

Nitin S Baliga

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1991864/publications.pdf>

Version: 2024-02-01

114
papers

43,355
citations

71004

43
h-index

25983

112
g-index

131
all docs

131
docs citations

131
times ranked

75252
citing authors

#	ARTICLE	IF	CITATIONS
1	MadR mediates acyl CoA-dependent regulation of mycolic acid desaturation in mycobacteria. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	0
2	Mathematical models to study the biology of pathogens and the infectious diseases they cause. IScience, 2022, 25, 104079.	1.9	8
3	A systems-level gene regulatory network model for <i>Plasmodium falciparum</i> . Nucleic Acids Research, 2021, 49, 4891-4906.	6.5	2
4	Synergistic epistasis enhances the co-operativity of mutualistic interspecies interactions. ISME Journal, 2021, 15, 2233-2247.	4.4	6
5	Lettuce (<i>Lactuca sativa</i>) productivity influenced by microbial inocula under nitrogen-limited conditions in aquaponics. PLoS ONE, 2021, 16, e0247534.	1.1	14
6	Sulfur Metabolites Play Key System-Level Roles in Modulating Denitrification. MSystems, 2021, 6, .	1.7	10
7	Mechanism Across Scales: A Holistic Modeling Framework Integrating Laboratory and Field Studies for Microbial Ecology. Frontiers in Microbiology, 2021, 12, 642422.	1.5	12
8	History and Future Perspectives on the Discipline of Quantitative Systems Pharmacology Modeling and Its Applications. Frontiers in Physiology, 2021, 12, 637999.	1.3	44
9	Diel Transcriptional Oscillations of a Plastid Antiporter Reflect Increased Resilience of <i>Thalassiosira pseudonana</i> in Elevated CO ₂ . Frontiers in Marine Science, 2021, 8, .	1.2	4
10	Genetic program activity delineates risk, relapse, and therapy responsiveness in multiple myeloma. Npj Precision Oncology, 2021, 5, 60.	2.3	5
11	A Systems Approach to Brain Tumor Treatment. Cancers, 2021, 13, 3152.	1.7	21
12	Contrasting heat stress response patterns of coral holobionts across the Red Sea suggest distinct mechanisms of thermal tolerance. Molecular Ecology, 2021, 30, 4466-4480.	2.0	68
13	Autophagy as a Mechanism for Adaptive Prediction-Mediated Emergence of Drug Resistance. Frontiers in Microbiology, 2021, 12, 712631.	1.5	1
14	Mycobacterium abscessus biofilms produce an extracellular matrix and have a distinct mycolic acid profile. Cell Surface, 2021, 7, 100051.	1.5	23
15	InÂvivo commensal control of <i>Clostridioides difficile</i> virulence. Cell Host and Microbe, 2021, 29, 1693-1708.e7.	5.1	62
16	Predictive regulatory and metabolic network models for systems analysis of <i>Clostridioides difficile</i> . Cell Host and Microbe, 2021, 29, 1709-1723.e5.	5.1	12
17	Transcriptome signature of cell viability predicts drug response and drug interaction in <i>Mycobacterium tuberculosis</i> . Cell Reports Methods, 2021, 1, 100123.	1.4	4
18	EPCO-23. A SINGLE-CELL BASED PRECISION MEDICINE APPROACH USING GLIOBLASTOMA PATIENT-SPECIFIC MODELS. Neuro-Oncology, 2021, 23, vi6-vi7.	0.6	0

#	ARTICLE	IF	CITATIONS
19	Quantitative prediction of conditional vulnerabilities in regulatory and metabolic networks using PRIME. <i>Npj Systems Biology and Applications</i> , 2021, 7, 43.	1.4	3
20	A comprehensive spectral assay library to quantify the <i>Escherichia coli</i> proteome by DIA/SWATH-MS. <i>Scientific Data</i> , 2020, 7, 389.	2.4	28
21	Biofilms of the non-tuberculous <i>Mycobacterium chelonae</i> form an extracellular matrix and display distinct expression patterns. <i>Cell Surface</i> , 2020, 6, 100043.	1.5	8
22	Selective Translation of Low Abundance and Upregulated Transcripts in <i>Halobacterium salinarum</i> . <i>MSystems</i> , 2020, 5, .	1.7	10
23	Transcriptional portrait of <i>M. bovis</i> BCG during biofilm production shows genes differentially expressed during intercellular aggregation and substrate attachment. <i>Scientific Reports</i> , 2020, 10, 12578.	1.6	12
24	Intricate Genetic Programs Controlling Dormancy in <i>Mycobacterium tuberculosis</i> . <i>Cell Reports</i> , 2020, 31, 107577.	2.9	31
25	Inference of Bacterial Small RNA Regulatory Networks and Integration with Transcription Factor-Driven Regulatory Networks. <i>MSystems</i> , 2020, 5, .	1.7	14
26	Crippling life support for SARS-CoV-2 and other viruses through synthetic lethality. <i>Journal of Cell Biology</i> , 2020, 219, .	2.3	20
27	PerSort Facilitates Characterization and Elimination of Persister Subpopulation in <i>Mycobacteria</i> . <i>MSystems</i> , 2020, 5, .	1.7	12
28	Use and abuse of correlation analyses in microbial ecology. <i>ISME Journal</i> , 2019, 13, 2647-2655.	4.4	193
29	EcoFABs: advancing microbiome science through standardized fabricated ecosystems. <i>Nature Methods</i> , 2019, 16, 567-571.	9.0	90
30	Temporal and metabolic overlap between lipid accumulation and programmed cell death due to nitrogen starvation in the unicellular chlorophyte <i>Chlamydomonas reinhardtii</i> . <i>Phycological Research</i> , 2019, 67, 173-183.	0.8	13
31	Pathâ€seq identifies an essential mycolate remodeling program for mycobacterial host adaptation. <i>Molecular Systems Biology</i> , 2019, 15, e8584.	3.2	51
32	Constraintâ€based modelling captures the metabolic versatility of <i>Desulfovibrio vulgaris</i> . <i>Environmental Microbiology Reports</i> , 2018, 10, 190-201.	1.0	11
33	Transcriptional regulatory networks underlying gene expression changes in Huntington's disease. <i>Molecular Systems Biology</i> , 2018, 14, e7435.	3.2	55
34	Stress response of a marine ammonia-oxidizing archaeon informs physiological status of environmental populations. <i>ISME Journal</i> , 2018, 12, 508-519.	4.4	82
35	The BCG ^{Î²} BCG1419c Vaccine Candidate Reduces Lung Pathology, IL-6, TNF-Î±, and IL-10 During Chronic TB Infection. <i>Frontiers in Microbiology</i> , 2018, 9, 1281.	1.5	25
36	Systems biology approaches towards predictive microbial ecology. <i>Environmental Microbiology</i> , 2018, 20, 4197-4209.	1.8	19

#	ARTICLE	IF	CITATIONS
37	Ocean acidification conditions increase resilience of marine diatoms. <i>Nature Communications</i> , 2018, 9, 2328.	5.8	38
38	The State of Systems Genetics in 2017. <i>Cell Systems</i> , 2017, 4, 7-15.	2.9	29
39	Robustness of a model microbial community emerges from population structure among single cells of a clonal population. <i>Environmental Microbiology</i> , 2017, 19, 3059-3069.	1.8	13
40	Mechanism for microbial population collapse in a fluctuating resource environment. <i>Molecular Systems Biology</i> , 2017, 13, 919.	3.2	22
41	Adaptive Prediction Emerges Over Short Evolutionary Time Scales. <i>Genome Biology and Evolution</i> , 2017, 9, 1616-1623.	1.1	14
42	A genome wide dosage suppressor network reveals genomic robustness. <i>Nucleic Acids Research</i> , 2017, 45, 255-270.	6.5	13
43	Combining inferred regulatory and reconstructed metabolic networks enhances phenotype prediction in yeast. <i>PLoS Computational Biology</i> , 2017, 13, e1005489.	1.5	46
44	The Transcription Factor Nfatc2 Regulates Î²-Cell Proliferation and Genes Associated with Type 2 Diabetes in Mouse and Human Islets. <i>PLoS Genetics</i> , 2016, 12, e1006466.	1.5	40
45	MiR-155â€œregulated molecular network orchestrates cell fate in the innate and adaptive immune response to <i>Mycobacterium tuberculosis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E6172-E6181.	3.3	109
46	Causal Mechanistic Regulatory Network for Glioblastoma Deciphered Using Systems Genetics Network Analysis. <i>Cell Systems</i> , 2016, 3, 172-186.	2.9	97
47	Network analysis identifies Rv0324 and Rv0880 as regulators of bedaquiline tolerance in <i>Mycobacterium tuberculosis</i> . <i>Nature Microbiology</i> , 2016, 1, 16078.	5.9	71
48	Pan-transcriptomic analysis identifies coordinated and orthologous functional modules in the diatoms <i>Thalassiosira pseudonana</i> and <i>Phaeodactylum tricornutum</i> . <i>Marine Genomics</i> , 2016, 26, 21-28.	0.4	40
49	Bicluster Sampled Coherence Metric (BSCM) provides an accurate environmental context for phenotype predictions. <i>BMC Systems Biology</i> , 2015, 9, S1.	3.0	4
50	A refined genome-scale reconstruction of <i>Chlamydomonas</i> metabolism provides a platform for systems-level analyses. <i>Plant Journal</i> , 2015, 84, 1239-1256.	2.8	70
51	Data-driven integration of genome-scale regulatory and metabolic network models. <i>Frontiers in Microbiology</i> , 2015, 6, 409.	1.5	49
52	cMonkey ₂ : Automated, systematic, integrated detection of co-regulated gene modules for any organism. <i>Nucleic Acids Research</i> , 2015, 43, e87-e87.	6.5	45
53	A comprehensive map of genome-wide gene regulation in <i>Mycobacterium tuberculosis</i> . <i>Scientific Data</i> , 2015, 2, 150010.	2.4	55
54	Transcriptional program for nitrogen starvation-induced lipid accumulation in <i>Chlamydomonas reinhardtii</i> . <i>Biotechnology for Biofuels</i> , 2015, 8, 207.	6.2	60

#	ARTICLE	IF	CITATIONS
55	Genome-wide CRISPR-Cas9 Screens Reveal Loss of Redundancy between PKMYT1 and WEE1 in Glioblastoma Stem-like Cells. Cell Reports, 2015, 13, 2425-2439.	2.9	146
56	The DNA-binding network of Mycobacterium tuberculosis s. Nature Communications, 2015, 6, 5829.	5.8	192
57	Diatom acclimation to elevated CO ₂ via cAMP signalling and coordinated gene expression. Nature Climate Change, 2015, 5, 761-765.	8.1	108
58	Sense overlapping transcripts in IS<i>1341</i>-type transposase genes are functional non-coding RNAs in archaea. RNA Biology, 2015, 12, 490-500.	1.5	27
59	A method to analyze, sort, and retain viability of obligate anaerobic microorganisms from complex microbial communities. Journal of Microbiological Methods, 2015, 117, 74-77.	0.7	13
60	Ocean Acidification. The Science Teacher, 2015, 082, .	0.1	2
61	Transcription Start Site Associated RNAs (TSSaRNAs) Are Ubiquitous in All Domains of Life. PLoS ONE, 2014, 9, e107680.	1.1	14
62	A high-resolution network model for global gene regulation in Mycobacterium tuberculosis. Nucleic Acids Research, 2014, 42, 11291-11303.	6.5	61
63	Molecular mechanisms of system responses to novel stimuli are predictable from public data. Nucleic Acids Research, 2014, 42, 1442-1460.	6.5	28
64	A system-level model for the microbial regulatory genome. Molecular Systems Biology, 2014, 10, 740.	3.2	64
65	An evolutionarily conserved <scp>RNase</scp>-based mechanism for repression of transcriptional positive autoregulation. Molecular Microbiology, 2014, 92, 369-382.	1.2	12
66	Model Organisms Retain an "Ecological Memory" of Complex Ecologically Relevant Environmental Variation. Applied and Environmental Microbiology, 2014, 80, 1821-1831.	1.4	16
67	Evolution of context dependent regulation by expansion of feast/famine regulatory proteins. BMC Systems Biology, 2014, 8, 122.	3.0	19
68	Mapping and manipulating the Mycobacterium tuberculosis transcriptome using a transcription factor overexpression-derived regulatory network. Genome Biology, 2014, 15, 502.	3.8	136
69	Community-integrated omics links dominance of a microbial generalist to fine-tuned resource usage. Nature Communications, 2014, 5, 5603.	5.8	75
70	Network portal: a database for storage, analysis and visualization of biological networks. Nucleic Acids Research, 2014, 42, D184-D190.	6.5	20
71	Structure-based predictions broadly link transcription factor mutations to gene expression changes in cancers. Nucleic Acids Research, 2014, 42, 12973-12983.	6.5	5
72	Erosion of functional independence early in the evolution of a microbial mutualism. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 14822-14827.	3.3	63

#	ARTICLE	IF	CITATIONS
73	Inference of Expanded Lrp-Like Feast/Famine Transcription Factor Targets in a Non-Model Organism Using Protein Structure-Based Prediction. PLoS ONE, 2014, 9, e107863.	1.1	5
74	A systems level predictive model for global gene regulation of methanogenesis in a hydrogenotrophic methanogen. Genome Research, 2013, 23, 1839-1851.	2.4	30
75	Genome-wide diel growth state transitions in the diatom <i>Thalassiosira pseudonana</i> . Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 7518-7523.	3.3	132
76	A Role for Programmed Cell Death in the Microbial Loop. PLoS ONE, 2013, 8, e62595.	1.1	57
77	A miRNA-regulatory network explains how dysregulated miRNAs perturb oncogenic processes across diverse cancers. Genome Research, 2012, 22, 2302-2314.	2.4	184
78	Adaptation of cells to new environments. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2011, 3, 544-561.	6.6	148
79	Parallel evolution of transcriptome architecture during genome reorganization. Genome Research, 2011, 21, 1892-1904.	2.4	58
80	miRvestigator: web application to identify miRNAs responsible for co-regulated gene expression patterns discovered through transcriptome profiling. Nucleic Acids Research, 2011, 39, W125-W131.	6.5	26
81	Niche adaptation by expansion and reprogramming of general transcription factors. Molecular Systems Biology, 2011, 7, 554.	3.2	39
82	Coordination of frontline defense mechanisms under severe oxidative stress. Molecular Systems Biology, 2010, 6, 393.	3.2	55
83	Large scale physiological readjustment during growth enables rapid, comprehensive and inexpensive systems analysis. BMC Systems Biology, 2010, 4, 64.	3.0	27
84	GTC: A web server for integrating systems biology data with web tools and desktop applications. Source Code for Biology and Medicine, 2010, 5, 7.	1.7	2
85	Diurnally Entrained Anticipatory Behavior in Archaea. PLoS ONE, 2009, 4, e5485.	1.1	59
86	A single transcription factor regulates evolutionarily diverse but functionally linked metabolic pathways in response to nutrient availability. Molecular Systems Biology, 2009, 5, 282.	3.2	55
87	Prevalence of transcription promoters within archaeal operons and coding sequences. Molecular Systems Biology, 2009, 5, 285.	3.2	114
88	The role of predictive modelling in rationally re-engineering biological systems. Nature Reviews Microbiology, 2009, 7, 297-305.	13.6	55
89	Halobacterium salinarum NRC-1 PeptideAtlas: Toward Strategies for Targeted Proteomics and Improved Proteome Coverage. Journal of Proteome Research, 2008, 7, 3755-3764.	1.8	46
90	The Scale of Prediction. Science, 2008, 320, 1297-1298.	6.0	16

#	ARTICLE	IF	CITATIONS
91	General transcription factor specified global gene regulation in archaea. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 4630-4635.	3.3	105
92	The anatomy of microbial cell state transitions in response to oxygen. Genome Research, 2007, 17, 1399-1413.	2.4	59
93	A Predictive Model for Transcriptional Control of Physiology in a Free Living Cell. Cell, 2007, 131, 1354-1365.	13.5	284
94	The Firegoose: two-way integration of diverse data from different bioinformatics web resources with desktop applications. BMC Bioinformatics, 2007, 8, 456.	1.2	30
95	Prokaryotic Systems Biology. Cell Engineering, 2007, , 395-423.	0.4	1
96	The Inferelator: an algorithm for learning parsimonious regulatory networks from systems-biology data sets de novo. Genome Biology, 2006, 7, R36.	13.9	456
97	An integrated systems approach for understanding cellular responses to gamma radiation. Molecular Systems Biology, 2006, 2, 47.	3.2	78
98	The Gaggle: an open-source software system for integrating bioinformatics software and data sources. BMC Bioinformatics, 2006, 7, 176.	1.2	135
99	Integrated biclustering of heterogeneous genome-wide datasets for the inference of global regulatory networks. BMC Bioinformatics, 2006, 7, 280.	1.2	221
100	A systems view of haloarchaeal strategies to withstand stress from transition metals. Genome Research, 2006, 16, 841-854.	2.4	101
101	Systems Level Insights Into the Stress Response to UV Radiation in the Halophilic Archaeon Halobacterium NRC-1. Genome Research, 2004, 14, 1025-1035.	2.4	130
102	Genome sequence of Haloarcula marismortui: A halophilic archaeon from the Dead Sea. Genome Research, 2004, 14, 2221-2234.	2.4	268
103	Low-pass sequencing for microbial comparative genomics. BMC Genomics, 2004, 5, 3.	1.2	40
104	Comprehensive de novo structure prediction in a systems-biology context for the archaea Halobacterium sp. NRC-1. Genome Biology, 2004, 5, R52.	13.9	45
105	Systems Biology Experimental Design - Considerations for Building Predictive Gene Regulatory Network Models for Prokaryotic Systems. Current Genomics, 2004, 5, 527-544.	0.7	18
106	Proteomic Analysis of an Extreme Halophilic Archaeon, Halobacterium sp. NRC-1. Molecular and Cellular Proteomics, 2003, 2, 506-524.	2.5	52
107	Cytoscape: A Software Environment for Integrated Models of Biomolecular Interaction Networks. Genome Research, 2003, 13, 2498-2504.	2.4	37,062
108	Coordinate regulation of energy transduction modules in Halobacterium sp. analyzed by a global systems approach. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 14913-14918.	3.3	123

#	ARTICLE	IF	CITATIONS
109	Genomic perspective on the photobiology of Halobacterium species NRC-1, a phototrophic, phototactic, and UV-tolerant haloarchaeon. <i>Photosynthesis Research</i> , 2001, 70, 3-17.	1.6	54
110	Promoter analysis by saturation mutagenesis. <i>Biological Procedures Online</i> , 2001, 3, 64-69.	1.4	6
111	Saturation mutagenesis of the haloarchaeal bop gene promoter: identification of DNA supercoiling sensitivity sites and absence of TFB recognition element and UAS enhancer activity. <i>Molecular Microbiology</i> , 2000, 36, 1175-1183.	1.2	26
112	Is gene expression in Halobacterium NRC-1 regulated by multiple TBP and TFB transcription factors?. <i>MicroCorrespondence. Molecular Microbiology</i> , 2000, 36, 1184-1185.	1.2	94
113	Saturation Mutagenesis of the TATA Box and Upstream Activator Sequence in the Haloarchaeal bop Gene Promoter. <i>Journal of Bacteriology</i> , 1999, 181, 2513-2518.	1.0	35
114	Context-Specific Regulation of Coupled Transcription-Translation Modules Predicts Pervasive Ribosome Specialization. <i>SSRN Electronic Journal</i> , 0, , .	0.4	2