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	Machine learning from *Pseudomonas aeruginosa* transcriptomes identifies independently modulated sets of genes associated with known transcriptional regulators. Nucleic Acids Research, 2022, 50, 3658-3672.	6.5	25
2	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
3	Mathematical models to study the biology of pathogens and the infectious diseases they cause. IScience, 2022, 25, 104079.	1.9	8
4	Machine-learning from Pseudomonas putida KT2440 transcriptomes reveals its transcriptional regulatory network. Metabolic Engineering, 2022, 72, 297-310.	3.6	28
5	Membrane transporter identification and modulation via adaptive laboratory evolution. Metabolic Engineering, 2022, 72, 376-390.	3.6	16
6	iModulonDB: a knowledgebase of microbial transcriptional regulation derived from machine learning. Nucleic Acids Research, 2021, 49, D112-D120.	6.5	67
7	Independent component analysis recovers consistent regulatory signals from disparate datasets. PLoS Computational Biology, 2021, 17, e1008647.	1.5	27
8	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
9	Machine Learning of Bacterial Transcriptomes Reveals Responses Underlying Differential Antibiotic Susceptibility. MSphere, 2021, 6, e0044321.	1.3	12
10	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
11	RiboRid: A low cost, advanced, and ultra-efficient method to remove ribosomal RNA for bacterial transcriptomics. PLoS Genetics, 2021, 17, e1009821.	1.5	16
12	Machine Learning Uncovers a Data-Driven Transcriptional Regulatory Network for the Crenarchaeal Thermoacidophile Sulfolobus acidocaldarius. Frontiers in Microbiology, 2021, 12, 753521.	1.5	20
13	Optimal dimensionality selection for independent component analysis of transcriptomic data. BMC Bioinformatics, 2021, 22, 584.	1.2	34
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	The Bitome: digitized genomic features reveal fundamental genome organization. Nucleic Acids Research, 2020, 48, 10157-10163.	6.5	11
16	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
17	Machine learning uncovers independently regulated modules in the Bacillus subtilis transcriptome. Nature Communications, 2020, 11, 6338.	5.8	54
18	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

#	ARTICLE	IF	CITATIONS
19	Adaptive laboratory evolution of Escherichia coli under acid stress. Microbiology (United Kingdom), 2020, 166, 141-148.	0.7	28
20	Elucidation of Regulatory Modes for Five Two-Component Systems in Escherichia coli Reveals Novel Relationships. MSystems, 2020, 5, .	1.7	25
21	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
22	Pseudogene repair driven by selection pressure applied in experimental evolution. Nature Microbiology, 2019, 4, 386-389.	5.9	21
23	BOFdat: Generating biomass objective functions for genome-scale metabolic models from experimental data. PLoS Computational Biology, 2019, 15, e1006971.	1.5	83
24	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
25	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
26	The Escherichia coli transcriptome mostly consists of independently regulated modules. Nature Communications, 2019, 10, 5536.	5.8	161
27	Recon3D enables a three-dimensional view of gene variation in human metabolism. Nature Biotechnology, 2018, 36, 272-281.	9.4	520
28	ssbio: a Python framework for structural systems biology. Bioinformatics, 2018, 34, 2155-2157.	1.8	36
29	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
30	Systematic discovery of uncharacterized transcription factors in Escherichia coli K-12 MG1655. Nucleic Acids Research, 2018, 46, 10682-10696.	6.5	65
31	Machine learning in computational biology to accelerate high-throughput protein expression. Bioinformatics, 2017, 33, 2487-2495.	1.8	8
32	iML1515, a knowledgebase that computes Escherichia coli traits. Nature Biotechnology, 2017, 35, 904-908.	9.4	425
33	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
34	Multi-omic data integration enables discovery of hidden biological regularities. Nature Communications, 2016, 7, 13091.	5.8	141