Jennifer L Reed

List of Publications by Year
in descending order

76 papers	11,072 citations	71102 41 h-index	82547 72 g-index
79 all docs	79 docs citations	79 times ranked	9079 citing authors

#	Article	IF	Citations
1	A genomeâ€scale metabolic reconstruction for Escherichia coli Kâ€12 MG1655 that accounts for 1260 ORFs and thermodynamic information. Molecular Systems Biology, 2007, 3, 121.	7.2	1,234
2	Genome-scale models of microbial cells: evaluating the consequences of constraints. Nature Reviews Microbiology, 2004, 2, 886-897.	28.6	935
3	An expanded genome-scale model of Escherichia coli K-12 (iJR904 GSM/GPR). Genome Biology, 2003, 4, R54.	9.6	880
4	Towards environmental systems biology of Shewanella. Nature Reviews Microbiology, 2008, 6, 592-603.	28.6	829
5	Reconstruction of biochemical networks in microorganisms. Nature Reviews Microbiology, 2009, 7, 129-143.	28.6	797
6	Integrating high-throughput and computational data elucidates bacterial networks. Nature, 2004, 429, 92-96.	27.8	796
7	Amyloid Fibril Formation by Aî²16-22, a Seven-Residue Fragment of the Alzheimer's Î²-Amyloid Peptide, and Structural Characterization by Solid State NMRâ€. Biochemistry, 2000, 39, 13748-13759.	2.5	683
8	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.	7.1	387
9	Towards multidimensional genome annotation. Nature Reviews Genetics, 2006, 7, 130-141.	16.3	321
10	Thirteen Years of Building Constraint-Based In Silico Models of Escherichia coli. Journal of Bacteriology, 2003, 185, 2692-2699.	2.2	280
11	Systems approach to refining genome annotation. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 17480-17484.	7.1	262
12	Experimental and Computational Assessment of Conditionally Essential Genes in<i>Escherichia coli</i>. Journal of Bacteriology, 2006, 188, 8259-8271.	2.2	237
13	Hierarchical thinking in network biology: the unbiased modularization of biochemical networks. Trends in Biochemical Sciences, 2004, 29, 641-647.	7.5	189
14	OptORF: Optimal metabolic and regulatory perturbations for metabolic engineering of microbial strains. BMC Systems Biology, 2010, 4, 53.	3.0	188
15	Genome-Scale In Silico Models of E. coli Have Multiple Equivalent Phenotypic States: Assessment of Correlated Reaction Subsets That Comprise Network States. Genome Research, 2004, 14, 1797-1805.	5.5	181
16	Transcriptional patterns in both host and bacterium underlie a daily rhythm of anatomical and metabolic change in a beneficial symbiosis. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 2259-2264.	7.1	149
17	Synergy between 13C-metabolic flux analysis and flux balance analysis for understanding metabolic adaption to anaerobiosis in E. coli. Metabolic Engineering, 2011, 13, 38-48.	7.0	143
18	A community effort towards a knowledge-base and mathematical model of the human pathogen Salmonella Typhimurium LT2. BMC Systems Biology, 2011, 5, 8.	3.0	128

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19	Pyruvate and Lactate Metabolism by Shewanella oneidensis MR-1 under Fermentation, Oxygen Limitation, and Fumarate Respiration Conditions. Applied and Environmental Microbiology, 2011, 77, 8234-8240.	3.1	126
20	Constraint-Based Model of Shewanella oneidensis MR-1 Metabolism: A Tool for Data Analysis and Hypothesis Generation. PLoS Computational Biology, 2010, 6, e1000822.	3.2	124
21	Computational methods in metabolic engineering for strain design. Current Opinion in Biotechnology, 2015, 34, 135-141.	6.6	121
22	The global transcriptional regulatory network for metabolism in Escherichia coli exhibits few dominant functional states. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 19103-19108.	7.1	90
23	Multi-platform â€™Omics Analysis of Human Ebola Virus Disease Pathogenesis. Cell Host and Microbe, 2017, 22, 817-829.e8.	11.0	88
24	Metabolic Reconstruction and Modeling of Nitrogen Fixation in Rhizobium etli. PLoS Computational Biology, 2007, 3, e192.	3.2	85
25	Shrinking the Metabolic Solution Space Using Experimental Datasets. PLoS Computational Biology, 2012, 8, e1002662.	3.2	81
26	Genome-Scale Modeling of Light-Driven Reductant Partitioning and Carbon Fluxes in Diazotrophic Unicellular Cyanobacterium Cyanothece sp. ATCC 51142. PLoS Computational Biology, 2012, 8, e1002460.	3.2	78
27	RELATCH: relative optimality in metabolic networks explains robust metabolic and regulatory responses to perturbations. Genome Biology, 2012, 13, R78.	9.6	78
28	Large-Scale Bi-Level Strain Design Approaches and Mixed-Integer Programming Solution Techniques. PLoS ONE, 2011, 6, e24162.	2.5	77
29	Directed Evolution Reveals Unexpected Epistatic Interactions That Alter Metabolic Regulation and Enable Anaerobic Xylose Use by Saccharomyces cerevisiae. PLoS Genetics, 2016, 12, e1006372.	3.5	75
30	Analysis of Metabolic Capabilities Using Singular Value Decomposition of Extreme Pathway Matrices. Biophysical Journal, 2003, 84, 794-804.	0.5	73
31	Software platforms to facilitate reconstructing genomeâ€scale metabolic networks. Environmental Microbiology, 2014, 16, 49-59.	3.8	69
32	iRsp1095: A genome-scale reconstruction of the Rhodobacter sphaeroides metabolic network. BMC Systems Biology, 2011, 5, 116.	3.0	68
33	Do genomeâ€scale models need exact solvers or clearer standards?. Molecular Systems Biology, 2015, 11, 831.	7.2	68
34	Network-based analysis of metabolic regulation in the human red blood cell. Journal of Theoretical Biology, 2003, 225, 185-194.	1.7	64
35	The evolution of metabolic networks of E. coli. BMC Systems Biology, 2011, 5, 182.	3.0	60
36	Computational evaluation of <i>Synechococcus</i> sp. PCC 7002 metabolism for chemical production. Biotechnology Journal, 2013, 8, 619-630.	3.5	58

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37	Complex Physiology and Compound Stress Responses during Fermentation of Alkali-Pretreated Corn Stover Hydrolysate by an Escherichia coli Ethanologen. Applied and Environmental Microbiology, 2012, 78, 3442-3457.	3.1	57
38	Integrating proteomic or transcriptomic data into metabolic models using linear bound flux balance analysis. Bioinformatics, 2018, 34, 3882-3888.	4.1	55
39	Quantitative Assessment of Thermodynamic Constraints on the Solution Space of Genome-Scale Metabolic Models. Biophysical Journal, 2013, 105, 512-522.	0.5	51
40	Advances in gap-filling genome-scale metabolic models and model-driven experiments lead to novel metabolic discoveries. Current Opinion in Biotechnology, 2018, 51, 103-108.	6.6	51
41	2H and 13C metabolic flux analysis elucidates in vivo thermodynamics of the ED pathway in Zymomonas mobilis. Metabolic Engineering, 2019, 54, 301-316.	7.0	51
42	Metabolic assessment of E. coli as a Biofactory for commercial products. Metabolic Engineering, 2016, 35, 64-74.	7.0	48
43	Adaptive Evolution of Synthetic Cooperating Communities Improves Growth Performance. PLoS ONE, 2014, 9, e108297.	2.5	47
44	An Automated Phenotype-Driven Approach (GeneForce) for Refining Metabolic and Regulatory Models. PLoS Computational Biology, 2010, 6, e1000970.	3.2	43
45	Light-optimized growth of cyanobacterial cultures: Growth phases and productivity of biomass and secreted molecules in light-limited batch growth. Metabolic Engineering, 2018, 47, 230-242.	7.0	43
46	Identification of Functional Differences in Metabolic Networks Using Comparative Genomics and Constraint-Based Models. PLoS ONE, 2012, 7, e34670.	2.5	41
47	Comparisons of Shewanella strains based on genome annotations, modeling, and experiments. BMC Systems Biology, 2014, 8, 31.	3.0	40
48	Mechanistic analysis of multi-omics datasets to generate kinetic parameters for constraint-based metabolic models. BMC Bioinformatics, 2013, 14, 32.	2.6	37
49	Constraintâ€based strain design using continuous modifications (CosMos) of flux bounds finds new strategies for metabolic engineering. Biotechnology Journal, 2013, 8, 595-604.	3.5	35
50	Genome â€"Scale Reconstruction of Metabolic Networks of Lactobacillus casei ATCC 334 and 12A. PLoS ONE, 2014, 9, e110785.	2.5	32
51	Flux balance analysis indicates that methane is the lowest cost feedstock for microbial cell factories. Metabolic Engineering Communications, 2017, 5, 26-33.	3.6	31
52	Predicting outcomes of steady-state 13C isotope tracing experiments using Monte Carlo sampling. BMC Systems Biology, 2012, 6, 9.	3.0	30
53	Thermodynamics and H2 Transfer in a Methanogenic, Syntrophic Community. PLoS Computational Biology, 2015, 11, e1004364.	3.2	25
54	Transcriptional characterization of <i>Vibrio fischeri</i> during colonization of juvenile <i>Euprymna scolopes</i>. Environmental Microbiology, 2017, 19, 1845-1856.	3.8	24

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55	Refining metabolic models and accounting for regulatory effects. Current Opinion in Biotechnology, 2014, 29, 34-38.	6.6	23
56	A framework for the identification of promising bioâ€based chemicals. Biotechnology and Bioengineering, 2018, 115, 2328-2340.	3.3	22
57	MapMaker and PathTracer for tracking carbon in genomeâ€scale metabolic models. Biotechnology Journal, 2016, 11, 648-661.	3.5	21
58	Computational Approaches in Metabolic Engineering. Journal of Biomedicine and Biotechnology, 2010, 2010, 1-7.	3.0	19
59	FOCAL: an experimental design tool for systematizing metabolic discoveries and model development. Genome Biology, 2012, 13, R116.	9.6	17
60	Active and machine learning-based approaches to rapidly enhance microbial chemical production. Metabolic Engineering, 2021, 67, 216-226.	7.0	15
61	Introduction of NADH-dependent nitrate assimilation in Synechococcus sp. PCC 7002 improves photosynthetic production of 2-methyl-1-butanol and isobutanol. Metabolic Engineering, 2022, 69, 87-97.	7.0	14
62	Model-driven analysis of mutant fitness experiments improves genome-scale metabolic models of Zymomonas mobilis ZM4. PLoS Computational Biology, 2020, 16, e1008137.	3.2	12
63	Inferring ancient metabolism using ancestral core metabolic models of enterobacteria. BMC Systems Biology, 2013, 7, 46.	3.0	11
64	Escherichia coli as a model organism for systems metabolic engineering. Current Opinion in Systems Biology, 2017, 6, 80-88.	2.6	11
65	Expanding metabolic engineering algorithms using feasible space and shadow price constraint modules. Metabolic Engineering Communications, 2014, 1, 1-11.	3.6	9
66	Improving flux predictions by integrating data from multiple strains. Bioinformatics, 2017, 33, 893-900.	4.1	9
67	Systems Metabolic Engineering of <i>Escherichia coli</i> Improves Coconversion of Lignocelluloseâ€Derived Sugars. Biotechnology Journal, 2019, 14, e1800441.	3.5	9
68	Model-enabled gene search (MEGS) allows fast and direct discovery of enzymatic and transport gene functions in the marine bacterium Vibrio fischeri. Journal of Biological Chemistry, 2017, 292, 10250-10261.	3.4	7
69	BioMog: A Computational Framework for the De Novo Generation or Modification of Essential Biomass Components. PLoS ONE, 2013, 8, e81322.	2.5	7
70	Evaluating the capabilities of microbial chemical production using genome-scale metabolic models. Current Opinion in Systems Biology, 2017, 2, 91-97.	2.6	6
71	Genome-Wide Analysis of RNA Decay in the Cyanobacterium <i>Synechococcus</i> sp. Strain PCC 7002. MSystems, 2020, 5, .	3.8	6
72	Descriptive and predictive applications of constraint-based metabolic models. , 2009, 2009, 5460-3.		1

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73	Applications of Constraint-Based Models for Biochemical Production. , 2016, , 201-226.		1
74	Microbial Strain Design for Biochemical Production Using Mixed-integer Programming Techniques. Computer Aided Chemical Engineering, 2011, , 1306-1310.	0.5	0
75	Phenomics. , 2014, , 280-287.		0
76	Cover Image, Volume 115, Number 9, September 2018. Biotechnology and Bioengineering, 2018, 115, i.	3.3	0