

Christopher S Henry

List of Publications by Year in descending order

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Version: 2024-02-01

62
papers

9,275
citations

126708

33
h-index

128067

60
g-index

72
all docs

72
docs citations

72
times ranked

9853
citing authors

#	ARTICLE	IF	CITATIONS
1	Improvements to PATRIC, the all-bacterial Bioinformatics Database and Analysis Resource Center. <i>Nucleic Acids Research</i> , 2017, 45, D535-D542.	6.5	1,445
2	A genome-scale metabolic reconstruction for <i>Escherichia coli</i> K12 MG1655 that accounts for 1260 ORFs and thermodynamic information. <i>Molecular Systems Biology</i> , 2007, 3, 121.	3.2	1,234
3	High-throughput generation, optimization and analysis of genome-scale metabolic models. <i>Nature Biotechnology</i> , 2010, 28, 977-982.	9.4	974
4	KBase: The United States Department of Energy Systems Biology Knowledgebase. <i>Nature Biotechnology</i> , 2018, 36, 566-569.	9.4	955
5	Thermodynamics-Based Metabolic Flux Analysis. <i>Biophysical Journal</i> , 2007, 92, 1792-1805.	0.2	560
6	Competitive and cooperative metabolic interactions in bacterial communities. <i>Nature Communications</i> , 2011, 2, 589.	5.8	413
7	Group Contribution Method for Thermodynamic Analysis of Complex Metabolic Networks. <i>Biophysical Journal</i> , 2008, 95, 1487-1499.	0.2	345
8	Exploring the diversity of complex metabolic networks. <i>Bioinformatics</i> , 2005, 21, 1603-1609.	1.8	322
9	MEMOTE for standardized genome-scale metabolic model testing. <i>Nature Biotechnology</i> , 2020, 38, 272-276.	9.4	314
10	Genome-Scale Thermodynamic Analysis of <i>Escherichia coli</i> Metabolism. <i>Biophysical Journal</i> , 2006, 90, 1453-1461.	0.2	195
11	MINEs: open access databases of computationally predicted enzyme promiscuity products for untargeted metabolomics. <i>Journal of Cheminformatics</i> , 2015, 7, 44.	2.8	172
12	SEED Servers: High-Performance Access to the SEED Genomes, Annotations, and Metabolic Models. <i>PLoS ONE</i> , 2012, 7, e48053.	1.1	169
13	Discovery and analysis of novel metabolic pathways for the biosynthesis of industrial chemicals: 3-hydroxypropanoate. <i>Biotechnology and Bioengineering</i> , 2010, 106, 462-473.	1.7	146
14	iBsu1103: a new genome-scale metabolic model of <i>Bacillus subtilis</i> based on SEED annotations. <i>Genome Biology</i> , 2009, 10, R69.	13.9	141
15	Automated Genome Annotation and Metabolic Model Reconstruction in the SEED and Model SEED. <i>Methods in Molecular Biology</i> , 2013, 985, 17-45.	0.4	124
16	The ModelSEED Biochemistry Database for the integration of metabolic annotations and the reconstruction, comparison and analysis of metabolic models for plants, fungi and microbes. <i>Nucleic Acids Research</i> , 2021, 49, D575-D588.	6.5	119
17	Metabolic Reconstruction and Modeling Microbial Electrosynthesis. <i>Scientific Reports</i> , 2017, 7, 8391.	1.6	117
18	Microbial Community Metabolic Modeling: A Community Data-Driven Network Reconstruction. <i>Journal of Cellular Physiology</i> , 2016, 231, 2339-2345.	2.0	107

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19	Frontiers in metabolic reconstruction and modeling of plant genomes. <i>Journal of Experimental Botany</i> , 2012, 63, 2247-2258.	2.4	79
20	Plant B Vitamin Pathways and their Compartmentation: a Guide for the Perplexed. <i>Journal of Experimental Botany</i> , 2012, 63, 5379-5395.	2.4	78
21	Building the repertoire of dispensable chromosome regions in <i>Bacillus subtilis</i> entails major refinement of cognate large-scale metabolic model. <i>Nucleic Acids Research</i> , 2013, 41, 687-699.	6.5	76
22	â€œNothing of chemistry disappears in biologyâ€™: the Top 30 damage-prone endogenous metabolites. <i>Biochemical Society Transactions</i> , 2016, 44, 961-971.	1.6	76
23	Long-term phenotypic evolution of bacteria. <i>Nature</i> , 2015, 517, 369-372.	13.7	75
24	Computational discovery of biochemical routes to specialty chemicals. <i>Chemical Engineering Science</i> , 2004, 59, 5051-5060.	1.9	73
25	High-throughput comparison, functional annotation, and metabolic modeling of plant genomes using the PlantSEED resource. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 9645-9650.	3.3	69
26	Likelihood-Based Gene Annotations for Gap Filling and Quality Assessment in Genome-Scale Metabolic Models. <i>PLoS Computational Biology</i> , 2014, 10, e1003882.	1.5	66
27	Comparative Genomics of Cultured and Uncultured Strains Suggests Genes Essential for Free-Living Growth of <i>Liberibacter</i> . <i>PLoS ONE</i> , 2014, 9, e84469.	1.1	64
28	Methods for automated genome-scale metabolic model reconstruction. <i>Biochemical Society Transactions</i> , 2018, 46, 931-936.	1.6	51
29	Improved evidence-based genome-scale metabolic models for maize leaf, embryo, and endosperm. <i>Frontiers in Plant Science</i> , 2015, 6, 142.	1.7	48
30	Metabolite Damage and Metabolite Damage Control in Plants. <i>Annual Review of Plant Biology</i> , 2016, 67, 131-152.	8.6	43
31	Metabolite damage and repair in metabolic engineering design. <i>Metabolic Engineering</i> , 2017, 44, 150-159.	3.6	43
32	Genome-wide metabolic network reconstruction of the picoalga <i>Ostreococcus</i> . <i>Journal of Experimental Botany</i> , 2012, 63, 2353-2362.	2.4	41
33	The number of catalytic cycles in an enzymeâ€™s lifetime and why it matters to metabolic engineering. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	41
34	A directed-overflow and damage-control <i><i>N</i></i> -glycosidase in riboflavin biosynthesis. <i>Biochemical Journal</i> , 2015, 466, 137-145.	1.7	38
35	Genome-scale bacterial transcriptional regulatory networks: reconstruction and integrated analysis with metabolic models. <i>Briefings in Bioinformatics</i> , 2014, 15, 592-611.	3.2	30
36	Connecting genotype to phenotype in the era of high-throughput sequencing. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2011, 1810, 967-977.	1.1	28

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37	Modeling central metabolism and energy biosynthesis across microbial life. BMC Genomics, 2016, 17, 568.	1.2	28
38	Metabolic multistability and hysteresis in a model aerobe-anaerobe microbiome community. Science Advances, 2020, 6, eaba0353.	4.7	27
39	PlantSEED enables automated annotation and reconstruction of plant primary metabolism with improved compartmentalization and comparative consistency. Plant Journal, 2018, 95, 1102-1113.	2.8	25
40	Generation and Validation of the iKp1289 Metabolic Model for Klebsiella pneumoniae KPPR1. Journal of Infectious Diseases, 2017, 215, S37-S43.	1.9	23
41	Evolution of substrate specificity in a retained enzyme driven by gene loss. ELife, 2017, 6, .	2.8	23
42	Building the blueprint of life. Biotechnology Journal, 2010, 5, 695-704.	1.8	21
43	Enzymes as Parts in Need of Replacement “ and How to Extend Their Working Life. Trends in Plant Science, 2020, 25, 661-669.	4.3	20
44	Systems-Wide Prediction of Enzyme Promiscuity Reveals a New Underground Alternative Route for Pyridoxal 5-Phosphate Production in E. coli. PLoS Computational Biology, 2016, 12, e1004705.	1.5	20
45	A pathway for every product? Tools to discover and design plant metabolism. Plant Science, 2018, 273, 61-70.	1.7	18
46	Reconstruction of the Regulatory Network for Bacillus subtilis and Reconciliation with Gene Expression Data. Frontiers in Microbiology, 2016, 7, 275.	1.5	14
47	Systematic identification and analysis of frequent gene fusion events in metabolic pathways. BMC Genomics, 2016, 17, 473.	1.2	13
48	A plastidial pantoate transporter with a potential role in pantothenate synthesis. Biochemical Journal, 2018, 475, 813-825.	1.7	13
49	Quantum Mechanical Methods Predict Accurate Thermodynamics of Biochemical Reactions. ACS Omega, 2021, 6, 9948-9959.	1.6	12
50	Draft Genome Sequence of a Multidrug-Resistant Klebsiella quasipneumoniae subsp. similipneumoniae Isolate from a Clinical Source. Genome Announcements, 2016, 4, .	0.8	10
51	Maximal Sum of Metabolic Exchange Fluxes Outperforms Biomass Yield as a Predictor of Growth Rate of Microorganisms. PLoS ONE, 2014, 9, e98372.	1.1	9
52	The microbiome as a source of new enterprises and job creation: Considering clinical faecal and synthetic microbiome-transplants and therapeutic regulation. Microbial Biotechnology, 2017, 10, 4-5.	2.0	9
53	Computing and Applying Atomic Regulons to Understand Gene Expression and Regulation. Frontiers in Microbiology, 2016, 7, 1819.	1.5	7
54	Co-occurrence of analogous enzymes determines evolution of a novel (1 ² ±)8-isomerase sub-family after non-conserved mutations in flexible loop. Biochemical Journal, 2016, 473, 1141-1152.	1.7	6

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55	Enabling comparative modeling of closely related genomes: example genus <i>Brucella</i> . <i>3 Biotech</i> , 2015, 5, 101-105.	1.1	5
56	The Moderately (D)efficient Enzyme: Catalysis-Related Damage <i>In Vivo</i> and Its Repair. <i>Biochemistry</i> , 2021, 60, 3555-3565.	1.2	5
57	Chemical-damage MINE: A database of curated and predicted spontaneous metabolic reactions. <i>Metabolic Engineering</i> , 2022, 69, 302-312.	3.6	5
58	Chemical composition of material extractives influences microbial growth and dynamics on wetted wood materials. <i>Scientific Reports</i> , 2020, 10, 14500.	1.6	4
59	Analysis of the Effect of Reversibility Constraints on the Predictions of Genome-Scale Metabolic Models. <i>Advances in Intelligent and Soft Computing</i> , 2010, , 209-215.	0.2	1
60	Implementing and evaluating a Gaussian mixture framework for identifying gene function from TnSeq data. , 2018, , .		1
61	Comparative analysis of genome-scale metabolic models for <i>Mycoplasma genitalium</i> , <i>Ureaplasma parvum</i> , and <i>Mycoplasma hominis</i> reveals novel routes through the Pentose Phosphate Pathway. <i>FASEB Journal</i> , 2010, 24, 899.1.	0.2	0
62	Tapping the Wealth of Microbial Data in High-Throughput Metabolic Model Reconstruction. <i>Methods in Molecular Biology</i> , 2014, 1191, 19-45.	0.4	0