Bernhard O Palsson

List of Publications by Year
in descending order

587 papers	78,753 citations	366 135 h-index	779 248 g-index
667 all docs	667 docs citations	667 times ranked	36836 citing authors

#	Article	IF	Citations
1	proChIPdb: a chromatin immunoprecipitation database for prokaryotic organisms. Nucleic Acids Research, 2022, 50, D1077-D1084.	6.5	9
2	Genome-scale analysis of genetic regulatory elements in Streptomyces avermitilis MA-4680 using transcript boundary information. BMC Genomics, 2022, 23, 68.	1.2	2
3	Comparative pangenomics: analysis of 12 microbial pathogen pangenomes reveals conserved global structures of genetic and functional diversity. BMC Genomics, 2022, 23, 7.	1.2	22
4	Regulatory perturbations of ribosome allocation in bacteria reshape the growth proteome with a trade-off in adaptation capacity. IScience, 2022, 25, 103879.	1.9	7
5	Is the kinetome conserved?. Molecular Systems Biology, 2022, 18, e10782.	3.2	6
6	System-Level Analysis of Transcriptional and Translational Regulatory Elements in Streptomyces griseus. Frontiers in Bioengineering and Biotechnology, 2022, 10, 844200.	2.0	1
7	Machine learning from <i>Pseudomonas aeruginosa</i> transcriptomes identifies independently modulated sets of genes associated with known transcriptional regulators. Nucleic Acids Research, 2022, 50, 3658-3672.	6.5	25
8	Synthetic 3â€²-UTR valves for optimal metabolic flux control in <i>Escherichia coli</i>. Nucleic Acids Research, 2022, 50, 4171-4186.	6.5	3
9	Machine Learning of All Mycobacterium tuberculosis H37Rv RNA-seq Data Reveals a Structured Interplay between Metabolism, Stress Response, and Infection. MSphere, 2022, 7, e0003322.	1.3	22
10	Systems biology approach to functionally assess the <i>Clostridioides difficile</i> pangenome reveals genetic diversity with discriminatory power. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2119396119.	3.3	5
11	A systems approach discovers the role and characteristics of seven LysR type transcription factors in Escherichia coli. Scientific Reports, 2022, 12, 7274.	1.6	5
12	Machine-learning from Pseudomonas putida KT2440 transcriptomes reveals its transcriptional regulatory network. Metabolic Engineering, 2022, 72, 297-310.	3.6	28
13	Laboratory evolution of synthetic electron transport system variants reveals a larger metabolic respiratory system and its plasticity. Nature Communications, 2022, 13, .	5.8	8
14	iModulonDB: a knowledgebase of microbial transcriptional regulation derived from machine learning. Nucleic Acids Research, 2021, 49, D112-D120.	6.5	67
15	Identifying the effect of vancomycin on health careâ€"associated methicillin-resistant <i>Staphylococcus aureus</i> strains using bacteriological and physiological media. GigaScience, 2021, 10, .	3.3	5
16	Bacterial fitness landscapes stratify based on proteome allocation associated with discrete aero-types. PLoS Computational Biology, 2021, 17, e1008596.	1.5	14
17	MASSpy: Building, simulating, and visualizing dynamic biological models in Python using mass action kinetics. PLoS Computational Biology, 2021, 17, e1008208.	1.5	20
18	Pangenome Analytics Reveal Two-Component Systems as Conserved Targets in ESKAPEE Pathogens. MSystems, 2021, 6, .	1.7	24

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19	Independent component analysis recovers consistent regulatory signals from disparate datasets. PLoS Computational Biology, 2021, 17, e1008647.	1.5	27
20	Blood donor exposome and impact of common drugs on red blood cell metabolism. JCI Insight, 2021, 6, .	2.3	39
21	Experimentally Validated Reconstruction and Analysis of a Genome-Scale Metabolic Model of an Anaerobic Neocallimastigomycota Fungus. MSystems, 2021, 6, .	1.7	33
22	Restoration of fitness lost due to dysregulation of the pyruvate dehydrogenase complex is triggered by ribosomal binding site modifications. Cell Reports, 2021, 35, 108961.	2.9	13
23	The quantitative metabolome is shaped by abiotic constraints. Nature Communications, 2021, 12, 3178.	5.8	15
24	Environmental conditions dictate differential evolution of vancomycin resistance in Staphylococcus aureus. Communications Biology, 2021, 4, 793.	2.0	18
25	Elucidating the Regulatory Elements for Transcription Termination and Posttranscriptional Processing in the Streptomyces clavuligerus Genome. MSystems, 2021, 6, .	1.7	6
26	Computation of condition-dependent proteome allocation reveals variability in the macro and micro nutrient requirements for growth. PLoS Computational Biology, 2021, 17, e1007817.	1.5	3
27	Genomeâ€scale metabolic modeling reveals key features of a minimal gene set. Molecular Systems Biology, 2021, 17, e10099.	3.2	15
28	Unraveling the functions of uncharacterized transcription factors in *Escherichia coli* using ChIP-exo. Nucleic Acids Research, 2021, 49, 9696-9710.	6.5	30
29	Machine Learning of Bacterial Transcriptomes Reveals Responses Underlying Differential Antibiotic Susceptibility. MSphere, 2021, 6, e0044321.	1.3	12
30	Generation of *Pseudomonas putida* KT2440 Strains with Efficient Utilization of Xylose and Galactose via Adaptive Laboratory Evolution. ACS Sustainable Chemistry and Engineering, 2021, 9, 11512-11523.	3.2	32
31	Identification of a transcription factor, PunR, that regulates the purine and purine nucleoside transporter punC in E. coli. Communications Biology, 2021, 4, 991.	2.0	13
32	RiboRid: A low cost, advanced, and ultra-efficient method to remove ribosomal RNA for bacterial transcriptomics. PLoS Genetics, 2021, 17, e1009821.	1.5	16
33	Systems and synthetic biology to elucidate secondary metabolite biosynthetic gene clusters encoded in *Streptomyces* genomes. Natural Product Reports, 2021, 38, 1330-1361.	5.2	35
34	Discovery of novel secondary metabolites encoded in actinomycete genomes through coculture. Journal of Industrial Microbiology and Biotechnology, 2021, 48, .	1.4	29
35	DeepTFactor: A deep learning-based tool for the prediction of transcription factors. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	45
36	Machine Learning Uncovers a Data-Driven Transcriptional Regulatory Network for the Crenarchaeal Thermoacidophile Sulfolobus acidocaldarius. Frontiers in Microbiology, 2021, 12, 753521.	1.5	20

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37	Re-classification of Streptomyces venezuelae strains and mining secondary metabolite biosynthetic gene clusters. IScience, 2021, 24, 103410.	1.9	2
38	<i>Escherichia coli</i> Data-Driven Strain Design Using Aggregated Adaptive Laboratory Evolution Mutational Data. ACS Synthetic Biology, 2021, 10, 3379-3395.	1.9	5
39	Optimal dimensionality selection for independent component analysis of transcriptomic data. BMC Bioinformatics, 2021, 22, 584.	1.2	34
40	Streptomyces as Microbial Chassis for Heterologous Protein Expression. Frontiers in Bioengineering and Biotechnology, 2021, 9, 804295.	2.0	12
41	BiGG Models 2020: multi-strain genome-scale models and expansion across the phylogenetic tree. Nucleic Acids Research, 2020, 48, D402-D406.	6.5	130
42	OxyR Is a Convergent Target for Mutations Acquired during Adaptation to Oxidative Stress-Prone Metabolic States. Molecular Biology and Evolution, 2020, 37, 660-667.	3.5	52
43	Highâ€quality genomeâ€scale metabolic modelling of <i>Pseudomonas putida</i> highlights its broad metabolic capabilities. Environmental Microbiology, 2020, 22, 255-269.	1.8	127
44	Genome-scale reconstructions of the mammalian secretory pathway predict metabolic costs and limitations of protein secretion. Nature Communications, 2020, 11, 68.	5.8	74
45	Metabolic Systems Analysis of Shock-Induced Endotheliopathy (SHINE) in Trauma. Annals of Surgery, 2020, 272, 1140-1148.	2.1	23
46	Structure of galactarate dehydratase, a new fold in an enolase involved in bacterial fitness after antibiotic treatment. Protein Science, 2020, 29, 711-722.	3.1	4
47	A workflow for generating multi-strain genome-scale metabolic models of prokaryotes. Nature Protocols, 2020, 15, 1-14.	5.5	62
48	The Bitome: digitized genomic features reveal fundamental genome organization. Nucleic Acids Research, 2020, 48, 10157-10163.	6.5	11
49	Redefining fundamental concepts of transcription initiation in bacteria. Nature Reviews Genetics, 2020, 21, 699-714.	7.7	100
50	High-Quality Genome-Scale Models From Error-Prone, Long-Read Assemblies. Frontiers in Microbiology, 2020, 11, 596626.	1.5	3
51	Generation of ionic liquid tolerant <i>Pseudomonas putida</i> KT2440 strains <i>via</i> adaptive laboratory evolution. Green Chemistry, 2020, 22, 5677-5690.	4.6	29
52	Synthetic cross-phyla gene replacement and evolutionary assimilation of major enzymes. Nature Ecology and Evolution, 2020, 4, 1402-1409.	3.4	13
53	Causal mutations from adaptive laboratory evolution are outlined by multiple scales of genome annotations and condition-specificity. BMC Genomics, 2020, 21, 514.	1.2	23
54	Independent component analysis of E. coli's transcriptome reveals the cellular processes that respond to heterologous gene expression. Metabolic Engineering, 2020, 61, 360-368.	3.6	36

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55	System-level understanding of gene expression and regulation for engineering secondary metabolite production in <i>Streptomyces</i>. Journal of Industrial Microbiology and Biotechnology, 2020, 47, 739-752.	1.4	10
56	Systems biology analysis of the Clostridioides difficile core-genome contextualizes microenvironmental evolutionary pressures leading to genotypic and phenotypic divergence. Npj Systems Biology and Applications, 2020, 6, 31.	1.4	15
57	Kinetic profiling of metabolic specialists demonstrates stability and consistency of in vivo enzyme turnover numbers. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 23182-23190.	3.3	65
58	Reconstructing organisms in silico: genome-scale models and their emerging applications. Nature Reviews Microbiology, 2020, 18, 731-743.	13.6	158
59	The Expanding Computational Toolbox for Engineering Microbial Phenotypes at the Genome Scale. Microorganisms, 2020, 8, 2050.	1.6	12
60	Machine learning uncovers independently regulated modules in the Bacillus subtilis transcriptome. Nature Communications, 2020, 11, 6338.	5.8	54
61	Genome Sequence Comparison of Staphylococcus aureus TX0117 and a Beta-Lactamase-Cured Derivative Shows Increased Cationic Peptide Resistance Accompanying Mutations in <i>relA</i> and <i>mnaA</i>. Microbiology Resource Announcements, 2020, 9, .	0.3	2
62	Metabolic and genetic basis for auxotrophies in Gram-negative species. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 6264-6273.	3.3	39
63	Transcriptome and translatome profiles of Streptomyces species in different growth phases. Scientific Data, 2020, 7, 138.	2.4	18
64	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.	1.9	106
65	Repurposing Modular Polyketide Synthases and Non-ribosomal Peptide Synthetases for Novel Chemical Biosynthesis. Frontiers in Molecular Biosciences, 2020, 7, 87.	1.6	29
66	Comparative Genomics Determines Strain-Dependent Secondary Metabolite Production in Streptomyces venezuelae Strains. Biomolecules, 2020, 10, 864.	1.8	9
67	Reconstruction and Validation of a Genome-Scale Metabolic Model of Streptococcus oralis (iCJ415), a Human Commensal and Opportunistic Pathogen. Frontiers in Genetics, 2020, 11, 116.	1.1	11
68	An atlas of human metabolism. Science Signaling, 2020, 13, .	1.6	223
69	Machine learning with random subspace ensembles identifies antimicrobial resistance determinants from pan-genomes of three pathogens. PLoS Computational Biology, 2020, 16, e1007608.	1.5	49
70	Revealing 29 sets of independently modulated genes in <i>Staphylococcus aureus</i>, their regulators, and role in key physiological response. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 17228-17239.	3.3	60
71	Impact of insertion sequences on convergent evolution of Shigella species. PLoS Genetics, 2020, 16, e1008931.	1.5	43
72	Synthesizing Systems Biology Knowledge from Omics Using Genomeâ€Scale Models. Proteomics, 2020, 20, e1900282.	1.3	22

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73	MEMOTE for standardized genome-scale metabolic model testing. Nature Biotechnology, 2020, 38, 272-276.	9.4	314
74	Thirty complete Streptomyces genome sequences for mining novel secondary metabolite biosynthetic gene clusters. Scientific Data, 2020, 7, 55.	2.4	67
75	STATR: A simple analysis pipeline of Ribo-Seq in bacteria. Journal of Microbiology, 2020, 58, 217-226.	1.3	9
76	Iron competition triggers antibiotic biosynthesis in *Streptomyces coelicolor* during coculture with *Myxococcus xanthus*. ISME Journal, 2020, 14, 1111-1124.	4.4	60
77	Adaptations of Escherichia coli strains to oxidative stress are reflected in properties of their structural proteomes. BMC Bioinformatics, 2020, 21, 162.	1.2	5
78	Multiplex secretome engineering enhances recombinant protein production and purity. Nature Communications, 2020, 11, 1908.	5.8	63
79	Genetic Determinants Enabling Medium-Dependent Adaptation to Nafcillin in Methicillin-Resistant Staphylococcus aureus. MSystems, 2020, 5, .	1.7	8
80	Pangenome Flux Balance Analysis Toward Panphenomes. , 2020, , 219-232.		7
81	A biochemically-interpretable machine learning classifier for microbial GWAS. Nature Communications, 2020, 11, 2580.	5.8	51
82	Genome-scale determination of 5´ and 3´ boundaries of RNA transcripts in Streptomyces genomes. Scientific Data, 2020, 7, 436.	2.4	6
83	Adaptive laboratory evolution of Escherichia coli under acid stress. Microbiology (United Kingdom), 2020, 166, 141-148.	0.7	28
84	Elucidation of Regulatory Modes for Five Two-Component Systems in Escherichia coli Reveals Novel Relationships. MSystems, 2020, 5, .	1.7	25
85	Genome-scale metabolic models highlight stage-specific differences in essential metabolic pathways in Trypanosoma cruzi. PLoS Neglected Tropical Diseases, 2020, 14, e0008728.	1.3	8
86	SBML Level 3: an extensible format for the exchange and reuse of biological models. Molecular Systems Biology, 2020, 16, e9110.	3.2	178
87	Construction of Minimal Genomes and Synthetic Cells. , 2020, , 45-67.		0
88	The Use of In Silico Genome-Scale Models for the Rational Design of Minimal Cells. , 2020, , 141-175.		0
89	Title is missing!. , 2020, 16, e1007608.		0
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94	Title is missing!. , 2020, 14, e0008728.		0
95	Title is missing!. , 2020, 14, e0008728.		0
96	Title is missing!. , 2020, 14, e0008728.		0
97	Title is missing!. , 2020, 14, e0008728.		0
98	Title is missing!. , 2020, 14, e0008728.		0
99	The emergence of adaptive laboratory evolution as an efficient tool for biological discovery and industrial biotechnology. Metabolic Engineering, 2019, 56, 1-16.	3.6	307
100	Cellular responses to reactive oxygen species are predicted from molecular mechanisms. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 14368-14373.	3.3	79
101	The Transcription Unit Architecture of Streptomyces lividans TK24. Frontiers in Microbiology, 2019, 10, 2074.	1.5	25
102	Inactivation of a Mismatch-Repair System Diversifies Genotypic Landscape of Escherichia coli During Adaptive Laboratory Evolution. Frontiers in Microbiology, 2019, 10, 1845.	1.5	17
103	Systems Biology and Pangenome of <i>Salmonella</i> O-Antigens. MBio, 2019, 10, .	1.8	26
104	Estimating Cellular Goals from High-Dimensional Biological Data. , 2019, , .		2
105	Strain-Specific Metabolic Requirements Revealed by a Defined Minimal Medium for Systems Analyses of <i>Staphylococcus aureus</i>. Applied and Environmental Microbiology, 2019, 85, .	1.4	21
106	Evolution and regulation of nitrogen flux through compartmentalized metabolic networks in a marine diatom. Nature Communications, 2019, 10, 4552.	5.8	116
107	Pseudogene repair driven by selection pressure applied in experimental evolution. Nature Microbiology, 2019, 4, 386-389.	5.9	21
108	A computational knowledge-base elucidates the response of Staphylococcus aureus to different media types. PLoS Computational Biology, 2019, 15, e1006644.	1.5	41

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109	DynamicME: dynamic simulation and refinement of integrated models of metabolism and protein expression. BMC Systems Biology, 2019, 13, 2.	3.0	45
110	Primary transcriptome and translatome analysis determines transcriptional and translational regulatory elements encoded in the Streptomyces clavuligerus genome. Nucleic Acids Research, 2019, 47, 6114-6129.	6.5	49
111	Laboratory evolution reveals a two-dimensional rate-yield tradeoff in microbial metabolism. PLoS Computational Biology, 2019, 15, e1007066.	1.5	33
112	A White-Box Machine Learning Approach for Revealing Antibiotic Mechanisms of Action. Cell, 2019, 177, 1649-1661.e9.	13.5	227
113	BOFdat: Generating biomass objective functions for genome-scale metabolic models from experimental data. PLoS Computational Biology, 2019, 15, e1006971.	1.5	83
114	Characterization of CA-MRSA TCH1516 exposed to nafcillin in bacteriological and physiological media. Scientific Data, 2019, 6, 43.	2.4	14
115	Coupling S-adenosylmethionine–dependent methylation to growth: Design and uses. PLoS Biology, 2019, 17, e2007050.	2.6	39
116	Enzyme promiscuity shapes adaptation to novel growth substrates. Molecular Systems Biology, 2019, 15, e8462.	3.2	52
117	Adaptive laboratory evolution of a genome-reduced Escherichia coli. Nature Communications, 2019, 10, 935.	5.8	114
118	The y-ome defines the 35% of *Escherichia coli* genes that lack experimental evidence of function. Nucleic Acids Research, 2019, 47, 2446-2454.	6.5	117
119	Expanding the uses of genome–scale models with protein structures. Molecular Systems Biology, 2019, 15, e8601.	3.2	7
120	Systems-level analysis of NalD mutation, a recurrent driver of rapid drug resistance in acute Pseudomonas aeruginosa infection. PLoS Computational Biology, 2019, 15, e1007562.	1.5	11
121	Profiling the effect of nafcillin on HA-MRSA D712 using bacteriological and physiological media. Scientific Data, 2019, 6, 322.	2.4	8
122	Adaptive evolution reveals a tradeoff between growth rate and oxidative stress during naphthoquinone-based aerobic respiration. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 25287-25292.	3.3	56
123	Genome-scale model of metabolism and gene expression provides a multi-scale description of acid stress responses in Escherichia coli. PLoS Computational Biology, 2019, 15, e1007525.	1.5	37
124	The Escherichia coli transcriptome mostly consists of independently regulated modules. Nature Communications, 2019, 10, 5536.	5.8	161
125	Predicting the metabolic capabilities of Synechococcus elongatus PCC 7942 adapted to different light regimes. Metabolic Engineering, 2019, 52, 42-56.	3.6	34
126	Sugar-stimulated CO_2 sequestration by the green microalga Chlorella vulgaris. Science of the Total Environment, 2019, 654, 275-283.	3.9	31

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127	ALEdb 1.0: a database of mutations from adaptive laboratory evolution experimentation. Nucleic Acids Research, 2019, 47, D1164-D1171.	6.5	93
128	Cross‐compartment metabolic coupling enables flexible photoprotective mechanisms in the diatom <i>Phaeodactylum tricornutum</i>. New Phytologist, 2019, 222, 1364-1379.	3.5	54
129	Dataset on economic analysis of mass production of algae in LED-based photobioreactors. Data in Brief, 2019, 22, 137-139.	0.5	0
130	Synthetic Biology Tools for Novel Secondary Metabolite Discovery in Streptomyces. Journal of Microbiology and Biotechnology, 2019, 29, 667-686.	0.9	64
131	Minimal cells, maximal knowledge. ELife, 2019, 8, .	2.8	26
132	Title is missing!. , 2019, 15, e1007525.		0
133	Title is missing!. , 2019, 15, e1007525.		0
134	Title is missing!. , 2019, 15, e1007525.		0
135	Title is missing!. , 2019, 15, e1007525.		0
136	Recon3D enables a three-dimensional view of gene variation in human metabolism. Nature Biotechnology, 2018, 36, 272-281.	9.4	520
137	Modeling the multi-scale mechanisms of macromolecular resource allocation. Current Opinion in Microbiology, 2018, 45, 8-15.	2.3	46
138	Systems assessment of transcriptional regulation on central carbon metabolism by Cra and CRP. Nucleic Acids Research, 2018, 46, 2901-2917.	6.5	62
139	Genome-scale analysis of Methicillin-resistant Staphylococcus aureus USA300 reveals a tradeoff between pathogenesis and drug resistance. Scientific Reports, 2018, 8, 2215.	1.6	28
140	ssbio: a Python framework for structural systems biology. Bioinformatics, 2018, 34, 2155-2157.	1.8	36
141	Quantitative -omic data empowers bottom-up systems biology. Current Opinion in Biotechnology, 2018, 51, 130-136.	3.3	28
142	Dissecting the genetic and metabolic mechanisms of adaptation to the knockout of a major metabolic enzyme in <i>Escherichia coli</i>. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 222-227.	3.3	70
143	Updated and standardized genome-scale reconstruction of Mycobacterium tuberculosis H37Rv, iEK1011, simulates flux states indicative of physiological conditions. BMC Systems Biology, 2018, 12, 25.	3.0	63
144	Systems biology as an emerging paradigm in transfusion medicine. BMC Systems Biology, 2018, 12, 31.	3.0	12

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145	High-Level dCas9 Expression Induces Abnormal Cell Morphology in <i>Escherichia coli</i>. ACS Synthetic Biology, 2018, 7, 1085-1094.	1.9	147
146	Reframing gene essentiality in terms of adaptive flexibility. BMC Systems Biology, 2018, 12, 143.	3.0	11
147	Metagenomics-Based, Strain-Level Analysis of Escherichia coli From a Time-Series of Microbiome Samples From a Crohn's Disease Patient. Frontiers in Microbiology, 2018, 9, 2559.	1.5	37
148	Revealing Key Determinants of Clonal Variation in Transgene Expression in Recombinant CHO Cells Using Targeted Genome Editing. ACS Synthetic Biology, 2018, 7, 2867-2878.	1.9	39
149	Machine learning applied to enzyme turnover numbers reveals protein structural correlates and improves metabolic models. Nature Communications, 2018, 9, 5252.	5.8	151
150	Modeling genome-wide enzyme evolution predicts strong epistasis underlying catalytic turnover rates. Nature Communications, 2018, 9, 5270.	5.8	16
151	Characterizing posttranslational modifications in prokaryotic metabolism using a multiscale workflow. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 11096-11101.	3.3	44
152	Thermodynamic favorability and pathway yield as evolutionary tradeoffs in biosynthetic pathway choice. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 11339-11344.	3.3	30
153	Escher-FBA: a web application for interactive flux balance analysis. BMC Systems Biology, 2018, 12, 84.	3.0	44
154	Estimating Metabolic Equilibrium Constants: Progress and Future Challenges. Trends in Biochemical Sciences, 2018, 43, 960-969.	3.7	15
155	Network-level allosteric effects are elucidated by detailing how ligand-binding events modulate utilization of catalytic potentials. PLoS Computational Biology, 2018, 14, e1006356.	1.5	3
156	Machine learning and structural analysis of Mycobacterium tuberculosis pan-genome identifies genetic signatures of antibiotic resistance. Nature Communications, 2018, 9, 4306.	5.8	126
157	Gapless, Unambiguous Genome Sequence for Escherichia coli C, a Workhorse of Industrial Biology. Microbiology Resource Announcements, 2018, 7, .	0.3	3
158	Identification of growth-coupled production strains considering protein costs and kinetic variability. Metabolic Engineering Communications, 2018, 7, e00080.	1.9	19
159	Genome-scale metabolic reconstructions of multiple Salmonella strains reveal serovar-specific metabolic traits. Nature Communications, 2018, 9, 3771.	5.8	109
160	Evolution of gene knockout strains of E. coli reveal regulatory architectures governed by metabolism. Nature Communications, 2018, 9, 3796.	5.8	59
161	Growth Adaptation of gnd and sdhCB Escherichia coli Deletion Strains Diverges From a Similar Initial Perturbation of the Transcriptome. Frontiers in Microbiology, 2018, 9, 1793.	1.5	23
162	Adaptation to the coupling of glycolysis to toxic methylglyoxal production in tpiA deletion strains of Escherichia coli requires synchronized and counterintuitive genetic changes. Metabolic Engineering, 2018, 48, 82-93.	3.6	38

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163	Multiple Optimal Phenotypes Overcome Redox and Glycolytic Intermediate Metabolite Imbalances in Escherichia coli pgi Knockout Evolutions. Applied and Environmental Microbiology, 2018, 84, .	1.4	22
164	Escherichia coli B2 strains prevalent in inflammatory bowel disease patients have distinct metabolic capabilities that enable colonization of intestinal mucosa. BMC Systems Biology, 2018, 12, 66.	3.0	39
165	iCN718, an Updated and Improved Genome-Scale Metabolic Network Reconstruction of Acinetobacter baumannii AYE. Frontiers in Genetics, 2018, 9, 121.	1.1	40
166	The Staphylococcus aureus Two-Component System AgrAC Displays Four Distinct Genomic Arrangements That Delineate Genomic Virulence Factor Signatures. Frontiers in Microbiology, 2018, 9, 1082.	1.5	26
167	COBRAme: A computational framework for genome-scale models of metabolism and gene expression. PLoS Computational Biology, 2018, 14, e1006302.	1.5	123
168	Systematic discovery of uncharacterized transcription factors in Escherichia coli K-12 MG1655. Nucleic Acids Research, 2018, 46, 10682-10696.	6.5	65
169	A unified resource for transcriptional regulation in Escherichia coli K-12 incorporating high-throughput-generated binding data into RegulonDB version 10.0. BMC Biology, 2018, 16, 91.	1.7	42
170	Functional interrogation of Plasmodium genus metabolism identifies species- and stage-specific differences in nutrient essentiality and drug targeting. PLoS Computational Biology, 2018, 14, e1005895.	1.5	24
171	ChIP-exo interrogation of Crp, DNA, and RNAP holoenzyme interactions. PLoS ONE, 2018, 13, e0197272.	1.1	20
172	Adaptive laboratory evolution resolves energy depletion to maintain high aromatic metabolite phenotypes in Escherichia coli strains lacking the Phosphotransferase System. Metabolic Engineering, 2018, 48, 233-242.	3.6	43
173	Temperature-Dependent Estimation of Gibbs Energies Using an Updated Group-Contribution Method. Biophysical Journal, 2018, 114, 2691-2702.	0.2	36
174	Systems analysis of metabolism in platelet concentrates during storage in platelet additive solution. Biochemical Journal, 2018, 475, 2225-2240.	1.7	20
175	Whole-Genome Sequencing of Invasion-Resistant Cells Identifies Laminin Î±2 as a Host Factor for Bacterial Invasion. MBio, 2017, 8, .	1.8	36
176	Systems biology analysis of drivers underlying hallmarks of cancer cell metabolism. Scientific Reports, 2017, 7, 41241.	1.6	87
177	Integrated Regulatory and Metabolic Networks of the Marine Diatom <i>Phaeodactylum tricornutum</i> Predict the Response to Rising CO ₂ Levels. MSystems, 2017, 2, .	1.7	40
178	A Model for Designing Adaptive Laboratory Evolution Experiments. Applied and Environmental Microbiology, 2017, 83, .	1.4	71
179	Reliable and efficient solution of genome-scale models of Metabolism and macromolecular Expression. Scientific Reports, 2017, 7, 40863.	1.6	30
180	Machine learning in computational biology to accelerate high-throughput protein expression. Bioinformatics, 2017, 33, 2487-2495.	1.8	8

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181	Laboratory Evolution to Alternating Substrate Environments Yields Distinct Phenotypic and Genetic Adaptive Strategies. Applied and Environmental Microbiology, 2017, 83, .	1.4	76
182	Revealing genome-scale transcriptional regulatory landscape of OmpR highlights its expanded regulatory roles under osmotic stress in Escherichia coli K-12 MG1655. Scientific Reports, 2017, 7, 2181.	1.6	35
183	Elucidating dynamic metabolic physiology through network integration of quantitative time-course metabolomics. Scientific Reports, 2017, 7, 46249.	1.6	121
184	Literature mining supports a next-generation modeling approach to predict cellular byproduct secretion. Metabolic Engineering, 2017, 39, 220-227.	3.6	34
185	Fast growth phenotype of E. coli K-12 from adaptive laboratory evolution does not require intracellular flux rewiring. Metabolic Engineering, 2017, 44, 100-107.	3.6	59
186	Thermosensitivity of growth is determined by chaperone-mediated proteome reallocation. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 11548-11553.	3.3	79
187	iML1515, a knowledgebase that computes Escherichia coli traits. Nature Biotechnology, 2017, 35, 904-908.	9.4	425
188	Quantitative time-course metabolomics in human red blood cells reveal the temperature dependence of human metabolic networks. Journal of Biological Chemistry, 2017, 292, 19556-19564.	1.6	45
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