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# Nitin S. Baliga

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## WORK HISTORY AND EXPERIENCE

<b>Senior Vice President &amp; Director</b> Institute for Systems Biology Seattle, WA USA	2013 – present
<b>Director of Integrative Biology</b> Institute for Systems Biology Seattle, WA USA	2012 – 2013
<b>Professor</b> Institute for Systems Biology Seattle, WA USA	2010 – present
<b>Associate Professor</b> Institute for Systems Biology Seattle, WA, USA	2008 – 2010
<b>Assistant Professor</b> Institute for Systems Biology Seattle, WA, USA	2005 – 2007
<b>Affiliate Faculty</b> Department of Microbiology, School of Medicine Department of Biology Molecular and Cellular Biology Program, Full Member University of Washington Seattle, WA, USA	2005 – present
<b>Affiliate Scientist</b> Lawrence Berkeley National Laboratory Berkeley, CA, USA	2010 – present
<b>Senior Research Scientist</b> Institute for Systems Biology Seattle, WA, USA	2002 – 2004
<b>Postdoctoral fellow</b> Advisor: Prof. Leroy Hood Institute for Systems Biology Seattle, WA, USA)	2000 – 2002
<b>Graduate Research Assistant</b> Advisor: Prof. Shiladitya DasSarma University of Massachusetts Amherst, MA, USA	1996 – 2000
<b>Council for Scientific and Industrial Research (CSIR) Junior Research Fellow</b> Advisor: Prof. Dileep Deobagkar University of Pune Pune, MH, India	1994 – 1996

**Department of Biotechnology (DBT)**

1992 – 1994

**Graduate Fellow**

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 Institute for Information Technology. Mumbai, India.***AWARDS AND RECOGNITION**

- ◆ 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.
- ◆ Daniel J. Zaffarano Lecture 2009. Recognition for contributions to interdisciplinary science, Iowa State University.
- ◆ Participant SciFoo Camp 2008, 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.
- ◆ Council for Scientific and Industrial Research (CSIR) Junior Research Fellowship for graduate research in India. Awarded by the Central Government of India. 1994-1996.
- ◆ Department of Biotechnology (DBT) scholarship for graduate study in Biotechnology. Awarded by the Central Government of India. 1992-1994.

**ADVISORY ROLES**

- ◆ Scientific Review Panels for federal funding agencies include NSF, NIH, and DOE
- ◆ Advisory Boards for EMSL at Pacific Northwest National Lab, Richmond, WA
- ◆ Lead Editor for special issue on Systems & Synthetic Biology of Archaea (2011 – current)
- ◆ Bio-ITEST Advisory Board. (2011-current)
- ◆ Advisory Board Member for NSF funded project at Northwest Association for Biomedical Research (2009-current)
- ◆ DoE ARPA-E – expert panel for evaluating future prospects for bioenergy (2009)
- ◆ Scientific Review Board member for NSF funded energy center at Iowa State University (2007-current)
- ◆ BMC Systems Biology Section Editor. (2007-current)
- ◆ DoE BER – chaired panels for planning a Systems Biology Knowledgebase for the Genomes to Life program (2007-2009)
- ◆ DoE ASCR – planning commission for identifying investments into biological problems requiring petascale computing (2009)
- ◆ DOE BER – planning commission for planning future energy investments into renewable energy technologies (2009)
- ◆ Reviewer. Review of the Department of Energy’s Genomics: GTL Program National Research Council of the National Academies (2006).

**GRANTS**

- ◆ ISB-Sapphire Strategic Partnership
- ◆ M.J. Murdock Charitable Trust 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. \$15,000. 02/28/13 - 02/27/15

- ◆ NSF: EAGER: Shared Principles of Adaptive Learning - Anticipatory behavior in *Halobacterium salinarum*. MCB-1237267. \$150,000. 7/1/12 – 6/30/14
- ◆ DOE (BER): ENIGMA: Ecosystems and Networks Integrated with Genes and Molecular Assemblies. Project: Experimental Design, Implementation, and Data Analysis for the Magic Project. GTL Foundational Science through contract DE-AC02-05CH11231 between Lawrence Berkeley National Laboratory and the U.S. Department of Energy. \$619,265 10/01/2011 – 9/30/2013
  - ❖ Discovery Project: Systems level investigation of network readjustments to support evolution of syntrophy. \$112,866 10/01/12 – 09/30/13
- ◆ DOE: Enabling a Systems Biology Knowledgebase with Gaggles and Firegoose. DE-SC0004877. Total awarded: \$1,500,000 for 8/05/10-08/14/14.
- ◆ NIH: Center for Systems Biology. GM076547. \$09/01/12 – 08/31/17
- ◆ Institutional start-up funds; Total awarded \$500,000 for FY2005-current.

#### Completed

- ◆ Strategic Partnership University of Luxembourg 1/1/2009-12/31/2014
  - ❖ Project 1: Personal Genome Sequencing and Systems Genetics
  - ❖ Project 2: Personal blood Proteomics, RNA, and Cell Analysis
- ◆ NSF: Award OCE 0928561; A systems biology approach of diatom response to ocean acidification and climate change; Total awarded \$ 846,025 for FY2008-2013
- ◆ DOE: Award DE-FG02-04ER63807; Hydrogen regulation and global responses to electron, carbon, and nitrogen sources in *Methanococcus maripaludis*. Total awarded \$750,000 for FY2008-2011.
- ◆ DOE: Program: MAGGIE Component 3; Award DE-FG02-07ER64327; Total Awarded: \$851,395 for FY2006-2011. Molecular Assemblies, Genes, and Genomics Integrated Efficiently (MAGGIE). Component 3: Systems Approach in a Multi-Organism Strategy to Understand Biomolecular Interactions in DOE Relevant Organisms.
- ◆ Battelle: Award 214610; Total awarded \$351,000 for FY2007-2009. ISB/ PNNL Software Collaboration.
- ◆ NIH: Award GM077398; DNA Repair Process. Total awarded \$335,920 for FY2007-2009.
- ◆ DOE: Program: Genomes to Life; Award DE-FG02-04ER63807; Total awarded: \$1,199,999 for FY2004-2007. Project title: Development of advanced tools for data management, integration, analysis and visualization through a comprehensive systems analysis of the halophilic archaeon *Halobacterium* sp.
- ◆ NASA: Program: Extreme Environmental Conditions; Award NNG05GN58G; Total awarded: \$286,341 for FY2005-2007. Project Title: Molecular basis for adaptation to extreme environmental conditions of halophilic microorganisms.
- ◆ DOE: ISB/PNNL Collaboration; Total awarded \$147,480 for FY2007.
- ◆ NSF: Program: Information Technology Research; Award 0220153; Total awarded: \$445,999 for FY2002-2004. Project title: Development of an integrated computational and experimental approach to predict biological networks in *Halobacterium* sp.
- ◆ NSF: Program: Biocomplexity in the Environment; Award 0220153; Total awarded: \$1,750,000 for FY2003-2006. Project title: The oxygen-stress response in the extremophile *Halobacterium* sp. *NRC-1*: systems analysis and development of supplemental high school instruction modules.
- ◆ NSF: Program: Quantitative Systems Biotechnology; Award 0425825; Total awarded: \$500,000 for FY2004-2007. Project Title: Modeling Predictive Biological Networks in *Halobacterium* sp.

## PUBLICATIONS

1. 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 Feb 24.
2. 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.
3. Beer KD, Wurtmann EJ, Pínel N, **Baliga NS**. Model organisms retain an "ecological memory" of complex ecologically relevant environmental variation. *Appl Environ Microbiol*. 2014 Mar;80(6):1821-31.
4. 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.
5. 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 1; 42(3):1442-60.
  6. 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.
  7. Beer KD, Orellana MV, **Baliga NS**. Modeling the evolution of C4 photosynthesis. *Cell.* 2013 Jun 20;153(7):1427-9.
  8. 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.
  9. 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.
  10. 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.
  11. Costa KC, Yoon SH, Pan M, Burn JA, **Baliga NS**, Leigh JA. Effects of H<sub>2</sub> and formate on growth yield and regulation of methanogenesis in *Methanococcus maripaludis*. *J Bacteriol.* 2013 Apr;195(7):1456-62
  12. Bare JC, **Baliga NS**. Architecture for interoperable software in biology. *Brief Bioinform.* 2012 Dec 11.
  13. Muller EE, Pinel N, Gillette 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.
  14. 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.
  15. 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.
  16. 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
  17. 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**, Meroow 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.
  18. 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.
  19. 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.
  20. Yoon SH, Reiss DJ, Bare JC, Tenenbaum D, Pan M, Slagel J, Moritz RL, Lim S, Hackett M, Menon AL, Adams MW, Barnebey A, Yannone SM, Leigh JA, **Baliga NS**. Parallel evolution of transcriptome architecture during genome reorganization. *Genome Res.* 2011 Nov;21(11):1892-904.
  21. 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
  22. 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.
  23. 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.
  24. 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.
  25. 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.
  26. 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.
  27. 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.
28. 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.
  29. 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.
  30. 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.
  31. 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.
  32. 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.
  33. Whitehead K, Pan M, Masumura K, Bonneau R, **Baliga NS**. Diurnally entrained anticipatory behavior in archaea. *PLoS One*. 2009;4(5):e5485.
  34. 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.
  35. 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.
  36. Rubio ED, Reiss DJ, Welch PL, Distchele 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.
  37. **Baliga NS**. Systems biology. The scale of prediction. *Science*. 2008 Jun 6;320(5881):1297-8.
  38. 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.
  39. 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.
  40. 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.
  41. 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.
  42. 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.
  43. 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.
  44. 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.
  45. 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.
  46. 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.
  47. Schmid, A, and **Baliga, NS**. Prokaryotic Systems Biology. In *Cell Engineering*. Vol. 5. El-Rubeai, M. (ed): Springer. 2006.
  48. Shannon PT, Reiss DJ, Bonneau R, **Baliga NS**. The Gagger: an open-source software system for integrating bioinformatics software and data sources. *BMC Bioinformatics*. 2006 Mar 28;7:176.
  49. Ramkumar I, **Baliga NS**, and Camilli A. Catabolite control protein A (CcpA) regulates sugar metabolism and virulence in *Streptococcus pneumoniae*. *Journal of Bacteriology*, 2005 Dec;187(24):8340-9.
  50. **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.
51. 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.
  52. 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.
  53. **Baliga NS**, Bjork SJ, Bonneau R, Pan M, Iloanusi C, Kottemann 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.
  54. Facciotti, MT, Bonneau, R, Hood, L, and **Baliga, N S** Systems Biology Experimental Design - Considerations for Building Predictive Gene Regulatory Network Models for Prokaryotic Systems. *Current 2004 Genomics* 5:527-544.
  55. 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.
  56. 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.
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  58. 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.
  59. **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.
  60. **Baliga NS**. Promoter analysis by saturation mutagenesis. *Biol Proced Online.* 2001 Dec 22;3:64-69.
  61. **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.
  62. 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.
  63. 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, Ehardt H, Lowe TM, Liang P, Riley M, Hood L, DasSarma S. Genome sequence of *Halobacterium* species NRC-I. *Proc Natl Acad Sci U S A.* 2000 Oct 24;97(22):12176-81.
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  65. **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.
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## PATENTS

Application Title: "Methods to Increase and Harvest Desired Metabolite Production in Algae"

Inventors: **Nitin Baliga**, Monica Orellana, Kenia Whitehead, Lee Pang

Assignee: Institute for Systems Biology

Patent Application No: 13/092,706

Filing Date: 4/22/2011

Publication No. 2012-0107866

Publication Date: 5/3/2012

## SELECTED INVITED PRESENTATIONS

1. Halophiles 2013, "An intricate program for dealing with salt", June 25, 2013, Storrs, CT
2. Special Seminar "Strange Microbes & Complex Diseases: Different Problems, One Approach", June 13, 2013, Birmingham, UK
3. LCSB / ISB Symposium, June 10, 2013, Luxembourg
4. ISB Bay Area Breakfast "Strange Microbes & Complex Diseases: Different Problems, One Approach", May 30, 2013, Palo Alto, CA KEYNOTE
5. Genome BC Genomics Forum, May 3, 2013, Vancouver, Canada KEYNOTE
6. The Gordon and Betty Moore Foundation Modeling Workshop, March 2013, Miami, FL.
7. Genomic Science Annual Contractor-Grantee Meeting/USDA-DOE, February 24 – 27, 2013, Bethesda, Maryland
8. UTK-ORNL, Knoxville, TN, October 10, 2012
9. Joint Genomics: GTL Awardee Workshop VI February 2010. PLENARY SPEAKER
10. Daniel J. Zaffarano Lecture 2009. Recognition for contributions to interdisciplinary science, Iowa State University.
11. Nordic Archaeal Network Conference 2009. Copenhagen, Denmark. KEYNOTE SPEAKER
12. Extremophiles 2008, September 2008, Cape Town, South Africa. KEYNOTE SPEAKER
13. The Gordon and Betty Moore Foundation 4th Annual Marine Microbiology Investigator Symposium, July 2008, San Francisco, CA. KEYNOTE SPEAKER
14. 6th International Conference on Pathways, Networks and Systems, June 2008, Crete, Greece.
15. UT-ORNL-KBRIN Bioinformatics Summit, March 2008, Kadiz, KY. PLENARY SPEAKER
16. Seventh International Systems Biology Symposium, April 2007, Seattle, WA.
17. Database Integration and Analysis in Proteomics. The Human Proteome (HUPO) Meeting, March 2007, Seattle, WA.
18. Systems Biology: Integrating Biology, Technology and Computation (C6), Keystone Symposium, March 2006, Taos, New Mexico.
19. Gordon Research Conference on Archea: Ecology, Metabolism & Molecular Biology, August 2005, Magdalen College, Oxford, UK.
20. HUGO's 10th International Human Genome Meeting, From Genome to Health, 2005, Kyoto, Japan.
21. Computational Biology Research Center, 2005, Tokyo, Japan.
22. 2nd International Conference on Pathways, Networks, and Systems: Theory and Experiments 2004, Crete, Greece.
23. International E. coli Alliance Systems Biology meeting 2004, Calgary, Alberta, Canada.
24. 1st International Conference on Pathways, Networks, and Systems: Theory and Experiments 2003, Santorini, Greece.
25. Gordon Research Conference on Arachaea: Ecology, Metabolism & Molecular Biology. August 2003, Proctor Academy, Andover, New Hampshire
26. Seventh Extremophile Symposium (sponsored by American Type Culture Collection). July 2003, Centre for Marine Biotechnology, University of Maryland, Baltimore, Maryland.
27. Sixth Extremophile Symposium (sponsored by American Type Culture Collection). July 2002, Centre for Marine Biotechnology, University of Maryland, Baltimore, Maryland.
28. Gordon Research Conference on Archea: Ecology, Metabolism & Molecular Biology, August 1999, Proctor Academy, Andover, New Hampshire.

## EDUCATION AND COMMUNITY LEADERSHIP

- Instructor. Graduate level systems biology course. University of Washington, Seattle, WA. 2007-current
- Instructor. 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>).

## COLLABORATORS

Michael W. Adams	University of Georgia, Athens, Georgia
John Aitchison	Seattle Biomedical Research Institute, Seattle, WA
Adam Arkin	Lawrence Berkeley National Laboratories, Berkeley, CA
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