

Kiran R Patil

List of Publications by Year in descending order

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Version: 2024-02-01

79
papers

9,455
citations

66234

42
h-index

62479

80
g-index

100
all docs

100
docs citations

100
times ranked

12071
citing authors

#	ARTICLE	IF	CITATIONS
1	Extensive impact of non-antibiotic drugs on human gut bacteria. <i>Nature</i> , 2018, 555, 623-628.	13.7	1,339
2	Metabolic dependencies drive species co-occurrence in diverse microbial communities. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 6449-6454.	3.3	588
3	Towards standards for human fecal sample processing in metagenomic studies. <i>Nature Biotechnology</i> , 2017, 35, 1069-1076.	9.4	581
4	Uncovering transcriptional regulation of metabolism by using metabolic network topology. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 2685-2689.	3.3	553
5	Fast automated reconstruction of genome-scale metabolic models for microbial species and communities. <i>Nucleic Acids Research</i> , 2018, 46, 7542-7553.	6.5	410
6	Evolutionary programming as a platform for in silico metabolic engineering. <i>BMC Bioinformatics</i> , 2005, 6, 308.	1.2	374
7	OptFlux: an open-source software platform for in silico metabolic engineering. <i>BMC Systems Biology</i> , 2010, 4, 45.	3.0	321
8	MEMOTE for standardized genome-scale metabolic model testing. <i>Nature Biotechnology</i> , 2020, 38, 272-276.	9.4	314
9	Yeast Creates a Niche for Symbiotic Lactic Acid Bacteria through Nitrogen Overflow. <i>Cell Systems</i> , 2017, 5, 345-357.e6.	2.9	247
10	The Metabolic Response of Heterotrophic Arabidopsis Cells to Oxidative Stress. <i>Plant Physiology</i> , 2007, 143, 312-325.	2.3	234
11	Finding Functional Differences Between Species in a Microbial Community: Case Studies in Wine Fermentation and Kefir Culture. <i>Frontiers in Microbiology</i> , 2019, 10, 1347.	1.5	229
12	Improved vanillin production in baker's yeast through in silico design. <i>Microbial Cell Factories</i> , 2010, 9, 84.	1.9	226
13	Metabolic interactions in microbial communities: untangling the Gordian knot. <i>Current Opinion in Microbiology</i> , 2015, 27, 37-44.	2.3	213
14	Enhancing sesquiterpene production in <i>Saccharomyces cerevisiae</i> through in silico driven metabolic engineering. <i>Metabolic Engineering</i> , 2009, 11, 328-334.	3.6	199
15	Nutritional preferences of human gut bacteria reveal their metabolic idiosyncrasies. <i>Nature Microbiology</i> , 2018, 3, 514-522.	5.9	196
16	Bioaccumulation of therapeutic drugs by human gut bacteria. <i>Nature</i> , 2021, 597, 533-538.	13.7	159
17	Unravelling the collateral damage of antibiotics on gut bacteria. <i>Nature</i> , 2021, 599, 120-124.	13.7	159
18	Use of genome-scale microbial models for metabolic engineering. <i>Current Opinion in Biotechnology</i> , 2004, 15, 64-69.	3.3	150

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19	Industrial Systems Biology of <i>Saccharomyces cerevisiae</i> Enables Novel Succinic Acid Cell Factory. PLoS ONE, 2013, 8, e54144.	1.1	142
20	Metabolic cooperation and spatiotemporal niche partitioning in a kefir microbial community. Nature Microbiology, 2021, 6, 196-208.	5.9	138
21	Integration of metabolome data with metabolic networks reveals reporter reactions. Molecular Systems Biology, 2006, 2, 50.	3.2	131
22	Polarization of microbial communities between competitive and cooperative metabolism. Nature Ecology and Evolution, 2021, 5, 195-203.	3.4	131
23	Metabolic shifts in residual breast cancer drive tumor recurrence. Journal of Clinical Investigation, 2017, 127, 2091-2105.	3.9	128
24	Architecture of transcriptional regulatory circuits is knitted over the topology of bio-molecular interaction networks. BMC Systems Biology, 2008, 2, 17.	3.0	121
25	Integration of Biomass Formulations of Genome-Scale Metabolic Models with Experimental Data Reveals Universally Essential Cofactors in Prokaryotes. Metabolic Engineering, 2017, 39, 200-208.	3.6	101
26	Reconstruction and analysis of genome-scale metabolic model of a photosynthetic bacterium. BMC Systems Biology, 2010, 4, 156.	3.0	100
27	BioMet Toolbox: genome-wide analysis of metabolism. Nucleic Acids Research, 2010, 38, W144-W149.	6.5	91
28	Natural computation meta-heuristics for the in silico optimization of microbial strains. BMC Bioinformatics, 2008, 9, 499.	1.2	90
29	Versatile Enzyme Expression and Characterization System for <i>Aspergillus nidulans</i> , with the <i>Penicillium brevicompactum</i> Polyketide Synthase Gene from the Mycophenolic Acid Gene Cluster as a Test Case. Applied and Environmental Microbiology, 2011, 77, 3044-3051.	1.4	86
30	Multimodal interactions of drugs, natural compounds and pollutants with the gut microbiota. Nature Reviews Microbiology, 2022, 20, 431-443.	13.6	77
31	The metabolic background is a global player in <i>Saccharomyces</i> gene expression epistasis. Nature Microbiology, 2016, 1, 15030.	5.9	76
32	Metabolic Network Topology Reveals Transcriptional Regulatory Signatures of Type 2 Diabetes. PLoS Computational Biology, 2010, 6, e1000729.	1.5	75
33	Antibiotics-induced monodominance of a novel gut bacterial order. Gut, 2019, 68, 1781-1790.	6.1	73
34	Single-cell transcriptomics identifies CD44 as a marker and regulator of endothelial to haematopoietic transition. Nature Communications, 2020, 11, 586.	5.8	69
35	Do genome-scale models need exact solvers or clearer standards?. Molecular Systems Biology, 2015, 11, 831.	3.2	68
36	Random sampling of elementary flux modes in large-scale metabolic networks. Bioinformatics, 2012, 28, i515-i521.	1.8	66

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37	Contribution of Network Connectivity in Determining the Relationship between Gene Expression and Metabolite Concentration Changes. <i>PLoS Computational Biology</i> , 2014, 10, e1003572.	1.5	64
38	Towards a mechanistic understanding of reciprocal drug-microbiome interactions. <i>Molecular Systems Biology</i> , 2021, 17, e10116.	3.2	64
39	Microbial communities form rich extracellular metabolomes that foster metabolic interactions and promote drug tolerance. <i>Nature Microbiology</i> , 2022, 7, 542-555.	5.9	58
40	Ecological modelling approaches for predicting emergent properties in microbial communities. <i>Nature Ecology and Evolution</i> , 2022, 6, 855-865.	3.4	54
41	Involvement of a Natural Fusion of a Cytochrome P450 and a Hydrolase in Mycophenolic Acid Biosynthesis. <i>Applied and Environmental Microbiology</i> , 2012, 78, 4908-4913.	1.4	53
42	Global Transcriptional and Physiological Responses of <i>Saccharomyces cerevisiae</i> to Ammonium, l-Alanine, or l-Glutamine Limitation. <i>Applied and Environmental Microbiology</i> , 2006, 72, 6194-6203.	1.4	52
43	Flux coupling and transcriptional regulation within the metabolic network of the photosynthetic bacterium <i>Synechocystis</i> sp. PCC6803. <i>Biotechnology Journal</i> , 2011, 6, 330-342.	1.8	51
44	Systems Biology Perspectives on Minimal and Simpler Cells. <i>Microbiology and Molecular Biology Reviews</i> , 2014, 78, 487-509.	2.9	51
45	metaGEM: reconstruction of genome scale metabolic models directly from metagenomes. <i>Nucleic Acids Research</i> , 2021, 49, e126-e126.	6.5	50
46	Laboratory evolution reveals regulatory and metabolic trade-offs of glycerol utilization in <i>Saccharomyces cerevisiae</i> . <i>Metabolic Engineering</i> , 2018, 47, 73-82.	3.6	47
47	A new class of IMP dehydrogenase with a role in self-resistance of mycophenolic acid producing fungi. <i>BMC Microbiology</i> , 2011, 11, 202.	1.3	44
48	Model microbial communities for ecosystems biology. <i>Current Opinion in Systems Biology</i> , 2017, 6, 51-57.	1.3	44
49	Overexpression of <i>O</i> -methyltransferase leads to improved vanillin production in baker's yeast only when complemented with model-guided network engineering. <i>Biotechnology and Bioengineering</i> , 2013, 110, 656-659.	1.7	42
50	<i>Saccharomyces cerevisiae</i> metabolism in ecological context. <i>FEMS Yeast Research</i> , 2016, 16, fow080.	1.1	37
51	Hap4 Is Not Essential for Activation of Respiration at Low Specific Growth Rates in <i>Saccharomyces cerevisiae</i> *. <i>Journal of Biological Chemistry</i> , 2006, 281, 12308-12314.	1.6	31
52	Impact of Stoichiometry Representation on Simulation of Genotype-Phenotype Relationships in Metabolic Networks. <i>PLoS Computational Biology</i> , 2012, 8, e1002758.	1.5	31
53	Prediction and identification of sequences coding for orphan enzymes using genomic and metagenomic neighbours. <i>Molecular Systems Biology</i> , 2012, 8, 581.	3.2	29
54	Yeast metabolic chassis designs for diverse biotechnological products. <i>Scientific Reports</i> , 2016, 6, 29694.	1.6	28

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55	Proteomic characterization of extracellular vesicles produced by several wine yeast species. <i>Microbial Biotechnology</i> , 2020, 13, 1581-1596.	2.0	26
56	Global transcriptional response of <i>Saccharomyces cerevisiae</i> to the deletion of SDH3. <i>BMC Systems Biology</i> , 2009, 3, 17.	3.0	23
57	Computational tools for modeling xenometabolism of the human gut microbiota. <i>Trends in Biotechnology</i> , 2014, 32, 157-165.	4.9	22
58	Adaptive laboratory evolution of microbial co-cultures for improved metabolite secretion. <i>Molecular Systems Biology</i> , 2021, 17, e10189.	3.2	21
59	High-throughput ultrastructure screening using electron microscopy and fluorescent barcoding. <i>Journal of Cell Biology</i> , 2019, 218, 2797-2811.	2.3	18
60	PHUSER (Primer Help for USER): a novel tool for USER fusion primer design. <i>Nucleic Acids Research</i> , 2011, 39, W61-W67.	6.5	17
61	Identification of Metabolic Engineering Targets through Analysis of Optimal and Sub-Optimal Routes. <i>PLoS ONE</i> , 2013, 8, e61648.	1.1	16
62	Metabolic models and gene essentiality data reveal essential and conserved metabolism in prokaryotes. <i>PLoS Computational Biology</i> , 2018, 14, e1006556.	1.5	16
63	CRISPRi screens reveal genes modulating yeast growth in lignocellulose hydrolysate. <i>Biotechnology for Biofuels</i> , 2021, 14, 41.	6.2	15
64	The role of high-throughput transcriptome analysis in metabolic engineering. <i>Biotechnology and Bioprocess Engineering</i> , 2005, 10, 385-399.	1.4	14
65	Optimal fed-batch cultivation when mass transfer becomes limiting. <i>Biotechnology and Bioengineering</i> , 2007, 98, 706-710.	1.7	14
66	Metabolic memory underlying minimal residual disease in breast cancer. <i>Molecular Systems Biology</i> , 2021, 17, e10141.	3.2	14
67	Metabolic anchor reactions for robust biorefining. <i>Metabolic Engineering</i> , 2017, 40, 1-4.	3.6	12
68	Yeast Genome-Scale Metabolic Models for Simulating Genotype-Phenotype Relations. <i>Progress in Molecular and Subcellular Biology</i> , 2019, 58, 111-133.	0.9	11
69	Bioactivity assessment of natural compounds using machine learning models trained on target similarity between drugs. <i>PLoS Computational Biology</i> , 2022, 18, e1010029.	1.5	10
70	Conjugative transposition of the vancomycin resistance carrying Tn ₁₅₄₉ : enzymatic requirements and target site preferences. <i>Molecular Microbiology</i> , 2018, 107, 639-658.	1.2	7
71	Model-guided development of an evolutionarily stable yeast chassis. <i>Molecular Systems Biology</i> , 2021, 17, e10253.	3.2	6
72	Draft Genome Sequence of <i>Corynebacterium kefirresidentii</i> SB, Isolated from Kefir. <i>Genome Announcements</i> , 2017, 5, .	0.8	5

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73	Low Phenotypic Penetrance and Technological Impact of Yeast [GAR+] Prion-Like Elements on Winemaking. <i>Frontiers in Microbiology</i> , 2018, 9, 3311.	1.5	5
74	Molecular biology for green recoveryâ€™A call for action. <i>PLoS Biology</i> , 2022, 20, e3001623.	2.6	5
75	Freeing Yeast from Alcohol Addiction (Just) to Make (It) Fat Instead. <i>Cell</i> , 2018, 174, 1342-1344.	13.5	2
76	Model-Guided Identification of Gene Deletion Targets for Metabolic Engineering in <i>Saccharomyces cerevisiae</i> . <i>Methods in Molecular Biology</i> , 2014, 1152, 281-294.	0.4	2
77	Quantification of Duloxetine in the Bacterial Culture and Medium to Study Drug-gut Microbiome Interactions. <i>Bio-protocol</i> , 2021, 11, e4214.	0.2	2
78	Draft Genome Sequences of Three Novel Low-Abundance Species Strains Isolated from Kefir Grain. <i>Genome Announcements</i> , 2017, 5, .	0.8	1
79	Draft Genome Sequences of Five Fungal Strains Isolated from Kefir. <i>Microbiology Resource Announcements</i> , 2021, 10, e0019521.	0.3	1