# Kiran R Patil

List of Publications by Year
in descending order

| 79 | 9,455 | 66234 | 62479 |
|---|---|---|---|
| papers | citations | 42 | 80 |
| | | h-index | g-index |

| 100 | 100 | 100 | 12071 |
|---|---|---|---|
| all docs | docs citations | times ranked | citing authors |

| # | ARTICLE | IF | CITATIONS |
|---|---------|-----|-----------|
| 1 | Multimodal interactions of drugs, natural compounds and pollutants with the gut microbiota. Nature Reviews Microbiology, 2022, 20, 431-443. | 13.6 | 77 |
| 2 | Microbial communities form rich extracellular metabolomes that foster metabolic interactions and promote drug tolerance. Nature Microbiology, 2022, 7, 542-555. | 5.9 | 58 |
| 3 | Molecular biology for green recoveryâ€"A call for action. PLoS Biology, 2022, 20, e3001623. | 2.6 | 5 |
| 4 | Bioactivity assessment of natural compounds using machine learning models trained on target similarity between drugs. PLoS Computational Biology, 2022, 18, e1010029. | 1.5 | 10 |
| 5 | Ecological modelling approaches for predicting emergent properties in microbial communities. Nature Ecology and Evolution, 2022, 6, 855-865. | 3.4 | 54 |
| 6 | metaGEM: reconstruction of genome scale metabolic models directly from metagenomes. Nucleic Acids Research, 2021, 49, e126-e126. | 6.5 | 50 |
| 7 | Polarization of microbial communities between competitive and cooperative metabolism. Nature Ecology and Evolution, 2021, 5, 195-203. | 3.4 | 131 |
| 8 | CRISPRi screens reveal genes modulating yeast growth in lignocellulose hydrolysate. Biotechnology for Biofuels, 2021, 14, 41. | 6.2 | 15 |
| 9 | Towards a mechanistic understanding of reciprocal drugâ€"microbiome interactions. Molecular Systems Biology, 2021, 17, e10116. | 3.2 | 64 |
| 10 | Draft Genome Sequences of Five Fungal Strains Isolated from Kefir. Microbiology Resource Announcements, 2021, 10, e0019521. | 0.3 | 1 |
| 11 | Modelâ€guided development of an evolutionarily stable yeast chassis. Molecular Systems Biology, 2021, 17, e10253. | 3.2 | 6 |
| 12 | Adaptive laboratory evolution of microbial coâ€cultures for improved metabolite secretion. Molecular Systems Biology, 2021, 17, e10189. | 3.2 | 21 |
| 13 | Bioaccumulation of therapeutic drugs by human gut bacteria. Nature, 2021, 597, 533-538. | 13.7 | 159 |
| 14 | Metabolic cooperation and spatiotemporal niche partitioning in a kefir microbial community. Nature Microbiology, 2021, 6, 196-208. | 5.9 | 138 |
| 15 | Metabolic memory underlying minimal residual disease in breast cancer. Molecular Systems Biology, 2021, 17, e10141. | 3.2 | 14 |
| 16 | Unravelling the collateral damage of antibiotics on gut bacteria. Nature, 2021, 599, 120-124. | 13.7 | 159 |
| 17 | Quantification of Duloxetine in the Bacterial Culture and Medium to Study Drug-gut Microbiome Interactions. Bio-protocol, 2021, 11, e4214. | 0.2 | 2 |
| 18 | Proteomic characterization of extracellular vesicles produced by several wine yeast species. Microbial Biotechnology, 2020, 13, 1581-1596. | 2.0 | 26 |

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|---|---------|----|-----------| 
| 19 | MEMOTE for standardized genome-scale metabolic model testing. Nature Biotechnology, 2020, 38, 272-276. | 9.4 | 314 |
| 20 | Single-cell transcriptomics identifies CD44 as a marker and regulator of endothelial to haematopoietic transition. Nature Communications, 2020, 11, 586. | 5.8 | 69 |
| 21 | Finding Functional Differences Between Species in a Microbial Community: Case Studies in Wine Fermentation and Kefir Culture. Frontiers in Microbiology, 2019, 10, 1347. | 1.5 | 229 |
| 22 | High-throughput ultrastructure screening using electron microscopy and fluorescent barcoding. Journal of Cell Biology, 2019, 218, 2797-2811. | 2.3 | 18 |
| 23 | Antibiotics-induced monodominance of a novel gut bacterial order. Gut, 2019, 68, 1781-1790. | 6.1 | 73 |
| 24 | Yeast Genome-Scale Metabolic Models for Simulating Genotype–Phenotype Relations. Progress in Molecular and Subcellular Biology, 2019, 58, 111-133. | 0.9 | 11 |
| 25 | Conjugative transposition of the vancomycin resistance carrying Tn*1549*: enzymatic requirements and target site preferences. Molecular Microbiology, 2018, 107, 639-658. | 1.2 | 7 |
| 26 | Extensive impact of non-antibiotic drugs on human gut bacteria. Nature, 2018, 555, 623-628. | 13.7 | 1,339 |
| 27 | Nutritional preferences of human gut bacteria reveal their metabolic idiosyncrasies. Nature Microbiology, 2018, 3, 514-522. | 5.9 | 196 |
| 28 | Laboratory evolution reveals regulatory and metabolic trade-offs of glycerol utilization in Saccharomyces cerevisiae. Metabolic Engineering, 2018, 47, 73-82. | 3.6 | 47 |
| 29 | Metabolic models and gene essentiality data reveal essential and conserved metabolism in prokaryotes. PLoS Computational Biology, 2018, 14, e1006556. | 1.5 | 16 |
| 30 | Freeing Yeast from Alcohol Addiction (Just) to Make (It) Fat Instead. Cell, 2018, 174, 1342-1344. | 13.5 | 2 |
| 31 | Fast automated reconstruction of genome-scale metabolic models for microbial species and communities. Nucleic Acids Research, 2018, 46, 7542-7553. | 6.5 | 410 |
| 32 | Low Phenotypic Penetrance and Technological Impact of Yeast [GAR+] Prion-Like Elements on Winemaking. Frontiers in Microbiology, 2018, 9, 3311. | 1.5 | 5 |
| 33 | Metabolic anchor reactions for robust biorefining. Metabolic Engineering, 2017, 40, 1-4. | 3.6 | 12 |
| 34 | 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 |
| 35 | Towards standards for human fecal sample processing in metagenomic studies. Nature Biotechnology, 2017, 35, 1069-1076. | 9.4 | 581 |
| 36 | Yeast Creates a Niche for Symbiotic Lactic Acid Bacteria through Nitrogen Overflow. Cell Systems, 2017, 5, 345-357.e6. | 2.9 | 247 |

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|---|---------|----|-----------|
| 37 | Model microbial communities for ecosystems biology. Current Opinion in Systems Biology, 2017, 6, 51-57. | 1.3 | 44 |
| 38 | Draft Genome Sequences of Three Novel Low-Abundance Species Strains Isolated from Kefir Grain. Genome Announcements, 2017, 5, . | 0.8 | 1 |
| 39 | Draft Genome Sequence of Corynebacterium kefirresidentii SB, Isolated from Kefir. Genome Announcements, 2017, 5, . | 0.8 | 5 |
| 40 | Metabolic shifts in residual breast cancer drive tumor recurrence. Journal of Clinical Investigation, 2017, 127, 2091-2105. | 3.9 | 128 |
| 41 | <i>Saccharomyces cerevisiae</i> metabolism in ecological context. FEMS Yeast Research, 2016, 16, fow080. | 1.1 | 37 |
| 42 | Yeast metabolic chassis designs for diverse biotechnological products. Scientific Reports, 2016, 6, 29694. | 1.6 | 28 |
| 43 | The metabolic background is a global player in Saccharomyces gene expression epistasis. Nature Microbiology, 2016, 1, 15030. | 5.9 | 76 |
| 44 | Do genome‐scale models need exact solvers or clearer standards?. Molecular Systems Biology, 2015, 11, 831. | 3.2 | 68 |
| 45 | Metabolic interactions in microbial communities: untangling the Gordian knot. Current Opinion in Microbiology, 2015, 27, 37-44. | 2.3 | 213 |
| 46 | Metabolic dependencies drive species co-occurrence in diverse microbial communities. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 6449-6454. | 3.3 | 588 |
| 47 | Contribution of Network Connectivity in Determining the Relationship between Gene Expression and Metabolite Concentration Changes. PLoS Computational Biology, 2014, 10, e1003572. | 1.5 | 64 |
| 48 | Computational tools for modeling xenometabolism of the human gut microbiota. Trends in Biotechnology, 2014, 32, 157-165. | 4.9 | 22 |
| 49 | Systems Biology Perspectives on Minimal and Simpler Cells. Microbiology and Molecular Biology Reviews, 2014, 78, 487-509. | 2.9 | 51 |
| 50 | Model-Guided Identification of Gene Deletion Targets for Metabolic Engineering in Saccharomyces cerevisiae. Methods in Molecular Biology, 2014, 1152, 281-294. | 0.4 | 2 |
| 51 | Overexpression of <i>O</i>‐methyltransferase leads to improved vanillin production in baker's yeast only when complemented with model‐guided network engineering. Biotechnology and Bioengineering, 2013, 110, 656-659. | 1.7 | 42 |
| 52 | Industrial Systems Biology of Saccharomyces cerevisiae Enables Novel Succinic Acid Cell Factory. PLoS ONE, 2013, 8, e54144. | 1.1 | 142 |
| 53 | Identification of Metabolic Engineering Targets through Analysis of Optimal and Sub-Optimal Routes. PLoS ONE, 2013, 8, e61648. | 1.1 | 16 |
| 54 | Random sampling of elementary flux modes in large-scale metabolic networks. Bioinformatics, 2012, 28, i515-i521. | 1.8 | 66 |

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|---|---------|-----|-----------|
| 55 | Prediction and identification of sequences coding for orphan enzymes using genomic and metagenomic neighbours. Molecular Systems Biology, 2012, 8, 581. | 3.2 | 29 |
| 56 | Impact of Stoichiometry Representation on Simulation of Genotype-Phenotype Relationships in Metabolic Networks. PLoS Computational Biology, 2012, 8, e1002758. | 1.5 | 31 |
| 57 | Involvement of a Natural Fusion of a Cytochrome P450 and a Hydrolase in Mycophenolic Acid Biosynthesis. Applied and Environmental Microbiology, 2012, 78, 4908-4913. | 1.4 | 53 |
| 58 | A new class of IMP dehydrogenase with a role in self-resistance of mycophenolic acid producing fungi. BMC Microbiology, 2011, 11, 202. | 1.3 | 44 |
| 59 | PHUSER (Primer Help for USER): a novel tool for USER fusion primer design. Nucleic Acids Research, 2011, 39, W61-W67. | 6.5 | 17 |
| 60 | Flux coupling and transcriptional regulation within the metabolic network of the photosynthetic bacterium <i>Synechocystis</i> sp. PCC6803. Biotechnology Journal, 2011, 6, 330-342. | 1.8 | 51 |
| 61 | Versatile Enzyme Expression and Characterization System for Aspergillus nidulans, with the Penicillium brevicompactum Polyketide Synthase Gene from the Mycophenolic Acid Gene Cluster as a Test Case. Applied and Environmental Microbiology, 2011, 77, 3044-3051. | 1.4 | 86 |
| 62 | Reconstruction and analysis of genome-scale metabolic model of a photosynthetic bacterium. BMC Systems Biology, 2010, 4, 156. | 3.0 | 100 |
| 63 | OptFlux: an open-source software platform for in silico metabolic engineering. BMC Systems Biology, 2010, 4, 45. | 3.0 | 321 |
| 64 | Metabolic Network Topology Reveals Transcriptional Regulatory Signatures of Type 2 Diabetes. PLoS Computational Biology, 2010, 6, e1000729. | 1.5 | 75 |
| 65 | BioMet Toolbox: genome-wide analysis of metabolism. Nucleic Acids Research, 2010, 38, W144-W149. | 6.5 | 91 |
| 66 | Improved vanillin production in baker's yeast through in silico design. Microbial Cell Factories, 2010, 9, 84. | 1.9 | 226 |
| 67 | Global transcriptional response of Saccharomyces cerevisiae to the deletion of SDH3. BMC Systems Biology, 2009, 3, 17. | 3.0 | 23 |
| 68 | Enhancing sesquiterpene production in Saccharomyces cerevisiae through in silico driven metabolic engineering. Metabolic Engineering, 2009, 11, 328-334. | 3.6 | 199 |
| 69 | Natural computation meta-heuristics for the in silico optimization of microbial strains. BMC Bioinformatics, 2008, 9, 499. | 1.2 | 90 |
| 70 | Architecture of transcriptional regulatory circuits is knitted over the topology of bio-molecular interaction networks. BMC Systems Biology, 2008, 2, 17. | 3.0 | 121 |
| 71 | The Metabolic Response of Heterotrophic Arabidopsis Cells to Oxidative Stress. Plant Physiology, 2007, 143, 312-325. | 2.3 | 234 |
| 72 | Optimal fed-batch cultivation when mass transfer becomes limiting. Biotechnology and Bioengineering, 2007, 98, 706-710. | 1.7 | 14 |

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|---|---------|----|-----------|
| 73 | Integration of metabolome data with metabolic networks reveals reporter reactions. Molecular Systems Biology, 2006, 2, 50. | 3.2 | 131 |
| 74 | Global Transcriptional and Physiological Responses of Saccharomyces cerevisiae to Ammonium, l-Alanine, or l-Glutamine Limitation. Applied and Environmental Microbiology, 2006, 72, 6194-6203. | 1.4 | 52 |
| 75 | Hap4 Is Not Essential for Activation of Respiration at Low Specific Growth Rates in Saccharomyces cerevisiae*. Journal of Biological Chemistry, 2006, 281, 12308-12314. | 1.6 | 31 |
| 76 | Evolutionary programming as a platform for in silico metabolic engineering. BMC Bioinformatics, 2005, 6, 308. | 1.2 | 374 |
| 77 | The role of high-throughput transcriptome analysis in metabolic engineering. Biotechnology and Bioprocess Engineering, 2005, 10, 385-399. | 1.4 | 14 |
| 78 | Uncovering transcriptional regulation of metabolism by using metabolic network topology. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 2685-2689. | 3.3 | 553 |
| 79 | Use of genome-scale microbial models for metabolic engineering. Current Opinion in Biotechnology, 2004, 15, 64-69. | 3.3 | 150 |