

Nitin S Baliga

List of Publications by Year in descending order

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114
papers

43,355
citations

57758

44
h-index

22832

112
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131
all docs

131
docs citations

131
times ranked

68470
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 1 | Cytoscape: A Software Environment for Integrated Models of Biomolecular Interaction Networks. <i>Genome Research</i> , 2003, 13, 2498-2504. | 5.5 | 37,062 |
| 2 | The Inferelator: an algorithm for learning parsimonious regulatory networks from systems-biology data sets de novo. <i>Genome Biology</i> , 2006, 7, R36. | 9.6 | 456 |
| 3 | A Predictive Model for Transcriptional Control of Physiology in a Free Living Cell. <i>Cell</i> , 2007, 131, 1354-1365. | 28.9 | 284 |
| 4 | Genome sequence of <i>Haloarcula marismortui</i> : A halophilic archaeon from the Dead Sea. <i>Genome Research</i> , 2004, 14, 2221-2234. | 5.5 | 268 |
| 5 | Integrated biclustering of heterogeneous genome-wide datasets for the inference of global regulatory networks. <i>BMC Bioinformatics</i> , 2006, 7, 280. | 2.6 | 221 |
| 6 | Use and abuse of correlation analyses in microbial ecology. <i>ISME Journal</i> , 2019, 13, 2647-2655. | 9.8 | 193 |
| 7 | The DNA-binding network of <i>Mycobacterium tuberculosis</i> s. <i>Nature Communications</i> , 2015, 6, 5829. | 12.8 | 192 |
| 8 | A miRNA-regulatory network explains how dysregulated miRNAs perturb oncogenic processes across diverse cancers. <i>Genome Research</i> , 2012, 22, 2302-2314. | 5.5 | 184 |
| 9 | Adaptation of cells to new environments. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 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. <i>Cell Reports</i> , 2015, 13, 2425-2439. | 6.4 | 146 |
| 11 | Mapping and manipulating the <i>Mycobacterium tuberculosis</i> transcriptome using a transcription factor overexpression-derived regulatory network. <i>Genome Biology</i> , 2014, 15, 502. | 8.8 | 136 |
| 12 | The Gaggles: an open-source software system for integrating bioinformatics software and data sources. <i>BMC Bioinformatics</i> , 2006, 7, 176. | 2.6 | 135 |
| 13 | Genome-wide diel growth state transitions in the diatom <i>Thalassiosira pseudonana</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 7518-7523. | 7.1 | 132 |
| 14 | Systems Level Insights Into the Stress Response to UV Radiation in the Halophilic Archaeon <i>Halobacterium</i> NRC-1. <i>Genome Research</i> , 2004, 14, 1025-1035. | 5.5 | 130 |
| 15 | Coordinate regulation of energy transduction modules in <i>Halobacterium</i> sp. analyzed by a global systems approach. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 14913-14918. | 7.1 | 123 |
| 16 | Prevalence of transcription promoters within archaeal operons and coding sequences. <i>Molecular Systems Biology</i> , 2009, 5, 285. | 7.2 | 114 |
| 17 | MiR-155 regulated 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. | 7.1 | 109 |
| 18 | Diatom acclimation to elevated CO ₂ via cAMP signalling and coordinated gene expression. <i>Nature Climate Change</i> , 2015, 5, 761-765. | 18.8 | 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. | 7.1 | 105 |
| 20 | A systems view of haloarchaeal strategies to withstand stress from transition metals. Genome Research, 2006, 16, 841-854. | 5.5 | 101 |
| 21 | Causal Mechanistic Regulatory Network for Glioblastoma Deciphered Using Systems Genetics Network Analysis. Cell Systems, 2016, 3, 172-186. | 6.2 | 97 |
| 22 | Is gene expression in Halobacterium NRC-1 regulated by multiple TBP and TFB transcription factors?. MicroCorrespondence. Molecular Microbiology, 2000, 36, 1184-1185. | 2.5 | 94 |
| 23 | EcoFABs: advancing microbiome science through standardized fabricated ecosystems. Nature Methods, 2019, 16, 567-571. | 19.0 | 90 |
| 24 | Stress response of a marine ammonia-oxidizing archaeon informs physiological status of environmental populations. ISME Journal, 2018, 12, 508-519. | 9.8 | 82 |
| 25 | An integrated systems approach for understanding cellular responses to gamma radiation. Molecular Systems Biology, 2006, 2, 47. | 7.2 | 78 |
| 26 | Community-integrated omics links dominance of a microbial generalist to fine-tuned resource usage. Nature Communications, 2014, 5, 5603. | 12.8 | 75 |
| 27 | Network analysis identifies Rv0324 and Rv0880 as regulators of bedaquiline tolerance in Mycobacterium tuberculosis. Nature Microbiology, 2016, 1, 16078. | 13.3 | 71 |
| 28 | A refined genome-scale reconstruction of <i>Chlamydomonas</i> metabolism provides a platform for systems-level analyses. Plant Journal, 2015, 84, 1239-1256. | 5.7 | 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. | 3.9 | 68 |
| 30 | A systems-level model for the microbial regulatory genome. Molecular Systems Biology, 2014, 10, 740. | 7.2 | 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. | 7.1 | 63 |
| 32 | InÂvivo commensal control of Clostridioides difficile virulence. Cell Host and Microbe, 2021, 29, 1693-1708.e7. | 11.0 | 62 |
| 33 | A high-resolution network model for global gene regulation in Mycobacterium tuberculosis. Nucleic Acids Research, 2014, 42, 11291-11303. | 14.5 | 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. | 5.5 | 59 |
| 36 | Diurnally Entrained Anticipatory Behavior in Archaea. PLoS ONE, 2009, 4, e5485. | 2.5 | 59 |

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|----|--|------|-----------|
| 37 | Parallel evolution of transcriptome architecture during genome reorganization. <i>Genome Research</i> , 2011, 21, 1892-1904. | 5.5 | 58 |
| 38 | A Role for Programmed Cell Death in the Microbial Loop. <i>PLoS ONE</i> , 2013, 8, e62595. | 2.5 | 57 |
| 39 | A single transcription factor regulates evolutionarily diverse but functionally linked metabolic pathways in response to nutrient availability. <i>Molecular Systems Biology</i> , 2009, 5, 282. | 7.2 | 55 |
| 40 | The role of predictive modelling in rationally re-engineering biological systems. <i>Nature Reviews Microbiology</i> , 2009, 7, 297-305. | 28.6 | 55 |
| 41 | Coordination of frontline defense mechanisms under severe oxidative stress. <i>Molecular Systems Biology</i> , 2010, 6, 393. | 7.2 | 55 |
| 42 | A comprehensive map of genome-wide gene regulation in <i>Mycobacterium tuberculosis</i> . <i>Scientific Data</i> , 2015, 2, 150010. | 5.3 | 55 |
| 43 | Transcriptional regulatory networks underlying gene expression changes in Huntington's disease. <i>Molecular Systems Biology</i> , 2018, 14, e7435. | 7.2 | 55 |
| 44 | Genomic perspective on the photobiology of <i>Halobacterium</i> species NRC-1, a phototrophic, phototactic, and UV-tolerant haloarchaeon. <i>Photosynthesis Research</i> , 2001, 70, 3-17. | 2.9 | 54 |
| 45 | Proteomic Analysis of an Extreme Halophilic Archaeon, <i>Halobacterium</i> sp. NRC-1. <i>Molecular and Cellular Proteomics</i> , 2003, 2, 506-524. | 3.8 | 52 |
| 46 | Pathâ€seq identifies an essential mycolate remodeling program for mycobacterial host adaptation. <i>Molecular Systems Biology</i> , 2019, 15, e8584. | 7.2 | 51 |
| 47 | Data-driven integration of genome-scale regulatory and metabolic network models. <i>Frontiers in Microbiology</i> , 2015, 6, 409. | 3.5 | 49 |
| 48 | <i>Halobacterium salinarum</i> NRC-1 PeptideAtlas: Toward Strategies for Targeted Proteomics and Improved Proteome Coverage. <i>Journal of Proteome Research</i> , 2008, 7, 3755-3764. | 3.7 | 46 |
| 49 | Combining inferred regulatory and reconstructed metabolic networks enhances phenotype prediction in yeast. <i>PLoS Computational Biology</i> , 2017, 13, e1005489. | 3.2 | 46 |
| 50 | Comprehensive de novo structure prediction in a systems-biology context for the archaea <i>Halobacterium</i> sp. NRC-1. <i>Genome Biology</i> , 2004, 5, R52. | 9.6 | 45 |
| 51 | cMonkey ₂ : Automated, systematic, integrated detection of co-regulated gene modules for any organism. <i>Nucleic Acids Research</i> , 2015, 43, e87-e87. | 14.5 | 45 |
| 52 | History and Future Perspectives on the Discipline of Quantitative Systems Pharmacology Modeling and Its Applications. <i>Frontiers in Physiology</i> , 2021, 12, 637999. | 2.8 | 44 |
| 53 | Low-pass sequencing for microbial comparative genomics. <i>BMC Genomics</i> , 2004, 5, 3. | 2.8 | 40 |
| 54 | 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. | 3.5 | 40 |

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|----|---|------|-----------|
| 55 | 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. | 1.1 | 40 |
| 56 | Niche adaptation by expansion and reprogramming of general transcription factors. <i>Molecular Systems Biology</i> , 2011, 7, 554. | 7.2 | 39 |
| 57 | Ocean acidification conditions increase resilience of marine diatoms. <i>Nature Communications</i> , 2018, 9, 2328. | 12.8 | 38 |
| 58 | 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. | 2.2 | 35 |
| 59 | Intricate Genetic Programs Controlling Dormancy in <i>Mycobacterium tuberculosis</i> . <i>Cell Reports</i> , 2020, 31, 107577. | 6.4 | 31 |
| 60 | The Firegoose: two-way integration of diverse data from different bioinformatics web resources with desktop applications. <i>BMC Bioinformatics</i> , 2007, 8, 456. | 2.6 | 30 |
| 61 | A systems level predictive model for global gene regulation of methanogenesis in a hydrogenotrophic methanogen. <i>Genome Research</i> , 2013, 23, 1839-1851. | 5.5 | 30 |
| 62 | The State of Systems Genetics in 2017. <i>Cell Systems</i> , 2017, 4, 7-15. | 6.2 | 29 |
| 63 | Molecular mechanisms of system responses to novel stimuli are predictable from public data. <i>Nucleic Acids Research</i> , 2014, 42, 1442-1460. | 14.5 | 28 |
| 64 | A comprehensive spectral assay library to quantify the <i>Escherichia coli</i> proteome by DIA/SWATH-MS. <i>Scientific Data</i> , 2020, 7, 389. | 5.3 | 28 |
| 65 | Large scale physiological readjustment during growth enables rapid, comprehensive and inexpensive systems analysis. <i>BMC Systems Biology</i> , 2010, 4, 64. | 3.0 | 27 |
| 66 | Sense overlapping transcripts in IS<i>1341</i>-type transposase genes are functional non-coding RNAs in archaea. <i>RNA Biology</i> , 2015, 12, 490-500. | 3.1 | 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. <i>Molecular Microbiology</i> , 2000, 36, 1175-1183. | 2.5 | 26 |
| 68 | miRvestigator: web application to identify miRNAs responsible for co-regulated gene expression patterns discovered through transcriptome profiling. <i>Nucleic Acids Research</i> , 2011, 39, W125-W131. | 14.5 | 26 |
| 69 | The BCGÎ”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. | 3.5 | 25 |
| 70 | <i>Mycobacterium abscessus</i> biofilms produce an extracellular matrix and have a distinct mycolic acid profile. <i>Cell Surface</i> , 2021, 7, 100051. | 3.0 | 23 |
| 71 | Mechanism for microbial population collapse in a fluctuating resource environment. <i>Molecular Systems Biology</i> , 2017, 13, 919. | 7.2 | 22 |
| 72 | A Systems Approach to Brain Tumor Treatment. <i>Cancers</i> , 2021, 13, 3152. | 3.7 | 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. | 14.5 | 20 |
| 74 | Crippling life support for SARS-CoV-2 and other viruses through synthetic lethality. Journal of Cell Biology, 2020, 219, . | 5.2 | 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. | 3.8 | 19 |
| 77 | Systems Biology Experimental Design - Considerations for Building Predictive Gene Regulatory Network Models for Prokaryotic Systems. Current Genomics, 2004, 5, 527-544. | 1.6 | 18 |
| 78 | The Scale of Prediction. Science, 2008, 320, 1297-1298. | 12.6 | 16 |
| 79 | Model Organisms Retain an “Ecological Memory” of Complex Ecologically Relevant Environmental Variation. Applied and Environmental Microbiology, 2014, 80, 1821-1831. | 3.1 | 16 |
| 80 | Transcription Start Site Associated RNAs (TSSaRNAs) Are Ubiquitous in All Domains of Life. PLoS ONE, 2014, 9, e107680. | 2.5 | 14 |
| 81 | Adaptive Prediction Emerges Over Short Evolutionary Time Scales. Genome Biology and Evolution, 2017, 9, 1616-1623. | 2.5 | 14 |
| 82 | Inference of Bacterial Small RNA Regulatory Networks and Integration with Transcription Factor-Driven Regulatory Networks. MSystems, 2020, 5, . | 3.8 | 14 |
| 83 | Lettuce (<i>Lactuca sativa</i>) productivity influenced by microbial inocula under nitrogen-limited conditions in aquaponics. PLoS ONE, 2021, 16, e0247534. | 2.5 | 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. | 1.6 | 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. | 3.8 | 13 |
| 86 | A genome wide dosage suppressor network reveals genomic robustness. Nucleic Acids Research, 2017, 45, 255-270. | 14.5 | 13 |
| 87 | Temporal and metabolic overlap between lipid accumulation and programmed cell death due to nitrogen starvation in the unicellular chlorophyte <i>Chlamydomonas reinhardtii</i> . Phycological Research, 2019, 67, 173-183. | 1.6 | 13 |
| 88 | An evolutionarily conserved <i>σ</i> ⁷⁰ -based mechanism for repression of transcriptional positive autoregulation. Molecular Microbiology, 2014, 92, 369-382. | 2.5 | 12 |
| 89 | Transcriptional portrait of <i>M. bovis</i> BCG during biofilm production shows genes differentially expressed during intercellular aggregation and substrate attachment. Scientific Reports, 2020, 10, 12578. | 3.3 | 12 |
| 90 | Mechanism Across Scales: A Holistic Modeling Framework Integrating Laboratory and Field Studies for Microbial Ecology. Frontiers in Microbiology, 2021, 12, 642422. | 3.5 | 12 |

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|-----|--|------|-----------|
| 91 | PerSort Facilitates Characterization and Elimination of Persister Subpopulation in Mycobacteria. MSystems, 2020, 5, . | 3.8 | 12 |
| 92 | Predictive regulatory and metabolic network models for systems analysis of Clostridioides difficile. Cell Host and Microbe, 2021, 29, 1709-1723.e5. | 11.0 | 12 |
| 93 | Constraint-based modelling captures the metabolic versatility of <i>Desulfovibrio vulgaris</i> . Environmental Microbiology Reports, 2018, 10, 190-201. | 2.4 | 11 |
| 94 | Selective Translation of Low Abundance and Upregulated Transcripts in Halobacterium salinarum. MSystems, 2020, 5, . | 3.8 | 10 |
| 95 | Sulfur Metabolites Play Key System-Level Roles in Modulating Denitrification. MSystems, 2021, 6, . | 3.8 | 10 |
| 96 | Biofilms of the non-tuberculous Mycobacterium chelonae form an extracellular matrix and display distinct expression patterns. Cell Surface, 2020, 6, 100043. | 3.0 | 8 |
| 97 | Mathematical models to study the biology of pathogens and the infectious diseases they cause. IScience, 2022, 25, 104079. | 4.1 | 8 |
| 98 | Promoter analysis by saturation mutagenesis. Biological Procedures Online, 2001, 3, 64-69. | 2.9 | 6 |
| 99 | Synergistic epistasis enhances the co-operativity of mutualistic interspecies interactions. ISME Journal, 2021, 15, 2233-2247. | 9.8 | 6 |
| 100 | Structure-based predictions broadly link transcription factor mutations to gene expression changes in cancers. Nucleic Acids Research, 2014, 42, 12973-12983. | 14.5 | 5 |
| 101 | Genetic program activity delineates risk, relapse, and therapy responsiveness in multiple myeloma. Npj Precision Oncology, 2021, 5, 60. | 5.4 | 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. | 2.5 | 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 CO ₂ . Frontiers in Marine Science, 2021, 8, . | 2.5 | 4 |
| 105 | Transcriptome signature of cell viability predicts drug response and drug interaction in Mycobacterium tuberculosis. Cell Reports Methods, 2021, 1, 100123. | 2.9 | 4 |
| 106 | Quantitative prediction of conditional vulnerabilities in regulatory and metabolic networks using PRIME. Npj Systems Biology and Applications, 2021, 7, 43. | 3.0 | 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. | 14.5 | 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. | 3.5 | 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, . | 7.1 | 0 |
| 114 | EPCO-23. A SINGLE-CELL BASED PRECISION MEDICINE APPROACH USING GLIOBLASTOMA PATIENT-SPECIFIC MODELS. Neuro-Oncology, 2021, 23, vi6-vi7. | 1.2 | 0 |