	64
310	Comprehensive characterization and evaluation of hepatocellular carcinoma by LC-MS based serum metabolomics. Metabolomics, 2015, 11, 1381-1393.	1.4	16
311	Membrane transporter engineering in industrial biotechnology and whole cell biocatalysis. Trends in Biotechnology, 2015, 33, 237-246.	4.9	167
312	Metabolic Pathway Databases: A Word of Caution. Methods in Pharmacology and Toxicology, 2015, , 27-63.	0.1	1
313	Network-based discovery through mechanistic systems biology. Implications for applications in SMEs and drug discovery: where the action is. Drug Discovery Today: Technologies, 2015, 15, 41-48.	4.0	12
314	Network Analysis Identifies Mitochondrial Regulation of Epidermal Differentiation by MPZL3 and FDXR. Developmental Cell, 2015, 35, 444-457.	3.1	50
315	Effects of CeO2 nanoparticles on microbial metabolism. Chemical Geology, 2015, 391, 33-41.	1.4	13
316	A workflow for bacterial metabolic fingerprinting and lipid profiling: application to Ciprofloxacin challenged Escherichia coli. Metabolomics, 2015, 11, 438-453.	1.4	10

#	ARTICLE	IF	CITATIONS
318	A Dormant Microbial Component in the Development of Preeclampsia. <i>Frontiers in Medicine</i> , 2016, 3, 60.	1.2	64
319	A Strategy for Functional Interpretation of Metabolomic Time Series Data in Context of Metabolic Network Information. <i>Frontiers in Molecular Biosciences</i> , 2016, 3, 6.	1.6	17
320	Mathematical Modeling and Dynamic Simulation of Metabolic Reaction Systems Using Metabolome Time Series Data. <i>Frontiers in Molecular Biosciences</i> , 2016, 3, 15.	1.6	19
321	Efficient Reconstruction of Predictive Consensus Metabolic Network Models. <i>PLoS Computational Biology</i> , 2016, 12, e1005085.	1.5	19
322	Integration and Validation of the Genome-Scale Metabolic Models of <i>Pichia pastoris</i> : A Comprehensive Update of Protein Glycosylation Pathways, Lipid and Energy Metabolism. <i>PLoS ONE</i> , 2016, 11, e0148031.	1.1	56
323	MetMaxStruct: A Tversky-Similarity-Based Strategy for Analysing the (Sub)Structural Similarities of Drugs and Endogenous Metabolites. <i>Frontiers in Pharmacology</i> , 2016, 7, 266.	1.6	26
324	Reconstruction and applications of consensus yeast metabolic network based on <scp>RNA</scp> sequencing. <i>FEBS Open Bio</i> , 2016, 6, 264-275.	1.0	4
325	A Bacterial Component to Alzheimer's-Type Dementia Seen via a Systems Biology Approach that Links Iron Dysregulation and Inflammagen Shedding to Disease. <i>Journal of Alzheimer's Disease</i> , 2016, 53, 1237-1256.	1.2	56
326	2Path: A terpenoid metabolic network modeled as graph database. , 2016, , .		0
327	Constraint-based stoichiometric modelling from single organisms to microbial communities. <i>Journal of the Royal Society Interface</i> , 2016, 13, 20160627.	1.5	96
328	Whole-genome metabolic model of <i>Trichoderma reesei</i> built by comparative reconstruction. <i>Biotechnology for Biofuels</i> , 2016, 9, 252.	6.2	21
329	Spectral consensus strategy for accurate reconstruction of large biological networks. <i>BMC Bioinformatics</i> , 2016, 17, 493.	1.2	10
330	Control analysis of the impact of allosteric regulation mechanism in a <i>Escherichia coli</i> kinetic model: Application to serine production. <i>Biochemical Engineering Journal</i> , 2016, 110, 59-70.	1.8	2
331	Microbial network for waste activated sludge cascade utilization in an integrated system of microbial electrolysis and anaerobic fermentation. <i>Biotechnology for Biofuels</i> , 2016, 9, 83.	6.2	82
333	Synthetic biology and regulatory networks: where metabolic systems biology meets control engineering. <i>Journal of the Royal Society Interface</i> , 2016, 13, 20151046.	1.5	47
334	Yeast Expression Systems for Industrial Biotechnology. <i>Fungal Biology</i> , 2016, , 227-237.	0.3	2
335	The metabolome 18 years on: a concept comes of age. <i>Metabolomics</i> , 2016, 12, 148.	1.4	95
338	Recon 2.2: from reconstruction to model of human metabolism. <i>Metabolomics</i> , 2016, 12, 109.	1.4	243

#	ARTICLE	IF	CITATIONS
339	<i>Saccharomyces cerevisiae</i> metabolism in ecological context. FEMS Yeast Research, 2016, 16, fow080.	1.1	37
340	Computational Metabolomics: A Framework for the Million Metabolome. Chemical Research in Toxicology, 2016, 29, 1956-1975.	1.7	191
341	<i>In Vivo</i> Analysis of NH ₄ ⁺ Transport and Central Nitrogen Metabolism in <i>Saccharomyces cerevisiae</i> during Aerobic Nitrogen-Limited Growth. Applied and Environmental Microbiology, 2016, 82, 6831-6845.	1.4	9
342	Network analyses based on comprehensive molecular interaction maps reveal robust control structures in yeast stress response pathways. Npj Systems Biology and Applications, 2016, 2, 15018.	1.4	27
343	The metabolic background is a global player in <i>Saccharomyces</i> gene expression epistasis. Nature Microbiology, 2016, 1, 15030.	5.9	76
344	Analytical Techniques and Methods for Biomass. , 2016, , .		15
345	Mass Spectrometry for Metabolomics and Biomass Composition Analyses. , 2016, , 115-141.		2
346	Computational Lipidomics and Lipid Bioinformatics: Filling In the Blanks. Journal of Integrative Bioinformatics, 2016, 13, 34-51.	1.0	3
347	Measuring the robustness of link prediction algorithms under noisy environment. Scientific Reports, 2016, 6, 18881.	1.6	26
348	libChEBI: an API for accessing the ChEBI database. Journal of Cheminformatics, 2016, 8, 11.	2.8	19
349	Say hello to Dr Warwick Dunn! Metabolomics™ new Reviews Editor. Metabolomics, 2016, 12, 1.	1.4	0
350	Improving the flux distributions simulated with genome-scale metabolic models of <i>Saccharomyces cerevisiae</i> . Metabolic Engineering Communications, 2016, 3, 153-163.	1.9	51
351	iSCHRUNK “ In Silico Approach to Characterization and Reduction of Uncertainty in the Kinetic Models of Genome-scale Metabolic Networks. Metabolic Engineering, 2016, 33, 158-168.	3.6	72
352	Technology development for natural product biosynthesis in <i>Saccharomyces cerevisiae</i> . Current Opinion in Biotechnology, 2016, 42, 74-83.	3.3	39
353	Metabolomics reveals the physiological response of <i>Pseudomonas putida</i> KT2440 (UWC1) after pharmaceutical exposure. Molecular BioSystems, 2016, 12, 1367-1377.	2.9	5
354	Network-based methods for identifying critical pathways of complex diseases: a survey. Molecular BioSystems, 2016, 12, 1082-1089.	2.9	15
355	ChEBI in 2016: Improved services and an expanding collection of metabolites. Nucleic Acids Research, 2016, 44, D1214-D1219.	6.5	752
356	Algorithms for modeling global and context-specific functional relationship networks. Briefings in Bioinformatics, 2016, 17, 686-695.	3.2	3

#	ARTICLE	IF	CITATIONS
357	An overview of bioinformatics methods for modeling biological pathways in yeast. Briefings in Functional Genomics, 2016, 15, 95-108.	1.3	18
358	Xylose-induced dynamic effects on metabolism and gene expression in engineered <i>Saccharomyces cerevisiae</i> in anaerobic glucose-xylose cultures. Applied Microbiology and Biotechnology, 2016, 100, 969-985.	1.7	25
359	Genome-Wide Semi-Automated Annotation of Transporter Systems. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2017, 14, 443-456.	1.9	14
360	The Pivotal Role of Protein Phosphorylation in the Control of Yeast Central Metabolism. G3: Genes, Genomes, Genetics, 2017, 7, 1239-1249.	0.8	18
361	Augmenting brain metabolism to increase macro- and chaperone-mediated autophagy for decreasing neuronal proteotoxicity and aging. Progress in Neurobiology, 2017, 156, 90-106.	2.8	52
362	Multi-omics approaches to disease. Genome Biology, 2017, 18, 83.	3.8	1,439
363	Supporting Biological Pathway Curation Through Text Mining. Communications in Computer and Information Science, 2017, , 59-73.	0.4	2
364	Leader-following exponential consensus of fractional order nonlinear multi-agents system with hybrid time-varying delay: A heterogeneous impulsive method. Physica A: Statistical Mechanics and Its Applications, 2017, 482, 158-172.	1.2	46
365	Genome-scale metabolic modelling common cofactors metabolism in microorganisms. Journal of Biotechnology, 2017, 251, 1-13.	1.9	15
368	Systems Biology of Metabolism. Annual Review of Biochemistry, 2017, 86, 245-275.	5.0	173
369	A terpenoid metabolic network modelled as graph database. International Journal of Data Mining and Bioinformatics, 2017, 18, 74.	0.1	6
370	Transporter engineering in biomass utilization by yeast. FEMS Yeast Research, 2017, 17, .	1.1	35
371	Metabolic modeling to identify engineering targets for <i>Komagataella phaffii</i> : The effect of biomass composition on gene target identification. Biotechnology and Bioengineering, 2017, 114, 2605-2615.	1.7	16
372	Genome-scale modeling of yeast: chronology, applications and critical perspectives. FEMS Yeast Research, 2017, 17, .	1.1	54
373	In silico design of anaerobic growth-coupled product formation in <i>Escherichia coli</i> : experimental validation using a simple polyol, glycerol. Bioprocess and Biosystems Engineering, 2017, 40, 361-372.	1.7	4
374	Enhancing Drug Efficacy and Therapeutic Index through Cheminformatics-Based Selection of Small Molecule Binary Weapons That Improve Transporter-Mediated Targeting: A Cytotoxicity System Based on Gemcitabine. Frontiers in Pharmacology, 2017, 8, 155.	1.6	18
375	Perspectives and Challenges of Microbial Application for Crop Improvement. Frontiers in Plant Science, 2017, 8, 49.	1.7	370
376	From Systems to Organisations. Systems, 2017, 5, 23.	1.2	2

#	ARTICLE	IF	CITATIONS
377	Systematic Analysis of Transcriptional and Post-transcriptional Regulation of Metabolism in Yeast. <i>PLoS Computational Biology</i> , 2017, 13, e1005297.	1.5	51
378	Metabolic adjustment upon repetitive substrate perturbations using dynamic ¹³ C-tracing in yeast. <i>Microbial Cell Factories</i> , 2017, 16, 161.	1.9	14
379	Reconstruction of genome-scale metabolic model of <i>Yarrowia lipolytica</i> and its application in overproduction of triacylglycerol. <i>Bioresources and Bioprocessing</i> , 2017, 4, .	2.0	38
380	Modeling Microbial Communities: A Call for Collaboration between Experimentalists and Theorists. <i>Processes</i> , 2017, 5, 53.	1.3	21
381	A comprehensive comparison of network similarities for link prediction and spurious link elimination. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2018, 500, 97-105.	1.2	14
382	Metabolic profiling of isolated mitochondria and cytoplasm reveals compartment-specific metabolic responses. <i>Metabolomics</i> , 2018, 14, 59.	1.4	23
383	Anaerobiosis revisited: growth of <i>Saccharomyces cerevisiae</i> under extremely low oxygen availability. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 2101-2116.	1.7	20
384	Genome-scale fluxes predicted under the guidance of enzyme abundance using a novel hyper-cube shrink algorithm. <i>Bioinformatics</i> , 2018, 34, 502-510.	1.8	0
385	Network Community Detection Based on the <i>Physarum</i> -Inspired Computational Framework. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 15, 1916-1928.	1.9	38
386	Phosphorus and nitrogen starvation reveal life-cycle specific responses in the metabolome of <i>Emiliana huxleyi</i> (Haptophyta). <i>Limnology and Oceanography</i> , 2018, 63, 203-226.	1.6	23
387	Light-driven fine chemical production in yeast biohybrids. <i>Science</i> , 2018, 362, 813-816.	6.0	251
388	Synthetic biology tools for engineering <i>Yarrowia lipolytica</i> . <i>Biotechnology Advances</i> , 2018, 36, 2150-2164.	6.0	120
389	Machine Learning Predicts the Yeast Metabolome from the Quantitative Proteome of Kinase Knockouts. <i>Cell Systems</i> , 2018, 7, 269-283.e6.	2.9	80
390	An appeal to magic? The discovery of a non-enzymatic metabolism and its role in the origins of life. <i>Biochemical Journal</i> , 2018, 475, 2577-2592.	1.7	69
391	Microkinetic modeling in homogeneous catalysis. <i>Wiley Interdisciplinary Reviews: Computational Molecular Science</i> , 2018, 8, e1372.	6.2	85
392	Strategy for Modern Research of Traditional Chinese Medicine Formulae. , 2018, , 3-18.		2
393	Selection of small plasma peptides for the auxiliary diagnosis and prognosis of epithelial ovarian cancer by using UPLC/MS-based nontargeted and targeted analyses. <i>International Journal of Cancer</i> , 2019, 144, 2033-2042.	2.3	18
394	Ample Arsenite Bio-Oxidation Activity in Bangladesh Drinking Water Wells: A Bonanza for Bioremediation?. <i>Microorganisms</i> , 2019, 7, 246.	1.6	9

#	ARTICLE	IF	CITATIONS
395	ChIP-exo analysis highlights Fkh1 and Fkh2 transcription factors as hubs that integrate multi-scale networks in budding yeast. <i>Nucleic Acids Research</i> , 2019, 47, 7825-7841.	6.5	11
397	SLIMER: probing flexibility of lipid metabolism in yeast with an improved constraint-based modeling framework. <i>BMC Systems Biology</i> , 2019, 13, 4.	3.0	43
398	Predicting Metabolism from Gene Expression in an Improved Whole-Genome Metabolic Network Model of <i>Danio rerio</i> . <i>Zebrafish</i> , 2019, 16, 348-362.	0.5	20
399	Protein-facilitated transport of hydrophobic molecules across the yeast plasma membrane. <i>FEBS Letters</i> , 2019, 593, 1508-1527.	1.3	31
400	Current status and applications of genome-scale metabolic models. <i>Genome Biology</i> , 2019, 20, 121.	3.8	463
401	A genome-scale metabolic network reconstruction of extremely halophilic bacterium <i>Salinibacter ruber</i> . <i>PLoS ONE</i> , 2019, 14, e0216336.	1.1	7
402	Systems Biology and Multi-Omics Integration: Viewpoints from the Metabolomics Research Community. <i>Metabolites</i> , 2019, 9, 76.	1.3	387
403	BOFdat: Generating biomass objective functions for genome-scale metabolic models from experimental data. <i>PLoS Computational Biology</i> , 2019, 15, e1006971.	1.5	83
404	A Data Integration Multi-Omics Approach to Study Calorie Restriction-Induced Changes in Insulin Sensitivity. <i>Frontiers in Physiology</i> , 2018, 9, 1958.	1.3	39
405	A comprehensive, mechanistically detailed, and executable model of the cell division cycle in <i>Saccharomyces cerevisiae</i> . <i>Nature Communications</i> , 2019, 10, 1308.	5.8	41
406	Yeast Genome-Scale Metabolic Models for Simulating Genotype-Phenotype Relations. <i>Progress in Molecular and Subcellular Biology</i> , 2019, 58, 111-133.	0.9	11
407	Consistency, Inconsistency, and Ambiguity of Metabolite Names in Biochemical Databases Used for Genome-Scale Metabolic Modelling. <i>Metabolites</i> , 2019, 9, 28.	1.3	28
408	Signaling pathways in context. <i>Current Opinion in Biotechnology</i> , 2019, 58, 155-160.	3.3	2
409	Yeast Systems Biology: Model Organism and Cell Factory. <i>Biotechnology Journal</i> , 2019, 14, e1800421.	1.8	159
410	Uncovering and resolving challenges of quantitative modeling in a simplified community of interacting cells. <i>PLoS Biology</i> , 2019, 17, e3000135.	2.6	34
411	Established and Upcoming Yeast Expression Systems. <i>Methods in Molecular Biology</i> , 2019, 1923, 1-74.	0.4	25
412	Toward a Unification of System-Theoretical Principles in Biology and Ecology—The Stochastic Lyapunov Matrix Equation and Its Inverse Application. <i>Frontiers in Applied Mathematics and Statistics</i> , 2019, 5, .	0.7	21
413	Evaluation of synthetic formaldehyde and methanol assimilation pathways in <i>Yarrowia lipolytica</i> . <i>Fungal Biology and Biotechnology</i> , 2019, 6, 27.	2.5	20

#	ARTICLE	IF	CITATIONS
414	Metabolic profiling analysis upon acylcarnitines in tissues of hepatocellular carcinoma revealed the inhibited carnitine shuttle system caused by the downregulated carnitine palmitoyltransferase 2. <i>Molecular Carcinogenesis</i> , 2019, 58, 749-759.	1.3	28
415	Modeling Lipid Metabolism in Yeast. , 2019, , 375-388.		2
416	Quantitative flux coupling analysis. <i>Journal of Mathematical Biology</i> , 2019, 78, 1459-1484.	0.8	5
417	Robustness of Link Prediction Under Network Attacks. <i>IEEE Transactions on Circuits and Systems II: Express Briefs</i> , 2020, 67, 1472-1476.	2.2	6
418	A mechanism-aware and multiomic machine-learning pipeline characterizes yeast cell growth. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 18869-18879.	3.3	62
419	Serum Metabolomics for Biomarker Screening of Esophageal Squamous Cell Carcinoma and Esophageal Squamous Dysplasia Using Gas Chromatography-Mass Spectrometry. <i>ACS Omega</i> , 2020, 5, 26402-26412.	1.6	21
420	Connecting the dots: Advances in modern metabolomics and its application in yeast system. <i>Biotechnology Advances</i> , 2020, 44, 107616.	6.0	12
421	Genome-scale metabolic reconstruction of the non-model yeast <i>Issatchenkia orientalis</i> SD108 and its application to organic acids production. <i>Metabolic Engineering Communications</i> , 2020, 11, e00148.	1.9	20
422	Evolutionary Markov Dynamics for Network Community Detection. <i>IEEE Transactions on Knowledge and Data Engineering</i> , 2022, 34, 1206-1220.	4.0	52
423	Towards model-driven characterization and manipulation of plant lipid metabolism. <i>Progress in Lipid Research</i> , 2020, 80, 101051.	5.3	28
424	A scalable method for parameter-free simulation and validation of mechanistic cellular signal transduction network models. <i>Npj Systems Biology and Applications</i> , 2020, 6, 2.	1.4	10
425	Methanotrophic microbial cell factory platform for simultaneous conversion of methane and xylose to value-added chemicals. <i>Chemical Engineering Journal</i> , 2021, 420, 127632.	6.6	12
426	Purification and identification of surface active amphiphilic candidates produced by <i>Geotrichum candidum</i> MK880487 possessing antifungal property. <i>Journal of Dispersion Science and Technology</i> , 2021, 42, 1082-1098.	1.3	3
427	Metabolic modeling predicts specific gut bacteria as key determinants for <i>Candida albicans</i> colonization levels. <i>ISME Journal</i> , 2021, 15, 1257-1270.	4.4	23
428	Evolution of Ca ²⁺ transporters in plants. , 2021, , 69-87.		0
429	The Robustness of Graph <i>k</i> -Shell Structure Under Adversarial Attacks. <i>IEEE Transactions on Circuits and Systems II: Express Briefs</i> , 2022, 69, 1797-1801.	2.2	1
430	Evaluating accessibility, usability and interoperability of genome-scale metabolic models for diverse yeasts species. <i>FEMS Yeast Research</i> , 2021, 21, .	1.1	6
431	Application of Systems Biology Approaches for Host-Fungal Interaction in Animals. <i>Fungal Biology</i> , 2021, , 49-62.	0.3	0

#	ARTICLE	IF	CITATIONS
432	Rare genetic variants affecting urine metabolite levels link population variation to inborn errors of metabolism. <i>Nature Communications</i> , 2021, 12, 964.	5.8	20
433	New Cross-Talks between Pathways Involved in Grapevine Infection with <i>Candidatus Phytoplasma solani</i> ™ Revealed by Temporal Network Modelling. <i>Plants</i> , 2021, 10, 646.	1.6	3
435	Modeling in postharvest: a multiscale perspective. <i>Acta Horticulturae</i> , 2021, , 375-384.	0.1	0
436	Review of Machine Learning Methods for the Prediction and Reconstruction of Metabolic Pathways. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 634141.	1.6	15
438	Multiscale models quantifying yeast physiology: towards a whole-cell model. <i>Trends in Biotechnology</i> , 2022, 40, 291-305.	4.9	20
439	A novel recovery strategy based on link prediction and hyperbolic geometry of complex networks. <i>Journal of Complex Networks</i> , 2021, 9, .	1.1	5
440	The yeastGemMap: A process diagram to assist yeast systemsâ€™metabolic studies. <i>Biotechnology and Bioengineering</i> , 2021, 118, 4800-4814.	1.7	1
441	Path to improving the life cycle and quality of genome-scale models of metabolism. <i>Cell Systems</i> , 2021, 12, 842-859.	2.9	16
442	Review of construction methods for whole-cell computational models. <i>Systems Microbiology and Biomanufacturing</i> , 0, , 1.	1.5	1
443	Zooming in on Yeast Osmoadaptation. <i>Advances in Experimental Medicine and Biology</i> , 2012, 736, 293-310.	0.8	10
444	Computational Prediction of Essential Metabolic Genes Using Constraint-Based Approaches. <i>Methods in Molecular Biology</i> , 2015, 1279, 183-204.	0.4	15
445	Genome-Scale Metabolic Modeling from Yeast to Human Cell Models of Complex Diseases: Latest Advances and Challenges. <i>Methods in Molecular Biology</i> , 2019, 2049, 329-345.	0.4	14
446	Yeast Systems Biology: The Challenge of Eukaryotic Complexity. <i>Methods in Molecular Biology</i> , 2011, 759, 3-28.	0.4	10
447	Integrative Information Management for Systems Biology. <i>Lecture Notes in Computer Science</i> , 2010, , 164-178.	1.0	6
448	Workflows for Information Integration in the Life Sciences. <i>Lecture Notes in Computer Science</i> , 2011, , 215-225.	1.0	1
449	Anaerobic Carbon Metabolism of <i>Saccharomyces cerevisiae</i> . , 2014, , 57-82.		1
451	Systems Biology: Developments and Applications. , 2014, , 83-96.		3
452	Reproducibility of Model-Based Results in Systems Biology. , 2013, , 301-320.		7

#	ARTICLE	IF	CITATIONS
454	Enzyme-Constrained Models and Omics Analysis of <i>Streptomyces coelicolor</i> Reveal Metabolic Changes that Enhance Heterologous Production. <i>IScience</i> , 2020, 23, 101525.	1.9	30
460	Colloidal hydrodynamics of biological cells: A frontier spanning two fields. <i>Physical Review Fluids</i> , 2019, 4, .	1.0	14
461	Combining inferred regulatory and reconstructed metabolic networks enhances phenotype prediction in yeast. <i>PLoS Computational Biology</i> , 2017, 13, e1005489.	1.5	46
462	Synthetic Biology: Mapping the Scientific Landscape. <i>PLoS ONE</i> , 2012, 7, e34368.	1.1	81
463	The Yin and Yang of Yeast Transcription: Elements of a Global Feedback System between Metabolism and Chromatin. <i>PLoS ONE</i> , 2012, 7, e37906.	1.1	42
464	Exploiting Genomic Knowledge in Optimising Molecular Breeding Programmes: Algorithms from Evolutionary Computing. <i>PLoS ONE</i> , 2012, 7, e48862.	1.1	15
465	Computational Analysis of Reciprocal Association of Metabolism and Epigenetics in the Budding Yeast: A Genome-Scale Metabolic Model (GSMM) Approach. <i>PLoS ONE</i> , 2014, 9, e111686.	1.1	12
466	Pathway-Consensus Approach to Metabolic Network Reconstruction for <i>Pseudomonas putida</i> KT2440 by Systematic Comparison of Published Models. <i>PLoS ONE</i> , 2017, 12, e0169437.	1.1	29
468	Methodology of Modernization Research in Traditional Chinese Medicine Based on Systems Biology and Network Biology. <i>Chinese Journal of Natural Medicines</i> , 2009, 7, 249-259.	0.7	15
470	Intelligent host engineering for metabolic flux optimisation in biotechnology. <i>Biochemical Journal</i> , 2021, 478, 3685-3721.	1.7	8
471	Genome-Scale Constraint-Based Models to Navigate the Microbial Landscape. , 2010, , 4329-4338.		0
472	Introduction to GRNs. , 2010, , 28-56.		0
473	Systems biology: a new paradigm for industrial yeast strain development. <i>Microbiology Australia</i> , 2011, 32, 151.	0.1	0
474	Heterogeneous Biological Network Visualization System: Case Study in Context of Medical Image Data. <i>Advances in Experimental Medicine and Biology</i> , 2012, 736, 95-118.	0.8	0
476	Kinetic Parameter Information Resource, KiPar. , 2013, , 1070-1072.		0
479	Analysis of Chaperone Network Throughput. , 2014, , 3-23.		1
480	Systems Metabolic Engineering of <i>Arabidopsis</i> for Increased Cellulose Production. <i>FASEB Journal</i> , 2015, 29, 887.26.	0.2	1
481	Modeling Lipid Metabolism in Yeast. , 2016, , 1-14.		0

#	ARTICLE	IF	CITATIONS
489	Microbial Production of Nutraceuticals: Challenges and Prospects. , 2019, , 203-208.		1
491	Recent Advances in Molecular Approaches for Mining Potential Candidate Genes of Trichoderma for Biofuel. Fungal Biology, 2020, , 163-186.	0.3	0
492	Artificial Intelligence in Biological Modelling. , 2020, , 265-302.		1
493	Unsupervised Data Analysis Methods used in Qualitative and Quantitative Metabolomics and Metabonomics. Advances in Bioinformatics and Biomedical Engineering Book Series, 0, , 1-28.	0.2	0
494	Systems Biology: Developments and Applications. , 2014, , 83-96.		0
496	Computational Lipidomics and Lipid Bioinformatics: Filling In the Blanks. Journal of Integrative Bioinformatics, 2016, 13, 299.	1.0	2
497	Community Detection in Graph: An Embedding Method. IEEE Transactions on Network Science and Engineering, 2022, 9, 689-702.	4.1	18
498	Exploring the transportome of the biosurfactant producing yeast Starmerella bombicola. BMC Genomics, 2022, 23, 22.	1.2	8
500	Genome-scale modeling of yeast metabolism: retrospectives and perspectives. FEMS Yeast Research, 2022, 22, .	1.1	20
501	Soil microorganisms facilitated the electrode-driven trichloroethene dechlorination to ethene by Dehalococcoides species in a bioelectrochemical system. Environmental Research, 2022, 209, 112801.	3.7	18
502	From Petri Plates to Petri Nets, a revolution in yeast biology. FEMS Yeast Research, 2022, , .	1.1	0
506	Analysis and modeling tools of metabolic flux. , 2022, , 45-68.		0
510	Network approach to understand biological systems: From single to multilayer networks. Journal of Biosciences, 2022, 47, .	0.5	1
511	Multi-Omics Approaches and Resources for Systems-Level Gene Function Prediction in the Plant Kingdom. Plants, 2022, 11, 2614.	1.6	3
512	Predictive evolution of metabolic phenotypes using modelâ€designed environments. Molecular Systems Biology, 2022, 18, .	3.2	10
513	Recent Advances In Microbe-Photocatalyst Hybrid Systems for Production of Bulk Chemicals: A Review. Applied Biochemistry and Biotechnology, 0, , .	1.4	0
514	Using Kinetic Modelling to Infer Adaptations in Saccharomyces cerevisiae Carbohydrate Storage Metabolism to Dynamic Substrate Conditions. Metabolites, 2023, 13, 88.	1.3	1
515	Parameter Identification in Metabolic Reaction Networks by Means of Multiple Steady-State Measurements. Symmetry, 2023, 15, 368.	1.1	0

#	ARTICLE	IF	CITATIONS
516	Standards, dissemination, and best practices in systems biology. <i>Current Opinion in Biotechnology</i> , 2023, 81, 102922.	3.3	4
518	Plant and microbial sciences as key drivers in the development of metabolomics research. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2023, 120, .	3.3	11
520	Inducible Synthetic Growth Regulation Using the ClpXP Proteasome Enhances <i>cis,cis</i> -Muconic Acid and Glycolic Acid Yields in <i>Saccharomyces cerevisiae</i> . <i>ACS Synthetic Biology</i> , 2023, 12, 1021-1033.	1.9	1