

Christopher S Henry

List of Publications by Year in descending order

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Version: 2024-02-01

62
papers

9,275
citations

126907

33
h-index

128289

60
g-index

72
all docs

72
docs citations

72
times ranked

9853
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 1 | Chemical-damage MINE: A database of curated and predicted spontaneous metabolic reactions. <i>Metabolic Engineering</i> , 2022, 69, 302-312. | 7.0 | 5 |
| 2 | 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. | 14.5 | 119 |
| 3 | The number of catalytic cycles in an enzyme'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, . | 7.1 | 41 |
| 4 | Quantum Mechanical Methods Predict Accurate Thermodynamics of Biochemical Reactions. <i>ACS Omega</i> , 2021, 6, 9948-9959. | 3.5 | 12 |
| 5 | The Moderately (D)efficient Enzyme: Catalysis-Related Damage <i>In Vivo</i> and Its Repair. <i>Biochemistry</i> , 2021, 60, 3555-3565. | 2.5 | 5 |
| 6 | Metabolic multistability and hysteresis in a model aerobe-anaerobe microbiome community. <i>Science Advances</i> , 2020, 6, eaba0353. | 10.3 | 27 |
| 7 | Chemical composition of material extractives influences microbial growth and dynamics on wetted wood materials. <i>Scientific Reports</i> , 2020, 10, 14500. | 3.3 | 4 |
| 8 | Enzymes as Parts in Need of Replacement and How to Extend Their Working Life. <i>Trends in Plant Science</i> , 2020, 25, 661-669. | 8.8 | 20 |
| 9 | MEMOTE for standardized genome-scale metabolic model testing. <i>Nature Biotechnology</i> , 2020, 38, 272-276. | 17.5 | 314 |
| 10 | A plastidial pantoate transporter with a potential role in pantothenate synthesis. <i>Biochemical Journal</i> , 2018, 475, 813-825. | 3.7 | 13 |
| 11 | A pathway for every product? Tools to discover and design plant metabolism. <i>Plant Science</i> , 2018, 273, 61-70. | 3.6 | 18 |
| 12 | Methods for automated genome-scale metabolic model reconstruction. <i>Biochemical Society Transactions</i> , 2018, 46, 931-936. | 3.4 | 51 |
| 13 | KBase: The United States Department of Energy Systems Biology Knowledgebase. <i>Nature Biotechnology</i> , 2018, 36, 566-569. | 17.5 | 955 |
| 14 | PlantSEED enables automated annotation and reconstruction of plant primary metabolism with improved compartmentalization and comparative consistency. <i>Plant Journal</i> , 2018, 95, 1102-1113. | 5.7 | 25 |
| 15 | Implementing and evaluating a Gaussian mixture framework for identifying gene function from TnSeq data. , 2018, , . | | 1 |
| 16 | The microbiome as a source of new enterprises and job creation: Considering clinical faecal and synthetic microbiome transplants and therapeutic regulation. <i>Microbial Biotechnology</i> , 2017, 10, 4-5. | 4.2 | 9 |
| 17 | Improvements to PATRIC, the all-bacterial Bioinformatics Database and Analysis Resource Center. <i>Nucleic Acids Research</i> , 2017, 45, D535-D542. | 14.5 | 1,445 |
| 18 | Generation and Validation of the iKp1289 Metabolic Model for <i>Klebsiella pneumoniae</i> KPPR1. <i>Journal of Infectious Diseases</i> , 2017, 215, S37-S43. | 4.0 | 23 |

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|----|---|------|-----------|
| 19 | Metabolite damage and repair in metabolic engineering design. <i>Metabolic Engineering</i> , 2017, 44, 150-159. | 7.0 | 43 |
| 20 | Metabolic Reconstruction and Modeling Microbial Electrosynthesis. <i>Scientific Reports</i> , 2017, 7, 8391. | 3.3 | 117 |
| 21 | Evolution of substrate specificity in a retained enzyme driven by gene loss. <i>ELife</i> , 2017, 6, . | 6.0 | 23 |
| 22 | Draft Genome Sequence of a Multidrug-Resistant <i>Klebsiella quasipneumoniae</i> subsp. <i>similipneumoniae</i> Isolate from a Clinical Source. <i>Genome Announcements</i> , 2016, 4, . | 0.8 | 10 |
| 23 | Reconstruction of the Regulatory Network for <i>Bacillus subtilis</i> and Reconciliation with Gene Expression Data. <i>Frontiers in Microbiology</i> , 2016, 7, 275. | 3.5 | 14 |
| 24 | Computing and Applying Atomic Regulons to Understand Gene Expression and Regulation. <i>Frontiers in Microbiology</i> , 2016, 7, 1819. | 3.5 | 7 |
| 25 | Co-occurrence of analogous enzymes determines evolution of a novel (Î²±)8-isomerase sub-family after non-conserved mutations in flexible loop. <i>Biochemical Journal</i> , 2016, 473, 1141-1152. | 3.7 | 6 |
| 26 | Microbial Community Metabolic Modeling: A Community Data-Driven Network Reconstruction. <i>Journal of Cellular Physiology</i> , 2016, 231, 2339-2345. | 4.1 | 107 |
| 27 | Systematic identification and analysis of frequent gene fusion events in metabolic pathways. <i>BMC Genomics</i> , 2016, 17, 473. | 2.8 | 13 |
| 28 | â€œNothing of chemistry disappears in biologyâ€™: the Top 30 damage-prone endogenous metabolites. <i>Biochemical Society Transactions</i> , 2016, 44, 961-971. | 3.4 | 76 |
| 29 | Modeling central metabolism and energy biosynthesis across microbial life. <i>BMC Genomics</i> , 2016, 17, 568. | 2.8 | 28 |
| 30 | Metabolite Damage and Metabolite Damage Control in Plants. <i>Annual Review of Plant Biology</i> , 2016, 67, 131-152. | 18.7 | 43 |
| 31 | Systems-Wide Prediction of Enzyme Promiscuity Reveals a New Underground Alternative Route for Pyridoxal 5â€™-Phosphate Production in <i>E. coli</i> . <i>PLoS Computational Biology</i> , 2016, 12, e1004705. | 3.2 | 20 |
| 32 | Improved evidence-based genome-scale metabolic models for maize leaf, embryo, and endosperm. <i>Frontiers in Plant Science</i> , 2015, 6, 142. | 3.6 | 48 |
| 33 | A directed-overflow and damage-control <i>N</i> -glycosidase in riboflavin biosynthesis. <i>Biochemical Journal</i> , 2015, 466, 137-145. | 3.7 | 38 |
| 34 | MINEs: open access databases of computationally predicted enzyme promiscuity products for untargeted metabolomics. <i>Journal of Cheminformatics</i> , 2015, 7, 44. | 6.1 | 172 |
| 35 | Long-term phenotypic evolution of bacteria. <i>Nature</i> , 2015, 517, 369-372. | 27.8 | 75 |
| 36 | Enabling comparative modeling of closely related genomes: example genus <i>Brucella</i> . <i>3 Biotech</i> , 2015, 5, 101-105. | 2.2 | 5 |

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|----|---|------|-----------|
| 37 | Maximal Sum of Metabolic Exchange Fluxes Outperforms Biomass Yield as a Predictor of Growth Rate of Microorganisms. <i>PLoS ONE</i> , 2014, 9, e98372. | 2.5 | 9 |
| 38 | Likelihood-Based Gene Annotations for Gap Filling and Quality Assessment in Genome-Scale Metabolic Models. <i>PLoS Computational Biology</i> , 2014, 10, e1003882. | 3.2 | 66 |
| 39 | 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. | 7.1 | 69 |
| 40 | Genome-scale bacterial transcriptional regulatory networks: reconstruction and integrated analysis with metabolic models. <i>Briefings in Bioinformatics</i> , 2014, 15, 592-611. | 6.5 | 30 |
| 41 | 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. | 2.5 | 64 |
| 42 | Tapping the Wealth of Microbial Data in High-Throughput Metabolic Model Reconstruction. <i>Methods in Molecular Biology</i> , 2014, 1191, 19-45. | 0.9 | 0 |
| 43 | Automated Genome Annotation and Metabolic Model Reconstruction in the SEED and Model SEED. <i>Methods in Molecular Biology</i> , 2013, 985, 17-45. | 0.9 | 124 |
| 44 | 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. | 14.5 | 76 |
| 45 | Frontiers in metabolic reconstruction and modeling of plant genomes. <i>Journal of Experimental Botany</i> , 2012, 63, 2247-2258. | 4.8 | 79 |
| 46 | Genome-wide metabolic network reconstruction of the picoalga <i>Ostreococcus</i> . <i>Journal of Experimental Botany</i> , 2012, 63, 2353-2362. | 4.8 | 41 |
| 47 | Plant B Vitamin Pathways and their Compartmentation: a Guide for the Perplexed. <i>Journal of Experimental Botany</i> , 2012, 63, 5379-5395. | 4.8 | 78 |
| 48 | SEED Servers: High-Performance Access to the SEED Genomes, Annotations, and Metabolic Models. <i>PLoS ONE</i> , 2012, 7, e48053. | 2.5 | 169 |
| 49 | Competitive and cooperative metabolic interactions in bacterial communities. <i>Nature Communications</i> , 2011, 2, 589. | 12.8 | 413 |
| 50 | Connecting genotype to phenotype in the era of high-throughput sequencing. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2011, 1810, 967-977. | 2.4 | 28 |
| 51 | Building the blueprint of life. <i>Biotechnology Journal</i> , 2010, 5, 695-704. | 3.5 | 21 |
| 52 | Discovery and analysis of novel metabolic pathways for the biosynthesis of industrial chemicals: 3-hydroxypropanoate. <i>Biotechnology and Bioengineering</i> , 2010, 106, 462-473. | 3.3 | 146 |
| 53 | High-throughput generation, optimization and analysis of genome-scale metabolic models. <i>Nature Biotechnology</i> , 2010, 28, 977-982. | 17.5 | 974 |
| 54 | 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 |

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|----|---|-----|-----------|
| 55 | 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. | 0.5 | 0 |
| 56 | iBsu1103: a new genome-scale metabolic model of <i>Bacillus subtilis</i> based on SEED annotations. <i>Genome Biology</i> , 2009, 10, R69. | 9.6 | 141 |
| 57 | Group Contribution Method for Thermodynamic Analysis of Complex Metabolic Networks. <i>Biophysical Journal</i> , 2008, 95, 1487-1499. | 0.5 | 345 |
| 58 | A genome-scale metabolic reconstruction for <i>Escherichia coli</i> K-12 MG1655 that accounts for 1260 ORFs and thermodynamic information. <i>Molecular Systems Biology</i> , 2007, 3, 121. | 7.2 | 1,234 |
| 59 | Thermodynamics-Based Metabolic Flux Analysis. <i>Biophysical Journal</i> , 2007, 92, 1792-1805. | 0.5 | 560 |
| 60 | Genome-Scale Thermodynamic Analysis of <i>Escherichia coli</i> Metabolism. <i>Biophysical Journal</i> , 2006, 90, 1453-1461. | 0.5 | 195 |
| 61 | Exploring the diversity of complex metabolic networks. <i>Bioinformatics</i> , 2005, 21, 1603-1609. | 4.1 | 322 |
| 62 | Computational discovery of biochemical routes to specialty chemicals. <i>Chemical Engineering Science</i> , 2004, 59, 5051-5060. | 3.8 | 73 |