

Zachary A King

List of Publications by Year in descending order

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Version: 2024-02-01

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	Genome-scale metabolic modeling reveals key features of a minimal gene set. <i>Molecular Systems Biology</i> , 2021, 17, e10099.	7.2	15
2	BiGG Models 2020: multi-strain genome-scale models and expansion across the phylogenetic tree. <i>Nucleic Acids Research</i> , 2020, 48, D402-D406.	14.5	130
3	The Bitome: digitized genomic features reveal fundamental genome organization. <i>Nucleic Acids Research</i> , 2020, 48, 10157-10163.	14.5	11
4	Escher-Trace: a web application for pathway-based visualization of stable isotope tracing data. <i>BMC Bioinformatics</i> , 2020, 21, 297.	2.6	12
5	Causal mutations from adaptive laboratory evolution are outlined by multiple scales of genome annotations and condition-specificity. <i>BMC Genomics</i> , 2020, 21, 514.	2.8	23
6	Visualizing metabolic network dynamics through time-series metabolomic data. <i>BMC Bioinformatics</i> , 2020, 21, 130.	2.6	13
7	MEMOTE for standardized genome-scale metabolic model testing. <i>Nature Biotechnology</i> , 2020, 38, 272-276.	17.5	314
8	Laboratory evolution reveals a two-dimensional rate-yield tradeoff in microbial metabolism. <i>PLoS Computational Biology</i> , 2019, 15, e1007066.	3.2	33
9	BOFdat: Generating biomass objective functions for genome-scale metabolic models from experimental data. <i>PLoS Computational Biology</i> , 2019, 15, e1006971.	3.2	83
10	The genetic basis for adaptation of model-designed syntrophic co-cultures. <i>PLoS Computational Biology</i> , 2019, 15, e1006213.	3.2	17
11	Enzyme promiscuity shapes adaptation to novel growth substrates. <i>Molecular Systems Biology</i> , 2019, 15, e8462.	7.2	52
12	The γ -ome defines the 35% of <i>Escherichia coli</i> genes that lack experimental evidence of function. <i>Nucleic Acids Research</i> , 2019, 47, 2446-2454.	14.5	117
13	The <i>Escherichia coli</i> transcriptome mostly consists of independently regulated modules. <i>Nature Communications</i> , 2019, 10, 5536.	12.8	161
14	Modeling the multi-scale mechanisms of macromolecular resource allocation. <i>Current Opinion in Microbiology</i> , 2018, 45, 8-15.	5.1	46
15	Escher-FBA: a web application for interactive flux balance analysis. <i>BMC Systems Biology</i> , 2018, 12, 84.	3.0	44
16	Identification of growth-coupled production strains considering protein costs and kinetic variability. <i>Metabolic Engineering Communications</i> , 2018, 7, e00080.	3.6	19
17	COBRAME: A computational framework for genome-scale models of metabolism and gene expression. <i>PLoS Computational Biology</i> , 2018, 14, e1006302.	3.2	123
18	Literature mining supports a next-generation modeling approach to predict cellular byproduct secretion. <i>Metabolic Engineering</i> , 2017, 39, 220-227.	7.0	34

#	ARTICLE	IF	CITATIONS
19	iML1515, a knowledgebase that computes Escherichia coli traits. Nature Biotechnology, 2017, 35, 904-908.	17.5	425
20	A Padawan Programmer's Guide to Developing Software Libraries. Cell Systems, 2017, 5, 431-437.	6.2	14
21	A Consensus Genome-scale Reconstruction of Chinese Hamster Ovary Cell Metabolism. Cell Systems, 2016, 3, 434-443.e8.	6.2	205
22	A Phaeodactylum tricornutum literature database for interactive annotation of content. Algal Research, 2016, 18, 241-243.	4.6	0
23	BiGG Models: A platform for integrating, standardizing and sharing genome-scale models. Nucleic Acids Research, 2016, 44, D515-D522.	14.5	746
24	Escher: A Web Application for Building, Sharing, and Embedding Data-Rich Visualizations of Biological Pathways. PLoS Computational Biology, 2015, 11, e1004321.	3.2	344
25	Next-generation genome-scale models for metabolic engineering. Current Opinion in Biotechnology, 2015, 35, 23-29.	6.6	144
26	A model-driven quantitative metabolomics analysis of aerobic and anaerobic metabolism in <i>E. coli</i> MG1655 that is biochemically and thermodynamically consistent. Biotechnology and Bioengineering, 2014, 111, 803-815.	3.3	53
27	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
28	Constraint-based models predict metabolic and associated cellular functions. Nature Reviews Genetics, 2014, 15, 107-120.	16.3	714
29	Optimizing Cofactor Specificity of Oxidoreductase Enzymes for the Generation of Microbial Production Strains OptSwap. Industrial Biotechnology, 2013, 9, 236-246.	0.8	30
30	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
31	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
32	The Morphology of Poly(3,4-Ethylenedioxythiophene). Polymer Reviews, 2010, 50, 340-384.	10.9	157