

Kiran R Patil

List of Publications by Year in Descending Order

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Version: 2024-04-23

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

86
papers

6,017
citations

36
h-index

77
g-index

100
ext. papers

7,921
ext. citations

12.1
avg, IF

5.9
L-index

#	Paper	IF	Citations
86	Multimodal interactions of drugs, natural compounds and pollutants with the gut microbiota.. <i>Nature Reviews Microbiology</i> , 2022 ,	22.2	6
85	Microbial communities form rich extracellular metabolomes that foster metabolic interactions and promote drug tolerance.. <i>Nature Microbiology</i> , 2022 ,	26.6	4
84	Molecular biology for green recovery-A call for action.. <i>PLoS Biology</i> , 2022 , 20, e3001623	9.7	0
83	Bioactivity assessment of natural compounds using machine learning models trained on target similarity between drugs.. <i>PLoS Computational Biology</i> , 2022 , 18, e1010029	5	2
82	Metabolic memory underlying minimal residual disease in breast cancer. <i>Molecular Systems Biology</i> , 2021 , 17, e10141	12.2	2
81	Unravelling the collateral damage of antibiotics on gut bacteria. <i>Nature</i> , 2021 , 599, 120-124	50.4	21
80	Quantification of Duloxetine in the Bacterial Culture and Medium to Study Drug-gut Microbiome Interactions. <i>Bio-protocol</i> , 2021 , 11, e4214	0.9	
79	Towards a mechanistic understanding of reciprocal drug-microbiome interactions. <i>Molecular Systems Biology</i> , 2021 , 17, e10116	12.2	15
78	Draft Genome Sequences of Five Fungal Strains Isolated from Kefir. <i>Microbiology Resource Announcements</i> , 2021 , 10, e0019521	1.3	
77	metaGEM: reconstruction of genome scale metabolic models directly from metagenomes. <i>Nucleic Acids Research</i> , 2021 , 49, e126	20.1	11
76	Polarization of microbial communities between competitive and cooperative metabolism. <i>Nature Ecology and Evolution</i> , 2021 , 5, 195-203	12.3	35
75	CRISPRi screens reveal genes modulating yeast growth in lignocellulose hydrolysate. <i>Biotechnology for Biofuels</i> , 2021 , 14, 41	7.8	5
74	Model-guided development of an evolutionarily stable yeast chassis. <i>Molecular Systems Biology</i> , 2021 , 17, e10253	12.2	3
73	Adaptive laboratory evolution of microbial co-cultures for improved metabolite secretion. <i>Molecular Systems Biology</i> , 2021 , 17, e10189	12.2	3
72	Bioaccumulation of therapeutic drugs by human gut bacteria. <i>Nature</i> , 2021 , 597, 533-538	50.4	29
71	Metabolic cooperation and spatiotemporal niche partitioning in a kefir microbial community. <i>Nature Microbiology</i> , 2021 , 6, 196-208	26.6	44
70	Proteomic characterization of extracellular vesicles produced by several wine yeast species. <i>Microbial Biotechnology</i> , 2020 , 13, 1581-1596	6.3	12

69	MEMOTE for standardized genome-scale metabolic model testing. <i>Nature Biotechnology</i> , 2020 , 38, 272-276	27.5	121
68	Single-cell transcriptomics identifies CD44 as a marker and regulator of endothelial to haematopoietic transition. <i>Nature Communications</i> , 2020 , 11, 586	17.4	33
67	Antibiotics-induced monodominance of a novel gut bacterial order. <i>Gut</i> , 2019 , 68, 1781-1790	19.2	33
66	Yeast Genome-Scale Metabolic Models for Simulating Genotype-Phenotype Relations. <i>Progress in Molecular and Subcellular Biology</i> , 2019 , 58, 111-133	3	8
65	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	5.7	52
64	High-throughput ultrastructure screening using electron microscopy and fluorescent barcoding. <i>Journal of Cell Biology</i> , 2019 , 218, 2797-2811	7.3	13
63	Low Phenotypic Penetrance and Technological Impact of Yeast [] Prion-Like Elements on Winemaking. <i>Frontiers in Microbiology</i> , 2018 , 9, 3311	5.7	3
62	Conjugative transposition of the vancomycin resistance carrying Tn1549: enzymatic requirements and target site preferences. <i>Molecular Microbiology</i> , 2018 , 107, 639-658	4.1	5
61	Extensive impact of non-antibiotic drugs on human gut bacteria. <i>Nature</i> , 2018 , 555, 623-628	50.4	834
60	Nutritional preferences of human gut bacteria reveal their metabolic idiosyncrasies. <i>Nature Microbiology</i> , 2018 , 3, 514-522	26.6	119
59	Laboratory evolution reveals regulatory and metabolic trade-offs of glycerol utilization in <i>Saccharomyces cerevisiae</i> . <i>Metabolic Engineering</i> , 2018 , 47, 73-82	9.7	33
58	Fast automated reconstruction of genome-scale metabolic models for microbial species and communities. <i>Nucleic Acids Research</i> , 2018 , 46, 7542-7553	20.1	185
57	Metabolic models and gene essentiality data reveal essential and conserved metabolism in prokaryotes. <i>PLoS Computational Biology</i> , 2018 , 14, e1006556	5	12
56	Freeing Yeast from Alcohol Addiction (Just) to Make (It) Fat Instead. <i>Cell</i> , 2018 , 174, 1342-1344	56.2	0
55	Metabolic anchor reactions for robust biorefining. <i>Metabolic Engineering</i> , 2017 , 40, 1-4	9.7	12
54	Integration of Biomass Formulations of Genome-Scale Metabolic Models with Experimental Data Reveals Universally Essential Cofactors in Prokaryotes. <i>Metabolic Engineering</i> , 2017 , 39, 200-208	9.7	51
53	Towards standards for human fecal sample processing in metagenomic studies. <i>Nature Biotechnology</i> , 2017 , 35, 1069-1076	44.5	355
52	Yeast Creates a Niche for Symbiotic Lactic Acid Bacteria through Nitrogen Overflow. <i>Cell Systems</i> , 2017 , 5, 345-357.e6	10.6	151

51	Model microbial communities for ecosystems biology. <i>Current Opinion in Systems Biology</i> , 2017 , 6, 51-57	3.2	21
50	Draft Genome Sequences of Three Novel Low-Abundance Species Strains Isolated from Kefir Grain. <i>Genome Announcements</i> , 2017 , 5,		1
49	Draft Genome Sequence of SB, Isolated from Kefir. <i>Genome Announcements</i> , 2017 , 5,		1
48	Metabolic shifts in residual breast cancer drive tumor recurrence. <i>Journal of Clinical Investigation</i> , 2017 , 127, 2091-2105	15.9	78
47	<i>Saccharomyces cerevisiae</i> metabolism in ecological context. <i>FEMS Yeast Research</i> , 2016 , 16,	3.1	28
46	Yeast metabolic chassis designs for diverse biotechnological products. <i>Scientific Reports</i> , 2016 , 6, 29694	4.9	22
45	The metabolic background is a global player in <i>Saccharomyces</i> gene expression epistasis. <i>Nature Microbiology</i> , 2016 , 1, 15030	26.6	53
44	Metabolic interactions in microbial communities: untangling the Gordian knot. <i>Current Opinion in Microbiology</i> , 2015 , 27, 37-44	7.9	147
43	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, 6449-54	11.5	366
42	Do genome-scale models need exact solvers or clearer standards?. <i>Molecular Systems Biology</i> , 2015 , 11, 831	12.2	41
41	Computational tools for modeling xenometabolism of the human gut microbiota. <i>Trends in Biotechnology</i> , 2014 , 32, 157-65	15.1	17
40	Systems biology perspectives on minimal and simpler cells. <i>Microbiology and Molecular Biology Reviews</i> , 2014 , 78, 487-509	13.2	42
39	Contribution of network connectivity in determining the relationship between gene expression and metabolite concentration changes. <i>PLoS Computational Biology</i> , 2014 , 10, e1003572	5	52
38	Model-guided identification of gene deletion targets for metabolic engineering in <i>Saccharomyces cerevisiae</i> . <i>Methods in Molecular Biology</i> , 2014 , 1152, 281-94	1.4	2
37	Overexpression of O-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, 656-9	4.9	32
36	Industrial systems biology of <i>Saccharomyces cerevisiae</i> enables novel succinic acid cell factory. <i>PLoS ONE</i> , 2013 , 8, e54144	3.7	125
35	Identification of metabolic engineering targets through analysis of optimal and sub-optimal routes. <i>PLoS ONE</i> , 2013 , 8, e61648	3.7	15
34	Impact of stoichiometry representation on simulation of genotype-phenotype relationships in metabolic networks. <i>PLoS Computational Biology</i> , 2012 , 8, e1002758	5	27

33	Involvement of a natural fusion of a cytochrome P450 and a hydrolase in mycophenolic acid biosynthesis. <i>Applied and Environmental Microbiology</i> , 2012 , 78, 4908-13	4.8	44
32	Random sampling of elementary flux modes in large-scale metabolic networks. <i>Bioinformatics</i> , 2012 , 28, i515-i521	7.2	53
31	Prediction and identification of sequences coding for orphan enzymes using genomic and metagenomic neighbours. <i>Molecular Systems Biology</i> , 2012 , 8, 581	12.2	25
30	A new class of IMP dehydrogenase with a role in self-resistance of mycophenolic acid producing fungi. <i>BMC Microbiology</i> , 2011 , 11, 202	4.5	38
29	PHUSER (Primer Help for USER): a novel tool for USER fusion primer design. <i>Nucleic Acids Research</i> , 2011 , 39, W61-7	20.1	14
28	Flux coupling and transcriptional regulation within the metabolic network of the photosynthetic bacterium <i>Synechocystis</i> sp. PCC6803. <i>Biotechnology Journal</i> , 2011 , 6, 330-42	5.6	45
27	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. <i>Applied and Environmental Microbiology</i> , 2011 , 77, 3044-51	4.8	76
26	Metabolic network topology reveals transcriptional regulatory signatures of type 2 diabetes. <i>PLoS Computational Biology</i> , 2010 , 6, e1000729	5	66
25	BioMet Toolbox: genome-wide analysis of metabolism. <i>Nucleic Acids Research</i> , 2010 , 38, W144-9	20.1	82
24	Improved vanillin production in baker's yeast through in silico design. <i>Microbial Cell Factories</i> , 2010 , 9, 84	6.4	196
23	Reconstruction and analysis of genome-scale metabolic model of a photosynthetic bacterium. <i>BMC Systems Biology</i> , 2010 , 4, 156	3.5	94
22	OptFlux: an open-source software platform for in silico metabolic engineering. <i>BMC Systems Biology</i> , 2010 , 4, 45	3.5	258
21	Global transcriptional response of <i>Saccharomyces cerevisiae</i> to the deletion of SDH3. <i>BMC Systems Biology</i> , 2009 , 3, 17	3.5	21
20	Enhancing sesquiterpene production in <i>Saccharomyces cerevisiae</i> through in silico driven metabolic engineering. <i>Metabolic Engineering</i> , 2009 , 11, 328-34	9.7	187
19	Natural computation meta-heuristics for the in silico optimization of microbial strains. <i>BMC Bioinformatics</i> , 2008 , 9, 499	3.6	75
18	Architecture of transcriptional regulatory circuits is knitted over the topology of bio-molecular interaction networks. <i>BMC Systems Biology</i> , 2008 , 2, 17	3.5	104
17	Optimal fed-batch cultivation when mass transfer becomes limiting. <i>Biotechnology and Bioengineering</i> , 2007 , 98, 706-10	4.9	13
16	The metabolic response of heterotrophic <i>Arabidopsis</i> cells to oxidative stress. <i>Plant Physiology</i> , 2007 , 143, 312-25	6.6	199

15	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, 6194-203	4.8	46
14	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, 12308-14	5.4	25
13	Integration of metabolome data with metabolic networks reveals reporter reactions. <i>Molecular Systems Biology</i> , 2006 , 2, 50	12.2	110
12	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, 2685-9	11.5	445
11	Evolutionary programming as a platform for in silico metabolic engineering. <i>BMC Bioinformatics</i> , 2005 , 6, 308	3.6	312
10	The role of high-throughput transcriptome analysis in metabolic engineering. <i>Biotechnology and Bioprocess Engineering</i> , 2005 , 10, 385-399	3.1	13
9	Use of genome-scale microbial models for metabolic engineering. <i>Current Opinion in Biotechnology</i> , 2004 , 15, 64-9	11.4	138
8	Dissecting the collateral damage of antibiotics on gut microbes		4
7	Polarization of microbial communities between competitive and cooperative metabolism		3
6	Fast automated reconstruction of genome-scale metabolic models for microbial species and communities		3
5	Single-cell transcriptomics identifies CD44 as a new marker and regulator of haematopoietic stem cells development		2
4	Memote: A community driven effort towards a standardized genome-scale metabolic model test suite		26
3	Emergence of stable coexistence in a complex microbial community through metabolic cooperation and spatio-temporal niche partitioning		8
2	Co-translational assembly counteracts promiscuous interactions		1
1	metaGEM: reconstruction of genome scale metabolic models directly from metagenomes		1