Radhakrishnan Mahadevan

List of Publications by Year
in descending order

132 papers	8,054 citations	57758 44 h-index	54911 84 g-index
152 all docs	152 docs citations	152 times ranked	7576 citing authors

#	Article	IF	Citations
1	The effects of alternate optimal solutions in constraint-based genome-scale metabolic models. Metabolic Engineering, 2003, 5, 264-276.	7.0	1,083
2	Dynamic Flux Balance Analysis of Diauxic Growth in Escherichia coli. Biophysical Journal, 2002, 83, 1331-1340.	0.5	806
3	Genome-scale Reconstruction of Metabolic Network in Bacillus subtilis Based on High-throughput Phenotyping and Gene Essentiality Data. Journal of Biological Chemistry, 2007, 282, 28791-28799.	3.4	387
4	MEMOTE for standardized genome-scale metabolic model testing. Nature Biotechnology, 2020, 38, 272-276.	17.5	314
5	Characterization of Metabolism in the Fe(III)-Reducing Organism Geobacter sulfurreducens by Constraint-Based Modeling. Applied and Environmental Microbiology, 2006, 72, 1558-1568.	3.1	290
6	Genome-scale dynamic modeling of the competition between <i>Rhodoferax</i> and <i>Geobacter</i> in anoxic subsurface environments. ISME Journal, 2011, 5, 305-316.	9.8	275
7	Heavy Metal Removal by Bioaccumulation Using Genetically Engineered Microorganisms. Frontiers in Bioengineering and Biotechnology, 2018, 6, 157.	4.1	203
8	Engineering metabolism through dynamic control. Current Opinion in Biotechnology, 2015, 34, 142-152.	6.6	176
9	Economics of membrane occupancy and respiroâ€fermentation. Molecular Systems Biology, 2011, 7, 500.	7.2	162
10	Reconstructing metabolic flux vectors from extreme pathways: defining the Î±-spectrum. Journal of Theoretical Biology, 2003, 224, 313-324.	1.7	148
11	In situ to in silico and back: elucidating the physiology and ecology of Geobacter spp. using genome-scale modelling. Nature Reviews Microbiology, 2011, 9, 39-50.	28.6	128
12	Synthetic biosystems for the production of high-value plant metabolites. Trends in Biotechnology, 2012, 30, 127-131.	9.3	128
13	Dynamic metabolic engineering for increasing bioprocess productivity. Metabolic Engineering, 2008, 10, 255-266.	7.0	126
14	Comparative genomics of the white-rot fungi, Phanerochaete carnosa and P. chrysosporium, to elucidate the genetic basis of the distinct wood types they colonize. BMC Genomics, 2012, 13, 444.	2.8	125
15	Genome-scale analysis ofSaccharomyces cerevisiae metabolism and ethanol production in fed-batch culture. Biotechnology and Bioengineering, 2007, 97, 1190-1204.	3.3	120
16	Genomeâ€scale metabolic modeling of a clostridial coâ€culture for consolidated bioprocessing. Biotechnology Journal, 2010, 5, 726-738.	3.5	115
17	A three-dimensional engineered tumour for spatial snapshot analysis of cell metabolism andÂphenotype in hypoxic gradients. Nature Materials, 2016, 15, 227-234.	27.5	113
18	EMILiO: A fast algorithm for genome-scale strain design. Metabolic Engineering, 2011, 13, 272-281.	7.0	112

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19	Geobacter sulfurreducens strain engineered for increased rates of respiration. Metabolic Engineering, 2008, 10, 267-275.	7.0	102
20	Metabolic engineering of a tyrosine-overproducing yeast platform using targeted metabolomics. Microbial Cell Factories, 2015, 14, 73.	4.0	98
21	Coupling a genome‐scale metabolic model with a reactive transport model to describe *in situ* uranium bioremediation. Microbial Biotechnology, 2009, 2, 274-286.	4.2	92
22	Using metabolic flux data to further constrain the metabolic solution space and predict internal flux patterns: theEscherichia coli spectrum. Biotechnology and Bioengineering, 2004, 86, 317-331.	3.3	85
23	Properties of Metabolic Networks: Structure versus Function. Biophysical Journal, 2005, 88, L07-L09.	0.5	83
24	On the feasibility of growth-coupled product synthesis in microbial strains. Metabolic Engineering, 2015, 30, 166-178.	7.0	83
25	k-Cone Analysis: Determining All Candidate Values for Kinetic Parameters on a Network Scale. Biophysical Journal, 2005, 88, 1616-1625.	0.5	79
26	Alkene hydrogenation activity of enoate reductases for an environmentally benign biosynthesis of adipic acid. Chemical Science, 2017, 8, 1406-1413.	7.4	77
27	Genome-scale comparison and constraint-based metabolic reconstruction of the facultative anaerobic Fe(III)-reducer Rhodoferax ferrireducens. BMC Genomics, 2009, 10, 447.	2.8	76
28	Exploring Bacterial Carboxylate Reductases for the Reduction of Bifunctional Carboxylic Acids. Biotechnology Journal, 2017, 12, 1600751.	3.5	74
29	Estimating optimal profiles of genetic alterations using constraint-based models. Biotechnology and Bioengineering, 2005, 89, 243-251.	3.3	72
30	Computational and Experimental Analysis of Redundancy in the Central Metabolism of Geobacter sulfurreducens. PLoS Computational Biology, 2008, 4, e36.	3.2	72
31	Constructing kinetic models of metabolism at genome‐scales: A review. Biotechnology Journal, 2015, 10, 1345-1359.	3.5	72
32	Biocatalytic production of adipic acid from glucose using engineered Saccharomyces cerevisiae. Metabolic Engineering Communications, 2018, 6, 28-32.	3.6	70
33	Do genome‐scale models need exact solvers or clearer standards?. Molecular Systems Biology, 2015, 11, 831.	7.2	68
34	Genome-scale constraint-based modeling of Geobacter metallireducens. BMC Systems Biology, 2009, 3, 15.	3.0	65
35	The design of long‐term effective uranium bioremediation strategy using a community metabolic model. Biotechnology and Bioengineering, 2012, 109, 2475-2483.	3.3	65
36	The Degree of Redundancy in Metabolic Genes Is Linked to Mode of Metabolism. Biophysical Journal, 2008, 94, 1216-1220.	0.5	63

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37	From elementary flux modes to elementary flux vectors: Metabolic pathway analysis with arbitrary linear flux constraints. PLoS Computational Biology, 2017, 13, e1005409.	3.2	60
38	Analysis and Design of a Genetic Circuit for Dynamic Metabolic Engineering. ACS Synthetic Biology, 2013, 2, 442-452.	3.8	59
39	Differential flatness based nonlinear predictive control of fed-batch bioreactors. Control Engineering Practice, 2001, 9, 889-899.	5.5	56
40	When Do Two–Stage Processes Outperform One–Stage Processes?. Biotechnology Journal, 2018, 13, 1700539.	3.5	52
41	Novel approach to engineer strains for simultaneous sugar utilization. Metabolic Engineering, 2013, 20, 63-72.	7.0	50
42	Dynamic strain scanning optimization: an efficient strain design strategy for balanced yield, titer, and productivity. DySScO strategy for strain design. BMC Biotechnology, 2013, 13, 8.	3.3	50
43	Engineering a short, aldolase-based pathway for (R)-1,3-butanediol production in Escherichia coli. Metabolic Engineering, 2018, 48, 13-24.	7.0	49
44	Redesigning metabolism based on orthogonality principles. Nature Communications, 2017, 8, 15188.	12.8	47
45	Control-relevant scheduling of polymer grade transitions. AICHE Journal, 2002, 48, 1754-1764.	3.6	46
46	Characterizing the Metabolism of Dehalococcoides with a Constraint-Based Model. PLoS Computational Biology, 2010, 6, e1000887.	3.2	46
47	In silico characterization of microbial electrosynthesis for metabolic engineering of biochemicals. Microbial Cell Factories, 2011, 10, 76.	4.0	46
48	A defined co–culture of <i>Geobacter sulfurreducens</i> and <i>Escherichia coli</i> in a membrane–less microbial fuel cell. Biotechnology and Bioengineering, 2014, 111, 709-718.	3.3	45
49	Biosynthesis and Activity of Prenylated FMN Cofactors. Cell Chemical Biology, 2018, 25, 560-570.e6.	5.2	45
50	Direct coupling of a genome-scale microbial in silico model and a groundwater reactive transport model. Journal of Contaminant Hydrology, 2011, 122, 96-103.	3.3	44
51	Metabolic modeling of spatial heterogeneity of biofilms in microbial fuel cells reveals substrate limitations in electrical current generation. Biotechnology Journal, 2014, 9, 1350-1361.	3.5	44
52	Characterization of Proton Production and Consumption Associated with Microbial Metabolism. BMC Biotechnology, 2010, 10, 2.	3.3	41
53	Characterizing metabolic interactions in a clostridial co-culture for consolidated bioprocessing. BMC Biotechnology, 2013, 13, 95.	3.3	41
54	Systems biology based metabolic engineering for non-natural chemicals. Biotechnology Advances, 2019, 37, 107379.	11.7	38

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55	MoVE identifies metabolic valves to switch between phenotypic states. Nature Communications, 2018, 9, 5332.	12.8	37
56	Applications of metabolic modeling to drive bioprocess development for the production of value-added chemicals. Biotechnology and Bioprocess Engineering, 2005, 10, 408-417.	2.6	33
57	Investigating Moorella thermoacetica metabolism with a genome-scale constraint-based metabolic model. Integrative Biology (United Kingdom), 2015, 7, 869-882.	1.3	33
58	Integrative analysis of &lt;i&gt;Geobacter&lt;/i&gt; spp. and sulfate-reducing bacteria during uranium bioremediation. Biogeosciences, 2012, 9, 1033-1040.	3.3	31
59	Ensemble Modeling of Cancer Metabolism. Frontiers in Physiology, 2012, 3, 135.	2.8	30
60	An Optimized Bistable Metabolic Switch To Decouple Phenotypic States during Anaerobic Fermentation. ACS Synthetic Biology, 2018, 7, 2854-2866.	3.8	28
61	Pore-scale simulation of microbial growth using a genome-scale metabolic model: Implications for Darcy-scale reactive transport. Advances in Water Resources, 2013, 59, 256-270.	3.8	26
62	Genome-scale strain designs based on regulatory minimal cut sets. Bioinformatics, 2015, 31, 2844-2851.	4.1	26
63	GENOME-BASED MODELING AND DESIGN OF METABOLIC INTERACTIONS IN MICROBIAL COMMUNITIES. Computational and Structural Biotechnology Journal, 2012, 3, e201210008.	4.1	25
64	Characterizing Regulation of Metabolism in *Geobacter sulfurreducens* through Genome-Wide Expression Data and Sequence Analysis. OMICS A Journal of Integrative Biology, 2008, 12, 33-59.	2.0	24
65	Novel Aldo-Keto Reductases for the Biocatalytic Conversion of 3-Hydroxybutanal to 1,3-Butanediol: Structural and Biochemical Studies. Applied and Environmental Microbiology, 2017, 83, .	3.1	24
66	Inactivation of the transcription factor *mig1* (*YGL035C*) in *Saccharomyces cerevisiae* improves tolerance towards monocarboxylic weak acids: acetic, formic and levulinic acid. Journal of Industrial Microbiology and Biotechnology, 2018, 45, 735-751.	3.0	23
67	Chemical and Synthetic Genetic Array Analysis Identifies Genes that Suppress Xylose Utilization and Fermentation in *Saccharomyces cerevisiae*. G3: Genes, Genomes, Genetics, 2011, 1, 247-258.	1.8	22
68	On-Line Optimization of Recombinant Product in a Fed-Batch Bioreactor. Biotechnology Progress, 2003, 19, 639-646.	2.6	21
69	Refined experimental annotation reveals conserved corrinoid autotrophy in chloroform-respiring *Dehalobacter* isolates. ISME Journal, 2017, 11, 626-640.	9.8	21
70	Characterizing metabolic pathway diversification in the context of perturbation size. Metabolic Engineering, 2015, 28, 114-122.	7.0	20
71	Model‐based analysis of the role of biological, hydrological and geochemical factors affecting uranium bioremediation. Biotechnology and Bioengineering, 2011, 108, 1537-1548.	3.3	19
72	Engineering Photosynthetic Bioprocesses for Sustainable Chemical Production: A Review. Frontiers in Bioengineering and Biotechnology, 2020, 8, 610723.	4.1	19

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73	Systems Biology: The synergistic interplay between biology and mathematics. Canadian Journal of Chemical Engineering, 2008, 86, 127-141.	1.7	18
74	Novel two-stage processes for optimal chemical production in microbes. Metabolic Engineering, 2020, 62, 186-197.	7.0	18
75	Engineering Escherichia coli for the utilization of ethylene glycol. Microbial Cell Factories, 2021, 20, 22.	4.0	18
76	Genetic engineering of extremely acidophilic Acidithiobacillus species for biomining: Progress and perspectives. Journal of Hazardous Materials, 2022, 438, 129456.	12.4	17
77	Modeling and sensitivity analysis of electron capacitance for Geobacter in sedimentary environments. Journal of Contaminant Hydrology, 2010, 112, 30-44.	3.3	16
78	Structure and activity of the NAD(P)$^+$â€dependent succinate semialdehyde dehydrogenase YneI from *Salmonella typhimurium*. Proteins: Structure, Function and Bioinformatics, 2013, 81, 1031-1041.	2.6	16
79	A Multi-Scale Model of the Whole Human Body based on Dynamic Parsimonious Flux Balance Analysis. IFAC-PapersOnLine, 2016, 49, 937-942.	0.9	16
80	Rational engineering of 2-deoxyribose-5-phosphate aldolases for the biosynthesis of (R)-1,3-butanediol. Journal of Biological Chemistry, 2020, 295, 597-609.	3.4	16
81	Optimal genetic manipulations in batch bioreactor control. Automatica, 2006, 42, 1723-1733.	5.0	15
82	A bilevel optimization algorithm to identify enzymatic capacity constraints in metabolic networks. Computers and Chemical Engineering, 2008, 32, 2072-2085.	3.8	15
83	An interspecies malateâ€"pyruvate shuttle reconciles redox imbalance in an anaerobic microbial community. ISME Journal, 2019, 13, 1042-1055.	9.8	15
84	Genomic Analysis of a Newly Isolated Acidithiobacillus ferridurans JAGS Strain Reveals Its Adaptation to Acid Mine Drainage. Minerals (Basel, Switzerland), 2021, 11, 74.	2.0	15
85	New Insights into Dehalococcoides mccartyi Metabolism from a Reconstructed Metabolic Network-Based Systems-Level Analysis of D. mccartyi Transcriptomes. PLoS ONE, 2014, 9, e94808.	2.5	14
86	Synthetic rescue couples NADPH generation to metabolite overproduction in Saccharomyces cerevisiae. Metabolic Engineering, 2017, 43, 64-70.	7.0	14
87	Thermodynamic analysis of regulation in metabolic networks using constraint-based modeling. BMC Research Notes, 2010, 3, 125.	1.4	13
88	Design principles for generating robust gene expression patterns in dynamic engineered tissues. Integrative Biology (United Kingdom), 2013, 5, 578-589.	1.3	12
89	Dynamic Cell Programming with Quorum Sensing-Controlled CRISPRi Circuit. ACS Synthetic Biology, 2020, 9, 1284-1291.	3.8	12
90	Macrophage Immunomodulation Through New Polymers that Recapitulate Functional Effects of Itaconate as a Power House of Innate Immunity. Advanced Functional Materials, 2021, 31, 2003341.	14.9	12

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91	SARS-CoV-2 receptor-binding mutations and antibody contact sites. Antibody Therapeutics, 2021, 4, 149-158.	1.9	12
92	Leaching characteristics of nickeliferous pyrrhotite tailings from the Sudbury, Ontario area. Canadian Metallurgical Quarterly, 2017, 56, 372-381.	1.2	11
93	Overcoming Challenges in Expressing Iron–Sulfur Enzymes in Yeast. Trends in Biotechnology, 2021, 39, 665-677.	9.3	11
94	Systematizing the different notions of growth–coupled product synthesis and a single framework for computing corresponding strain designs. Biotechnology Journal, 2021, 16, e2100236.	3.5	10
95	Multiscale Metabolic Modeling Approach for Predicting Blood Alcohol Concentration. IEEE Life Sciences Letters, 2016, 2, 59-62.	1.2	9
96	AYbRAH: a curated ortholog database for yeasts and fungi spanning 600 million years of evolution. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	3.0	9
97	Pan–Genome–Scale Network Reconstruction: Harnessing Phylogenomics Increases the Quantity and Quality of Metabolic Models. Biotechnology Journal, 2020, 15, e1900519.	3.5	9
98	Toward a systematic design of smart probiotics. Current Opinion in Biotechnology, 2020, 64, 199-209.	6.6	9
99	Integration of a physiologically-based pharmacokinetic model with a whole-body, organ-resolved genome-scale model for characterization of ethanol and acetaldehyde metabolism. PLoS Computational Biology, 2021, 17, e1009110.	3.2	9
100	A multi-scale model for low-density lipoprotein cholesterol (LDL-C) regulation in the human body: Application to quantitative systems pharmacology. Computers and Chemical Engineering, 2019, 130, 106507.	3.8	8
101	Speeding up the core algorithm for the dual calculation of minimal cut sets in large metabolic networks. BMC Bioinformatics, 2020, 21, 510.	2.6	8
102	A microplate screen to estimate metal-binding affinities of metalloproteins. Analytical Biochemistry, 2020, 609, 113836.	2.4	8
103	A novel C-terminal degron identified in bacterial aldehyde decarbonylases using directed evolution. Biotechnology for Biofuels, 2020, 13, 114.	6.2	8
104	Advancing undergraduate synthetic biology education: insights from a Canadian iGEM student perspective. Canadian Journal of Microbiology, 2021, 67, 749-770.	1.7	7
105	Model-driven design of a Saccharomyces cerevisiae platform strain with improved tyrosine production capabilities. IFAC Postprint Volumes IPPV / International Federation of Automatic Control, 2013, 46, 221-226.	0.4	6
106	Model-based design of bistable cell factories for metabolic engineering. Bioinformatics, 2018, 34, 1363-1371.	4.1	5
107	Impact framework: A python package for writing data analysis workflows to interpret microbial physiology. Metabolic Engineering Communications, 2019, 9, e00089.	3.6	5
108	Engineering *Escherichia coli* for D-Ribose Production from Glucose-Xylose Mixtures. Industrial Biotechnology, 2014, 10, 106-114.	0.8	4

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109	Sub-optimal phenotypes of double-knockout mutants of Escherichia coli depend on the order of gene deletions. Integrative Biology (United Kingdom), 2015, 7, 930-939.	1.3	4
110	A scalable method for parameter identification in kinetic models of metabolism using steady-state data. Bioinformatics, 2019, 35, 5216-5225.	4.1	4
111	Complete Genome Sequence of Acidithiobacillus ferridurans JAGS, Isolated from Acidic Mine Drainage. Microbiology Resource Announcements, 2020, 9, .	0.6	4
112	Automation assisted anaerobic phenotyping for metabolic engineering. Microbial Cell Factories, 2021, 20, 184.	4.0	4
113	A gap-filling algorithm for prediction of metabolic interactions in microbial communities. PLoS Computational Biology, 2021, 17, e1009060.	3.2	4
114	Prediction of Weak Acid Toxicity inSaccharomyces cerevisiaeUsing Genome-Scale Metabolic Models. Industrial Biotechnology, 2013, 9, 229-235.	0.8	3
115	Metabolically engineered recombinant Saccharomyces cerevisiae for the production of 2-Deoxy-scyllo-inosose (2-DOI). Metabolic Engineering Communications, 2020, 11, e00134.	3.6	3
116	Could open science stimulate industry partnerships in <scp>chemical engineering</scp> university research?. Canadian Journal of Chemical Engineering, 2021, 99, 2186-2194.	1.7	3
117	Metabolic Modeling of Spatial Heterogeneity of Biofilms in Microbial Fuel Cells. IFAC Postprint Volumes IPPV / International Federation of Automatic Control, 2010, 43, 215-220.	0.4	2
118	â€˜Omicsâ€™ technologies and systems biology for engineeringSaccharomyces cerevisiaestrains for lignocellulosic bioethanol production. Biofuels, 2011, 2, 659-675.	2.4	2
119	Metabolic Model Refinement Using Phenotypic Microarray Data. Methods in Molecular Biology, 2013, 985, 47-59.	0.9	2
120	Opportunities and Challenges for Microbial Synthesis of Fatty Acid-Derived Chemicals (FACs). Frontiers in Bioengineering and Biotechnology, 2021, 9, 613322.	4.1	2
121	Rapid design of system-wide metabolic network modifications using iterative linear programming. IFAC Postprint Volumes IPPV / International Federation of Automatic Control, 2010, 43, 391-396.	0.4	1
122	Experimental validation of in silico modelâ€predicted isocitrate dehydrogenase and phosphomannose isomerase from D ehalococcoides mccartyi. Microbial Biotechnology, 2016, 9, 47-60.	4.2	1
123	Efficient Biochemical Pathway Prediction Using Simulated Annealing. IFAC-PapersOnLine, 2018, 51, 56-57.	0.9	1
124	Physiologically-based pharmacokinetic model for predicting blood and tissue tetrahydrocannabinol concentrations. Computers and Chemical Engineering, 2021, 154, 107461.	3.8	1
125	Model-driven design based on sensitivity analysis for a synthetic biology application. Computer Aided Chemical Engineering, 2011, 29, 1446-1450.	0.5	1
126	On the design principles of metabolic flux sensing. Biophysical Journal, 2022, 121, 237-247.	0.5	1

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127	Efficient Enumeration of Branched Novel Biochemical Pathways Using a Probabilistic Technique. Industrial & Engineering Chemistry Research, 0, , .	3.7	1
128	Genome Regions Involved in Multiple Regulatory Pathways Identified Using GSEL, A Genome-Wide Database of Regulatory Sequence Elements of Geobacter sulfurreducens. , 2008, , .		0
129	Protein-Level Control of Metabolism: Design Principles and Prospects from a Representative System. IFAC-PapersOnLine, 2016, 49, 165-170.	0.9	0
130	Evaluating the performance of a post-translational dynamic metabolic control system. IFAC-PapersOnLine, 2019, 52, 225-230.	0.9	0
131	A Personalized Multiscale Modeling Framework for Dose Selection in Precision Medicine. Industrial & Engineering Chemistry Research, 2020, 59, 9819-9829.	3.7	0
132	REVOLVER: A low-cost automated protein purifier based on parallel preparative gravity column workflows. HardwareX, 2022, 11, e00291.	2.2	0