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News

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WORK HISTORY AND EXPERIENCE

Senior Vice President & Director

Institute for Systems Biology, Seattle, WA USA

2013 – present

Director of Integrative Biology

Institute for Systems Biology, Seattle, WA USA

2012 – 2013

Visiting Scientist

Lawrence Berkeley National Laboratory, Berkeley, CA

2010 – present

Professor

Institute for Systems Biology, Seattle, WA USA

2010 – present

Associate Professor

Institute for Systems Biology, Seattle, WA USA

2008 – 2010

Assistant Professor

Institute for Systems Biology, Seattle, WA USA

2005 – 2007

Affiliate Faculty

Department of Microbiology, School of Medicine

Department of Biology

Molecular and Cellular Biology Program, Full Member

University of Washington, Seattle, WA USA

2005 – present

Senior Research Scientist

Institute for Systems Biology, Seattle, WA USA

2002 – 2004

Postdoctoral Fellow	2000 – 2002
Advisor: Prof. Leroy Hood, Institute for Systems Biology Seattle, WA, USA	
Graduate Research Assistant	1996 – 2000
Advisor: Prof. Shiladitya DasSarma, University of Massachusetts Amherst, MA, USA	
Junior Research Fellow	1994 – 1996
Council for Scientific and Industrial Research (CSIR)	
Advisor: Prof. Dileep Deobagkar University of Pune, Pune, MH, India	
Graduate Fellow	1992 – 1994
Department of Biotechnology	
Advisor: Prof. Uday Sangodkar, Goa University, Panaji, GA, India	

EDUCATION

- Ph.D.** Microbiology (2000), University of Massachusetts, Amherst, MA, USA
- M.Sc.** Marine Biotechnology (1994), Goa University, Panaji, GA, India
- B.Sc.** Microbiology (1992), University of Bombay, Mumbai, MH, India
- Diploma.** Systems Management (1991) National Inst. for Information Technology. Mumbai, India.

AWARDS, RECOGNITION, MEMBERSHIPS

- 2021 Member, Board of Studies of School of Biotechnology, Kalinga Institute of Industrial Technology Deemed to be University, Bhubaneswar.
- 2018-present. Board member, Climate Solutions (2018-present)
- 2012 Alvin J. Thompson award and recognition for “fostering public trust in biomedical research through education and dialogue” from the Northwest Association for Biomedical Research.
- 2009 Daniel J. Zaffarano Lecture. Recognition for contributions to interdisciplinary science, Iowa State University.
- 2008 SciFoo Camp, hosted by Google, Nature Publishing Group and O’reilly Publishing @ Googleplex, Mountain View, CA.
- Washington State LASER (Leadership and Assistance for Science Education Reform) recognition for outreach.
- 1994-1996 Council for Scientific and Industrial Research (CSIR) Junior Research Fellowship for graduate research in India. Awarded by the Central Government of India.
- 1992-1994 Department of Biotechnology (DBT) scholarship for graduate study in Biotechnology. Awarded by the Central Government of India.
- American Association for Advancement of Sciences (AAAS)
- American Society of Microbiologists (ASM)

EXECUTIVE ACCOMPLISHMENTS (selected)

- **Organization and Leadership**
 - Successfully steered ISB through leadership reorganization towards stability and sustainability
 - Crafted and led the development of Scientific Strategic Plan for ISB
 - Coordinated institutional fundraising, communications, and grant-writing for education and research
 - Developed and executed strategy to cover \$17M annual gap by coordinating financial projections, streamlining operations, and increasing fund raising through traditional and new channels
 - Established [Systems Research Scholars Program \(SRSP\)](#) and [Translational Research Program](#) program to train and recruit outstanding young investigators at ISB
 - Created ISB [Innovator Award Program](#) to promote transformational, cross-disciplinary, and collaborative activities among junior scientists across faculty groups

- **Mentorship and Training**
 - Developed career tracks for junior scientists
 - Recruited and developed faculty, and senior scientists
 - Mentored three SRSP scholars, two TRFP fellows, and seven Innovator awardees.
 - Through the [Systems Education Experiences \(SEE\)](#) program and [PROJECT FEED 1010](#), I have mentored high school teachers and students (high school and undergraduates) focusing on underrepresented groups including minorities and women in STEM careers

- **Outreach and fundraising**
 - Organized high profile events to increase ISB visibility worldwide: ISB annual symposia, ISB-Town Hall science discussions, ISB Systems Biology Course
 - Established processes to streamline internal and external science communications within ISB
 - Introduced crowdfunding into the spectrum of fund raising efforts at ISB

OTHER ADVISORY AND LEADERSHIP ROLES (selected)

- Sygnomics, Co-founder and CSO
- Hitachi, Hi Tech, Scientific Advisory Board
- Blue Nalu, Scientific Advisory Board
- SYAPSE, Scientific Advisory Board
- ENIGMA, \$60M DOE Science Focus Area, Director of Computation Component
- NSF, NIH, and DOE, Scientific Review Panels, federal funding agencies
- EMSL at Pacific Northwest National Lab, Richmond, WA, Advisory Boards
- Royal Society Open Science, Associate Editor (2018 - present)
- Nature Scientific Data, Editorial Board Member (2014 - present)
- Archaea, Special Issue, Systems & Synthetic Biology, Lead Editor (2011 - present)
- Bio-ITEST Advisory Board. Northwest Association for Biomedical Research (2009-2013)
- DoE ARPA-E – expert panel for evaluating future prospects for bioenergy (2009)
- DoE ASCR, Planning Commission, Identifying investments into biological problems requiring petascale computing (2009)
- DOE BER, Planning Commission, Planning future energy investments into renewable energy technologies (2009)
- Center for BioRenewable Chemicals (CBiRC) NSF ERC, Iowa State University, Scientific Review Board member (2007- present)

- BMC Systems Biology and BMC Bioinformatics Section Editor (2007- present)
- DoE BER, Planning Systems Biology Knowledgebase for Genomes to Life program, Chaired Panels (2007-2009)
- DOE Genomics: GTL Program National Research Council of the National Academies, Reviewer (2006)

PUBLICATIONS and BOOK CHAPTERS

2025

1. Murie C, Turkarslan S, Patel AP, Coffey DG, Becker PS, **Baliga NS**. Individualized dynamic risk assessment and treatment selection for multiple myeloma. *Br J Cancer*. 2025 Apr 1. doi: 10.1038/s41416-025-02987-6. Epub ahead of print. PMID: 40169765.
2. **Baliga NS**, Stankiewicz K, Valenzuela J, Turkarslan S, Wu W-J, Gomez-Campo K, Locatelli N, Conn T, Radice V, Parker K, Alderdice , Bay L, Voolstra C, Barshis D, Baums I. Alternative splicing in a coral during heat stress acclimation and recovery. 02 April 2025, PREPRINT (Version 1), Research Square. [https://doi.org/10.21203/rs.3.rs-6025431/v1]
3. Stankiewicz KH, Valenzuela JJ, Turkarslan S, Wu WJ, Gomez-Campo K, Locatelli NS, Conn TL, Radice VZ, Parker KE, Alderdice R, Bay LK, Voolstra CR, Barshis DJ, Baums IB, **Baliga NS**. Heat-responsive dynamic shifts in alternative splicing of the coral *Acropora cervicornis*. *bioRxiv* [Preprint] bioRxiv 2025.01.21.634199; doi: https://doi.org/10.1101/2025.01.21.634199.

2024

4. Carr AV, Otwell AE, Hunt KA, Chen Y, Wilson J, Faria JP, Liu F, Edirisinghe JN, Valenzuela JJ, Turkarslan S, Lui LM, Nielsen TN, Arkin AP, Henry CS, Petzold CJ, Stahl DA, **Baliga NS**. Emergence and disruption of cooperativity in a denitrifying microbial community. *bioRxiv* 2024.10.24.620115; doi: https://doi.org/10.1101/2024.10.24.620115
5. Valenzuela JJ, Immanuel SRC, Wilson J, Turkarslan S, Ruiz M, Gibbons SM, Hunt KA, Auer M, Zemla M, Stahl DA, **Baliga NS**. Origin of biogeographically distinct ecotypes during laboratory evolution. *Nat Commun*. 2024 Aug 28;15:7451. https://doi.org/10.1038/s41467-024-51759-y.
6. Park JH, Hothi P, de Lomana ALG, Pan M, Calder R, Turkarslan S, Wu WJ, Lee H, Patel AP, Cobbs C, Huang S, **Baliga NS**. Gene regulatory network topology governs resistance and treatment escape in glioma stem-like cells. *Sci Adv*. 2024 Jun 7;10(23):eadj7706. doi: 10.1126/sciadv.adj7706. Epub 2024 Jun 7. PMID: 38848360.
7. Flores-Valdez MA, Peterson EJR, Aceves-Sánchez MJ, **Baliga NS**, Morita YS, Sparks IL, Saini DK, Yadav R, Lang R, Mata-Espinosa D, León-Contreras JC, Hernández-Pando R. Comparison of the transcriptome, lipidome, and c-di-GMP production between BCGΔBCG1419c and BCG, with Mincle- and Myd88-dependent induction of proinflammatory cytokines in murine macrophages. *Sci Rep*. 2024 May 24;14(1):11898. doi: 10.1038/s41598-024-61815-8. PMID: 38789479.
8. Gupta VK, Vaishnavi VV, Arrieta-Ortiz ML, Abhirami PS, Jyothsnaj KM, Jeyasankar S, Raghunathan V, **Baliga NS**, Agarwal R. 3D Hydrogel Culture System Recapitulates Key Tuberculosis Phenotypes and Demonstrates Pyrazinamide Efficacy. *Adv Healthc Mater*. 2024; Apr 24:e2304299. doi: 10.1002/adhm.202304299. Epub ahead of print. PMID: 38655817.
9. Hunt KA, Carr AV, Otwell AE, Valenzuela JJ, Walker KS, Dixon ER, Lui LM, Nielsen TN, Bowman S, von Netzer F, Moon J, Schadt CW, Rodriguez Jr M, Lowe K, Joyner D, Davis KJ, Wu X, Chakraborty R, Fields MW, Zhou J, Hazen TC, Arkin AP, Wankel SD, **Baliga NS**, Stahl DA. Contribution of Microorganisms with the Clade II Nitrous Oxide Reductase to Suppression of Surface Emissions of Nitrous Oxide. *Environmental Science & Technology*. 2024;58:16(7056–7065). DOI: 10.1021/acs.est.3c07972. Epub 2024 Apr 12. PMID: 38608141.

10. Turkarslan S, He Y, Hothi P, Murie C, Nicolas A, Kannan K, Park JH, Pan M, Awawda A, Cole ZD, Shapiro MA, Stuhlmiller TJ, Lee H, Patel AP, Cobbs C, **Baliga NS**. An atlas of causal and mechanistic drivers of interpatient heterogeneity in glioma. medRxiv [Preprint]. 2024:Apr 7:2024.04.05.24305380. doi: 10.1101/2024.04.05.24305380. PMID: 38633778.
11. Murie C, Turkarslan S, Patel A, Coffey DG, Becker PS, **Baliga NS**. Individualized dynamic risk assessment for multiple myeloma. medRxiv [Preprint]. 2024; Apr 3:2024.04.01.24305024. doi: 10.1101/2024.04.01.24305024. PMID: 38633807.
12. Ludwig CM, Howsmon RA, Stromholt S, Valenzuela JJ, Calder R, **Baliga NS**. Consequential insights for advancing informal STEM learning and outcomes for students from historically marginalized communities. Humanit Soc Sci Commun. 2024;11(1):351. doi: 10.1057/s41599-024-02797-w. Epub 2024 Mar 2. PMID: 39035098.

2023

13. Turkarslan S, He Y, Hothi P, Murie C, Nicolas A, Kannan K, Park JH, Pan M, Patel A, Cobbs C, **Baliga NS**, EPCO-42. A systems scale model for personalized precision oncology applications to GBM. Neuro-Oncology. 2023;25(Supplement 5:v133. <https://doi.org/10.1093/neuonc/noad179.0504>.
14. Kusebauch U, Lorenzetti APR, Campbell DS, Pan M, Shteynberg D, Kapil C, Midha MK, García de Lomana AL, **Baliga NS** & Moritz RL. A comprehensive spectral assay library to quantify the Halobacterium salinarum NRC-1 proteome by DIA/SWATH-MS. Sci Data. 2023 Oct 13;10(1):697. doi: 10.1038/s41597-023-02590-5. PMID: 37833331.
15. Lim JJ, Diener C, Wilson J, Valenzuela JJ, **Baliga NS** and Gibbons SM. Growth phase estimation for abundant bacterial populations sampled longitudinally from human stool metagenomes. Nat Commun. 2023;Sep 14;14(1):5682. doi: 10.1038/s41467-023-41424-1. PMID: 37709733.
16. Wang Y, Gallagher LA, Andrade PA, Liu A, Humphreys IR, Turkarslan S, Cutler KJ, Arrieta-Ortiz ML, Li Y, Radey MC, McLean JS, Cong Q, Baker D, **Baliga NS**, Peterson SB, Mougous JD. Genetic manipulation of Patescibacteria provides mechanistic insights into microbial dark matter and the epibiotic lifestyle. Cell. 2023;Oct 26;186(22):4803-4817.e13. doi: 10.1016/j.cell.2023.08.017. Epub 2023 Sep 7. PMID: 37683634.
17. Peterson EJR, Brooks AN, Reiss DJ, Kaur A, Do J, Pan M, Wu W, Morrison R, Srinivas V, Carter W, Arrieta-Ortiz ML, Ruiz RA, Bhatt A, **Baliga NS**. MtrA modulates Mycobacterium tuberculosis cell division in host microenvironments to mediate intrinsic resistance and drug tolerance. Cell Rep. 2023 Aug 29;42(8):112875. doi: 10.1016/j.celrep.2023.112875. Epub 2023 Aug 4. PMID: 37542718.
18. Wang Y, Ledvina HE, Tower CA, Kambarev S, Liu E, Charity JC, Kreuk LSM, Tang Q, Chen Q, Gallagher LA, Radey MC, Rerolle GF, Li Y, Penewit KM, Turkarslan S, Skerrett SJ, Salipante SJ, **Baliga NS**, Woodward JJ, Dove SL, Peterson SB, Celli J, Mougous JD. Discovery of a glutathione utilization pathway in Francisella that shows functional divergence between environmental and pathogenic species. Cell Host Microbe. 2023 Aug 9;31(8):1359-1370.e7. doi: 10.1016/j.chom.2023.06.010. Epub 2023 Jul 14. PMID: 37453420.
19. Wang Y, Gallagher LA, Andrade PA, Liu A, Humphreys IR, Turkarslan S, Cutler KJ, Arrieta-Ortiz ML, Li Y, Radey MC, McLean JS, Cong Q, Baker D, **Baliga NS**, Peterson SB, Mougous JD. Genetic manipulation of candidate phyla radiation bacteria provides functional insights into microbial dark matter. bioRxiv. 2023 May 11; doi: 10.1101/2023.05.02.539146. PMID: 37205512.
20. Carr A, **Baliga NS**, Diener C, Gibbons SM. Personalized Clostridioides difficile engraftment risk prediction and probiotic therapy assessment in the human gut. bioRxiv. 2023 May 9; doi: 10.1101/2023.04.28.538771. PMID: 37162960.
21. Lorenzetti APR, Kusebauch U, Zaramela LS, Wu WJ, de Almeida JPP, Turkarslan S, L G de Lomana A, Gomes-Filho JV, Vêncio RZN, Moritz RL, Koide T, **Baliga NS**. A Genome-Scale Atlas Reveals Complex Interplay of Transcription and Translation in an Archaeon. mSystems. 2023 Mar 13; 8(2):e0081622. doi: 10.1128/mSystems.00816-22. PMID: 36912639.

2022

22. Arrieta-Ortiz ML, Pan M, Kaur A, Pepper-Tunick E, Srinivas V, Dash A, Immanuel SRC, Brooks AN, Shepherd TR, **Baliga NS**. Disrupting the ArcA Regulatory Network Amplifies the Fitness Cost of Tetracycline Resistance in *Escherichia coli*. *mSystems*. 2023 Feb 23;8(1):e0090422. doi: 10.1128/msystems.00904-22. Epub 2022 Dec 20. PMID: 36537814.
23. Stuhlmiller T, Turkarslan S, Friedland J, Shapiro M, Kesari S, Patel A, **Baliga N**. Epco-10. Systems Biology-Based Therapeutic Predictions With Gbmsygnal And Clinical Correlates In The Real-World Longitudinal Outcomes Registry Xcelsior. *Neuro-Oncology*. 2022; 24(Suppl 7): viii117. <https://doi.org/10.1093/neuonc/noac209.445>.
24. Lorenzetti APR, Kusebauch U, Zaramela LS, Wu WJ, de Almeida JPP, Turkarslan S, L G de Lomana A, Gomes-Filho JV, Vêncio RZN, Moritz RL, Koide T, **Baliga NS**. A Genome-Scale Atlas Reveals Complex Interplay of Transcription and Translation in an Archaeon. *mSystems*. 2023 Mar 13:e0081622. doi: 10.1128/msystems.00816-22. Epub ahead of print. PMID: 36912639.
25. Park JH, Feroze AH, Emerson SN, Mihalas AB, Keene CD, Cimino PJ, de Lomana ALG, Kannan K, Wu WJ, Turkarslan S, **Baliga NS**, Patel AP. A single-cell based precision medicine approach using glioblastoma patient-specific models. *NPJ Precis Oncol*. 2022 Aug 8;6(1):55. doi: 10.1038/s41698-022-00294-4. PMID: 35941215.
26. Pavao A, Graham M, Arrieta-Ortiz ML, Immanuel SRC, **Baliga NS**, Bry L. Reconsidering the in vivo functions of Clostridial Stickland amino acid fermentations. *Anaerobe*. 2022 Aug;76:102600. doi: 10.1016/j.anaerobe.2022.102600. Epub 2022 Jun 13. PMID: 35709938.
27. Akhade AS, Mosquera GV, Arrieta-Ortiz ML, Kaur A, Peterson EJR, **Baliga NS**, Hughes KT, Subramanian N. A non-canonical role of caspase-1 in regulating bacterial physiology and antimicrobial resistance. *J Immunol* 1 May 2022; 208 (1_Supplement): 51.05. <https://doi.org/10.4049/jimmunol.208.Supp.51.05>
28. Xavier JB, Monk JM, Poudel S, Norsigian CJ, Sastry AV, Liao C, Bento J, Suchard MA, Arrieta-Ortiz ML, Peterson EJR, **Baliga NS**, Stoeger T, Ruffin F, Richardson RAK, Gao CA, Horvath TD, Haag AM, Wu Q, Savidge T, Yeaman MR. Mathematical models to study the biology of pathogens and the infectious diseases they cause. *iScience*. 2022 Mar 15;25(4):104079. doi: 10.1016/j.isci.2022.104079. PMID: 35359802.
29. Cooper C, Peterson EJR, Bailo R, Pan M, Singh A, Moynihan P, Nakaya M, Fujiwara N, **Baliga N**, Bhatt A. MadR mediates acyl CoA-dependent regulation of mycolic acid desaturation in mycobacteria. *Proc Natl Acad Sci U S A*. 2022 Feb 22;119(8):e2111059119. doi: 10.1073/pnas.2111059119. PMID: 35165190.

2021

30. Immanuel SRC, Arrieta-Ortiz ML, Ruiz RA, Pan M, Lopez Garcia de Lomana A, Peterson EJR, **Baliga NS**. Quantitative prediction of conditional vulnerabilities in regulatory and metabolic networks using PRIME. *NPJ Syst Biol Appl*. 2021 Dec 6;7(1):43. doi: 10.1038/s41540-021-00205-6. PMID: 34873198.
31. Srinivas V, Ruiz RA, Pan M, Immanuel SRC, Peterson EJR, **Baliga NS**. Transcriptome signature of cell viability predicts drug response and drug interaction in *Mycobacterium tuberculosis*. *Cell Rep Methods*. 2021 Dec 20;1(8):None. doi: 10.1016/j.crmeth.2021.100123. PMID: 34977849.
32. Girinathan BP, DiBenedetto N, Worley JN, Peltier J, Arrieta-Ortiz ML, Immanuel SRC, Lavin R, Delaney ML, Cummins CK, Hoffman M, Luo Y, Gonzalez-Escalona N, Allard M, Onderdonk AB, Gerber GK, Sonenshein AL, **Baliga NS**, Dupuy B, Bry L. In vivo commensal control of *Clostridioides difficile* virulence. *Cell Host Microbe*. 2021 Nov 10;29(11):1693-1708.e7. doi: 10.1016/j.chom.2021.09.007. Epub 2021 Oct 11. PMID: 34637781.
33. Arrieta-Ortiz ML, Immanuel SRC, Turkarslan S, Wu WJ, Girinathan BP, Worley JN, DiBenedetto N, Soutourina O, Peltier J, Dupuy B, Bry L, **Baliga NS**. Predictive regulatory and metabolic network models for systems analysis of *Clostridioides difficile*. *Cell Host Microbe*. 2021 Nov 10;29(11):1709-1723.e5. doi: 10.1016/j.chom.2021.09.008. Epub 2021 Oct 11. PMID: 34637780.

34. Nivedita N, Aitchison JD, **Baliga NS**. Autophagy as a Mechanism for Adaptive Prediction-Mediated Emergence of Drug Resistance. *Front Microbiol.* 2021 Sep 10;12:712631. doi: 10.3389/fmicb.2021.712631. PMID: 34566920.
35. Voolstra CR, Valenzuela JJ, Turkarslan S, Cárdenas A, Hume BCC, Perna G, Buitrago-López C, Rowe K, Orellana MV, **Baliga NS**, Paranjape S, Banc-Prandi G, Bellworthy J, Fine M, Frias-Torres S, Barshis DJ. Contrasting heat stress response patterns of coral holobionts across the Red Sea suggest distinct mechanisms of thermal tolerance. *Mol Ecol.* 2021 Sep;30(18):4466-4480. doi: 10.1111/mec.16064. Epub 2021 Aug 3. PMID: 34342082.
36. Park JH, de Lomana ALG, Marzese DM, Juarez T, Feroze A, Hothi P, Cobbs C, Patel AP, Kesari S, Huang S, **Baliga NS**. A Systems Approach to Brain Tumor Treatment. *Cancers.* 2021 Jun 24;13(13). doi: 10.3390/cancers1313152. PMID: 34202449.
37. Peterson, EJR, Abidi AA, Arrieta-Ortiz ML, Aguilar B, Yurkovich JT, Kaur A, Pan M, Srinivas V, Shmulevich I, **Baliga NS**. CORRECTION. Intricate Genetic Programs Controlling Dormancy in *Mycobacterium tuberculosis*. *Cell Reports.* 2021;35(11). <https://doi.org/10.1016/j.celrep.2021.109287>.
38. Wall M, Turkarslan S, Wu W, Danziger S, Reiss D, Mason M, Dervan A, Trotter M, Bassett D, Hershberg R, López García de Lomana Adrián, Ratushny A, **Baliga NS**. Genetic program activity delineates risk, relapse, and therapy responsiveness in multiple myeloma. *NPJ Precis Oncol.* 2021 Jun 28;5(1):60. doi: 10.1038/s41698-021-00185-0. PMID: 34183722.
39. Valenzuela JJ, Ashworth J, Cusick A, Abbriano RM, Armbrust EV, Hildebrand M, Orellana MV, **Baliga NS**. Diel Transcriptional Oscillations of a Plastid Antiporter Reflect Increased Resilience of *Thalassiosira pseudonana* in Elevated CO₂. *Front Mar Sci.* 2021; 8:441. DOI=10.3389/fmars.2021.633225
40. Lui LM, Majumder ELW, Smith HJ, Carlson HK, **Baliga NS**, von Netzer F, Fields MW, Stahl DA, Zhou J, Hazen TC, Adams PD, Arkin AP. Mechanism across scales: a holistic modeling framework integrating laboratory and field studies for microbial ecology. *Front Microbiol.* 2021;12:642422. doi: 10.3389/fmicb.2021.642422. eCollection. PMID: 33841364.
41. Turkarslan S, Stopnisek N, Thompson A, Arens C, Valenzuela J, Wilson J, Hunt K, Hardwicke J, Lim S, Seah YM, Fu Y, Wu L, Lopez García de Lomana, A, Zhou J, Hillesland K, Stahl DA and **Baliga NS**. Synergistic epistasis enhances cooperativity of mutualistic interspecies interactions. *ISME J.* 2021 Aug;15(8):2233-2247. doi: 10.1038/s41396-021-00919-9. PMID: 33612833.
42. Azer K, Kaddi CD, Barrett JS, Bai P, McQuade S, Merrill N, Piccoli B, Zaph SN, Marchetti L, Lombardo R, Parolo S, Immanuel SRC and **Baliga N**. History and future perspectives on the discipline of Quantitative Systems Pharmacology modeling and its applications. *Front Physiol.* 2021;12:637999. doi: 10.3389/fphys.2021.637999. eCollection. PMID: 33841175.
43. Dokic A, Peterson E, Arrieta-Ortiz ML, Pan M, Di Maio A, **Baliga NS**, Bhatt A. *Mycobacterium abscessus* biofilms produce an extracellular matrix and have a distinct mycolic acid profile. *Cell Surf.* 2021 Dec;7:100051. doi: 10.1016/j.tcsu.2021.100051. eCollection. PMID: 33912773.
44. Day JA, Diener C, Otwell AE, Tams KE, Bebout B, Detweiler AM, Lee MD, Scott MT, Ta W, Ha M, Carreon SA, Tong K, Ali AA, Gibbons SM, **Baliga NS**. Lettuce (*Lactuca sativa*) productivity influenced by microbial inocula under nitrogen-limited conditions in aquaponics. *PLoS One.* 2021;16(2):e0247534. doi: 10.1371/journal.pone.0247534. eCollection 2021. PMID: 33621265.
45. Girinathan BP, DiBenedetto N, Worley JN, Peltier J, Arrieta-Ortiz ML, Immanuel SRC, Lavin R, Delaney ML, Cummins CK, Hoffman M, Luo Y, Gonzalez-Escalona N, Allard M, Onderdonk AB, Gerber GK, Sonenshein AI, **Baliga NS**, Dupuy B, Bry L. In vivo commensal control of *Clostridioides difficile* virulence. *Cell Host Microbe.* 2021 Nov 10;29(11):1693-1708.e7. doi: 10.1016/j.chom.2021.09.007. Epub 2021 Oct 11. PMID: 34637781.
46. Immanuel, SRC, Arrieta-Ortiz ML, Ruiz RA, Pan M, Garcia de Lomana, AL, Peterson EJR and **Baliga NS**. Quantitative prediction of conditional vulnerabilities in regulatory and metabolic networks using PRIME. *NPJ Syst Biol Appl.* 2021 Dec 6;7(1):43. doi: 10.1038/s41540-021-00205-6. PMID: 34873198.
47. Neal ML, Wei L, Peterson E, Arrieta-Ortiz ML, Danziger SA, **Baliga NS**, Kaushansky A, Aitchison JD. A

systems-level gene regulatory network model for *Plasmodium falciparum*. *Nucleic Acids Res.* 2021 May 21;49(9):4891-4906. doi: 10.1093/nar/gkaa1245. PMID: 33450011.

48. Day JA, Ludwig CM, **Baliga NS**. Cultivating Environmental Sustainable Food through a Community Ambassador Program. *Clearing: Journal of Community-Based Environmental Literacy Education*. 2021 Winter Edition: 12-16.
49. Otwell AE, Carr AV, Majumder ELW, Ruiza MK, Wilpiseski RL, Hoang LT, Webb B, Turkarslan S, Gibbons SM, Elias DA, Stahl DA, Siuzdak G, **Baliga NS**. Sulfur Metabolites Play Key System-Level Roles in Modulating Denitrification. 2021 Feb 9;6(1). doi: 10.1128/mSystems.01025-20. PMID: 33563788.
50. Srinivas V, Ruiz RA, Pan M, Immanuel SRC, Peterson EJR, **Baliga NS**. Transcriptome signature of cell viability predicts drug response and drug interaction in *Mycobacterium tuberculosis*. *Cell Rep Methods*. 2021 Dec 20;1(8):None. doi: 10.1016/j.crmeth.2021.100123. PMID: 34977849.
51. Voolstra C, Valenzuela J, Turkarslan S, Cardenas A, Hume B, Perna G, Buitrago-López C, Rowe K, Orellana M, **Baliga N**, Paranjabe S, Banc-Prandi G, Bellworthy J, Fine M, Frias-Torres S, Barshis D. Contrasting heat stress response patterns of coral holobionts across the Red Sea suggest distinct mechanisms of thermal tolerance. *Mol Ecol*. 2021 Sep;30(18):4466-4480. doi: 10.1111/mec.16064. Epub 2021 Aug 3. PMID: 34342082

2020

52. Srinivas V, Arrieta-Ortiz ML, Kaur A, Peterson EJR, **Baliga NS**. PerSort Facilitates Characterization and Elimination of Persister Subpopulation in *Mycobacteria*. *mSystems*. 2020 Dec 1;5(6):e01127-20. doi: 10.1128/mSystems.01127-20. PMID: 33262242.
53. Midha MK, Kusebauch U, Shteynberg D, Kapil C, Bader SL, Reddy PJ, Campbell DS, **Baliga NS**, Moritz RL. A comprehensive spectral assay library to quantify the *Escherichia coli* proteome by DIA/SWATH-MS. *Sci Data*. 2020 Nov 12;7(1):389. doi: 10.1038/s41597-020-00724-7. PMID: 33184295.
54. Mast FD, Navare AT, van der Sloot AM, Coulombe-Huntington J, Rout MP, **Baliga NS**, Kaushansky A, Chait BT, Aderem A, Rice CM, Sali A, Tyers M, Aitchison JD. Crippling life support for SARS-CoV-2 and other viruses through synthetic lethality. *J Cell Biol*. 2020 Oct 5;219(10):e202006159. doi: 10.1083/jcb.202006159. PMID: 32785687.
55. Vega-Dominguez, P., E. Peterson, M. Pan, A. Di Maio, S. Singh, S. Umapathy, D. K. Saini, **Baliga N** and A. Bhatt (2020). Biofilms of the non-tuberculous *Mycobacterium chelonae* form an extracellular matrix and display distinct expression patterns. *Cell Surf*. 2020 Aug 5;6:100043. doi: 10.1016/j.tcsu.2020.100043. PMID: 32803022.
56. López García de Lomana A, Kusebauch U, Raman AV, Pan M, Turkarslan S, Lorenzetti APR, Moritz RL, **Baliga NS**. (2020) Selective Translation of Low Abundance and Upregulated Transcripts in *Halobacterium salinarum*. *mSystems*. 2020 Jul 28;5(4):e00329-20. doi: 10.1128/mSystems.00329-20. PMID: 32723790.
57. Flores-Valdez, M. A., M. d. J. Aceves-Sánchez, E. J. R. Peterson, **Baliga N**, J. Bravo-Madrigal, M. Á. De la Cruz-Villegas, M. A. Ares, S. Born, M. Voskuil, N. A. Pérez-Padilla, M. Burciaga-Flores, T. A. Camacho-Villegas and M. G. Espinoza-Jorge (2020). "Transcriptional portrait of *M. bovis* BCG during biofilm production shows genes differentially expressed during intercellular aggregation and substrate attachment." *Sci Rep*. 2020 Jul 28;10(1):12578. doi: 10.1038/s41598-020-69152-2. PMID: 32724037.
58. Arrieta-Ortiz ML, Hafemeister C, Shuster B, **Baliga NS**, Bonneau R, Eichenberger P. (2020) Inference of Bacterial Small RNA Regulatory Networks and Integration with Transcription Factor-Driven Regulatory Networks. *mSystems*. 2020 Jun 2;5(3):e00057-20. doi: 10.1128/mSystems.00057-20. PMID: 32487739
59. Peterson EJR, Abidi AA, Arrieta-Ortiz ML, Aguilar B, Yurkovich JT, Kaur A, Pan M, Srinivas V, Shmulevich I, **Baliga NS**. (2020) Intricate Genetic Programs Controlling Dormancy in *Mycobacterium tuberculosis*. *Cell Rep*. 2020 Apr 28;31(4):107577. doi: 10.1016/j.celrep.2020.107577. PMID: 32348771.

60. Orellana MV, Ludwig CM, Thompson AW, **Baliga, NS**. Integrating oceanographic research into high school curricula: Achieving broader impacts through systems education experiences modules. *Oceanography* 33(3):16-20, <https://doi.org/10.5670/oceanog.2020.304>.

2019

61. Carr A, Diener C, **Baliga NS**, Gibbons SM (2019). Use and abuse of correlation analyses in microbial ecology. *ISME J.* 2019 Nov;13(11):2647-2655. doi: 10.1038/s41396-019-0459-z. Epub 2019 Jun 28. Review. PMID: 31253856
62. Zengler K, Hofmockel K, **Baliga NS**, Behie SW, Bernstein HC, Brown JB, Dinneny JR, Floge SA, Forry SP, Hess M, Jackson SA, Jansson C, Lindemann SR, Pett-Ridge J, Maranas C, Venturelli OS, Wallenstein MD, Shank EA, Northen TR (2019). EcoFABs: advancing microbiome science through standardized fabricated ecosystems. *Nat Methods.* 2019 Jul;16(7):567-571. doi: 10.1038/s41592-019-0465-0. No abstract available. PMID: 31227812
63. Peterson EJ, Bailo R, Rothchild AC, Arrieta-Ortiz ML, Kaur A, Pan M, Mai D, Abidi AA, Cooper C, Aderem A, Bhatt A, **Baliga NS** (2019). Path-seq identifies an essential mycolate remodeling program for mycobacterial host adaptation. *Mol Syst Biol.* 2019 Mar 4;15(3):e8584. doi: 10.15252/msb.20188584. PMID: 30833303

2018

64. Otwell AE, López García de Lomana A, Gibbons SM, Orellana MV, Baliga NS (2018). Systems biology approaches towards predictive microbial ecology. *Environ Microbiol.* 2018 Dec;20(12):4197-4209. doi: 10.1111/1462-2920.14378. Epub 2018 Oct 19. PMID: 30106224.
65. Flores-Valdez, M.A., Pedroza-Roldán, C., Aceves-Sánchez, M.d.J., Peterson, E.J.R., **Baliga, N.S.**, Hernández-Pando, R., Troudt, J., Creissen, E., Izzo, L., Bielefeldt-Ohmann, H., et al. (2018). The BCGΔBCG1419c Vaccine Candidate Reduces Lung Pathology, IL-6, TNF-α, and IL-10 During Chronic TB Infection. *Front Microbiol.* 2018;9:1281. doi: 10.3389/fmicb.2018.01281. eCollection 2018. PMID: 29946316.
66. Ament, S.A., Pearl, J.R., Cantle, J.P., Bragg, R.M., Skene, P.J., Coffey, S.R., Bergey, D.E., Wheeler, V.C., MacDonald, M.E., **Baliga, N.S.**, et al. (2018). Transcriptional regulatory networks underlying gene expression changes in Huntington's disease. *Mol Syst Biol.* 2018 Mar 26;14(3):e7435. doi: 10.15252/msb.20167435. PMID: 29581148.
67. Valenzuela, J.J., López García de Lomana, A., Lee, A., Armbrust, E.V., Orellana, M.V., and **Baliga, N.S.** (2018). Ocean acidification conditions increase resilience of marine diatoms. *Nat Commun.* 2018 Jun 13;9(1):2328. doi: 10.1038/s41467-018-04742-3. PMID: 29899534.
68. Qin W, Amin SA, Lundeen RA, Heal KR, Martens-Habbena W, Turkarslan S, Urakawa H, Costa KC, Hendrickson EL, Wang T, Beck DA, Tiquia-Arashiro SM, Taub F, Holmes AD, Vajrala N, Berube PM, Lowe TM, Moffett JW, Devol AH, **Baliga NS**, Arp DJ, Sayavedra-Soto LA, Hackett M, Armbrust EV, Ingalls AE, Stahl DA. Stress response of a marine ammonia-oxidizing archaeon informs physiological status of environmental populations. *ISME J.* 2018 Feb;12(2):508-519. doi: 10.1038/ismej.2017.186. Epub 2017 Oct 20. PMID: 29053148.

2017

69. Thompson AW, Turkarslan S, Arens CE, López García de Lomana A, Raman AV, Stahl DA, **Baliga NS**. Robustness of a model microbial community emerges from population structure among single cells of

a clonal population. *Environ Microbiol.* 2017 Aug;19(8):3059-3069. doi: 10.1111/1462-2920.13764. Epub 2017 May 29. PMID: 28419704.

70. López García de Lomana A, Kaur A, Turkarslan S, Beer KD, Mast FD, Smith JJ, Aitchison JD, **Baliga NS**. Adaptive Prediction Emerges Over Short Evolutionary Time Scales. *Genome Biol Evol.* 2017 Jun 1;9(6):1616-1623. doi: 10.1093/gbe/evx116. PMID: 28854640.
71. Wang Z, Danziger SA, Heavner BD, Ma S, Smith JJ, Li S, Herricks T, Simeonidis E, **Baliga NS**, Aitchison JD, Price ND. Combining inferred regulatory and reconstructed metabolic networks enhances phenotype prediction in yeast. *PLoS Comput Biol.* 2017 May 17;13(5):e1005489. doi: 10.1371/journal.pcbi.1005489. eCollection 2017 May. PMID: 28520713.
72. Turkarslan S, Raman AV, Thompson AW, Arens CE, Gillespie MA, von Netzer F, Hillesland KL, Stolyar S, López García de Lomana A, Reiss DJ, Gorman-Lewis D, Zane GM, Ranish JA, Wall JD, Stahl DA, **Baliga NS**. Mechanism for microbial population collapse in a fluctuating resource environment. *Mol Syst Biol.* 2017 Mar 20;13(3):919. doi: 10.15252/msb.20167058. PMID: 28320772.
73. **Baliga NS**, Björkegren JL, Boeke JD, Boutros M, Crawford NP, Dudley AM, Farber CR, Jones A, Levey AI, Lusis AJ, Mak HC, Nadeau JH, Noyes MB, Petretto E, Seyfried NT, Steinmetz LM, Vonesch SC. The State of Systems Genetics in 2017. *Cell Syst.* 2017 Jan 25;4(1):7-15. doi: 10.1016/j.cels.2017.01.005. PMID: 28125793.
74. Patra B, Kon Y, Yadav G, Sevdal AW, Frumkin JP, Vallabhajosyula RR, Hintze A, Østman B, Schossau J, Bhan A, Marzolf B, Tamashiro JK, Kaur A, **Baliga NS**, Grayhack EJ, Adami C, Galas DJ, Raval A, Phizicky EM, Ray A. A genome wide dosage suppressor network reveals genomic robustness. *Nucleic Acids Res.* 2017 Jan 9;45(1):255-270. doi: 10.1093/nar/gkw1148. Epub 2016 Nov 29. PMID: 27899637.

2016

75. Keller MP, Paul PK, Rabaglia ME, Stapleton DS, Schueler KL, Broman AT, Ye SI, Leng N, Brandon CJ, Neto EC, Plaisier CL, Simonett SP, Kebede MA, Sheynkman GM, Klein MA, **Baliga NS**, Smith LM, Broman KW, Yandell BS, Kendziora C, Attie AD. The Transcription Factor Nfatc2 Regulates β -Cell Proliferation and Genes Associated with Type 2 Diabetes in Mouse and Human Islets. *PLoS Genet.* 2016 Dec 9;12(12):e1006466. doi: 10.1371/journal.pgen.1006466. eCollection 2016 Dec. PMID: 27935966.
76. Rothchild AC, Sissons JR, Shafiani S, Plaisier C, Min D, Mai D, Gilchrist M, Peschon J, Larson RP, Bergthaler A, **Baliga NS**, Urdahl KB, Aderem A. MiR-155-regulated molecular network orchestrates cell fate in the innate and adaptive immune response to Mycobacterium tuberculosis. *Proc Natl Acad Sci U S A.* 2016 Oct 11;113(41):E6172-E6181. Epub 2016 Sep 28. PMID: 27681624.
77. Plaisier CL, O'Brien S, Bernard B, Reynolds S, Simon Z, Toledo CM, Ding Y, Reiss DJ, Paddison PJ, **Baliga NS**. Causal Mechanistic Regulatory Network for Glioblastoma Deciphered Using Systems Genetics Network Analysis. *Cell Syst.* 2016 Aug;3(2):172-186. doi: 10.1016/j.cels.2016.06.006. Epub 2016 Jul 14. PMID: 27426982.
78. Peterson EJR, Ma S, Sherman DR, **Baliga NS**. Network analysis identifies Rv0324 and Rv0880 as regulators of bedaquiline tolerance in Mycobacterium tuberculosis. *Nat Microbiol.* 2016 Jun 6;1(8):16078. doi: 10.1038/nmicrobiol.2016.78. PMID: 27573104.
79. Ashworth J, Turkarslan S, Harris M, Orellana MV, **Baliga NS**. Pan-transcriptomic analysis identifies coordinated and orthologous functional modules in the diatoms *Thalassiosira pseudonana* and *Phaeodactylum tricornutum*. *Mar Genomics.* 2016 Apr;26:21-8. doi: 10.1016/j.margen.2015.10.011. Epub 2015 Nov 10. PMID: 26560047.

2015

80. Hennon GMM, Ashworth J, Groussman RD, Berthiaume C, Morales RL, **Baliga NS**, Orellana MV and Armbrust EV. (2015) Diatom acclimation to elevated co2 via camp signalling and coordinated gene expression. *Nature Clim Change*. 2015;5:761–765. <https://doi.org/10.1038/nclimate2683>.
81. Ludwig C, Orellana MV, DeVault M, Simon Z, and **Baliga N**. Ocean acidification: Engaging students in solving a systems-level, global problem. *The Science Teacher*. 2015 82(6):41-48
82. Toledo CM, Ding Y, Hoellerbauer P, Davis RJ, Basom R, Girard EJ, Lee E, Corrin P, Hart T, Bolouri H, Davison J, Zhang Q, Hardcastle J, Aronow BJ, Plaisier CL, **Baliga NS**, Moffat J, Lin Q, Li XN, Nam DH, Lee J, Pollard SM, Zhu J, Delrow JJ, Clurman BE, Olson JM, Paddison PJ. Genome-wide CRISPR-Cas9 Screens Reveal Loss of Redundancy between PKMYT1 and WEE1 in Glioblastoma Stem-like Cells. *Cell Rep*. 2015 Dec 22;13(11):2425-2439. doi: 10.1016/j.celrep.2015.11.021. Epub 2015 Dec 7. PMID: 26673326.
83. Imam S, Schäuble S, Valenzuela J, López García de Lomana A, Carter W, Price ND, **Baliga NS**. A refined genome-scale reconstruction of Chlamydomonas metabolism provides a platform for systems-level analyses. *Plant J*. 2015 Dec;84(6):1239-56. doi: 10.1111/tpj.13059. Epub 2015 Nov 30. PMID: 26485611.
84. Thompson AW, Crow MJ, Wadey B, Arens C, Turkarslan S, Stolyar S, Elliott N, Petersen TW, van den Engh G, Stahl DA, **Baliga NS**. A method to analyze, sort, and retain viability of obligate anaerobic microorganisms from complex microbial communities. *J Microbiol Methods*. 2015 Oct;117:74-7. doi: 10.1016/j.mimet.2015.07.009. Epub 2015 Jul 14. PMID: 26187776.
85. Reiss DJ, Plaisier CL, Wu WJ, **Baliga NS**. cMonkey2: Automated, systematic, integrated detection of co-regulated gene modules for any organism. *Nucleic Acids Res*. 2015 Jul 27;43(13):e87. doi: 10.1093/nar/gkv300. Epub 2015 Apr 14. PMID: 25873626.
86. Raman AV, **Baliga NS**. The universe under a microscope. *Environ Microbiol Rep*. 2015 Feb;7(1):11-2. doi: 10.1111/1758-2229.12225. PMID: 25721591.
87. Minch KJ, Rustad TR, Peterson EJ, Winkler J, Reiss DJ, Ma S, Hickey M, Brabant W, Morrison B, Turkarslan S, Mawhinney C, Galagan JE, Price ND, **Baliga NS**, Sherman DR. The DNA-binding network of Mycobacterium tuberculosis. *Nat Commun*. 2015 Jan 12;6:5829. doi: 10.1038/ncomms6829. PMID: 25581030.
88. Gomes-Filho JV, Zaramela LS, Italiani VC, **Baliga NS**, Vêncio RZ, Koide T. Sense overlapping transcripts in IS1341-type transposase genes are functional non-coding RNAs in archaea. *RNA Biol*. 2015;12(5):490-500. doi: 10.1080/15476286.2015.1019998. PMID: 25806405
89. Danziger SA, Reiss DJ, Ratushny AV, Smith JJ, Plaisier CL, Aitchison JD, **Baliga NS**. Biclust Sampled Coherence Metric (BSCM) provides an accurate environmental context for phenotype predictions. *BMC Syst Biol*. 2015;9 Suppl 2:S1. doi: 10.1186/1752-0509-9-S2-S1. Epub 2015 Apr 15. PMID: 25881257
90. Turkarslan S, Peterson EJ, Rustad TR, Minch KJ, Reiss DJ, Morrison R, Ma S, Price ND, Sherman DR, **Baliga NS**. A comprehensive map of genome-wide gene regulation in Mycobacterium tuberculosis. *Sci Data*. 2015 Mar 31;2:150010. doi: 10.1038/sdata.2015.10. eCollection 2015. PMID: 25977815
91. Imam S, Schäuble S, Brooks AN, **Baliga NS**, Price ND. Data-driven integration of genome-scale regulatory and metabolic network models. *Front Microbiol*. 2015 May 5;6:409. doi: 10.3389/fmicb.2015.00409. eCollection 2015. Review. PMID: 25999934
92. López García de Lomana A, Schäuble S, Valenzuela J, Imam S, Carter W, Bilgin DD, Yohn CB, Turkarslan S, Reiss DJ, Orellana MV, Price ND, **Baliga NS**. Transcriptional program for nitrogen starvation-induced lipid accumulation in Chlamydomonas reinhardtii. *Biotechnol Biofuels*. 2015 Dec 2;8:207. doi: 10.1186/s13068-015-0391-z. eCollection 2015. PMID: 26633994

2014

93. Ashworth J, Bernard B, Reynolds S, Plaisier CL, Shmulevich I, **Baliga NS**. Structure-based predictions broadly link transcription factor mutations to gene expression changes in cancers. *Nucleic Acids Res*. 2014 Dec 1;42(21):12973-83. doi: 10.1093/nar/gku1031. Epub 2014 Nov 5. PMID: 25378323.

94. Muller EE, Pinel N, Laczny CC, Hoopmann MR, Narayanasamy S, Lebrun LA, Roume H, Lin J, May P, Hicks ND, Heintz-Buschart A, Wampach L, Liu CM, Price LB, Gillece JD, Guignard C, Schupp JM, Vlassis N, **Baliga NS**, Moritz RL, Keim PS, Wilmes P. Community-integrated omics links dominance of a microbial generalist to fine-tuned resource usage. *Nat Commun.* 2014 Nov 26;5:5603. doi: 10.1038/ncomms6603. PMID: 25424998
95. Plaisier CL, Lo FY, Ashworth J, Brooks AN, Beer KD, Kaur A, Pan M, Reiss DJ, Facciotti MT, **Baliga NS**. Evolution of context dependent regulation by expansion of feast/famine regulatory proteins. *BMC Syst Biol.* 2014 Nov 14;8:122. doi: 10.1186/s12918-014-0122-2. PMID: 25394904
96. Hillesland KL, Lim S, Flowers JJ, Turkarslan S, Pinel N, Zane GM, Elliott N, Qin Y, Wu L, **Baliga NS**, Zhou J, Wall JD, Stahl DA. Erosion of functional independence early in the evolution of a microbial mutualism. *Proc Natl Acad Sci U S A.* 2014 Oct 14;111(41):14822-7. doi: 10.1073/pnas.1407986111. Epub 2014 Sep 29. PMID: 25267659
97. Peterson EJ, Reiss DJ, Turkarslan S, Minch KJ, Rustad T, Plaisier CL, Longabaugh WJ, Sherman DR, **Baliga NS**. A high-resolution network model for global gene regulation in *Mycobacterium tuberculosis*. *Nucleic Acids Res.* 2014 Oct;42(18):11291-303. doi: 10.1093/nar/gku777. Epub 2014 Sep 17. PMID: 25232098.
98. Brooks AN, Reiss DJ, Allard A, Wu WJ, Salvanha DM, Plaisier CL, Chandrasekaran S, Pan M, Kaur A, **Baliga NS**. A system-level model for the microbial regulatory genome. *Mol Syst Biol.* 2014 Jul 15;10:740. doi: 10.15252/msb.20145160. PMID: 25028489.
99. Bare JC, **Baliga NS**. Architecture for interoperable software in biology. *Brief Bioinform.* 2014 Jul;15(4):626-36. doi: 10.1093/bib/bbs074. Epub 2012 Dec 11. PMID: 23235920.
100. Wurtmann EJ, Ratushny AV, Pan M, Beer KD, Aitchison JD, **Baliga NS**. An evolutionarily conserved RNase-based mechanism for repression of transcriptional positive autoregulation. *Mol Microbiol.* 2014 Apr;92(2):369-82. doi: 10.1111/mmi.12564. Epub 2014 Mar 19. PMID: 24612392.
101. Beer KD, Wurtmann EJ, Pinel N, **Baliga NS**. Model organisms retain an "ecological memory" of complex ecologically relevant environmental variation. *Appl Environ Microbiol.* 2014 Mar;80(6):1821-31. doi: 10.1128/AEM.03280-13. Epub 2014 Jan 10. PMID: 24413600.
102. Danziger SA, Ratushny AV, Smith JJ, Saleem RA, Wan Y, Arens CE, Armstrong AM, Sitko K, Chen WM, Chiang JH, Reiss DJ, **Baliga NS**, Aitchison JD. Molecular mechanisms of system responses to novel stimuli are predictable from public data. *Nucleic Acids Res.* 2014 Feb;42(3):1442-60. doi: 10.1093/nar/gkt938. Epub 2013 Oct 31. PMID: 24185701.
103. Ekici S, Turkarslan S, Pawlik G, Dancis A, **Baliga NS**, Koch HG, Daldal F. Intracytoplasmic copper homeostasis controls cytochrome c oxidase production. *MBio.* 2014 Jan 14;5(1):e01055-13. doi: 10.1128/mBio.01055-13. PMID: 24425735.
104. Turkarslan S, Wurtmann EJ, Wu WJ, Jiang N, Bare JC, Foley K, Reiss DJ, Novichkov P, **Baliga NS**. Network portal: a database for storage, analysis and visualization of biological networks. *Nucleic Acids Res.* 2014 Jan;42(Database issue):D184-90. doi: 10.1093/nar/gkt1190. Epub 2013 Nov 23. PMID: 24271392.
105. Zaramela LS, Vêncio RZ, ten-Caten F, **Baliga NS**, Koide T. Transcription start site associated RNAs (TSSaRNAs) are ubiquitous in all domains of life. *PLoS One.* 2014 Sep 19;9(9):e107680. doi: 10.1371/journal.pone.0107680. eCollection 2014. PMID: 25238539.
106. Ashworth J, Plaisier CL, Lo FY, Reiss DJ, **Baliga NS**. Inference of expanded Lrp-like feast/famine transcription factor targets in a non-model organism using protein structure-based prediction. *PLoS One.* 2014 Sep 25;9(9):e107863. doi: 10.1371/journal.pone.0107863. eCollection 2014. Erratum in: *PLoS One.* 2014;9(11):e114450. PMID: 25255272.
107. Rustad TR, Minch KJ, Ma S, Winkler JK, Hobbs S, Hickey M, Brabant W, Turkarslan S, Price ND, **Baliga NS**, Sherman DR. Mapping and manipulating the *Mycobacterium tuberculosis* transcriptome using a transcription factor overexpression-derived regulatory network. *Genome Biol.* 2014;15(11):502. PMID: 25380655.

2013

108. Ballereau S, Glaab E, Kolodkin A, Chaiboonchoe A, Biryukov M, Vlassis N, Ahmed H, Pellet J, **Baliga NS**, Hood L, Schneider S, Balling R, Auffray C. Systems Biology: Integrative Biology and Simulation Tools (Chapter) in Functional Genomics and bioinformatics for systems biology. Eds, Prokop A and Csukas B. Springer. 2013.
109. Yoon SH, Turkarslan S, Reiss DJ, Pan M, Burn JA, Costa KC, Lie TJ, Slagel J, Moritz RL, Hackett M, Leigh JA, **Baliga NS**. A systems level predictive model for global gene regulation of methanogenesis in a hydrogenotrophic methanogen. *Genome Res.* 2013 Nov;23(11):1839-51. doi: 10.1101/gr.153916.112. Epub 2013 Oct 2. PubMed PMID: 24089473; PubMed Central PMCID: PMC3814884.
110. Beer KD, Orellana MV, **Baliga NS**. Modeling the evolution of C4 photosynthesis. *Cell.* 2013 Jun 20;153(7):1427-9. doi: 10.1016/j.cell.2013.05.058. PubMed PMID: 23791172; PubMed Central PMCID: PMC3832052.
111. Ashworth J, Coesel S, Lee A, Armbrust EV, Orellana MV, **Baliga NS**. Genome-wide diel growth state transitions in the diatom *Thalassiosira pseudonana*. *Proc Natl Acad Sci U S A.* 2013 Apr 30;110(18):7518-23. doi: 10.1073/pnas.1300962110. Epub 2013 Apr 17. PubMed PMID: 23596211; PubMed Central PMCID: PMC3645528.
112. Costa KC, Yoon SH, Pan M, Burn JA, **Baliga NS**, Leigh JA. Effects of H₂ and formate on growth yield and regulation of methanogenesis in *Methanococcus maripaludis*. *J Bacteriol.* 2013 Apr;195(7):1456-62. doi: 10.1128/JB.02141-12. Epub 2013 Jan 18. PubMed PMID: 23335420; PubMed Central PMCID: PMC3624518.
113. Rustad TR, Minch KJ, Brabant W, Winkler JK, Reiss DJ, **Baliga NS**, Sherman DR. Global analysis of mRNA stability in *Mycobacterium tuberculosis*. *Nucleic Acids Res.* 2013 Jan 7;41(1):509-17. doi: 10.1093/nar/gks1019. Epub 2012 Nov 3. PubMed PMID: 23125364; PubMed Central PMCID: PMC3592478.
114. Pang WL, Kaur A, Ratushny AV, Cvetkovic A, Kumar S, Pan M, Arkin AP, Aitchison JD, Adams MW, **Baliga NS**. Metallochaperones regulate intracellular copper levels. *PLoS Comput Biol.* 2013;9(1):e1002880. doi: 10.1371/journal.pcbi.1002880. Epub 2013 Jan 17. PubMed PMID: 23349626; PubMed Central PMCID: PMC3551603.
115. Orellana MV, Pang WL, Durand PM, Whitehead K, **Baliga NS**. A role for programmed cell death in the microbial loop. *PLoS One.* 2013 May 8;8(5):e62595. doi: 10.1371/journal.pone.0062595. Print 2013. PubMed PMID: 23667496; PubMed Central PMCID: PMC3648572.

2012

116. Muller EE, Pinel N, Gillece JD, Schupp JM, Price LB, Engelthaler DM, Levantesi C, Tandoi V, Luong K, **Baliga NS**, Korlach J, Keim PS, Wilmes P. Genome sequence of "Candidatus *Microthrix parvicella*" Bio17-1, a long-chain-fatty-acid-accumulating filamentous actinobacterium from a biological wastewater treatment plant. *J Bacteriol.* 2012 Dec;194(23):6670-1. doi: 10.1128/JB.01765-12. PubMed PMID: 23144412; PubMed Central PMCID: PMC3497503.
117. Plaisier CL, Pan M, **Baliga NS**. A miRNA-regulatory network explains how dysregulated miRNAs perturb oncogenic processes across diverse cancers. *Genome Res.* 2012 Nov;22(11):2302-14. doi: 10.1101/gr.133991.111. Epub 2012 Jun 28. PubMed PMID: 22745231; PubMed Central PMCID: PMC3483559.
118. Ashworth J, Wurtmann EJ, **Baliga NS**. Reverse engineering systems models of regulation: discovery, prediction and mechanisms. *Curr Opin Biotechnol.* 2012 Aug;23(4):598-603. doi: 10.1016/j.copbio.2011.12.005. Epub 2011 Dec 28. Review. PubMed PMID: 22209016; PubMed Central PMCID: PMC3477774.

119. Plaisier CL, **Baliga NS**. Harnessing the power of human tumor-derived cell lines for the rational design of cancer therapies. *Pigment Cell Melanoma Res.* 2012 Jul;25(4):406-8. doi: 10.1111/j.1755-148X.2012.01020.x. PubMed PMID: 22781216; PubMed Central PMCID: PMC3825090.
120. Edgar RS, Green EW, Zhao Y, van Ooijen G, Olmedo M, Qin X, Xu Y, Pan M, Valekunja UK, Feeney KA, Maywood ES, Hastings MH, **Baliga NS**, Merrow M, Millar AJ, Johnson CH, Kyriacou CP, O'Neill JS, Reddy AB. Peroxiredoxins are conserved markers of circadian rhythms. *Nature.* 2012 May 16;485(7399):459-64. doi: 10.1038/nature11088. Erratum in: *Nature.* 2012 Sep 27;489(7417):590. PubMed PMID: 22622569; PubMed Central PMCID: PMC3398137.

2011

121. Turkarslan S, Reiss DJ, Gibbins G, Su WL, Pan M, Bare JC, Plaisier CL, **Baliga NS**. Niche adaptation by expansion and reprogramming of general transcription factors. *Mol Syst Biol.* 2011 Nov 22;7:554. doi: 10.1038/msb.2011.87. PubMed PMID: 22108796; PubMed Central PMCID: PMC3261711.
122. Yoon SH, Reiss DJ, Bare JC, Tenenbaum D, Pan M, Slagel J, Moritz RL, Lim S, Hackett M, Menon AL, Adams MW, Barnebey A, Yannoni SM, Leigh JA, **Baliga NS**. Parallel evolution of transcriptome architecture during genome reorganization. *Genome Res.* 2011 Nov;21(11):1892-904. doi: 10.1101/gr.122218.111. Epub 2011 Jul 12. PubMed PMID: 21750103; PubMed Central PMCID: PMC3205574.
123. Brooks AN, Turkarslan S, Beer KD, Lo FY, **Baliga NS**. Adaptation of cells to new environments. *Wiley Interdiscip Rev Syst Biol Med.* 2011 Sep-Oct;3(5):544-61. doi: 10.1002/wsbm.136. Epub 2010 Dec 31. Review. PubMed PMID: 21197660; PubMed Central PMCID: PMC3081528.
124. Plaisier CL, Bare JC, **Baliga NS**. miRvestigator: web application to identify miRNAs responsible for co-regulated gene expression patterns discovered through transcriptome profiling. *Nucleic Acids Res.* 2011 Jul;39(Web Server issue):W125-31. doi: 10.1093/nar/gkr374. Epub 2011 May 20. PubMed PMID: 21602264; PubMed Central PMCID: PMC3125776.
125. Schmid AK, Pan M, Sharma K, **Baliga NS**. Two transcription factors are necessary for iron homeostasis in a salt-dwelling archaeon. *Nucleic Acids Res.* 2011 Apr;39(7):2519-33. doi: 10.1093/nar/gkq1211. Epub 2010 Nov 24. PubMed PMID: 21109526; PubMed Central PMCID: PMC3074139.
126. Robinson CK, Webb K, Kaur A, Jaruga P, Dizdaroglu M, **Baliga NS**, Place A, Diruggiero J. A major role for nonenzymatic antioxidant processes in the radioresistance of *Halobacterium salinarum*. *J Bacteriol.* 2011 Apr;193(7):1653-62. doi: 10.1128/JB.01310-10. Epub 2011 Jan 28. PubMed PMID: 21278285; PubMed Central PMCID: PMC3067647.
127. Tautenhahn R, Patti GJ, Kalisiak E, Miyamoto T, Schmidt M, Lo FY, McBee J, **Baliga NS**, Siuzdak G. metaXCMS: second-order analysis of untargeted metabolomics data. *Anal Chem.* 2011 Feb 1;83(3):696-700. doi: 10.1021/ac102980g. Epub 2010 Dec 21. PubMed PMID: 21174458; PubMed Central PMCID: PMC3654666.

2010

128. Bare JC, Koide T, Reiss DJ, Tenenbaum D, **Baliga NS**. Integration and visualization of systems biology data in context of the genome. *BMC Bioinformatics.* 2010 Jul 19;11:382. doi: 10.1186/1471-2105-11-382. PubMed PMID: 20642854; PubMed Central PMCID: PMC2912892.
129. Tenenbaum D, Bare JC, **Baliga NS**. GTC: A web server for integrating systems biology data with web tools and desktop applications. *Source Code Biol Med.* 2010 Jul 13;5:7. doi: 10.1186/1751-0473-5-7. PubMed PMID: 20626906; PubMed Central PMCID: PMC2917411.
130. Kaur A, Van PT, Busch CR, Robinson CK, Pan M, Pang WL, Reiss DJ, DiRuggiero J, **Baliga NS**. Coordination of frontline defense mechanisms under severe oxidative stress. *Mol Syst Biol.* 2010 Jul;6:393. doi: 10.1038/msb.2010.50. PubMed PMID: 20664639; PubMed Central PMCID: PMC2925529.

131. Facciotti MT, Pang WL, Lo FY, Whitehead K, Koide T, Masumura K, Pan M, Kaur A, Larsen DJ, Reiss DJ, Hoang L, Kalisiak E, Northen T, Trauger SA, Siuzdak G, **Baliga NS**. Large scale physiological readjustment during growth enables rapid, comprehensive and inexpensive systems analysis. *BMC Syst Biol*. 2010 May 14;4:64. doi: 10.1186/1752-0509-4-64. PubMed PMID: 20470417; PubMed Central PMCID: PMC2880973.
132. Gehlenborg N, O'Donoghue SI, **Baliga NS**, Goesmann A, Hibbs MA, Kitano H, Kohlbacher O, Neuweger H, Schneider R, Tenenbaum D, Gavin AC. Visualization of omics data for systems biology. *Nat Methods*. 2010 Mar;7(3 Suppl):S56-68. doi: 10.1038/nmeth.1436. Review. PubMed PMID: 20195258.

2009

133. Koide T, Pang WL, **Baliga NS**. The role of predictive modelling in rationally re-engineering biological systems. *Nat Rev Microbiol*. 2009 Apr;7(4):297-305. doi: 10.1038/nrmicro2107. Epub 2009 Mar 2. Review. PubMed PMID: 19252506; PubMed Central PMCID: PMC2734281.
134. Whitehead K, Pan M, Masumura K, Bonneau R, **Baliga NS**. Diurnally entrained anticipatory behavior in archaea. *PLoS One*. 2009;4(5):e5485. doi: 10.1371/journal.pone.0005485. Epub 2009 May 8. PubMed PMID: 19424498; PubMed Central PMCID: PMC2675056.
135. Schmid AK, Reiss DJ, Pan M, Koide T, **Baliga NS**. A single transcription factor regulates evolutionarily diverse but functionally linked metabolic pathways in response to nutrient availability. *Mol Syst Biol*. 2009;5:282. doi: 10.1038/msb.2009.40. Epub 2009 Jun 16. PubMed PMID: 19536205; PubMed Central PMCID: PMC2710871.
136. Koide T, Reiss DJ, Bare JC, Pang WL, Facciotti MT, Schmid AK, Pan M, Marzolf B, Van PT, Lo FY, Pratap A, Deutsch EW, Peterson A, Martin D, **Baliga NS**. Prevalence of transcription promoters within archaeal operons and coding sequences. *Mol Syst Biol*. 2009;5:285. doi: 10.1038/msb.2009.42. Epub 2009 Jun 16. PubMed PMID: 19536208; PubMed Central PMCID: PMC2710873.

2008

137. Ludwig CM, **Baliga NS**. Systems concepts effectively taught using systems practices. *Science Scope*. 2008 31(9).
138. Van PT, Schmid AK, King NL, Kaur A, Pan M, Whitehead K, Koide T, Facciotti MT, Goo YA, Deutsch EW, Reiss DJ, Mallick P, **Baliga NS**. Halobacterium salinarum NRC-1 PeptideAtlas: toward strategies for targeted proteomics and improved proteome coverage. *J Proteome Res*. 2008 Sep;7(9):3755-64. doi: 10.1021/pr800031f. Epub 2008 Jul 25. PubMed PMID: 18652504; PubMed Central PMCID: PMC2643335.
139. Rubio ED, Reiss DJ, Welsh PL, Distche CM, Filippova GN, **Baliga NS**, Aebersold R, Ranish JA, Krumm A. CTCF physically links cohesin to chromatin. *Proc Natl Acad Sci U S A*. 2008 Jun 17;105(24):8309-14. doi: 10.1073/pnas.0801273105. Epub 2008 Jun 11. PubMed PMID: 18550811; PubMed Central PMCID: PMC2448833.
140. **Baliga NS**. Systems biology. The scale of prediction. *Science*. 2008 Jun 6;320(5881):1297-8. doi: 10.1126/science.1159485. PubMed PMID: 18535232.
141. Reiss DJ, Facciotti MT, **Baliga NS**. Model-based deconvolution of genome-wide DNA binding. *Bioinformatics*. 2008 Feb 1;24(3):396-403. Epub 2007 Dec 1. PubMed PMID: 18056063.

2007

142. Schmid AK, **Baliga NS**. Prokaryotic Systems Biology (Chapter). *Cell Engineering Series: Systems Biology*, Volume 5, 2007, p 395-423.
143. Bonneau R, Facciotti MT, Reiss DJ, Schmid AK, Pan M, Kaur A, Thorsson V, Shannon P, Johnson MH, Bare JC, Longabaugh W, Vuthoori M, Whitehead K, Madar A, Suzuki L, Mori T, Chang DE, Diruggiero J, Johnson

- CH, Hood L, **Baliga NS**. A predictive model for transcriptional control of physiology in a free living cell. *Cell*. 2007 Dec 28;131(7):1354-65. PubMed PMID: 18160043.
144. Bare JC, Shannon PT, Schmid AK, **Baliga NS**. The Firegoose: two-way integration of diverse data from different bioinformatics web resources with desktop applications. *BMC Bioinformatics*. 2007 Nov 19;8:456. PubMed PMID: 18021453; PubMed Central PMCID: PMC2211326.
145. Schmid AK, Reiss DJ, Kaur A, Pan M, King N, Van PT, Hohmann L, Martin DB, **Baliga NS**. The anatomy of microbial cell state transitions in response to oxygen. *Genome Res*. 2007 Oct;17(10):1399-413. Epub 2007 Sep 4. PubMed PMID: 17785531; PubMed Central PMCID: PMC1987344.
146. Facciotti MT, Reiss DJ, Pan M, Kaur A, Vuthoori M, Bonneau R, Shannon P, Srivastava A, Donohoe SM, Hood LE, **Baliga NS**. General transcription factor specified global gene regulation in archaea. *Proc Natl Acad Sci U S A*. 2007 Mar 13;104(11):4630-5. Epub 2007 Mar 7. PubMed PMID: 17360575; PubMed Central PMCID: PMC1838652.

2006

147. Kaur A, Pan M, Meislin M, Facciotti MT, El-Gewely R, **Baliga NS**. A systems view of haloarchaeal strategies to withstand stress from transition metals. *Genome Res*. 2006 Jul;16(7):841-54. Epub 2006 Jun 2. PubMed PMID: 16751342; PubMed Central PMCID: PMC1484451.
148. Reiss DJ, **Baliga NS**, Bonneau R. Integrated biclustering of heterogeneous genome-wide datasets for the inference of global regulatory networks. *BMC Bioinformatics*. 2006 Jun 2;7:280. PubMed PMID: 16749936; PubMed Central PMCID: PMC1502140.
149. Shannon PT, Reiss DJ, Bonneau R, **Baliga NS**. The Gaggles: an open-source software system for integrating bioinformatics software and data sources. *BMC Bioinformatics*. 2006 Mar 28;7:176. PubMed PMID: 16569235; PubMed Central PMCID: PMC1464137.
150. Bonneau R, Reiss DJ, Shannon P, Facciotti M, Hood L, **Baliga NS**, Thorsson V. The Inferelator: an algorithm for learning parsimonious regulatory networks from systems-biology data sets de novo. *Genome Biol*. 2006;7(5):R36. Epub 2006 May 10. PubMed PMID: 16686963; PubMed Central PMCID: PMC1779511.
151. Whitehead K, Kish A, Pan M, Kaur A, Reiss DJ, King N, Hohmann L, DiRuggiero J, **Baliga NS**. An integrated systems approach for understanding cellular responses to gamma radiation. *Mol Syst Biol*. 2006;2:47. Epub 2006 Sep 12. PubMed PMID: 16969339; PubMed Central PMCID: PMC1681521.

2005

152. Iyer R, **Baliga NS**, Camilli A. Catabolite control protein A (CcpA) contributes to virulence and regulation of sugar metabolism in *Streptococcus pneumoniae*. *J Bacteriol*. 2005 Dec;187(24):8340-9. PubMed PMID: 16321938; PubMed Central PMCID: PMC1317011.

2004

153. **Baliga NS**, Bonneau R, Facciotti MT, Pan M, Glusman G, Deutsch EW, Shannon P, Chiu Y, Weng RS, Gan RR, Hung P, Date SV, Marcotte E, Hood L, Ng WV. Genome sequence of *Haloarcula marismortui*: a halophilic archaeon from the Dead Sea. *Genome Res*. 2004 Nov;14(11):2221-34. Erratum in: *Genome Res*. 2004 Dec;14(12):2510. PubMed PMID: 15520287; PubMed Central PMCID: PMC525680.

154. **Baliga NS**, Bjork SJ, Bonneau R, Pan M, Iloanusi C, Kottmann MC, Hood L, DiRuggiero J. Systems level insights into the stress response to UV radiation in the halophilic archaeon Halobacterium NRC-I. *Genome Res.* 2004 Jun;14(6):1025-35. Epub 2004 May 12. PubMed PMID: 15140832; PubMed Central PMCID: PMC419780.
155. Facciotti MT, Cheung VS, Lunde CS, Rouhani S, **Baliga NS**, Glaeser RM. Specificity of anion binding in the substrate pocket of bacteriorhodopsin. *Biochemistry.* 2004 May 4;43(17):4934-43. PubMed PMID: 15109251.
156. Goo YA, Roach J, Glusman G, **Baliga NS**, Deutsch K, Pan M, Kennedy S, DasSarma S, Ng WV, Hood L. Low-pass sequencing for microbial comparative genomics. *BMC Genomics.* 2004 Jan 12;5(1):3. PubMed PMID: 14718067; PubMed Central PMCID: PMC331400.
157. Bonneau R, **Baliga NS**, Deutsch EW, Shannon P, Hood L. Comprehensive de novo structure prediction in a systems-biology context for the archaea Halobacterium sp. NRC-I. *Genome Biol.* 2004;5(8):R52. Epub 2004 Jul 12. PubMed PMID: 15287974; PubMed Central PMCID: PMC507877.

2003

158. Shannon P, Markiel A, Ozier O, **Baliga NS**, Wang JT, Ramage D, Amin N, Schwikowski B, Ideker T. Cytoscape: a software environment for integrated models of biomolecular interaction networks. *Genome Res.* 2003 Nov;13(11):2498-504. PubMed PMID: 14597658; PubMed Central PMCID: PMC403769.
159. Goo YA, Yi EC, **Baliga NS**, Tao WA, Pan M, Aebersold R, Goodlett DR, Hood L, Ng WV. Proteomic analysis of an extreme halophilic archaeon, Halobacterium sp. NRC-I. *Mol Cell Proteomics.* 2003 Aug;2(8):506-24. Epub 2003 Jul 18. PubMed PMID: 12872007.
160. Weston AD, **Baliga NS**, Bonneau R, Hood L. Systems approaches applied to the study of Saccharomyces cerevisiae and Halobacterium sp. *Cold Spring Harb Symp Quant Biol.* 2003;68:345-57. PubMed PMID: 15338636.

2002

161. **Baliga NS**, Pan M, Goo YA, Yi EC, Goodlett DR, Dimitrov K, Shannon P, Aebersold R, Ng WV, Hood L. Coordinate regulation of energy transduction modules in Halobacterium sp. analyzed by a global systems approach. *Proc Natl Acad Sci U S A.* 2002 Nov 12;99(23):14913-8. Epub 2002 Oct 28. PubMed PMID: 12403819; PubMed Central PMCID: PMC137519.

2001

162. **Baliga NS**. Promoter analysis by saturation mutagenesis. *Biol Proced Online.* 2001 Dec 22;3:64-69. PubMed PMID: 12734578; PubMed Central PMCID: PMC145547.
163. **Baliga NS**, Kennedy SP, Ng WV, Hood L, DasSarma S. Genomic and genetic dissection of an archaeal regulon. *Proc Natl Acad Sci U S A.* 2001 Feb 27;98(5):2521-5. Epub 2001 Feb 20. PubMed PMID: 11226271; PubMed Central PMCID: PMC30170.
164. Dassarma S, Kennedy SP, Berquist B, Victor Ng W, **Baliga NS**, Spudich JL, Krebs MP, Eisen JA, Johnson CH, Hood L. Genomic perspective on the photobiology of Halobacterium species NRC-I, a phototrophic, phototactic, and UV-tolerant haloarchaeon. *Photosynth Res.* 2001;70(1):3-17. PubMed PMID: 16228359.

2000

165. Ng WV, Kennedy SP, Mahairas GG, Berquist B, Pan M, Shukla HD, Lasky SR, **Baliga NS**, Thorsson V, Sbrogna J, Swartzell S, Weir D, Hall J, Dahl TA, Welti R, Goo YA, Leithauser B, Keller K, Cruz R, Danson

MJ, Hough DW, Maddocks DG, Jablonski PE, Krebs MP, Angevine CM, Dale H, Isenbarger TA, Peck RF, Pohlschroder M, Spudich JL, Jung KW, Alam M, Freitas T, Hou S, Daniels CJ, Dennis PP, Omer AD, Ebhardt H, Lowe TM, Liang P, Riley M, Hood L, DasSarma S. Genome sequence of Halobacterium species NRC-1. Proc Natl Acad Sci U S A. 2000 Oct 24;97(22):12176-81. PubMed PMID: 11016950; PubMed Central PMCID: PMC17314.

166. **Baliga NS**, DasSarma S. Saturation mutagenesis of the haloarchaeal bop gene promoter: identification of DNA supercoiling sensitivity sites and absence of TFB recognition element and UAS enhancer activity. Mol Microbiol. 2000 Jun;36(5):1175-83. PubMed PMID: 10844701.

167. **Baliga NS**, Goo YA, Ng WV, Hood L, Daniels CJ, DasSarma S. Is gene expression in Halobacterium NRC-1 regulated by multiple TBP and TFB transcription factors? Mol Microbiol. 2000 Jun;36(5):1184-5. PubMed PMID: 10844702.

1999

168. **Baliga NS**, DasSarma S. Saturation mutagenesis of the TATA box and upstream activator sequence in the haloarchaeal bop gene promoter. J Bacteriol. 1999 Apr;181(8):2513-8. PubMed PMID: 10198017; PubMed Central PMCID: PMC93679.

PATENTS

US Patent No:	10,006,071
Entitled:	"Methods to Increase and Harvest Desired Metabolite Production in Algae to enhance recovery of said byproducts"
Inventors:	Nitin Baliga, Monica Orellana, Kenia Whitehead, W. Lee Pang
Issue Date:	06/26/2018
Application No:	14/901,707
Entitled:	"Products and Methods Relating to Micro RNAs and Cancer"
Inventors:	Chris Plaisier, Nitin Baliga
Filing Date:	12/18/2015
Status:	Pending
US Patent No:	10,472,687
Entitled:	"Methods to Identify Antituberculosis Compounds"
Inventors:	Eliza Peterson, Nitin Baliga
Filing Date:	1/6/2017
Issue Date:	11/12/2019
US Patent No:	11,657,895
Entitled:	"Methods for Identifying Treatment Targets Based on Multiomics Data"
Inventors:	Chris Plaisier, Nitin Baliga
Filing Date:	5/3/2017
Issue Date:	5/23/2023
Application No:	US 18/168,056
Entitled:	"Determining viability and treatment of disease agents"
Inventors:	Nitin S. BALIGA, Vivek Srinivas
Filing Date:	2/13/2023

Status:

Pending

SELECTED INVITED TALKS AND PRESENTATIONS

1. UW 7th Annual TB Symposium, Data Science Challenges and Opportunities in TB Research. May 2023. PANELIST.
2. Tuberculosis Research and Training Center (TRTC), Advanced TB Research Training Course. September 2022. Virtual. SPEAKER.
3. 2021 Grand Challenges Annual Meeting, Optimizing Drug Discovery & Translation Track, Grand Challenges Partners, BMGF. November 2021, Hybrid - SPEAKER
4. Tuberculosis Research and Training Center (TRTC) & Mycobacterium Interest Group (MIG) Seminar Series, University of Washington. September 2021, Hybrid - SPEAKER
5. Tuberculosis Drug Accelerator (TBDA) Science Meeting. July 2021. Virtual - SPEAKER
6. BioSystems Science and Engineering (BSSE) Annual Research Symposium 2021. February 2021, Virtual - SPEAKER
7. Lawrence Berkeley National Laboratory (Environmental Genomics and Systems Biology) Annual Meeting, Emergence of complex behaviors from spatiotemporal heterogeneity, January 2021, Virtual – KEYNOTE
8. EMBO MTB Symposium, A multiscale paradigm shift for winning the arms race against TB, February 2020, New Delhi, India – SPEAKER
9. TB Human Infection (HIS) Consortium, Systems Biology of Host-Pathogen interactions, September 2019, Liverpool, UK - SPEAKER
10. TCGA India 2019 Conference, Systems approach to Precision Medicine, September 2019, Pune, India - SPEAKER
11. Life Sciences Symposium at University of British Columbia, Systems approach to Precision Medicine, June 2019, Vancouver BC, Canada – SPEAKER
12. TB QSP Drug Regimen Symposium, Generating mechanism data on TB drug combinations and EGRIN application, June 2019, CDI, Nutley, NJ – SPEAKER
13. NetSci19 conference, Getting connected: Systems Medicine and Networks, May 2019, Burlington, VT – KEYNOTE
14. ICSB 2018: Systems Biology Solutions/Tools for Applied research, October 2018, Lyon, France - SPEAKER
15. EMBO: Molecular Biology of Archaea 2018 – MBoA6: Multiscale systems analysis of microbial community structure, function, and resilience, September 2018, Vienna, Austria - SPEAKER
16. CARIS SAB Meeting: Systems Biology and Molecular Network Architectures in Optimization of Oncology Drug Action, June 2018, Park City, UT - KEYNOTE
17. NBDA ThinkTank II - Connecting the Dots: Big Data, Artificial Intelligence, and Biomarkers: May 2018, Scottsdale, AZ - PANELIST
18. India EMBO Symposia: Big Data in Biomedicine: Will small signals have big impact?, Systems medicine strategies in infectious diseases and cancers, February 2018 New Delhi, India - SEMINAR
19. India EMBO Symposia: Big Data in Biomedicine: Will small signals have big impact?, Will Big Data Break Classical RCTs in Evidence-based Medicine?, February 2018 New Delhi, India - PANELIST (Chair)
20. Seminar, Big Data to Actionable Insights, CISR Institute of Genomics and Integrative Biology, February 2018 New Delhi, India - KEYNOTE
21. BioSparks Student organized conference, Big Data to Insights, February 2018 New Delhi, India. Led discussion and advised students re: Education and Research for setting up big data research efforts.
22. Systems Approach to Cancer, Infectious Disease, the Environment, and Education, Indian Institute of Science (IISc), December, 2017, Bangalore, India - SEMINAR

23. Systems Approach to Cancer, Infectious Disease, the Environment, and Education, National Centre for Cell Science (NCCS), December, 2017 Pune, India - SEMINAR
24. NBDA Think Tank, "Connecting the Dots: Big Data, Artificial Intelligence, and Biomarkers," , November, 2018, Washington DC - PANELIST
25. Systems Approach to Cancer, Infectious Disease, the Environment, and Education, National Centre for Biological Sciences (NCBS), December, 2017, Bangalore, India - SEMINAR
26. SSC 2017: International Symposium on Systems, Synthetic & Chemical Biology, December, 2017, Kolkata, India - KEYNOTE
27. Alda 2017 Senior Management Conference, The Outlook for Omics Technologies and their Role in Advancing Medicine, October, 2017, Half Moon Bay, CA
28. Boston University Bioinformatics Symposium, June, 2017, Boston, MA
29. SchlossGeister Seminar Series, Predictive Models of Biological Networks - Strategies for Personalized Medicine and for Sustainable Environments, June, 2017, Stuttgart, German
30. Tuberculosis Drug Discovery & Development, June, 2017, Barga, Italy
31. 2017 EcoFAB Summit: Developing a community strategy to advance standardized model ecosystems, April, 2017, Washington DC
32. Seattle Science Foundation: Multimodal Spinal Tumors , April, 2017, Seattle, WA
33. Annual Meeting, American Burn Association (ABA), March, 2017, Boston, MA
34. NGS Data Analysis & Informatics, February, 2017, San Diego, CA
35. Seattle Science Foundation: Approaches to Brain Tumor Management, February, 2017, Seattle, WA
36. PepTalk - The Protein Science Week, January, 2017, San Diego, CA KEYNOTE
37. Roche MIT Think Tank (MIT³), October, 2016, Boston, MA
38. Broad Institute: Systems Biology of Human Disease (SPHD), June, 2016, Cambridge, MA
39. Seminar, Systems biology, environment, and health, New York University , February, 2016, New York City, NY
40. CTW: Modeling and Inference from Single Molecule to Cells Workshop, January, 2016, Columbus, OH
41. Partners in Science National Conference, January, 2016, San Diego, CA
42. IHES - Cellular and Molecular Biotechnology Seminar, December, 2015, Paris, France
43. Northeastern University: Xconomy - Cities of the future - Seattle 2035, October, 2015, Seattle WA
44. Boston College Seminar, Memory of environmental history and its influence on biological behaviors across scales, April, 2015, Boston, MA
45. Molecular Basis of Disease Area of Focus (MBDAF), June, 2014, Atlanta, GA
46. Theodore L. Badger Lectures in Network Medicine, April, 2014, Cambridge, MA
47. Lawrence Berkeley National Lab - Biological Sciences Division Retreat. November 2014, Berkeley, CA - KEYNOTE
48. Halophiles 2013, "An intricate program for dealing with salt", June, 2013, Storrs, CT
49. Special Seminar "Strange Microbes & Complex Diseases: Different Problems, One Approach", June, 2013, Birmingham, UK
50. LCSB/ISB Symposium, June, 2013
51. ISB Bay Area Breakfast "Strange Microbes & Complex Diseases: Different Problems, One Approach", May 30, 2013, Palo Alto, CA - KEYNOTE
52. Genome BC Genomics Forum, May 3, 2013, Vancouver, Canada - KEYNOTE
53. The Gordon and Betty Moore Foundation Modeling Workshop, March 2013, Miami, FL.
54. Genomic Science Annual Contractor-Grantee Meeting/USDA-DOE, February, 2013, Bethesda, Maryland
55. UTK-ORNL, Knoxville, TN, October, 2012
56. Joint Genomics: GTL Awardee Workshop VI February, 2010. - PLENARY
57. Daniel J. Zaffarano Lecture 2009. Recognition for contributions to interdisciplinary science, Iowa State University.
58. Nordic Archaeal Network Conference 2009. Copenhagen, Denmark. - KEYNOTE

59. Extremophiles 2008, September, 2008, Cape Town, South Africa, - KEYNOTE
60. The Gordon and Betty Moore Foundation 4th Annual Marine Microbiology Investigator Symposium, July 2008, San Francisco, CA KEYNOTE
61. 6th International Conference on Pathways, Networks and Systems, June 2008, Crete, Greece.
62. IT-ORNL-KBRIN Bioinformatics Summit, March, 2008, Kadi, KY - PLENARY
63. Database Integration and Analysis in Proteomics. The Human Proteome (HUPO) Meeting, March 2007, Seattle, WA.
64. Systems Biology: Integrating Biology, Technology and Computation (C6), Keystone Symposium, March 2006, Taos, New Mexico.
65. Gordon Research Conference on Archaea: Ecology, Metabolism & Molecular Biology, August 2005, Magdalen College, Oxford, UK.
66. HUGO's 10th International Human Genome Meeting, From Genome to Health, 2005, Kyoto, Japan.
67. Computational Biology Research Center, 2005, Tokyo, Japan.
68. 2nd International Conference on Pathways, Networks, and Systems: Theory and Experiments 2004, Crete, Greece.
69. International E. coli Alliance Systems Biology meeting 2004, Calgary, Alberta, Canada.
70. 1st International Conference on Pathways, Networks, and Systems: Theory and Experiments 2003, Santorini, Greece.
71. Gordon Research Conference on Archaea: Ecology, Metabolism & Molecular Biology. August 2003, Proctor Academy, Andover, New Hampshire.
72. Seventh Extremophile Symposium (sponsored by American Type Culture Collection). July 2003, Centre for
73. Marine Biotechnology, University of Maryland, Baltimore, Maryland.
74. Sixth Extremophile Symposium (sponsored by American Type Culture Collection). July 2002, Centre for
75. Marine Biotechnology, University of Maryland, Baltimore, Maryland.
75. Gordon Research Conference on Archaea: Ecology, Metabolism & Molecular Biology, August 1999, Proctor Academy, Andover, New Hampshire.

EDUCATION AND COMMUNITY LEADERSHIP

- Invited to establish Single Cell Biology Research Area S&T strategy at Pacific Northwest National Laboratory's Environmental Molecular Sciences Laboratory's workshop. Virtual. April 28, 2022.
- Established Internships and Scientist-Educator-Student Partnerships to transfer authentic scientific practice and content from laboratories to classrooms (Systems Education Experiences): 2003-current
- Created a crowdsourced network to coordinate training and research on food security issues (Project Feed 1010): 2015-current.
- Developed Next Generation Standards-aligned High School curriculum on systems biology, technology, computation, food security, ocean acidification
- Instructor. Graduate level systems biology course. University of Washington, Seattle, WA. 2007-current
- Organizer. Systems biology workshop. Institute for Systems Biology, Seattle, WA. 2004-current
- Instructor. ATCC sponsored workshop on extremophile biology. 1997-1999 and 2002.
- Lecturer. Graduate level immunology course. University of Massachusetts, Amherst
- Lecturer. Undergraduate level microbiology course. University of Massachusetts, Amherst
- Lead Organizer. Gaggle Workshop for coordinating multi-institutional systems biology software development (<http://gaggle.systemsbiology.net>)

CURRENT GRADUATE STUDENTS, POSTDOCS and SCIENTISTS

Evan Pepper

Graduate Student, University of Washington

Caner Karaca	Graduate Student, Dokuz Eylül University
Zac Cooper	Postdoctoral Fellow
Ishita Mukherjee	Postdoctoral Fellow
Kathryn Stankiewicz	Postdoctoral Fellow
Henry Brinkerhoff	Lee Hood Systems Fellow
Wei-Ju Wu	Software Engineer II
Chris Deutsch	Research Associate III
Julie Do	Research Associate III
Amardeep Kaur	Research Associate IV
Min Pan	Research Associate IV
Kris Hunt	Research Scientist I
Yu He	Research Scientist I
Rupa Immanuel	Research Scientist I
Carl Murie	Research Scientist II
Mario Arrieta-Ortiz	Senior Research Scientist I
Jacob Valenzuela	Senior Research Scientist I
Serdar Turkarslan	Senior Research Scientist II
Sepideh Pakpour	Visiting Faculty on Sabbatical, Univ. of British Columbia
Michael Zhao	Visiting Undergraduate Student w/ Dr. Pakpour, UBC
Claudia Ludwig	Director, Systems Education Experiences
Monica Orellana	Principal Scientist, University of Washington

LAB ALUMNI

	Lab Position	Subsequent Position
Amy Zamora	SRSP Fellow	Graduate Student, Harvard University
David Reiss	Senior Research Scientist	Research Scientist, University of Washington
Amy Schmid	Senior Research Scientist	Assistant Professor, Duke University
Kenia Whitehead	Research Scientist	Staff Res. Associate, Scripps Inst of Oceanography
Tie Koide	Postdoctoral Fellow	Professor, Universidade de São Paulo
Lee Pang	Postdoctoral Fellow	Research Scientist, Genomata
Phu T. Van	Research Associate	Ph.D, Biological Sciences, Carnegie Mellon University
Ricardo Vencio	Postdoctoral Fellow	Professor, Universidade de São Paulo
Aaron Brooks	Postdoctoral Fellow	Postdoc Fellow, Steinmetz gp, Gen Biol Unit, EMBL
Sung Ho Yoon	Postdoctoral Fellow	Senior Researcher, KRIBB
Allison Lee	Research Associate	Senior Research Associate, Synthetic Genomics
Elisabeth Wurtmann	Research Scientist	Associate Faculty, Cascadia College
Nicolas Pinel	Postdoctoral Fellow	Professor, Universidad EAFIT, Medellín, Colombia
Anne Thompson	Senior Research Scientist	Res.Assistant Professor, Portland State University
Saheed Imam	Postdoctoral Fellow	Scientist, Synthetic Genomics
Christopher Plaisier	Senior Research Scientist	Assistant Professor, Arizona State University
Rene Ruiz	Research Associate III	Research Scientist, University of Washington
Vivek Srinivas	Research Scientist I	self-employed
Nivedita Nivedita	Research Scientist I	Scientist, Allen Institute
Rachel Calder	Education Coordinator	Grad Student, Georgia Institute of Technology
John Guittar	Research Scientist I	Tempus Labs, Chicago, IL
Kavya Kannan	Postdoctoral Fellow	Senior Bioinformatics Engineer, Datma

Reino Carlson	Laboratory Technician	Teachers Aide, Seattle Preparatory School
Sasha Coesel	Postdoctoral Fellow	Research Scientist, University of Washington
Jane Timberlake	Research Associate	Research Associate, Allen Institute
Dina Kovarik	Project Manager	Professor, Shoreline Community College
Aimee Desaki	Research Associate I	Interaction Designer, Stratos
Katherine Johnson	Research Associate I	Research Technician, FHCRC
Jessica Hale	Lab Assistant	Grad Student, University of Washington
Maryann Ruiz	Research Associate	Dietician, UW Medicine
A. L. Garcia de Lomana	Senior Research Scientist	Research Specialist, University of Iceland
Saheed Imam	Postdoctoral Fellow	Assoc. Principal Scientist, LifeMine Therapeutics
Warren Carter	Research Associate II	Nanostring, Research Associate
Matthew Wall	Postdoctoral Fellow	Research Scientist, Sage Bionetworks
Rebecca Howsmon	Program Manager	Teacher, Ballard High School
Arjun Raman	Postdoctoral Fellow	MD, Univ of Texas at Southwestern
Marc Facciotti	Research Scientist	Assistant Professor, UC Davis
Madhavi Vuthoori	Research Associate I	Accounting Svcs. Professional, Peterson Sullivan LLP
Micheleen Harris	Software Engineer	R Programmer, Revolution Analytics
Dan Tenenbaum	Software Engineer	Systems Analyst/Programmer, FHCRC
Alex Carr	Graduate Student	Postdoctoral Fellow
James Wilson	Research Associate III	Business Owner, Castaway Ceramics
Yaqiao Li	Bioinformatics Scientist	Software Engineer, UW
James Park	Research Scientist I	Assistant Professor, Tulane Univ.
Eliza Peterson	Senior Research Scientist II	In Process
Brittany Spanier-Marson	Grad. Student, Maastricht Univ.	Maastricht University

IMPACT

Scientific Impact

- Authored over 100 peer reviewed articles, in top tier journals such as Science and Cell
- Filed for five patents, one issued, four pending
- Invited as a speaker to over 50 conferences, including as a keynote or a plenary speaker and as a panelist to over 10 conferences.
- Established over 30 collaborations that span across the USA and internationally in countries, including the United Kingdom, India, Canada, Mexico, including both academia and industry.

Mentoring Impact

- Mentored 100+ researchers including, postdoctoral scientists, graduate students, and undergraduates.
- Developed the Systems Biology Course at ISB (offered annually), from inception in 2003, Leading and mentoring young ISB researchers and faculty to organize the course.

Education impact

SEE: Through its innovative scientist-educator-student partnership program, SEE has enhanced student competency and engagement in STEM careers, and since 2003, has impacted over 60,000 teachers and 2.5 million students. Furthermore, SEE's standards-aligned, open-access curriculum is in use across all 50 states in the US and part of the official curriculum in the state of California. Moreover, the curriculum is also used across 144 countries, with approximately 62,000 web users. 80% of those are teachers who have used these resources with students. The other 20% are interested students and the public who access our career and internship resources.

PROJECT Feed 1010: To date, PF1010 has provided training to **430** educators, **545** citizens, and **55** interns, and has reached over **20,000** students through its open-access, standards-aligned curriculum. In addition, data from over **160** unique citizen science aquaponic systems has been monitored across the world through PF1010's [data portal](#), **300** members joined the [Facebook page](#), and since April 2015, [PF1010 website](#) resources have been viewed by nearly **60,000** users across all 50 states and **150** countries.

WEB RESOURCES, TOOLS, AND ALGORITHMS

Tools / Software

cmonkey2

An algorithm that detects putative co-regulated gene groupings by integrating the bi-clustering of gene expression data and various functional associations with the de novo detection of sequence motifs.

- Source code: <https://github.com/baliga-lab/cmonkey2>
- PyPI.org project: [cmonkey2](#)

EGRIN2 tools

A model that delineates the complex relationship between environment, gene regulation, and phenotype in prokaryotes

- Website: <http://egrin2.systemsbiology.net/>
- Source code: <https://github.com/baliga-lab/egrin2-tools>

sequencelogo.js

Simple sequence logo visualization in Javascript. Website developers can use this simple, small library to render sequence logos as a dynamic vector based graphics within a web page.

- Source code: <https://github.com/baliga-lab/sequencelogo.js>
- NPM package: [@baliga-lab/sequencelogo.js](#)

SYGNAL

SYstems Genetic Network AnaLysis (SYGNAL) pipeline. SYGNAL integrates correlative, causal and mechanistic inference approaches into a framework that systematically infers the causal flow of information from mutations to TFs and miRNAs to perturbed gene expression patterns across patients.

- Source code: <https://github.com/baliga-lab/sygnal>

FIRM

Framework for Inference of regulation by miRNAs. FIRM integrates three best performing algorithms to infer miRNA mediate regulation from co-expression signatures.

- Source code: <https://github.com/baliga-lab/firm2> (original: <https://github.com/baliga-lab/FIRM>)
- PyPI.org project: isb-firm

MINER

An algorithm to map mutations within tumors that causally perturb the regulators to drive downstream changes in disease phenotype.

- Source code: <https://github.com/baliga-lab/miner3>
- PyPI.org project: isb-miner3

Network Portal

The Network Portal is a database of gene transcription regulatory networks and enables exploration, annotation and comparative analysis.

- Website: <http://networks.systemsbiology.net>
- Source code: https://github.com/baliga-lab/network_portal

miRvestigator

Framework designed to take a list of co-expressed genes as input and will return the most likely regulatory miRNAs.

- Website: <https://mirvestigator.systemsbiology.net/>
- Source code: https://github.com/baliga-lab/miRvestigator_www

MTB Network Portal

A database of gene transcription regulatory networks and enables exploration, annotation and comparative analysis. This database is customized to the specifics of *Mycobacterium tuberculosis*.

- Website: <http://networks.systemsbiology.net/mtb/>

Syntrophy Portal

A database of gene transcription regulatory networks and enables exploration, annotation and comparative analysis. This database is customized to explore *Methylobacterium extorquens* AM1 *Methanococcus maripaludis* S2, *Desulfovibrio vulgaris* H and .

- Website: <http://networks.systemsbiology.net/syntrophy/>

Diatom Portal

A database of gene transcription regulatory networks and enables exploration, annotation and comparative analysis. This database is customized to diatoms, at the moment, *T. pseudonana* and *P. tricornutum*.

- Website: <https://baliga.systemsbiology.net/projects/diatom-portal/>

Chlamy Portal

A database of gene transcription regulatory networks and enables exploration, annotation and comparative analysis. This database is customized to *Chlamydomonas reinhardtii*.

- Website: <http://networks.systemsbiology.net/chlamy-portal/>

Publications

Gaggle

- “The Gaggle: An open-source software system for integrating bioinformatics software and data sources” (03/2006) <https://bmcbioinformatics.biomedcentral.com/articles/10.1186/1471-2105-7-176>

cmonkey 1 and 2

- “Integrated biclustering of heterogeneous genome-wide datasets for the inference of global regulatory networks” (06/2006) <https://link.springer.com/article/10.1186/1471-2105-7-280>
- “cMonkey₂: Automated, systematic, integrated detection of co-regulated gene modules for any organism” (07/2015) <https://academic.oup.com/nar/article/43/13/e87/2414187>

Inferelator

- “The Inferelator: an algorithm for learning parsimonious regulatory networks from systems-biology data sets *de novo*” (05/2006) <https://link.springer.com/article/10.1186/gb-2006-7-5-r36>

EGRIN 1 and 2

- “A Predictive Model for Transcriptional Control of Physiology in a Free Living Cell” (12/2007) <https://www.sciencedirect.com/science/article/pii/S009286740701416X>
- “A system-level model for the microbial regulatory genome” (07/2014) <https://www.embopress.org/doi/full/10.15252/msb.20145160>

miRvestigator

- “miRvestigator: web application to identify miRNAs responsible for co-regulated gene expression patterns discovered through transcriptome profiling” (07/2011) https://academic.oup.com/nar/article/39/suppl_2/W125/2506547

FIRM

- “A miRNA-regulatory network explains how dysregulated miRNAs perturb oncogenic processes across diverse cancers” (06/2012) <https://genome.cshlp.org/content/22/11/2302.short>

Network Portal

- “Network portal: a database for storage, analysis and visualization of biological networks” (01/2014) <https://academic.oup.com/nar/article/42/D1/D184/1058860>

MTB Network Portal

- “A comprehensive map of genome-wide gene regulation in *Mycobacterium tuberculosis*” (03/2015) <https://www.nature.com/articles/sdata201510>

Chlamydomonas Portal

- “A refined genome-scale reconstruction of *Chlamydomonas* metabolism provides a platform for systems-level analyses” (10/2015) <https://onlinelibrary.wiley.com/doi/full/10.1111/tpj.13059>

Diatom Portal

- “Pan-transcriptomic analysis identifies coordinated and orthologous functional modules in the diatoms *Thalassiosira pseudonana* and *Phaeodactylum tricornutum*” (04/2016)
<https://www.sciencedirect.com/science/article/abs/pii/S1874778715300441>

Syntrophy Portal

- “Mechanism for microbial population collapse in a fluctuating resource environment” (03/2017)
<https://www.emboPress.org/doi/full/10.15252/msb.20167058>

SUPPORT

Active Support

1. A systems analysis of drug tolerance in *Mycobacterium tuberculosis*. NIH. 2R01AI128215. PI: Baliga. \$4,323,974. 07/2022 - 06/2027.
2. Systems biology of intratumoral heterogeneity in glioblastoma. NIH. R01CA259469. PI: Baliga. \$3,699,285. 01/2022 - 12/2026.
3. Host Pathogen Variation & TB Pathogenesis Project #3 title: Mtb strain-dependent mechanisms of pathogenesis in mouse models. NIH. U19AI162583. PI: Urdahl. \$423,680. 08/2021 - 05/2026.
4. Host innate immune mechanisms control temporal expression of flagellin by pathogenic *Salmonella*. NIH. R01AI155685. PI: Subramanian. \$2,532,632. 06/2021 - 05/2026.
5. Ecosystems and Networks Integrated with Genes and Molecular Assemblies (ENIGMA): Environmental Simulations: Using Field Isolate to Create Synthetic Communities to Characterize/Simulate Ecological Phenomena. DOE. DE-AC02-05CH11231. PI: Adams. \$4,314,995. 01/2021 - 12/2025.
6. IIBR RoL: A systems biology framework to uncover rules governing robustness of a microbial community. NSF. 20429848. PI: Baliga. \$1,552,327. 08/2021 - 07/2025.
7. Translating Single Cell Analysis into Actionable Therapeutic Strategies for Glioblastoma. Kuni Foundation. PI: Patel. \$95,145. 01/2021 - 12/2024.
8. Modular interplay of transcription and translation. NSF. 2105570. PI: Baliga. \$1,424,000. 07/2021 - 06/2024.
9. A systems approach to manipulate microbial adaptation to structured environments. NIH. R01AI141953. PI: Baliga. \$4,440,707. 06/2019 - 05/2024.
10. Global Search for Genetic Regulators of Coral Resilience of Thermal Stress. Allen Foundation. PI: Baliga. \$979,176. 05/2021 - 05/2024.
11. Collaborative Research: IMAGiNE: Quantifying Diatom Resilience in an Acidified Ocean. NSF. 2050550. PI: Baliga. \$1,101,964. 06/2021 - 05/2024.
12. Omics for TB: Response to Infection and Treatment. NIH. U19AI135976-01. PI: Aderem. \$2,206,310. 02/2018 - 01/2024.
13. Discovery Project: Initialization of a real-time emissions network by developing novel N₂O sensor probes. LBNL. PI: Baliga. \$144,329. 01/2022 - 12/2023.
14. Systems Biology enabled ML/AI to Accelerate TB Drug Discovery. Gates Foundation. INV-046460. PI: Baliga. \$199,911. 06/2022 - 12/2023.

Closed Support

1. Systems Biology approach to TB treatment shortening. Gates Foundation. OPP1197573. PI: Baliga. \$1,900,169. 12/2018 - 03/2023.
2. SYGNAL commercialization for Personalized Medicine Applications. WRF. PI: Baliga. \$189,993. 06/01/20 - 01/31/22.
3. Physiologic state modulation by conditional translational complexes. NSF. 1616955. PI: Baliga. \$1,199,383. 09/1/2016 - 8/31/2021.
4. ABI Innovation: A framework to predictably manipulate a microbial gene regulatory program. NSF. 1565166. PI: Baliga. \$1,541,850. 05/01/16 - 04/30/21.
5. Bilateral BBSRC-NSF/BIO: Identifying Mechanisms for Environmental Adaptation in CMNR Bacteria: A Systems Analysis of Gene Regulation of Alternative Substrate Metabolism. NSF. 1518261. PI: Baliga. \$929,994. 08/01/15 - 07/31/20.
6. Bilateral BBSRC-NSF/BIO: Identifying Mechanisms for Environmental Adaptation in Bacteria. NSF. 1518261. PI: Baliga. \$29,994. 08/01/15 - 07/31/20.
7. Model-guided systems re-engineering of *Chlamydomonas reinhardtii*. NSF. 1606206. PI: Baliga. \$298,700. 08/01/16 - 01/31/20.
8. Omics for TB Disease Progression (OTB) - Data Core. NIH. 1U19AI135976-01. PI: Aderem. \$2,206,310. 02/12/18 - 01/31/20.
9. Exploratory Systems Analyses to Coral Resilience ("Phase 0"). Vulcan. 39914. PI: Baliga. \$45,000. 12/07/18 - 04/15/19.
10. Microbial ecology of coexisting ecotypes: Are all *Prochlorococcus* equal?. NSF. 1558924. PI: Thompson. \$102,780. 06/01/16 - 03/31/19.
11. Transcriptional Regulatory Network to Inform Multiple Myeloma Clinical Studies. Celgene. PI: Baliga. \$350,000. 12/01/16 - 01/31/19.
12. Omics for TB Disease Progression (OTB): Data Dissemination Core. NIH. 1U19AI106761. PI: Aderem. \$802,949. 06/21/13 - 05/31/18.
13. Omics for TB Disease Progression (OTB): Modeling Core. NIH. 1U19AI106761. PI: Aderem. \$2,400,905. 06/21/13 - 05/31/18.
14. Stress test for assaying resilience of nitrogen cycling microbial communities. DOE. DE-AC02-05CH11231. PI: Adams. \$170,000. 10/01/16 - 09/30/17.
15. Interplay of Transcriptional, Translational Regulatory Mechanisms and Kinetics of an Environmental Response. NSF. MCB-1330912. PI: Baliga. \$1,199,999. 09/15/13 - 08/31/17.
16. Electron flow and energy conservation in a hydrogenotrophic methanogen. DOE. DE-FG02-05ER15709. PI: Leigh. \$44,495. 09/01/16 - 08/31/17.
17. ABI Innovation: An approach to construct a systems scale predictive model of a gene regulatory network complete with mechanisms at nucleotide-resolution. DB-1262637. PI: Baliga. \$1,047,098. 04/01/13 - 03/31/17.
18. aGRN-Seq: High-throughput characterization of active gene regulatory networks. DOE. 6953601. PI: Adams. \$140,000. 10/01/15 - 09/30/16.
19. A novel approach to leverage laboratory-based gene regulatory network models to decipher active physiological states of keystone organisms in the field. DOE. DE-AC02-05CH11231. PI: Adams. \$303,476. 10/01/13 - 09/30/15.

20. ENIGMA KBase Integration. DOE. DE-AC02-05CH11231. PI: Adams. \$214,000. 10/01/14 - 09/30/15.
21. ISB-Sapphire Strategic Partnership. Sapphire. Collaboration Agmt. \$900,000. 07/17/12 - 09/16/15.
22. Biomass productivity technology advancement towards a commercially viable, integrated algal biomass production unit. DOE. DE-EE0006315. PI: Behnke. \$1,977,005. 03/01/14 - 06/30/15.
23. Partners in Science Program: Employing systems models to accurately predict the biological consequences of sequence variation and small 3D structural changes in the P53 protein. MJ Murdock Charitable Trust. 2012312:BAH:2/28/2013. PI: Baliga. \$15,000. 02/28/13 - 02/27/15.
24. Project Biotech Summer Camp. Shoreline Community College. PI: Baliga. \$3,305. 05/16/14 - 08/31/14.
25. Enabling a Systems Biology Knowledgebase with Gaggles and Firegoose. DOE. DE-SC0004877. PI: Baliga. \$1,495,501. 08/15/10 - 08/14/14.
26. EAGER: Shared Principles of Adaptive Learning Drive Advancements in Biology and Computer Science. NSF. MCB-1237267. PI: Baliga. \$300,000. 07/01/12 - 06/30/14.
27. Systems level investigation of network readjustments to support evolution of syntrophy. DOE. DE-AC02-05CH11231. PI: Adams. \$203,159. 10/01/12 - 09/30/13.
28. 2012 Systems Bioinformatics Workshop. DOE. DE-AC02-05CH11231. PI: Adams. \$203,159.00. 10/01/12 - 09/30/13.
29. Design and Implementation of an effective solution for archiving and processing systems biology data. NSF. DBI-0640950. PI: Baliga. \$1,845,336. 07/01/07 - 09/30/12.
30. Interrogation of Systems Level Mechanisms Controlling DNA Repair Processes (Renewal). NIH. R01 GM077398. PI: Baliga. \$1,343,680.00. 8/1/2007 - 7/31/2012.
31. Interrogation of Systems level mechanisms controlling DNA repair processes. NIH. R01 PI: Baliga. GM077398. \$1,343,680.00. 08/01/07 - 07/31/12.
32. Hydrogen regulation and global responses to electron, carbon and nitrogen sources in *Methanococcus Maripaludis*. DOE. DE-FG02-08ER64685. PI: Leigh.
33. Molecular Assemblies, genes, and Genomics Integrated Efficiently (MAGGIE). DOE. DE-AC02-05CH11231. PI: Adams. \$1,570,279.00. 01/20/06 - 02/28/11.
34. ISB/PNNL Software Collaboration (Continuation). Battelle. PI: Baliga. \$200,000.00. 10/01/08 - 09/30/09.
35. ISB-PNNL Software Collaboration. Battelle. PI: Baliga. 214610 / PNNL #39527. \$550,998.77. 10/01/08 - 09/30/09.
36. Development of advanced tools for data management, integration, analysis and visualization through a comprehensive systems analysis of the halophilic archaeon *Halobacterium* sp. DOE. DE-FG02-04ER63807. PI: Baliga. \$1,199,606.04. 05/15/04 - 05/31/08.
37. ISB / PNNL Collaboration. DOE: 39527. PI: Baliga. \$147,480.00. 03/01/07 - 09/30/07.
38. Molecular Basis for Adaptation to Extreme Environmental Conditions of Halophilic Microorganisms. NASA. NNG05GN58G. PI: DiRuggiero. \$286,341.00. 08/15/05 - 08/14/07.
39. BE/GEN-EN: The oxygen-stress response in the extremophile *Halobacterium* sp. NRC-I: systems analysis and development of supplemental high school instruction modules. NSF. DE-FG02-04ER63807. \$1,750,000.00. 09/01/03 - 08/31/06.
40. QSB: Modeling Predictive Biological Networks in *Halobacterium* sp. NSF. MCB-0425825. PI: Baliga. \$510,000.00. 09/01/04 - 08/31/06.