

Jennifer L Reed

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1367294/publications.pdf>

Version: 2024-02-01

76
papers

11,072
citations

71061

41
h-index

82499

72
g-index

79
all docs

79
docs citations

79
times ranked

9079
citing authors

#	ARTICLE	IF	CITATIONS
1	Introduction of NADH-dependent nitrate assimilation in <i>Synechococcus</i> sp. PCC 7002 improves photosynthetic production of 2-methyl-1-butanol and isobutanol. <i>Metabolic Engineering</i> , 2022, 69, 87-97.	3.6	14
2	Active and machine learning-based approaches to rapidly enhance microbial chemical production. <i>Metabolic Engineering</i> , 2021, 67, 216-226.	3.6	15
3	Genome-Wide Analysis of RNA Decay in the Cyanobacterium <i>Synechococcus</i> sp. Strain PCC 7002. <i>MSystems</i> , 2020, 5, .	1.7	6
4	Model-driven analysis of mutant fitness experiments improves genome-scale metabolic models of <i>Zymomonas mobilis</i> ZM4. <i>PLoS Computational Biology</i> , 2020, 16, e1008137.	1.5	12
5	Systems Metabolic Engineering of <i>Escherichia coli</i> Improves Coconversion of Lignocellulose-Derived Sugars. <i>Biotechnology Journal</i> , 2019, 14, e1800441.	1.8	9
6	² H and ¹³ C metabolic flux analysis elucidates in vivo thermodynamics of the ED pathway in <i>Zymomonas mobilis</i> . <i>Metabolic Engineering</i> , 2019, 54, 301-316.	3.6	51
7	Advances in gap-filling genome-scale metabolic models and model-driven experiments lead to novel metabolic discoveries. <i>Current Opinion in Biotechnology</i> , 2018, 51, 103-108.	3.3	51
8	Light-optimized growth of cyanobacterial cultures: Growth phases and productivity of biomass and secreted molecules in light-limited batch growth. <i>Metabolic Engineering</i> , 2018, 47, 230-242.	3.6	43
9	Cover Image, Volume 115, Number 9, September 2018. <i>Biotechnology and Bioengineering</i> , 2018, 115, i.	1.7	0
10	A framework for the identification of promising bio-based chemicals. <i>Biotechnology and Bioengineering</i> , 2018, 115, 2328-2340.	1.7	22
11	Integrating proteomic or transcriptomic data into metabolic models using linear bound flux balance analysis. <i>Bioinformatics</i> , 2018, 34, 3882-3888.	1.8	55
12	Improving flux predictions by integrating data from multiple strains. <i>Bioinformatics</i> , 2017, 33, 893-900.	1.8	9
13	Transcriptional characterization of <i>Vibrio fischeri</i> during colonization of juvenile <i>Euprymna scolopes</i> . <i>Environmental Microbiology</i> , 2017, 19, 1845-1856.	1.8	24
14	Model-enabled gene search (MEGS) allows fast and direct discovery of enzymatic and transport gene functions in the marine bacterium <i>Vibrio fischeri</i> . <i>Journal of Biological Chemistry</i> , 2017, 292, 10250-10261.	1.6	7
15	Evaluating the capabilities of microbial chemical production using genome-scale metabolic models. <i>Current Opinion in Systems Biology</i> , 2017, 2, 91-97.	1.3	6
16	Multi-platform ¹ H NMR Omics Analysis of Human Ebola Virus Disease Pathogenesis. <i>Cell Host and Microbe</i> , 2017, 22, 817-829.e8.	5.1	88
17	<i>Escherichia coli</i> as a model organism for systems metabolic engineering. <i>Current Opinion in Systems Biology</i> , 2017, 6, 80-88.	1.3	11
18	Flux balance analysis indicates that methane is the lowest cost feedstock for microbial cell factories. <i>Metabolic Engineering Communications</i> , 2017, 5, 26-33.	1.9	31

#	ARTICLE	IF	CITATIONS
19	Directed Evolution Reveals Unexpected Epistatic Interactions That Alter Metabolic Regulation and Enable Anaerobic Xylose Use by <i>Saccharomyces cerevisiae</i> . <i>PLoS Genetics</i> , 2016, 12, e1006372.	1.5	75
20	Applications of Constraint-Based Models for Biochemical Production. , 2016, , 201-226.		1
21	MapMaker and PathTracer for tracking carbon in genome-scale metabolic models. <i>Biotechnology Journal</i> , 2016, 11, 648-661.	1.8	21
22	Metabolic assessment of <i>E. coli</i> as a Biofactory for commercial products. <i>Metabolic Engineering</i> , 2016, 35, 64-74.	3.6	48
23	Do genome-scale models need exact solvers or clearer standards?. <i>Molecular Systems Biology</i> , 2015, 11, 831.	3.2	68
24	Thermodynamics and H ₂ Transfer in a Methanogenic, Syntrophic Community. <i>PLoS Computational Biology</i> , 2015, 11, e1004364.	1.5	25
25	Computational methods in metabolic engineering for strain design. <i>Current Opinion in Biotechnology</i> , 2015, 34, 135-141.	3.3	121
26	Genome Scale Reconstruction of Metabolic Networks of <i>Lactobacillus casei</i> ATCC 334 and 12A. <i>PLoS ONE</i> , 2014, 9, e110785.	1.1	32
27	Phenomix. , 2014, , 280-287.		0
28	Comparisons of <i>Shewanella</i> strains based on genome annotations, modeling, and experiments. <i>BMC Systems Biology</i> , 2014, 8, 31.	3.0	40
29	Expanding metabolic engineering algorithms using feasible space and shadow price constraint modules. <i>Metabolic Engineering Communications</i> , 2014, 1, 1-11.	1.9	9
30	Refining metabolic models and accounting for regulatory effects. <i>Current Opinion in Biotechnology</i> , 2014, 29, 34-38.	3.3	23
31	Software platforms to facilitate reconstructing genome-scale metabolic networks. <i>Environmental Microbiology</i> , 2014, 16, 49-59.	1.8	69
32	Adaptive Evolution of Synthetic Cooperating Communities Improves Growth Performance. <i>PLoS ONE</i> , 2014, 9, e108297.	1.1	47
33	Quantitative Assessment of Thermodynamic Constraints on the Solution Space of Genome-Scale Metabolic Models. <i>Biophysical Journal</i> , 2013, 105, 512-522.	0.2	51
34	Mechanistic analysis of multi-omics datasets to generate kinetic parameters for constraint-based metabolic models. <i>BMC Bioinformatics</i> , 2013, 14, 32.	1.2	37
35	Inferring ancient metabolism using ancestral core metabolic models of enterobacteria. <i>BMC Systems Biology</i> , 2013, 7, 46.	3.0	11
36	Constraint-based strain design using continuous modifications (CosMos) of flux bounds finds new strategies for metabolic engineering. <i>Biotechnology Journal</i> , 2013, 8, 595-604.	1.8	35

#	ARTICLE	IF	CITATIONS
37	Computational evaluation of <i>Synechococcus</i> sp. PCC 7002 metabolism for chemical production. <i>Biotechnology Journal</i> , 2013, 8, 619-630.	1.8	58
38	BioMog: A Computational Framework for the De Novo Generation or Modification of Essential Biomass Components. <i>PLoS ONE</i> , 2013, 8, e81322.	1.1	7
39	Complex Physiology and Compound Stress Responses during Fermentation of Alkali-Pre-treated Corn Stover Hydrolysate by an <i>Escherichia coli</i> Ethanologen. <i>Applied and Environmental Microbiology</i> , 2012, 78, 3442-3457.	1.4	57
40	Genome-Scale Modeling of Light-Driven Reductant Partitioning and Carbon Fluxes in Diazotrophic Unicellular Cyanobacterium <i>Cyanothece</i> sp. ATCC 51142. <i>PLoS Computational Biology</i> , 2012, 8, e1002460.	1.5	78
41	RELATCH: relative optimality in metabolic networks explains robust metabolic and regulatory responses to perturbations. <i>Genome Biology</i> , 2012, 13, R78.	13.9	78
42	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
43	FOCAL: an experimental design tool for systematizing metabolic discoveries and model development. <i>Genome Biology</i> , 2012, 13, R116.	13.9	17
44	Identification of Functional Differences in Metabolic Networks Using Comparative Genomics and Constraint-Based Models. <i>PLoS ONE</i> , 2012, 7, e34670.	1.1	41
45	Shrinking the Metabolic Solution Space Using Experimental Datasets. <i>PLoS Computational Biology</i> , 2012, 8, e1002662.	1.5	81
46	Microbial Strain Design for Biochemical Production Using Mixed-integer Programming Techniques. <i>Computer Aided Chemical Engineering</i> , 2011, , 1306-1310.	0.3	0
47	iRsp1095: A genome-scale reconstruction of the <i>Rhodobacter sphaeroides</i> metabolic network. <i>BMC Systems Biology</i> , 2011, 5, 116.	3.0	68
48	The evolution of metabolic networks of <i>E. coli</i> . <i>BMC Systems Biology</i> , 2011, 5, 182.	3.0	60
49	A community effort towards a knowledge-base and mathematical model of the human pathogen <i>Salmonella Typhimurium</i> LT2. <i>BMC Systems Biology</i> , 2011, 5, 8.	3.0	128
50	Synergy between ¹³ C-metabolic flux analysis and flux balance analysis for understanding metabolic adaption to anaerobiosis in <i>E. coli</i> . <i>Metabolic Engineering</i> , 2011, 13, 38-48.	3.6	143
51	Pyruvate and Lactate Metabolism by <i>Shewanella oneidensis</i> MR-1 under Fermentation, Oxygen Limitation, and Fumarate Respiration Conditions. <i>Applied and Environmental Microbiology</i> , 2011, 77, 8234-8240.	1.4	126
52	Large-Scale Bi-Level Strain Design Approaches and Mixed-Integer Programming Solution Techniques. <i>PLoS ONE</i> , 2011, 6, e24162.	1.1	77
53	OptORF: Optimal metabolic and regulatory perturbations for metabolic engineering of microbial strains. <i>BMC Systems Biology</i> , 2010, 4, 53.	3.0	188
54	Transcriptional patterns in both host and bacterium underlie a daily rhythm of anatomical and metabolic change in a beneficial symbiosis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 2259-2264.	3.3	149

#	ARTICLE	IF	CITATIONS
55	Constraint-Based Model of <i>Shewanella oneidensis</i> MR-1 Metabolism: A Tool for Data Analysis and Hypothesis Generation. <i>PLoS Computational Biology</i> , 2010, 6, e1000822.	1.5	124
56	An Automated Phenotype-Driven Approach (GeneForce) for Refining Metabolic and Regulatory Models. <i>PLoS Computational Biology</i> , 2010, 6, e1000970.	1.5	43
57	Computational Approaches in Metabolic Engineering. <i>Journal of Biomedicine and Biotechnology</i> , 2010, 2010, 1-7.	3.0	19
58	Descriptive and predictive applications of constraint-based metabolic models. , 2009, 2009, 5460-3.		1
59	Reconstruction of biochemical networks in microorganisms. <i>Nature Reviews Microbiology</i> , 2009, 7, 129-143.	13.6	797
60	Towards environmental systems biology of <i>Shewanella</i> . <i>Nature Reviews Microbiology</i> , 2008, 6, 592-603.	13.6	829
61	Metabolic Reconstruction and Modeling of Nitrogen Fixation in <i>Rhizobium etli</i> . <i>PLoS Computational Biology</i> , 2007, 3, e192.	1.5	85
62	A genome-scale metabolic reconstruction for <i>Escherichia coli</i> K12 MG1655 that accounts for 1260 ORFs and thermodynamic information. <i>Molecular Systems Biology</i> , 2007, 3, 121.	3.2	1,234
63	Towards multidimensional genome annotation. <i>Nature Reviews Genetics</i> , 2006, 7, 130-141.	7.7	321
64	Systems approach to refining genome annotation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 17480-17484.	3.3	262
65	Experimental and Computational Assessment of Conditionally Essential Genes in <i>Escherichia coli</i> . <i>Journal of Bacteriology</i> , 2006, 188, 8259-8271.	1.0	237
66	The global transcriptional regulatory network for metabolism in <i>Escherichia coli</i> exhibits few dominant functional states. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 19103-19108.	3.3	90
67	Genome-Scale In Silico Models of <i>E. coli</i> Have Multiple Equivalent Phenotypic States: Assessment of Correlated Reaction Subsets That Comprise Network States. <i>Genome Research</i> , 2004, 14, 1797-1805.	2.4	181
68	Integrating high-throughput and computational data elucidates bacterial networks. <i>Nature</i> , 2004, 429, 92-96.	13.7	796
69	Hierarchical thinking in network biology: the unbiased modularization of biochemical networks. <i>Trends in Biochemical Sciences</i> , 2004, 29, 641-647.	3.7	189
70	Genome-scale models of microbial cells: evaluating the consequences of constraints. <i>Nature Reviews Microbiology</i> , 2004, 2, 886-897.	13.6	935
71	Network-based analysis of metabolic regulation in the human red blood cell. <i>Journal of Theoretical Biology</i> , 2003, 225, 185-194.	0.8	64
72	Thirteen Years of Building Constraint-Based In Silico Models of <i>Escherichia coli</i> . <i>Journal of Bacteriology</i> , 2003, 185, 2692-2699.	1.0	280

#	ARTICLE	IF	CITATIONS
73	Analysis of Metabolic Capabilities Using Singular Value Decomposition of Extreme Pathway Matrices. Biophysical Journal, 2003, 84, 794-804.	0.2	73
74	An expanded genome-scale model of Escherichia coli K-12 (ijR904 GSM/GPR). Genome Biology, 2003, 4, R54.	13.9	880
75	Amyloid Fibril Formation by A β 16-22, a Seven-Residue Fragment of the Alzheimer's β -Amyloid Peptide, and Structural Characterization by Solid State NMR. Biochemistry, 2000, 39, 13748-13759.	1.2	683
76	Multiple quantum solid-state NMR indicates a parallel, not antiparallel, organization of beta -sheets in Alzheimer's beta -amyloid fibrils. Proceedings of the National Academy of Sciences of the United States of America, 2000, 97, 13045-13050.	3.3	387