Anand V Sastry

List of Publications by Year
in descending order

34 papers	2,540 citations	393982 19 h-index	377514 34 g-index
57 all docs	57 docs citations	57 times ranked	2691 citing authors

#	Article	IF	Citations
1	Recon3D enables a three-dimensional view of gene variation in human metabolism. Nature Biotechnology, 2018, 36, 272-281.	9.4	520
2	iML1515, a knowledgebase that computes Escherichia coli traits. Nature Biotechnology, 2017, 35, 904-908.	9.4	425
3	The Escherichia coli transcriptome mostly consists of independently regulated modules. Nature Communications, 2019, 10, 5536.	5.8	161
4	Multi-omic data integration enables discovery of hidden biological regularities. Nature Communications, 2016, 7, 13091.	5.8	141
5	The y-ome defines the 35% of *Escherichia coli* genes that lack experimental evidence of function. Nucleic Acids Research, 2019, 47, 2446-2454.	6.5	117
6	Global transcriptional regulatory network for *Escherichia coli* robustly connects gene expression to transcription factor activities. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 10286-10291.	3.3	89
7	BOFdat: Generating biomass objective functions for genome-scale metabolic models from experimental data. PLoS Computational Biology, 2019, 15, e1006971.	1.5	83
8	Cellular responses to reactive oxygen species are predicted from molecular mechanisms. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 14368-14373.	3.3	79
9	iModulonDB: a knowledgebase of microbial transcriptional regulation derived from machine learning. Nucleic Acids Research, 2021, 49, D112-D120.	6.5	67
10	Systematic discovery of uncharacterized transcription factors in Escherichia coli K-12 MG1655. Nucleic Acids Research, 2018, 46, 10682-10696.	6.5	65
11	Revealing 29 sets of independently modulated genes in *Staphylococcus aureus* , their regulators, and role in key physiological response. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 17228-17239.	3.3	60
12	Adaptive evolution reveals a tradeoff between growth rate and oxidative stress during naphthoquinone-based aerobic respiration. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 25287-25292.	3.3	56
13	Machine learning uncovers independently regulated modules in the Bacillus subtilis transcriptome. Nature Communications, 2020, 11, 6338.	5.8	54
14	OxyR Is a Convergent Target for Mutations Acquired during Adaptation to Oxidative Stress-Prone Metabolic States. Molecular Biology and Evolution, 2020, 37, 660-667.	3.5	52
15	Escherichia coli B2 strains prevalent in inflammatory bowel disease patients have distinct metabolic capabilities that enable colonization of intestinal mucosa. BMC Systems Biology, 2018, 12, 66.	3.0	39
16	ssbio: a Python framework for structural systems biology. Bioinformatics, 2018, 34, 2155-2157.	1.8	36
17	Independent component analysis of E. coli's transcriptome reveals the cellular processes that respond to heterologous gene expression. Metabolic Engineering, 2020, 61, 360-368.	3.6	36
18	Optimal dimensionality selection for independent component analysis of transcriptomic data. BMC Bioinformatics, 2021, 22, 584.	1.2	34

#	Article	IF	Citations
19	Adaptive laboratory evolution of Escherichia coli under acid stress. Microbiology (United Kingdom), 2020, 166, 141-148.	0.7	28
20	Machine-learning from Pseudomonas putida KT2440 transcriptomes reveals its transcriptional regulatory network. Metabolic Engineering, 2022, 72, 297-310.	3.6	28
21	Independent component analysis recovers consistent regulatory signals from disparate datasets. PLoS Computational Biology, 2021, 17, e1008647.	1.5	27
22	Elucidation of Regulatory Modes for Five Two-Component Systems in Escherichia coli Reveals Novel Relationships. MSystems, 2020, 5, .	1.7	25
23	Machine learning from<i>Pseudomonas aeruginosa</i>transcriptomes identifies independently modulated sets of genes associated with known transcriptional regulators. Nucleic Acids Research, 2022, 50, 3658-3672.	6.5	25
24	Machine Learning of All Mycobacterium tuberculosis H37Rv RNA-seq Data Reveals a Structured Interplay between Metabolism, Stress Response, and Infection. MSphere, 2022, 7, e0003322.	1.3	22
25	Pseudogene repair driven by selection pressure applied in experimental evolution. Nature Microbiology, 2019, 4, 386-389.	5.9	21
26	Machine Learning Uncovers a Data-Driven Transcriptional Regulatory Network for the Crenarchaeal Thermoacidophile Sulfolobus acidocaldarius. Frontiers in Microbiology, 2021, 12, 753521.	1.5	20
27	RiboRid: A low cost, advanced, and ultra-efficient method to remove ribosomal RNA for bacterial transcriptomics. PLoS Genetics, 2021, 17, e1009821.	1.5	16
28	Membrane transporter identification and modulation via adaptive laboratory evolution. Metabolic Engineering, 2022, 72, 376-390.	3.6	16
29	Restoration of fitness lost due to dysregulation of the pyruvate dehydrogenase complex is triggered by ribosomal binding site modifications. Cell Reports, 2021, 35, 108961.	2.9	13
30	Identification of a transcription factor, PunR, that regulates the purine and purine nucleoside transporter punC in E. coli. Communications Biology, 2021, 4, 991.	2.0	13
31	Machine Learning of Bacterial Transcriptomes Reveals Responses Underlying Differential Antibiotic Susceptibility. MSphere, 2021, 6, e0044321.	1.3	12
32	The Bitome: digitized genomic features reveal fundamental genome organization. Nucleic Acids Research, 2020, 48, 10157-10163.	6.5	11
33	Machine learning in computational biology to accelerate high-throughput protein expression. Bioinformatics, 2017, 33, 2487-2495.	1.8	8
34	Mathematical models to study the biology of pathogens and the infectious diseases they cause. IScience, 2022, 25, 104079.	1.9	8