Nitin S Baliga

List of Publications by Year
in descending order

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	Cytoscape: A Software Environment for Integrated Models of Biomolecular Interaction Networks. Genome Research, 2003, 13, 2498-2504.	2.4	37,062
2	The Inferelator: an algorithm for learning parsimonious regulatory networks from systems-biology data sets de novo. Genome Biology, 2006, 7, R36.	13.9	456
3	A Predictive Model for Transcriptional Control of Physiology in a Free Living Cell. Cell, 2007, 131, 1354-1365.	13.5	284
4	Genome sequence of Haloarcula marismortui: A halophilic archaeon from the Dead Sea. Genome Research, 2004, 14, 2221-2234.	2.4	268
5	Integrated biclustering of heterogeneous genome-wide datasets for the inference of global regulatory networks. BMC Bioinformatics, 2006, 7, 280.	1.2	221
6	Use and abuse of correlation analyses in microbial ecology. ISME Journal, 2019, 13, 2647-2655.	4.4	193
7	The DNA-binding network of Mycobacterium tuberculosi s. Nature Communications, 2015, 6, 5829.	5.8	192
8	A miRNA-regulatory network explains how dysregulated miRNAs perturb oncogenic processes across diverse cancers. Genome Research, 2012, 22, 2302-2314.	2.4	184
9	Adaptation of cells to new environments. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2011, 3, 544-561.	6.6	148
10	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
11	Mapping and manipulating the Mycobacterium tuberculosis transcriptome using a transcription factor overexpression-derived regulatory network. Genome Biology, 2014, 15, 502.	3.8	136
12	The Gaggle: an open-source software system for integrating bioinformatics software and data sources. BMC Bioinformatics, 2006, 7, 176.	1.2	135
13	Genome-wide diel growth state transitions in the diatom *Thalassiosira pseudonana*. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 7518-7523.	3.3	132
14	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
15	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
16	Prevalence of transcription promoters within archaeal operons and coding sequences. Molecular Systems Biology, 2009, 5, 285.	3.2	114
17	MiR-155â€"regulated molecular network orchestrates cell fate in the innate and adaptive immune response to *Mycobacterium tuberculosis*. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E6172-E6181.	3.3	109
18	Diatom acclimation to elevated CO2 via cAMP signalling and coordinated gene expression. Nature Climate Change, 2015, 5, 761-765.	8.1	108

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19	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
20	A systems view of haloarchaeal strategies to withstand stress from transition metals. Genome Research, 2006, 16, 841-854.	2.4	101
21	Causal Mechanistic Regulatory Network for Glioblastoma Deciphered Using Systems Genetics Network Analysis. Cell Systems, 2016, 3, 172-186.	2.9	97
22	Is gene expression in Halobacterium NRC-1 regulated by multiple TBP and TFB transcription factors?. MicroCorrespondence. Molecular Microbiology, 2000, 36, 1184-1185.	1.2	94
23	EcoFABs: advancing microbiome science through standardized fabricated ecosystems. Nature Methods, 2019, 16, 567-571.	9.0	90
24	Stress response of a marine ammonia-oxidizing archaeon informs physiological status of environmental populations. ISME Journal, 2018, 12, 508-519.	4.4	82
25	An integrated systems approach for understanding cellular responses to gamma radiation. Molecular Systems Biology, 2006, 2, 47.	3.2	78
26	Community-integrated omics links dominance of a microbial generalist to fine-tuned resource usage. Nature Communications, 2014, 5, 5603.	5.8	75
27	Network analysis identifies Rv0324 and Rv0880 as regulators of bedaquiline tolerance in Mycobacterium tuberculosis. Nature Microbiology, 2016, 1, 16078.	5.9	71
28	A refined genomeâ€scale reconstruction of *Chlamydomonas* metabolism provides a platform for systemsâ€level analyses. Plant Journal, 2015, 84, 1239-1256.	2.8	70
29	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
30	A systemâ€level model for the microbial regulatory genome. Molecular Systems Biology, 2014, 10, 740.	3.2	64
31	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
32	InÂ vivo commensal control of Clostridioides difficile virulence. Cell Host and Microbe, 2021, 29, 1693-1708.e7.	5.1	62
33	A high-resolution network model for global gene regulation in Mycobacterium tuberculosis. Nucleic Acids Research, 2014, 42, 11291-11303.	6.5	61
34	Transcriptional program for nitrogen starvation-induced lipid accumulation in Chlamydomonas reinhardtii. Biotechnology for Biofuels, 2015, 8, 207.	6.2	60
35	The anatomy of microbial cell state transitions in response to oxygen. Genome Research, 2007, 17, 1399-1413.	2.4	59
36	Diurnally Entrained Anticipatory Behavior in Archaea. PLoS ONE, 2009, 4, e5485.	1.1	59

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37	Parallel evolution of transcriptome architecture during genome reorganization. Genome Research, 2011, 21, 1892-1904.	2.4	58
38	A Role for Programmed Cell Death in the Microbial Loop. PLoS ONE, 2013, 8, e62595.	1.1	57
39	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
40	The role of predictive modelling in rationally re-engineering biological systems. Nature Reviews Microbiology, 2009, 7, 297-305.	13.6	55
41	Coordination of frontline defense mechanisms under severe oxidative stress. Molecular Systems Biology, 2010, 6, 393.	3.2	55
42	A comprehensive map of genome-wide gene regulation in Mycobacterium tuberculosis. Scientific Data, 2015, 2, 150010.	2.4	55
43	Transcriptional regulatory networks underlying gene expression changes in Huntington's disease. Molecular Systems Biology, 2018, 14, e7435.	3.2	55
44	Genomic perspective on the photobiology of Halobacterium species NRC-1, a phototrophic, phototactic, and UV-tolerant haloarchaeon. Photosynthesis Research, 2001, 70, 3-17.	1.6	54
45	Proteomic Analysis of an Extreme Halophilic Archaeon, Halobacterium sp. NRC-1. Molecular and Cellular Proteomics, 2003, 2, 506-524.	2.5	52
46	Path–seq identifies an essential mycolate remodeling program for mycobacterial host adaptation. Molecular Systems Biology, 2019, 15, e8584.	3.2	51
47	Data-driven integration of genome-scale regulatory and metabolic network models. Frontiers in Microbiology, 2015, 6, 409.	1.5	49
48	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
49	Combining inferred regulatory and reconstructed metabolic networks enhances phenotype prediction in yeast. PLoS Computational Biology, 2017, 13, e1005489.	1.5	46
50	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
51	cMonkey$_2$: Automated, systematic, integrated detection of co-regulated gene modules for any organism. Nucleic Acids Research, 2015, 43, e87-e87.	6.5	45
52	History and Future Perspectives on the Discipline of Quantitative Systems Pharmacology Modeling and Its Applications. Frontiers in Physiology, 2021, 12, 637999.	1.3	44
53	Low-pass sequencing for microbial comparative genomics. BMC Genomics, 2004, 5, 3.	1.2	40
54	The Transcription Factor Nfatc2 Regulates Î²-Cell Proliferation and Genes Associated with Type 2 Diabetes in Mouse and Human Islets. PLoS Genetics, 2016, 12, e1006466.	1.5	40

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55	Pan-transcriptomic analysis identifies coordinated and orthologous functional modules in the diatoms Thalassiosira pseudonana and Phaeodactylum tricornutum. Marine Genomics, 2016, 26, 21-28.	0.4	40
56	Niche adaptation by expansion and reprogramming of general transcription factors. Molecular Systems Biology, 2011, 7, 554.	3.2	39
57	Ocean acidification conditions increase resilience of marine diatoms. Nature Communications, 2018, 9, 2328.	5.8	38
58	Saturation Mutagenesis of the TATA Box and Upstream Activator Sequence in the Haloarchaeal bop Gene Promoter. Journal of Bacteriology, 1999, 181, 2513-2518.	1.0	35
59	Intricate Genetic Programs Controlling Dormancy in Mycobacterium tuberculosis. Cell Reports, 2020, 31, 107577.	2.9	31
60	The Firegoose: two-way integration of diverse data from different bioinformatics web resources with desktop applications. BMC Bioinformatics, 2007, 8, 456.	1.2	30
61	A systems level predictive model for global gene regulation of methanogenesis in a hydrogenotrophic methanogen. Genome Research, 2013, 23, 1839-1851.	2.4	30
62	The State of Systems Genetics in 2017. Cell Systems, 2017, 4, 7-15.	2.9	29
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 comprehensive spectral assay library to quantify the Escherichia coli proteome by DIA/SWATH-MS. Scientific Data, 2020, 7, 389.	2.4	28
65	Large scale physiological readjustment during growth enables rapid, comprehensive and inexpensive systems analysis. BMC Systems Biology, 2010, 4, 64.	3.0	27
66	Sense overlapping transcripts in IS*1341*-type transposase genes are functional non-coding RNAs in archaea. RNA Biology, 2015, 12, 490-500.	1.5	27
67	Saturation mutagenesis of the haloarchaeal bop gene promoter: identification of DNA supercoiling sensitivity sites and absence of TFB recognition element and UAS enhancer activity. Molecular Microbiology, 2000, 36, 1175-1183.	1.2	26
68	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
69	The BCGÎ"BCG1419c Vaccine Candidate Reduces Lung Pathology, IL-6, TNF-Î±, and IL-10 During Chronic TB Infection. Frontiers in Microbiology, 2018, 9, 1281.	1.5	25
70	Mycobacterium abscessus biofilms produce an extracellular matrix and have a distinct mycolic acid profile. Cell Surface, 2021, 7, 100051.	1.5	23
71	Mechanism for microbial population collapse in a fluctuating resource environment. Molecular Systems Biology, 2017, 13, 919.	3.2	22
72	A Systems Approach to Brain Tumor Treatment. Cancers, 2021, 13, 3152.	1.7	21

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73	Network portal: a database for storage, analysis and visualization of biological networks. Nucleic Acids Research, 2014, 42, D184-D190.	6.5	20
74	Crippling life support for SARS-CoV-2 and other viruses through synthetic lethality. Journal of Cell Biology, 2020, 219, .	2.3	20
75	Evolution of context dependent regulation by expansion of feast/famine regulatory proteins. BMC Systems Biology, 2014, 8, 122.	3.0	19
76	Systems biology approaches towards predictive microbial ecology. Environmental Microbiology, 2018, 20, 4197-4209.	1.8	19
77	Systems Biology Experimental Design - Considerations for Building Predictive Gene Regulatory Network Models for Prokaryotic Systems. Current Genomics, 2004, 5, 527-544.	0.7	18
78	The Scale of Prediction. Science, 2008, 320, 1297-1298.	6.0	16
79	Model Organisms Retain an â€œEcological Memoryâ€•of Complex Ecologically Relevant Environmental Variation. Applied and Environmental Microbiology, 2014, 80, 1821-1831.	1.4	16
80	Transcription Start Site Associated RNAs (TSSaRNAs) Are Ubiquitous in All Domains of Life. PLoS ONE, 2014, 9, e107680.	1.1	14
81	Adaptive Prediction Emerges Over Short Evolutionary Time Scales. Genome Biology and Evolution, 2017, 9, 1616-1623.	1.1	14
82	Inference of Bacterial Small RNA Regulatory Networks and Integration with Transcription Factor-Driven Regulatory Networks. MSystems, 2020, 5, .	1.7	14
83	Lettuce (Lactuca sativa) productivity influenced by microbial inocula under nitrogen-limited conditions in aquaponics. PLoS ONE, 2021, 16, e0247534.	1.1	14
84	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
85	Robustness of a model microbial community emerges from population structure among single cells of a clonal population. Environmental Microbiology, 2017, 19, 3059-3069.	1.8	13
86	A genome wide dosage suppressor network reveals genomic robustness. Nucleic Acids Research, 2017, 45, 255-270.	6.5	13
87	Temporal and metabolic overlap between lipid accumulation and programmed cell death due to nitrogen starvation in the unicellular chlorophyte Chlamydomonas reinhardtii. Phycological Research, 2019, 67, 173-183.	0.8	13
88	An evolutionarily conserved <scp>RNase</scp>â€•based mechanism for repression of transcriptional positive autoregulation. Molecular Microbiology, 2014, 92, 369-382.	1.2	12
89	Transcriptional portrait of M. bovis BCG during biofilm production shows genes differentially expressed during intercellular aggregation and substrate attachment. Scientific Reports, 2020, 10, 12578.	1.6	12
90	Mechanism Across Scales: A Holistic Modeling Framework Integrating Laboratory and Field Studies for Microbial Ecology. Frontiers in Microbiology, 2021, 12, 642422.	1.5	12

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91	PerSort Facilitates Characterization and Elimination of Persister Subpopulation in Mycobacteria. MSystems, 2020, 5, .	1.7	12
92	Predictive regulatory and metabolic network models for systems analysis of Clostridioides difficile. Cell Host and Microbe, 2021, 29, 1709-1723.e5.	5.1	12
93	Constraintâ€based modelling captures the metabolic versatility of <i>Desulfovibrio vulgaris</i>. Environmental Microbiology Reports, 2018, 10, 190-201.	1.0	11
94	Selective Translation of Low Abundance and Upregulated Transcripts in Halobacterium salinarum. MSystems, 2020, 5, .	1.7	10
95	Sulfur Metabolites Play Key System-Level Roles in Modulating Denitrification. MSystems, 2021, 6, .	1.7	10
96	Biofilms of the non-tuberculous Mycobacterium chelonae form an extracellular matrix and display distinct expression patterns. Cell Surface, 2020, 6, 100043.	1.5	8
97	Mathematical models to study the biology of pathogens and the infectious diseases they cause. IScience, 2022, 25, 104079.	1.9	8
98	Promoter analysis by saturation mutagenesis. Biological Procedures Online, 2001, 3, 64-69.	1.4	6
99	Synergistic epistasis enhances the co-operativity of mutualistic interspecies interactions. ISME Journal, 2021, 15, 2233-2247.	4.4	6
100	Structure-based predictions broadly link transcription factor mutations to gene expression changes in cancers. Nucleic Acids Research, 2014, 42, 12973-12983.	6.5	5
101	Genetic program activity delineates risk, relapse, and therapy responsiveness in multiple myeloma. Npj Precision Oncology, 2021, 5, 60.	2.3	5
102	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
103	Bicluster Sampled Coherence Metric (BSCM) provides an accurate environmental context for phenotype predictions. BMC Systems Biology, 2015, 9, S1.	3.0	4
104	Diel Transcriptional Oscillations of a Plastid Antiporter Reflect Increased Resilience of Thalassiosira pseudonana in Elevated CO2. Frontiers in Marine Science, 2021, 8, .	1.2	4
105	Transcriptome signature of cell viability predicts drug response and drug interaction in Mycobacterium tuberculosis. Cell Reports Methods, 2021, 1, 100123.	1.4	4
106	Quantitative prediction of conditional vulnerabilities in regulatory and metabolic networks using PRIME. Npj Systems Biology and Applications, 2021, 7, 43.	1.4	3
107	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
108	A systems-level gene regulatory network model for <i>Plasmodium falciparum</i>. Nucleic Acids Research, 2021, 49, 4891-4906.	6.5	2

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109	Context-Specific Regulation of Coupled Transcription-Translation Modules Predicts Pervasive Ribosome Specialization. SSRN Electronic Journal, 0, , .	0.4	2
110	Ocean Acidification. The Science Teacher, 2015, 082, .	0.1	2
111	Autophagy as a Mechanism for Adaptive Prediction-Mediated Emergence of Drug Resistance. Frontiers in Microbiology, 2021, 12, 712631.	1.5	1
112	Prokaryotic Systems Biology. Cell Engineering, 2007, , 395-423.	0.4	1
113	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
114	EPCO-23. A SINGLE-CELL BASED PRECISION MEDICINE APPROACH USING GLIOBLASTOMA PATIENT-SPECIFIC MODELS. Neuro-Oncology, 2021, 23, vi6-vi7.	0.6	0