

# Anand V Sastry

## List of Publications by Year in descending order

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Version: 2024-02-01

34  
papers

2,540  
citations

394421

19  
h-index

377865

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. <i>Nature Biotechnology</i> , 2018, 36, 272-281.	17.5	520
2	iML1515, a knowledgebase that computes <i>Escherichia coli</i> traits. <i>Nature Biotechnology</i> , 2017, 35, 904-908.	17.5	425
3	The <i>Escherichia coli</i> transcriptome mostly consists of independently regulated modules. <i>Nature Communications</i> , 2019, 10, 5536.	12.8	161
4	Multi-omic data integration enables discovery of hidden biological regularities. <i>Nature Communications</i> , 2016, 7, 13091.	12.8	141
5	The $\gamma$ -ome defines the 35% of <i>Escherichia coli</i> genes that lack experimental evidence of function. <i>Nucleic Acids Research</i> , 2019, 47, 2446-2454.	14.5	117
6	Global transcriptional regulatory network for <i>Escherichia coli</i> robustly connects gene expression to transcription factor activities. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 10286-10291.	7.1	89
7	BOFdat: Generating biomass objective functions for genome-scale metabolic models from experimental data. <i>PLoS Computational Biology</i> , 2019, 15, e1006971.	3.2	83
8	Cellular responses to reactive oxygen species are predicted from molecular mechanisms. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 14368-14373.	7.1	79
9	iModulonDB: a knowledgebase of microbial transcriptional regulation derived from machine learning. <i>Nucleic Acids Research</i> , 2021, 49, D112-D120.	14.5	67
10	Systematic discovery of uncharacterized transcription factors in <i>Escherichia coli</i> K-12 MG1655. <i>Nucleic Acids Research</i> , 2018, 46, 10682-10696.	14.5	65
11	Revealing 29 sets of independently modulated genes in <i>Staphylococcus aureus</i> , their regulators, and role in key physiological response. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 17228-17239.	7.1	60
12	Adaptive evolution reveals a tradeoff between growth rate and oxidative stress during naphthoquinone-based aerobic respiration. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 25287-25292.	7.1	56
13	Machine learning uncovers independently regulated modules in the <i>Bacillus subtilis</i> transcriptome. <i>Nature Communications</i> , 2020, 11, 6338.	12.8	54
14	OxyR Is a Convergent Target for Mutations Acquired during Adaptation to Oxidative Stress-Prone Metabolic States. <i>Molecular Biology and Evolution</i> , 2020, 37, 660-667.	8.9	52
15	<i>Escherichia coli</i> B2 strains prevalent in inflammatory bowel disease patients have distinct metabolic capabilities that enable colonization of intestinal mucosa. <i>BMC Systems Biology</i> , 2018, 12, 66.	3.0	39
16	ssbio: a Python framework for structural systems biology. <i>Bioinformatics</i> , 2018, 34, 2155-2157.	4.1	36
17	Independent component analysis of <i>E. coli</i> 's transcriptome reveals the cellular processes that respond to heterologous gene expression. <i>Metabolic Engineering</i> , 2020, 61, 360-368.	7.0	36
18	Optimal dimensionality selection for independent component analysis of transcriptomic data. <i>BMC Bioinformatics</i> , 2021, 22, 584.	2.6	34

#	ARTICLE	IF	CITATIONS
19	Adaptive laboratory evolution of <i>Escherichia coli</i> under acid stress. <i>Microbiology (United Kingdom)</i> , 2020, 166, 141-148.	1.8	28
20	Machine-learning from <i>Pseudomonas putida</i> KT2440 transcriptomes reveals its transcriptional regulatory network. <i>Metabolic Engineering</i> , 2022, 72, 297-310.	7.0	28
21	Independent component analysis recovers consistent regulatory signals from disparate datasets. <i>PLoS Computational Biology</i> , 2021, 17, e1008647.	3.2	27
22	Elucidation of Regulatory Modes for Five Two-Component Systems in <i>Escherichia coli</i> Reveals Novel Relationships. <i>MSystems</i> , 2020, 5, .	3.8	25
23	Machine learning from <i>Pseudomonas aeruginosa</i> transcriptomes identifies independently modulated sets of genes associated with known transcriptional regulators. <i>Nucleic Acids Research</i> , 2022, 50, 3658-3672.	14.5	25
24	Machine Learning of All <i>Mycobacterium tuberculosis</i> H37Rv RNA-seq Data Reveals a Structured Interplay between Metabolism, Stress Response, and Infection. <i>MSphere</i> , 2022, 7, e0003322.	2.9	22
25	Pseudogene repair driven by selection pressure applied in experimental evolution. <i>Nature Microbiology</i> , 2019, 4, 386-389.	13.3	21
26	Machine Learning Uncovers a Data-Driven Transcriptional Regulatory Network for the Crenarchaeal Thermoacidophile <i>Sulfolobus acidocaldarius</i> . <i>Frontiers in Microbiology</i> , 2021, 12, 753521.	3.5	20
27	RiboRid: A low cost, advanced, and ultra-efficient method to remove ribosomal RNA for bacterial transcriptomics. <i>PLoS Genetics</i> , 2021, 17, e1009821.	3.5	16
28	Membrane transporter identification and modulation via adaptive laboratory evolution. <i>Metabolic Engineering</i> , 2022, 72, 376-390.	7.0	16
29	Restoration of fitness lost due to dysregulation of the pyruvate dehydrogenase complex is triggered by ribosomal binding site modifications. <i>Cell Reports</i> , 2021, 35, 108961.	6.4	13
30	Identification of a transcription factor, PunR, that regulates the purine and purine nucleoside transporter punC in <i>E. coli</i> . <i>Communications Biology</i> , 2021, 4, 991.	4.4	13
31	Machine Learning of Bacterial Transcriptomes Reveals Responses Underlying Differential Antibiotic Susceptibility. <i>MSphere</i> , 2021, 6, e0044321.	2.9	12
32	The Bitome: digitized genomic features reveal fundamental genome organization. <i>Nucleic Acids Research</i> , 2020, 48, 10157-10163.	14.5	11
33	Machine learning in computational biology to accelerate high-throughput protein expression. <i>Bioinformatics</i> , 2017, 33, 2487-2495.	4.1	8
34	Mathematical models to study the biology of pathogens and the infectious diseases they cause. <i>IScience</i> , 2022, 25, 104079.	4.1	8