Zachary A King

List of Publications by Year
in descending order

32 papers	4,540 citations	279798 23 h-index	414414 32 g-index
44 all docs	44 docs citations	44 times ranked	5142 citing authors

#	Article	IF	Citations
1	BiGG Models: A platform for integrating, standardizing and sharing genome-scale models. Nucleic Acids Research, 2016, 44, D515-D522.	14.5	746
2	Constraint-based models predict metabolic and associated cellular functions. Nature Reviews Genetics, 2014, 15, 107-120.	16.3	714
3	iML1515, a knowledgebase that computes Escherichia coli traits. Nature Biotechnology, 2017, 35, 904-908.	17.5	425
4	Escher: A Web Application for Building, Sharing, and Embedding Data-Rich Visualizations of Biological Pathways. PLoS Computational Biology, 2015, 11, e1004321.	3.2	344
5	MEMOTE for standardized genome-scale metabolic model testing. Nature Biotechnology, 2020, 38, 272-276.	17.5	314
6	In Vitro and In Vivo Evaluation of PEDOT Microelectrodes for Neural Stimulation and Recording. IEEE Transactions on Neural Systems and Rehabilitation Engineering, 2011, 19, 307-316.	4.9	258
7	A Consensus Genome-scale Reconstruction of Chinese Hamster Ovary Cell Metabolism. Cell Systems, 2016, 3, 434-443.e8.	6.2	205
8	The Escherichia coli transcriptome mostly consists of independently regulated modules. Nature Communications, 2019, 10, 5536.	12.8	161
9	The Morphology of Poly(3,4-Ethylenedioxythiophene). Polymer Reviews, 2010, 50, 340-384.	10.9	157
10	Next-generation genome-scale models for metabolic engineering. Current Opinion in Biotechnology, 2015, 35, 23-29.	6.6	144
11	BiGG Models 2020: multi-strain genome-scale models and expansion across the phylogenetic tree. Nucleic Acids Research, 2020, 48, D402-D406.	14.5	130
12	COBRAme: A computational framework for genome-scale models of metabolism and gene expression. PLoS Computational Biology, 2018, 14, e1006302.	3.2	123
13	The y-ome defines the 35% of *Escherichia coli* genes that lack experimental evidence of function. Nucleic Acids Research, 2019, 47, 2446-2454.	14.5	117
14	BOFdat: Generating biomass objective functions for genome-scale metabolic models from experimental data. PLoS Computational Biology, 2019, 15, e1006971.	3.2	83
15	Structural, chemical and electrochemical characterization of poly(3,4-Ethylenedioxythiophene) (PEDOT) prepared with various counter-ions and heat treatments. Polymer, 2011, 52, 1302-1308.	3.8	77
16	A model-driven quantitative metabolomics analysis of aerobic and anaerobic metabolism in *E. coli* K-12 MG1655 that is biochemically and thermodynamically consistent. Biotechnology and Bioengineering, 2014, 111, 803-815.	3.3	53
17	Enzyme promiscuity shapes adaptation to novel growth substrates. Molecular Systems Biology, 2019, 15, e8462.	7.2	52
18	Modeling the multi-scale mechanisms of macromolecular resource allocation. Current Opinion in Microbiology, 2018, 45, 8-15.	5.1	46

#	Article	IF	Citations
19	Escher-FBA: a web application for interactive flux balance analysis. BMC Systems Biology, 2018, 12, 84.	3.0	44
20	Optimal cofactor swapping can increase the theoretical yield for chemical production in Escherichia coli and Saccharomyces cerevisiae. Metabolic Engineering, 2014, 24, 117-128.	7.0	40
21	Literature mining supports a next-generation modeling approach to predict cellular byproduct secretion. Metabolic Engineering, 2017, 39, 220-227.	7.0	34
22	Laboratory evolution reveals a two-dimensional rate-yield tradeoff in microbial metabolism. PLoS Computational Biology, 2019, 15, e1007066.	3.2	33
23	Optimizing Cofactor Specificity of Oxidoreductase Enzymes for the Generation of Microbial Production Strains—OptSwap. Industrial Biotechnology, 2013, 9, 236-246.	0.8	30
24	Causal mutations from adaptive laboratory evolution are outlined by multiple scales of genome annotations and condition-specificity. BMC Genomics, 2020, 21, 514.	2.8	23
25	Identification of growth-coupled production strains considering protein costs and kinetic variability. Metabolic Engineering Communications, 2018, 7, e00080.	3.6	19
26	The genetic basis for adaptation of model-designed syntrophic co-cultures. PLoS Computational Biology, 2019, 15, e1006213.	3.2	17
27	Genome‐scale metabolic modeling reveals key features of a minimal gene set. Molecular Systems Biology, 2021, 17, e10099.	7.2	15
28	A Padawan Programmer's Guide to Developing Software Libraries. Cell Systems, 2017, 5, 431-437.	6.2	14
29	Visualizing metabolic network dynamics through time-series metabolomic data. BMC Bioinformatics, 2020, 21, 130.	2.6	13
30	Escher-Trace: a web application for pathway-based visualization of stable isotope tracing data. BMC Bioinformatics, 2020, 21, 297.	2.6	12
31	The Bitome: digitized genomic features reveal fundamental genome organization. Nucleic Acids Research, 2020, 48, 10157-10163.	14.5	11
32	A Phaeodactylum tricornutum literature database for interactive annotation of content. Algal Research, 2016, 18, 241-243.	4.6	0