

Daniel C Zielinski

List of Publications by Year in descending order

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Version: 2024-02-01

24
papers

3,535
citations

471061

17
h-index

642321

23
g-index

26
all docs

26
docs citations

26
times ranked

4551
citing authors

#	ARTICLE	IF	CITATIONS
1	MASSpy: Building, simulating, and visualizing dynamic biological models in Python using mass action kinetics. <i>PLoS Computational Biology</i> , 2021, 17, e1008208.	1.5	20
2	The quantitative metabolome is shaped by abiotic constraints. <i>Nature Communications</i> , 2021, 12, 3178.	5.8	15
3	<i>Escherichia coli</i> Data-Driven Strain Design Using Aggregated Adaptive Laboratory Evolution Mutational Data. <i>ACS Synthetic Biology</i> , 2021, 10, 3379-3395.	1.9	5
4	Recon3D enables a three-dimensional view of gene variation in human metabolism. <i>Nature Biotechnology</i> , 2018, 36, 272-281.	9.4	520
5	Machine learning applied to enzyme turnover numbers reveals protein structural correlates and improves metabolic models. <i>Nature Communications</i> , 2018, 9, 5252.	5.8	151
6	Modeling genome-wide enzyme evolution predicts strong epistasis underlying catalytic turnover rates. <i>Nature Communications</i> , 2018, 9, 5270.	5.8	16
7	Thermodynamic favorability and pathway yield as evolutionary tradeoffs in biosynthetic pathway choice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 11339-11344.	3.3	30
8	Estimating Metabolic Equilibrium Constants: Progress and Future Challenges. <i>Trends in Biochemical Sciences</i> , 2018, 43, 960-969.	3.7	15
9	Temperature-Dependent Estimation of Gibbs Energies Using an Updated Group-Contribution Method. <i>Biophysical Journal</i> , 2018, 114, 2691-2702.	0.2	36
10	Systems biology analysis of drivers underlying hallmarks of cancer cell metabolism. <i>Scientific Reports</i> , 2017, 7, 41241.	1.6	87
11	A Systematic Evaluation of Methods for Tailoring Genome-Scale Metabolic Models. <i>Cell Systems</i> , 2017, 4, 318-329.e6.	2.9	178
12	Quantitative time-course metabolomics in human red blood cells reveal the temperature dependence of human metabolic networks. <i>Journal of Biological Chemistry</i> , 2017, 292, 19556-19564.	1.6	45
13	Topological and kinetic determinants of the modal matrices of dynamic models of metabolism. <i>PLoS ONE</i> , 2017, 12, e0189880.	1.1	1
14	Evaluation of rate law approximations in bottom-up kinetic models of metabolism. <i>BMC Systems Biology</i> , 2016, 10, 40.	3.0	26
15	Genome-Scale Metabolic Model for the Green Alga <i>Chlorella vulgaris</i> UTEX 395 Accurately Predicts Phenotypes under Autotrophic, Heterotrophic, and Mixotrophic Growth Conditions. <i>Plant Physiology</i> , 2016, 172, 589-602.	2.3	86
16	A Consensus Genome-scale Reconstruction of Chinese Hamster Ovary Cell Metabolism. <i>Cell Systems</i> , 2016, 3, 434-443.e8.	2.9	205
17	Recon 2.2: from reconstruction to model of human metabolism. <i>Metabolomics</i> , 2016, 12, 109.	1.4	243
18	Metabolic Analysis of Red Blood Cells Stored at High Temperature. <i>Blood</i> , 2016, 128, 3848-3848.	0.6	0

#	ARTICLE	IF	CITATIONS
19	Pharmacogenomic and clinical data link non-pharmacokinetic metabolic dysregulation to drug side effect pathogenesis. <i>Nature Communications</i> , 2015, 6, 7101.	5.8	41
20	Personalized Whole-Cell Kinetic Models of Metabolism for Discovery in Genomics and Pharmacodynamics. <i>Cell Systems</i> , 2015, 1, 283-292.	2.9	92
21	A Systems Approach to Predict Oncometabolites via Context-Specific Genome-Scale Metabolic Networks. <i>PLoS Computational Biology</i> , 2014, 10, e1003837.	1.5	63
22	Predicting outcomes of steady-state ¹³ C isotope tracing experiments using Monte Carlo sampling. <i>BMC Systems Biology</i> , 2012, 6, 9.	3.0	30
23	Quantitative prediction of cellular metabolism with constraint-based models: the COBRA Toolbox v2.0. <i>Nature Protocols</i> , 2011, 6, 1290-1307.	5.5	1,408
24	Model-driven evaluation of the production potential for growth-coupled products of <i>Escherichia coli</i> . <i>Metabolic Engineering</i> , 2010, 12, 173-186.	3.6	221