Daniel C Zielinski

List of Publications by Year
in descending order

24	3,535	471509	642732
papers	citations	17	23
		h-index	g-index

26	26	26	4551
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Quantitative prediction of cellular metabolism with constraint-based models: the COBRA Toolbox v2.0. Nature Protocols, 2011, 6, 1290-1307.	12.0	1,408
2	Recon3D enables a three-dimensional view of gene variation in human metabolism. Nature Biotechnology, 2018, 36, 272-281.	17.5	520
3	Recon 2.2: from reconstruction to model of human metabolism. Metabolomics, 2016, 12, 109.	3.0	243
4	Model-driven evaluation of the production potential for growth-coupled products of Escherichia coli. Metabolic Engineering, 2010, 12, 173-186.	7.0	221
5	A Consensus Genome-scale Reconstruction of Chinese Hamster Ovary Cell Metabolism. Cell Systems, 2016, 3, 434-443.e8.	6.2	205
6	A Systematic Evaluation of Methods for Tailoring Genome-Scale Metabolic Models. Cell Systems, 2017, 4, 318-329.e6.	6.2	178
7	Machine learning applied to enzyme turnover numbers reveals protein structural correlates and improves metabolic models. Nature Communications, 2018, 9, 5252.	12.8	151
8	Personalized Whole-Cell Kinetic Models of Metabolism for Discovery in Genomics and Pharmacodynamics. Cell Systems, 2015, 1, 283-292.	6.2	92
9	Systems biology analysis of drivers underlying hallmarks of cancer cell metabolism. Scientific Reports, 2017, 7, 41241.	3.3	87
10	Genome-Scale Metabolic Model for the Green Alga *Chlorella vulgaris* UTEX 395 Accurately Predicts Phenotypes under Autotrophic, Heterotrophic, and Mixotrophic Growth Conditions. Plant Physiology, 2016, 172, 589-602.	4.8	86
11	A Systems Approach to Predict Oncometabolites via Context-Specific Genome-Scale Metabolic Networks. PLoS Computational Biology, 2014, 10, e1003837.	3.2	63
12	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.	3.4	45
13	Pharmacogenomic and clinical data link non-pharmacokinetic metabolic dysregulation to drug side effect pathogenesis. Nature Communications, 2015, 6, 7101.	12.8	41
14	Temperature-Dependent Estimation of Gibbs Energies Using an Updated Group-Contribution Method. Biophysical Journal, 2018, 114, 2691-2702.	0.5	36
15	Predicting outcomes of steady-state 13C isotope tracing experiments using Monte Carlo sampling. BMC Systems Biology, 2012, 6, 9.	3.0	30
16	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.	7.1	30
17	Evaluation of rate law approximations in bottom-up kinetic models of metabolism. BMC Systems Biology, 2016, 10, 40.	3.0	26
18	MASSpy: Building, simulating, and visualizing dynamic biological models in Python using mass action kinetics. PLoS Computational Biology, 2021, 17, e1008208.	3.2	20

#	Article	IF	Citations
19	Modeling genome-wide enzyme evolution predicts strong epistasis underlying catalytic turnover rates. Nature Communications, 2018, 9, 5270.	12.8	16
20	Estimating Metabolic Equilibrium Constants: Progress and Future Challenges. Trends in Biochemical Sciences, 2018, 43, 960-969.	7.5	15
21	The quantitative metabolome is shaped by abiotic constraints. Nature Communications, 2021, 12, 3178.	12.8	15
22	*Escherichia coli* Data-Driven Strain Design Using Aggregated Adaptive Laboratory Evolution Mutational Data. ACS Synthetic Biology, 2021, 10, 3379-3395.	3.8	5
23	Topological and kinetic determinants of the modal matrices of dynamic models of metabolism. PLoS ONE, 2017, 12, e0189880.	2.5	1
24	Metabolic Analysis of Red Blood Cells Stored at High Temperature. Blood, 2016, 128, 3848-3848.	1.4	0