Bernhard O Palsson

List of Publications by Year
in descending order

587 papers	78,753 citations	369 135 h-index	784 248 g-index
667 all docs	667 docs citations	667 times ranked	36836 citing authors

#	Article	IF	Citations
1	What is flux balance analysis?. Nature Biotechnology, 2010, 28, 245-248.	17.5	3,233
2	Sharing and community curation of mass spectrometry data with Global Natural Products Social Molecular Networking. Nature Biotechnology, 2016, 34, 828-837.	17.5	2,802
3	A protocol for generating a high-quality genome-scale metabolic reconstruction. Nature Protocols, 2010, 5, 93-121.	12.0	1,568
4	Quantitative prediction of cellular metabolism with constraint-based models: the COBRA Toolbox v2.0. Nature Protocols, 2011, 6, 1290-1307.	12.0	1,408
5	Global reconstruction of the human metabolic network based on genomic and bibliomic data. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 1777-1782.	7.1	1,259
6	A genomeâ€scale metabolic reconstruction for Escherichia coli Kâ€12 MG1655 that accounts for 1260 ORFs and thermodynamic information. Molecular Systems Biology, 2007, 3, 121.	7.2	1,234
7	COBRApy: COnstraints-Based Reconstruction and Analysis for Python. BMC Systems Biology, 2013, 7, 74.	3.0	973
8	Genome-scale models of microbial cells: evaluating the consequences of constraints. Nature Reviews Microbiology, 2004, 2, 886-897.	28.6	935
9	Genome-Scale Reconstruction of the Saccharomyces cerevisiae Metabolic Network. Genome Research, 2003, 13, 244-253.	5.5	931
10	A community-driven global reconstruction of human metabolism. Nature Biotechnology, 2013, 31, 419-425.	17.5	920
11	A comprehensive genomeâ€scale reconstruction of Escherichia coli metabolismâ€"2011. Molecular Systems Biology, 2011, 7, 535.	7.2	917
12	An expanded genome-scale model of Escherichia coli K-12 (iJR904 GSM/GPR). Genome Biology, 2003, 4, R54.	9.6	880
13	In silico predictions of Escherichia coli metabolic capabilities are consistent with experimental data. Nature Biotechnology, 2001, 19, 125-130.	17.5	877
14	The Escherichia coli MG1655 in silico metabolic genotype: Its definition, characteristics, and capabilities. Proceedings of the National Academy of Sciences of the United States of America, 2000, 97, 5528-5533.	7.1	833
15	Escherichia coli K-12 undergoes adaptive evolution to achieve in silico predicted optimal growth. Nature, 2002, 420, 186-189.	27.8	797
16	Reconstruction of biochemical networks in microorganisms. Nature Reviews Microbiology, 2009, 7, 129-143.	28.6	797
17	Integrating high-throughput and computational data elucidates bacterial networks. Nature, 2004, 429, 92-96.	27.8	796
18	Metabolic Flux Balancing: Basic Concepts, Scientific and Practical Use. Bio/technology, 1994, 12, 994-998.	1.5	786

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19	Applications of genomeâ€scale metabolic reconstructions. Molecular Systems Biology, 2009, 5, 320.	7.2	759
20	Quantitative prediction of cellular metabolism with constraint-based models: the COBRA Toolbox. Nature Protocols, 2007, 2, 727-738.	12.0	757
21	BiGG Models: A platform for integrating, standardizing and sharing genome-scale models. Nucleic Acids Research, 2016, 44, D515-D522.	14.5	746
22	Constraining the metabolic genotypeâ€"phenotype relationship using a phylogeny of in silico methods. Nature Reviews Microbiology, 2012, 10, 291-305.	28.6	721
23	Constraint-based models predict metabolic and associated cellular functions. Nature Reviews Genetics, 2014, 15, 107-120.	16.3	714
24	The genomic sequence of the Chinese hamster ovary (CHO)-K1 cell line. Nature Biotechnology, 2011, 29, 735-741.	17.5	699
25	The model organism as a system: integrating 'omics' data sets. Nature Reviews Molecular Cell Biology, 2006, 7, 198-210.	37.0	678
26	Theory for the Systemic Definition of Metabolic Pathways and their use in Interpreting Metabolic Function from a Pathway-Oriented Perspective. Journal of Theoretical Biology, 2000, 203, 229-248.	1.7	649
27	Omic data from evolved E. coli are consistent with computed optimal growth from genomeâ€scale models. Molecular Systems Biology, 2010, 6, 390.	7.2	615
28	Network-based prediction of human tissue-specific metabolism. Nature Biotechnology, 2008, 26, 1003-1010.	17.5	594
29	Using Genome-scale Models to Predict Biological Capabilities. Cell, 2015, 161, 971-987.	28.9	590
30	Reconstruction and Validation of Saccharomyces cerevisiae iND750, a Fully Compartmentalized Genome-Scale Metabolic Model. Genome Research, 2004, 14, 1298-1309.	5.5	557
31	The biomass objective function. Current Opinion in Microbiology, 2010, 13, 344-349.	5.1	540
32	A consensus yeast metabolic network reconstruction obtained from a community approach to systems biology. Nature Biotechnology, 2008, 26, 1155-1160.	17.5	530
33	Recon3D enables a three-dimensional view of gene variation in human metabolism. Nature Biotechnology, 2018, 36, 272-281.	17.5	520
34	Context-Specific Metabolic Networks Are Consistent with Experiments. PLoS Computational Biology, 2008, 4, e1000082.	3.2	509
35	The growing scope of applications of genome-scale metabolic reconstructions using Escherichia coli. Nature Biotechnology, 2008, 26, 659-667.	17.5	491
36	Reconstruction of cellular signalling networks and analysis of their properties. Nature Reviews Molecular Cell Biology, 2005, 6, 99-111.	37.0	472

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37	The evolution of molecular biology into systems biology. Nature Biotechnology, 2004, 22, 1249-1252.	17.5	460
38	iML1515, a knowledgebase that computes Escherichia coli traits. Nature Biotechnology, 2017, 35, 904-908.	17.5	425
39	Genomeâ€scale models of metabolism and gene expression extend and refine growth phenotype prediction. Molecular Systems Biology, 2013, 9, 693.	7.2	411
40	Internal Model Control: extension to nonlinear system. Industrial & Engineering Chemistry Process Design and Development, 1986, 25, 403-411.	0.6	405
41	Regulation of Gene Expression in Flux Balance Models of Metabolism. Journal of Theoretical Biology, 2001, 213, 73-88.	1.7	399
42	Connecting extracellular metabolomic measurements to intracellular flux states in yeast. BMC Systems Biology, 2009, 3, 37.	3.0	391
43	Genome-scale Reconstruction of Metabolic Network in Bacillus subtilis Based on High-throughput Phenotyping and Gene Essentiality Data. Journal of Biological Chemistry, 2007, 282, 28791-28799.	3.4	387
44	Genome-scale microbial in silico models: the constraints-based approach. Trends in Biotechnology, 2003, 21, 162-169.	9.3	365
45	Comparative genome sequencing of Escherichia coli allows observation of bacterial evolution on a laboratory timescale. Nature Genetics, 2006, 38, 1406-1412.	21.4	354
46	Metabolic pathways in the post-genome era. Trends in Biochemical Sciences, 2003, 28, 250-258.	7.5	347
47	Comparison of network-based pathway analysis methods. Trends in Biotechnology, 2004, 22, 400-405.	9.3	347
48	In silico design and adaptive evolution ofEscherichia colifor production of lactic acid. Biotechnology and Bioengineering, 2005, 91, 643-648.	3.3	346
49	Saccharomyces cerevisiae phenotypes can be predicted by using constraint-based analysis of a genome-scale reconstructed metabolic network. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 13134-13139.	7.1	345
50	Escher: A Web Application for Building, Sharing, and Embedding Data-Rich Visualizations of Biological Pathways. PLoS Computational Biology, 2015, 11, e1004321.	3.2	344
51	Genomic landscapes of Chinese hamster ovary cell lines as revealed by the Cricetulus griseus draft genome. Nature Biotechnology, 2013, 31, 759-765.	17.5	340
52	Metabolic modelling of microbes: the flux-balance approach. Environmental Microbiology, 2002, 4, 133-140.	3.8	335
53	Systems Properties of the Haemophilus influenzaeRd Metabolic Genotype. Journal of Biological Chemistry, 1999, 274, 17410-17416.	3.4	333
54	Effects of ammonia and lactate on hybridoma growth, metabolism, and antibody production. Biotechnology and Bioengineering, 1992, 39, 418-431.	3.3	328

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55	Towards multidimensional genome annotation. Nature Reviews Genetics, 2006, 7, 130-141.	16.3	321
56	Genome-Scale Metabolic Model of Helicobacter pylori 26695. Journal of Bacteriology, 2002, 184, 4582-4593.	2.2	317
57	MEMOTE for standardized genome-scale metabolic model testing. Nature Biotechnology, 2020, 38, 272-276.	17.5	314
58	The emergence of adaptive laboratory evolution as an efficient tool for biological discovery and industrial biotechnology. Metabolic Engineering, 2019, 56, 1-16.	7.0	307
59	Metabolic Pathway Analysis: Basic Concepts and Scientific Applications in the Post-genomic Era. Biotechnology Progress, 1999, 15, 296-303.	2.6	303
60	Transcriptional Regulation in Constraints-based Metabolic Models of Escherichia coli. Journal of Biological Chemistry, 2002, 277, 28058-28064.	3.4	301
61	Metabolic modeling of microbial strains in silico. Trends in Biochemical Sciences, 2001, 26, 179-186.	7.5	291
62	Characterization of Metabolism in the Fe(III)-Reducing Organism Geobacter sulfurreducens by Constraint-Based Modeling. Applied and Environmental Microbiology, 2006, 72, 1558-1568.	3.1	290
63	Basic and applied uses of genomeâ€scale metabolic network reconstructions of Escherichia coli. Molecular Systems Biology, 2013, 9, 661.	7.2	290
64	Metabolic geneâ€"deletion strains of Escherichia coli evolve to computationally predicted growth phenotypes. Nature Genetics, 2004, 36, 1056-1058.	21.4	282
65	Thirteen Years of Building Constraint-Based In Silico Models of Escherichia coli. Journal of Bacteriology, 2003, 185, 2692-2699.	2.2	280
66	Ion Mobility Derived Collision Cross Sections to Support Metabolomics Applications. Analytical Chemistry, 2014, 86, 3985-3993.	6.5	279
67	Genome-scale metabolic reconstructions of multiple Escherichia coli strains highlight strain-specific adaptations to nutritional environments. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 20338-20343.	7.1	270
68	Detailing the optimality of photosynthesis in cyanobacteria through systems biology analysis. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 2678-2683.	7.1	266
69	Metabolic network reconstruction of Chlamydomonas offers insight into lightâ€driven algal metabolism. Molecular Systems Biology, 2011, 7, 518.	7.2	264
70	Systems approach to refining genome annotation. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 17480-17484.	7.1	262
71	The challenges of in silico biology. Nature Biotechnology, 2000, 18, 1147-1150.	17.5	260
72	What Makes a Bacterial Species Pathogenic?:Comparative Genomic Analysis of the Genus Leptospira. PLoS Neglected Tropical Diseases, 2016, 10, e0004403.	3.0	253

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73	The transcription unit architecture of the Escherichia coli genome. Nature Biotechnology, 2009, 27, 1043-1049.	17.5	251
74	MS/MS networking guided analysis of molecule and gene cluster families. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E2611-20.	7.1	250
75	Metabolic Capabilities of Escherichia coli: I. Synthesis of Biosynthetic Precursors and Cofactors. Journal of Theoretical Biology, 1993, 165, 477-502.	1.7	249
76	Network Context and Selection in the Evolution to Enzyme Specificity. Science, 2012, 337, 1101-1104.	12.6	249
77	Network analysis of intermediary metabolism using linear optimization. I. Development of mathematical formalism. Journal of Theoretical Biology, 1992, 154, 421-454.	1.7	246
78	Parallel adaptive evolution cultures of Escherichia coli lead to convergent growth phenotypes with different gene expression states. Genome Research, 2005, 15, 1365-1372.	5.5	246
79	Insight into human alveolar macrophage and M. tuberculosis interactions via metabolic reconstructions. Molecular Systems Biology, 2010, 6, 422.	7.2	246
80	Large-scale in silico modeling of metabolic interactions between cell types in the human brain. Nature Biotechnology, 2010, 28, 1279-1285.	17.5	246
81	Microbial laboratory evolution in the era of genomeâ€scale science. Molecular Systems Biology, 2011, 7, 509.	7.2	245
82	Ion Mobility-Derived Collision Cross Section As an Additional Measure for Lipid Fingerprinting and Identification. Analytical Chemistry, 2015, 87, 1137-1144.	6.5	245
83	Deciphering Fur transcriptional regulatory network highlights its complex role beyond iron metabolism in Escherichia coli. Nature Communications, 2014, 5, 4910.	12.8	241
84	Metabolic Capabilities of Escherichia coli II. Optimal Growth Patterns. Journal of Theoretical Biology, 1993, 165, 503-522.	1.7	238
85	In silico method for modelling metabolism and gene product expression at genome scale. Nature Communications, 2012, 3, 929.	12.8	238
86	Experimental and Computational Assessment of Conditionally Essential Genes inEscherichia coli. Journal of Bacteriology, 2006, 188, 8259-8271.	2.2	237
87	Use of Adaptive Laboratory Evolution To Discover Key Mutations Enabling Rapid Growth of Escherichia coli K-12 MG1655 on Glucose Minimal Medium. Applied and Environmental Microbiology, 2015, 81, 17-30.	3.1	235
88	Enhancement of carotenoid biosynthesis in the green microalga Dunaliella salina with light-emitting diodes and adaptive laboratory evolution. Applied Microbiology and Biotechnology, 2013, 97, 2395-2403.	3.6	227
89	A White-Box Machine Learning Approach for Revealing Antibiotic Mechanisms of Action. Cell, 2019, 177, 1649-1661.e9.	28.9	227
90	An atlas of human metabolism. Science Signaling, 2020, 13, .	3.6	223

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91	Metabolic flux balance analysis and the in silico analysis of Escherichia coli K-12 gene deletions. BMC Bioinformatics, 2000, 1, 1.	2.6	221
92	Use of Randomized Sampling for Analysis of Metabolic Networks. Journal of Biological Chemistry, 2009, 284, 5457-5461.	3.4	221
93	Model-driven evaluation of the production potential for growth-coupled products of Escherichia coli. Metabolic Engineering, 2010, 12, 173-186.	7.0	221
94	RNA polymerase mutants found through adaptive evolution reprogram Escherichia coli for optimal growth in minimal media. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 20500-20505.	7.1	219
95	Assessment of the Metabolic Capabilities of Haemophilus influenzae Rd through a Genome-scale Pathway Analysis. Journal of Theoretical Biology, 2000, 203, 249-283.	1.7	216
96	A Consensus Genome-scale Reconstruction of Chinese Hamster Ovary Cell Metabolism. Cell Systems, 2016, 3, 434-443.e8.	6.2	205
97	Elimination of Thermodynamically Infeasible Loops in Steady-State Metabolic Models. Biophysical Journal, 2011, 100, 544-553.	0.5	203
98	Integrated analysis of regulatory and metabolic networks reveals novel regulatory mechanisms in Saccharomyces cerevisiae. Genome Research, 2006, 16, 627-635.	5.5	202
99	Systems biology and biotechnology of Streptomyces species for the production of secondary metabolites. Biotechnology Advances, 2014, 32, 255-268.	11.7	199
100	Effective intercellular communication distances are determined by the relative time constants for cyto/chemokine secretion and diffusion. Proceedings of the National Academy of Sciences of the United States of America, 1997, 94, 12258-12262.	7.1	191
101	Hierarchical thinking in network biology: the unbiased modularization of biochemical networks. Trends in Biochemical Sciences, 2004, 29, 641-647.	7.5	189
102	Optimizing genome-scale network reconstructions. Nature Biotechnology, 2014, 32, 447-452.	17.5	185
103	Biochemical production capabilities ofescherichia coli. Biotechnology and Bioengineering, 1993, 42, 59-73.	3.3	184
104	Drug Off-Target Effects Predicted Using Structural Analysis in the Context of a Metabolic Network Model. PLoS Computational Biology, 2010, 6, e1000938.	3.2	183
105	Genome-Scale In Silico Models of E. coli Have Multiple Equivalent Phenotypic States: Assessment of Correlated Reaction Subsets That Comprise Network States. Genome Research, 2004, 14, 1797-1805.	5.5	181
106	Robustness Analysis of the Escherichia coli Metabolic Network. Biotechnology Progress, 2000, 16, 927-939.	2.6	179
107	Effect of medium osmolarity on hybridoma growth, metabolism, and antibody production. Biotechnology and Bioengineering, 1991, 37, 989-993.	3.3	178
108	Antibiotic-Induced Changes to the Host Metabolic Environment Inhibit Drug Efficacy and Alter Immune Function. Cell Host and Microbe, 2017, 22, 757-765.e3.	11.0	178

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109	<scp>SBML</scp> Level 3: an extensible format for the exchange and reuse of biological models. Molecular Systems Biology, 2020, 16, e9110.	7.2	178
110	Elemental balancing of biomass and medium composition enhances growth capacity in high-densityChlorella vulgaris cultures. , 1998, 59, 605-611.		177
111	Three-Dimensional Structural View of the Central Metabolic Network of Thermotoga maritima. Science, 2009, 325, 1544-1549.	12.6	176
112	Analysis of omics data with genome-scale models of metabolism. Molecular BioSystems, 2013, 9, 167-174.	2.9	176
113	Genome-wide Reconstruction of OxyR and SoxRS Transcriptional Regulatory Networks under Oxidative Stress in Escherichia coli K-12 MG1655. Cell Reports, 2015, 12, 1289-1299.	6.4	174
114	Genome-scale reconstruction of the Lrp regulatory network in Escherichia coli. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 19462-19467.	7.1	169
115	Proteomic Analysis of Chinese Hamster Ovary Cells. Journal of Proteome Research, 2012, 11, 5265-5276.	3.7	168
116	Toward Metabolic Phenomics: Analysis of Genomic Data Using Flux Balances. Biotechnology Progress, 1999, 15, 288-295.	2.6	166
117	Characterizing the metabolic phenotype: A phenotype phase plane analysis. Biotechnology and Bioengineering, 2002, 77, 27-36.	3.3	166
118	A multi-tissue type genome-scale metabolic network for analysis of whole-body systems physiology. BMC Systems Biology, 2011, 5, 180.	3.0	166
119	Latent Pathway Activation and Increased Pathway Capacity Enable Escherichia coli Adaptation to Loss of Key Metabolic Enzymes. Journal of Biological Chemistry, 2006, 281, 8024-8033.	3.4	165
120	High-density algal photobioreactors using light-emitting diodes. Biotechnology and Bioengineering, 1994, 44, 1161-1167.	3.3	164
121	Genome-wide analysis of Fis binding in Escherichia coli indicates a causative role for A-/AT-tracts. Genome Research, 2008, 18, 900-910.	5.5	164
122	Genome-scale reconstruction and in silico analysis of the Clostridium acetobutylicum ATCC 824 metabolic network. Applied Microbiology and Biotechnology, 2008, 80, 849-862.	3.6	161
123	Genome-Scale Reconstruction of Escherichia coli's Transcriptional and Translational Machinery: A Knowledge Base, Its Mathematical Formulation, and Its Functional Characterization. PLoS Computational Biology, 2009, 5, e1000312.	3.2	161
124	The Escherichia coli transcriptome mostly consists of independently regulated modules. Nature Communications, 2019, 10, 5536.	12.8	161
125	Growth, metabolic, and antibody production kinetics of hybridoma cell culture: 2. Effects of serum concentration, dissolved oxygen concentration, and medium pH in a batch reactor. Biotechnology Progress, 1991, 7, 481-494.	2.6	159
126	The underlying pathway structure of biochemical reaction networks. Proceedings of the National Academy of Sciences of the United States of America, 1998, 95, 4193-4198.	7.1	158

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127	Reconstructing organisms in silico: genome-scale models and their emerging applications. Nature Reviews Microbiology, 2020, 18, 731-743.	28.6	158
128	Metabolic dynamics in the human red cell. Journal of Theoretical Biology, 1989, 141, 515-528.	1.7	157
129	Constraints-based models: Regulation of Gene Expression Reduces the Steady-state Solution Space. Journal of Theoretical Biology, 2003, 221, 309-325.	1.7	157
130	Extreme Pathway Analysis of Human Red Blood Cell Metabolism. Biophysical Journal, 2002, 83, 808-818.	0.5	156
131	The challenges of integrating multi-omic data sets. Nature Chemical Biology, 2010, 6, 787-789.	8.0	154
132	Generation of an atlas for commodity chemical production in Escherichia coli and a novel pathway prediction algorithm, GEM-Path. Metabolic Engineering, 2014, 25, 140-158.	7.0	152
133	Machine learning applied to enzyme turnover numbers reveals protein structural correlates and improves metabolic models. Nature Communications, 2018, 9, 5252.	12.8	151
134	Formulating genomeâ€scale kinetic models in the postâ€genome era. Molecular Systems Biology, 2008, 4, 171.	7.2	150
135	Reconstruction of microbial transcriptional regulatory networks. Current Opinion in Biotechnology, 2004, 15, 70-77.	6.6	149
136	Reconstructing metabolic flux vectors from extreme pathways: defining the Î±-spectrum. Journal of Theoretical Biology, 2003, 224, 313-324.	1.7	148
137	Engineering synergy in biotechnology. Nature Chemical Biology, 2014, 10, 319-322.	8.0	147
138	High-Level dCas9 Expression Induces Abnormal Cell Morphology in Escherichia coli. ACS Synthetic Biology, 2018, 7, 1085-1094.	3.8	147
139	Evolution of Escherichia coli to 42 Â°C and Subsequent Genetic Engineering Reveals Adaptive Mechanisms and Novel Mutations. Molecular Biology and Evolution, 2014, 31, 2647-2662.	8.9	145
140	Next-generation genome-scale models for metabolic engineering. Current Opinion in Biotechnology, 2015, 35, 23-29.	6.6	144
141	Modelâ€driven multiâ€omic data analysis elucidates metabolic immunomodulators of macrophage activation. Molecular Systems Biology, 2012, 8, 558.	7.2	142
142	Multi-omic data integration enables discovery of hidden biological regularities. Nature Communications, 2016, 7, 13091.	12.8	141
143	Chemical decomposition of glutamine in cell culture media: effect of media type, pH, and serum concentration. Biotechnology Progress, 1990, 6, 121-128.	2.6	140
144	Constraint-based analysis of metabolic capacity of Salmonella typhimurium during host-pathogen interaction. BMC Systems Biology, 2009, 3, 38.	3.0	140

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145	Adaptive Evolution ofEscherichia coliK-12 MG1655 during Growth on a Nonnative Carbon Source,<scp>l</scp>-1,2-Propanediol. Applied and Environmental Microbiology, 2010, 76, 4158-4168.	3.1	140
146	Reconstruction and Functional Characterization of the Human Mitochondrial Metabolic Network Based on Proteomic and Biochemical Data. Journal of Biological Chemistry, 2004, 279, 39532-39540.	3.4	139
147	Candidate Metabolic Network States in Human Mitochondria. Journal of Biological Chemistry, 2005, 280, 11683-11695.	3.4	138
148	Flux-balance analysis of mitochondrial energy metabolism: consequences of systemic stoichiometric constraints. American Journal of Physiology - Regulatory Integrative and Comparative Physiology, 2001, 280, R695-R704.	1.8	136
149	Mechanism of release from pellets coated with an ethylcellulose-based film. Journal of Controlled Release, 1990, 14, 203-213.	9.9	135
150	Large-Scale Evaluation ofIn SilicoGene Deletions inSaccharomyces cerevisiae. OMICS A Journal of Integrative Biology, 2003, 7, 193-202.	2.0	135
151	A road map for the development of community systems (CoSy) biology. Nature Reviews Microbiology, 2012, 10, 366-372.	28.6	135
152	High-density photoautotrophic algal cultures: Design, construction, and operation of a novel photobioreactor system. Biotechnology and Bioengineering, 1991, 38, 1182-1189.	3.3	132
153	An Experimentally Validated Genome-Scale Metabolic Reconstruction of Klebsiella pneumoniae MGH 78578, i YL1228. Journal of Bacteriology, 2011, 193, 1710-1717.	2.2	132
154	Uniform Sampling of Steady-State Flux Spaces: Means to Design Experiments and to Interpret Enzymopathies. Biophysical Journal, 2004, 87, 2172-2186.	0.5	130
155	Systematizing the generation of missing metabolic knowledge. Biotechnology and Bioengineering, 2010, 107, 403-412.	3.3	130
156	BiGG Models 2020: multi-strain genome-scale models and expansion across the phylogenetic tree. Nucleic Acids Research, 2020, 48, D402-D406.	14.5	130
157	Maximizing biomass productivity and cell density of Chlorella vulgaris by using light-emitting diode-based photobioreactor. Journal of Biotechnology, 2012, 161, 242-249.	3.8	129
158	In situ to in silico and back: elucidating the physiology and ecology of Geobacter spp. using genome-scale modelling. Nature Reviews Microbiology, 2011, 9, 39-50.	28.6	128
159	A community effort towards a knowledge-base and mathematical model of the human pathogen Salmonella Typhimurium LT2. BMC Systems Biology, 2011, 5, 8.	3.0	128
160	Highâ€quality genomeâ€scale metabolic modelling of Pseudomonas putida highlights its broad metabolic capabilities. Environmental Microbiology, 2020, 22, 255-269.	3.8	127
161	Machine learning and structural analysis of Mycobacterium tuberculosis pan-genome identifies genetic signatures of antibiotic resistance. Nature Communications, 2018, 9, 4306.	12.8	126
162	Consistent and High Rates of Gene Transfer Can Be Obtained Using Flow-Through Transduction over a Wide Range of Retroviral Titers. Human Gene Therapy, 1996, 7, 743-750.	2.7	125

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163	Extreme Pathway Lengths and Reaction Participation in Genome-Scale Metabolic Networks. Genome Research, 2002, 12, 1889-1900.	5.5	125
164	Multi-omics Quantification of Species Variation of Escherichia coli Links Molecular Features with Strain Phenotypes. Cell Systems, 2016, 3, 238-251.e12.	6.2	124
165	COBRAme: A computational framework for genome-scale models of metabolism and gene expression. PLoS Computational Biology, 2018, 14, e1006302.	3.2	123
166	Retroviral Infection Is Limited by Brownian Motion. Human Gene Therapy, 1996, 7, 1527-1534.	2.7	121
167	Genetic Basis of Growth Adaptation of Escherichia coli after Deletion of pgi, a Major Metabolic Gene. PLoS Genetics, 2010, 6, e1001186.	3.5	121
168	Elucidating dynamic metabolic physiology through network integration of quantitative time-course metabolomics. Scientific Reports, 2017, 7, 46249.	3.3	121
169	Monte Carlo sampling can be used to determine the size and shape of the steady-state flux space. Journal of Theoretical Biology, 2004, 228, 437-447.	1.7	117
170	The JAK-STAT Signaling Network in the Human B-Cell: An Extreme Signaling Pathway Analysis. Biophysical Journal, 2004, 87, 37-46.	0.5	117
171	The y-ome defines the 35% ofEscherichia coligenes that lack experimental evidence of function. Nucleic Acids Research, 2019, 47, 2446-2454.	14.5	117
172	Biomass as a Source of Chemical Feedstocks: An Economic Evaluation. Science, 1981, 213, 513-517.	12.6	116
173	Evolution and regulation of nitrogen flux through compartmentalized metabolic networks in a marine diatom. Nature Communications, 2019, 10, 4552.	12.8	116
174	The Genome-Scale Metabolic Extreme Pathway Structure in Haemophilus influenzae Shows Significant Network Redundancy. Journal of Theoretical Biology, 2002, 215, 67-82.	1.7	115
175	Biomarkers defining the metabolic age of red blood cells during cold storage. Blood, 2016, 128, e43-e50.	1.4	115
176	Description and Interpretation of Adaptive Evolution of Escherichia coli K-12 MG1655 by Using a Genome-Scale In Silico Metabolic Model. Journal of Bacteriology, 2003, 185, 6400-6408.	2.2	114
177	Adaptive laboratory evolution of a genome-reduced Escherichia coli. Nature Communications, 2019, 10, 935.	12.8	114
178	Unique attributes of cyanobacterial metabolism revealed by improved genome-scale metabolic modeling and essential gene analysis. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E8344-E8353.	7.1	113
179	Towards genome-scale signalling-network reconstructions. Nature Reviews Genetics, 2010, 11, 297-307.	16.3	111
180	Structural Systems Biology Evaluation of Metabolic Thermotolerance in Escherichia coli. Science, 2013, 340, 1220-1223.	12.6	111

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181	Genome-scale reconstruction of the sigma factor network in Escherichia coli: topology and functional states. BMC Biology, 2014, 12, 4.	3.8	111
182	Systems biology as a foundation for genome-scale synthetic biology. Current Opinion in Biotechnology, 2006, 17, 488-492.	6.6	109
183	Genome-scale metabolic reconstructions of multiple Salmonella strains reveal serovar-specific metabolic traits. Nature Communications, 2018, 9, 3771.	12.8	109
184	Global Rebalancing of Cellular Resources by Pleiotropic Point Mutations Illustrates a Multi-scale Mechanism of Adaptive Evolution. Cell Systems, 2016, 2, 260-271.	6.2	107
185	Expansion of Human Bone Marrow Progenitor Cells in a High Cell Density Continuous Perfusion System. Bio/technology, 1993, 11, 368-372.	1.5	106
186	Mini review: Genome mining approaches for the identification of secondary metabolite biosynthetic gene clusters in Streptomyces. Computational and Structural Biotechnology Journal, 2020, 18, 1548-1556.	4.1	106
187	Immobilization of Escherichia coli RNA Polymerase and Location of Binding Sites by Use of Chromatin Immunoprecipitation and Microarrays. Journal of Bacteriology, 2005, 187, 6166-6174.	2.2	105
188	Identification of Genome-Scale Metabolic Network Models Using Experimentally Measured Flux Profiles. PLoS Computational Biology, 2006, 2, e72.	3.2	105
189	Identified metabolic signature for assessing red blood cell unit quality is associated with endothelial damage markers and clinical outcomes. Transfusion, 2016, 56, 852-862.	1.6	105
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