

**JOEL S. BADER, PH.D.
CURRICULUM VITAE**

Current Appointments

Academic Departments

Associate Professor (with tenure), Department of Biomedical Engineering, Whiting School of Engineering (2010–present)

Assistant Professor, Department of Biomedical Engineering, Whiting School of Engineering (2003–2010)

Secondary Appointment, Department of Computer Science, Whiting School of Engineering (2005–present)

Research Centers

Interim Director, High-Throughput Biology Center, Institute for Basic Biomedical Sciences, School of Medicine (01/2014–present)

Member, High-Throughput Biology Center, Institute for Basic Biomedical Sciences, School of Medicine (2003–present)

Affiliated Faculty, Institute for Computational Medicine (Affiliated Faculty, 2006–present)

Affiliated Faculty, Institute of Genetic Medicine (2006–present)

Graduate Programs

Preceptor, Human Genetics Graduate Program (2005–present)

Program Faculty, Institute in Multiscale Modeling of Biological Interactions (2005–2007)

Personal Data

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Address, Medical School Campus

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EDUCATION AND TRAINING (in chronological order)

<u>Year</u>	<u>Degree</u>	<u>Institution</u>	<u>Discipline</u>
1986	B.S.	Lehigh University	Biochemistry (Phi Beta Kappa, Tau Beta Pi)
1991	Ph.D.	University of California, Berkeley	Theoretical Chemistry (NSF Pre-Doctoral Fellow) Advisor: Dr. David Chandler
1992–1995	Postdoc	Columbia University	Theoretical Chemistry Advisor: Dr. Bruce J. Berne

ACADEMIC EXPERIENCE

<u>Dates</u>	<u>Position</u>	<u>Institution</u>
2010–present	Associate Professor, Department of Biomedical Engineering	Whiting School of Engineering, Johns Hopkins University
2003–2010	Assistant Professor, Department of Biomedical Engineering	Whiting School of Engineering, Johns Hopkins University (NSF CAREER Award)

BIOTECH EXPERIENCE

<u>Date</u>	<u>Position</u>	<u>Company (Sector)</u>
2015–present	Co-Founder and Director	Neochromosome, Inc. (synthetic biology)
2014–present	Scientific Advisory Board	LAM Therapeutics, Inc. (cancer and rare disease therapeutics and biomarkers, with candidates for lymphangioleiomyomatosis, TSC, and non-Hodgkin B-cell lymphoma)
2014–present	Scientific Advisory Board	CDI Laboratories, Inc. (monoclonal antibodies, protein biomarkers)
1999–2003	Director of Bioinformatics	CuraGen Corporation, New Haven, CT (functional genomics, proteomics, human genetics, co-inventor 454 Genome Sequencer)
1995–1999	Project Leader	CuraGen Corporation, New Haven, CT (DNA sequencing, IPO team)

RESEARCH ACTIVITIES

Peer-Reviewed Publications

(in chronological order, Google Scholar H-index = 47, total citations = 17,310)

Graduate and Postdoctoral Training

1. Kuharski RA, **Bader JS**, Chandler D, Sprik M, Impey RW. 1988. Molecular model for aqueous ferrous–ferric electron transfer. *Journal of Chemical Physics* 89: 3248-3256.
2. **Bader JS**, Chander D. 1989. Computer simulation of photochemically induced electron transfer. *Chemical Physics Letters* 157: 501-504.
3. **Bader JS**, Kuharski RA, Chandler D. 1990. Role of nuclear tunneling in aqueous ferrous-ferric electron transfer. *Journal of Chemical Physics* 93: 230-236.
4. **Bader JS**, Chandler D. 1992. Computer simulation study of the mean forces between ferrous and ferric ions in water. *Journal of Physical Chemistry* 96: 6423-6427.
5. Pollak E, **Bader JS**, Berne BJ, Talkner P. 1993. Theory of correlated hops in surface diffusion. *Physical Review Letters* 70: 3299-3302.
6. **Bader JS**, Berne BJ. 1994. Quantum and classical relaxation rates from classical simulations. *Journal of Chemical Physics* 100: 8359-8366.

7. **Bader JS**, Berne BJ. 1995. The energy-dependent transmission coefficient and the energy distribution of classical particles escaping from a metastable well. *Journal of Chemical Physics* 102: 7953-7965.
8. **Bader JS**, Berne BJ, Pollak E. 1995. Activated rate processes: The reactive flux method for one-dimensional surface diffusion. *Journal of Chemical Physics* 102: 4037-4055.
9. Rick SW, Stuart SJ, **Bader JS**, Berne BJ. 1995. Fluctuating charge force fields for aqueous solutions. *Journal of Molecular Liquids* 65: 31-40.
10. Deem MW, **Bader JS**. 1996. A configurational bias Monte Carlo method for linear and cyclic peptides. *Molecular Physics* 87: 1245-1260.
11. **Bader JS**, Berne BJ, Pollack E, Hanggi P. 1996. The energy relaxation of a nonlinear oscillator coupled to a linear bath. *Journal of Chemical Physics* 104: 1111-1119.
12. **Bader JS**, Berne BJ. 1996. Solvation energies and electronic spectra in polar, polarizable media - simulation tests of dielectric continuum theory. *Journal of Chemical Physics* 104: 1293-1308.
13. **Bader JS**, Cortis CM, Berne BJ. 1997. Solvation and reorganization energies in polarizable molecular and continuum solvents. *Journal of Chemical Physics* 106: 2372-2387.

CuraGen Corporation, Director of Bioinformatics

14. **Bader JS**, Hammond RW, Henck SA, Deem MW, McDermott GA, Bustillo JM, Simpson JW, Mulhern GT, Rothberg JM. Nov 1999. DNA transport by a micromachined Brownian ratchet device. *Proceedings of the National Academy of Sciences USA* 96: 13165-13169.
15. Hammond RW, **Bader JS**, Henck SA, Deem MW, McDermott GA, Bustillo JM, Rothberg JM. 2000. Differential transport of DNA by a rectified Brownian motion device. *Electrophoresis* 21: 74-80.
16. **Bader JS**. 2001. The relative power of SNPs and haplotype as genetic markers for association tests. *Pharmacogenomics* 2: 11-24.
17. **Bader JS**, Bansal A, Sham P. 2001. Efficient SNP-based tests of association for quantitative phenotypes using pooled DNA. *Genescreen* 1: 143-150.
18. **Bader JS**, Deem MW, Hammond RW, Henck SA, Simpson JW, Rothberg JM. 2002. A Brownian-ratchet DNA pump with applications to single-nucleotide polymorphism genotyping. *Applied Physics A* 74: 1-4.
19. Jawaid A, **Bader JS**, Purcell S, Cherny SS, Sham P. Feb 2002. Optimal selection strategies for QTL mapping using pooled DNA samples. *European Journal of Human Genetics* 10: 125-132.
20. **Bader JS**, Sham P. 2002. Family-based association tests for quantitative traits using pooled DNA. *European Journal of Human Genetics* 10: 868-876.
21. Sham P, **Bader JS**, Craig I, O'Donovan M, Owen M. 2002. DNA Pooling: a tool for large-scale association studies. *Nature Reviews Genetics* 3: 862-871.
22. Giot L, **Bader JS** (contributing equally), Brouwer C, Chaudhuri A, Kuang B, Li Y, Hao YL, Ooi CE, Godwin B, Vitols E, Govindan V, Pochart P, Machineni H, Welsh M, Kong Y, Zerhusen B, Malcolm R, Varrone Z, Collis A, Minto M, Burgess S, McDaniel L, Stimpson E, Spriggs F, Williams J, Neurath K, Ioime N, Agee M, Voss E, Furtak K, Renzulli R, Aanensen N, Carrola S, Bickelhaupt E, Lazovatsk Y, DaSilva A, Zhong J, Stanyon CA, Finley RL,

White KP, Braverman M, Jarvie T, Gold S, Leach M, Knight J, Shimkets. RA, McKenna MP, Chant J, Rothberg JM. 2003. A genome-scale protein interaction map of *Drosophila melanogaster*. *Science* 302: 1727-1736. (Cover article)

23. **Bader JS**. 2003. Greedily building protein networks with confidence. *Bioinformatics* 19: 1869-1874. Accepted through the Fourth Georgia Tech – University of Georgia International Conference in Bioinformatics.

Assistant Professor, Johns Hopkins Appointment (2004–2009)

24. **Bader JS**, Chaudhuri A, Rothberg JM, Chant J. 2004. Gaining confidence in high-throughput protein interaction networks. *Nature Biotechnology* 22: 78-85.
25. Iossifov I, Krauthammer M, Friedman C, Hatzivassiloglou V, **Bader JS**, White KP, Rzhetsky A. 2004. Probabilistic inference of molecular networks from noisy data sources. *Bioinformatics* 20: 1205-1213.
26. Pan X, Yuan DS, Xiang D, Wang X, Sookhai-Mahadeo S, **Bader JS**, Hieter P, Spencer F, Boeke JD. 2004. A robust toolkit for functional profiling of the yeast genome. *Molecular Cell* 16: 487-496.
27. Margulies M, Egholm M, Altman WE, Attiya S, **Bader JS**, Bembien LA, Berka J, Braverman MS, Chen YJ, Chen Z, Dewell SB, Du L, Fierro JM, Gomes XV, Godwin BC, He W, Helgesen S, Ho CH, Irzyk GP, Jando SC, Alenquer ML, Jarvie TP, Jirage KB, Kim JB, Knight JR, Lanza JR, Leamon JH, Lefkowitz SM, Lei M, Li J, Lohman KL, Lu H, Makhijani VB, McDade KE, McKenna MP, Myers EW, Nickerson E, Nobile JR, Plant R, Puc BP, Ronan MT, Roth GT, Sarkis GJ, Simons JF, Simpson JW, Srinivasan M, Tartaro KR, Tomasz A, Vogt KA, Volkmer GA, Wang SH, Wang Y, Weiner MP, Yu P, Begley RF, Rothberg JM. 2005. Genome sequencing in microfabricated high-density picolitre reactors. *Nature* 437: 376-380.
28. Ye P, Peyser BP, Spencer FA, **Bader JS**. 2005. Commensurate distances and similar motifs in genetic congruence and protein interaction networks in yeast. *BMC Bioinformatics* 6: 270.
29. Ye P, Peyser BP, Pan X, Boeke JD, Spencer FA, **Bader JS**. 2005. Gene function prediction from congruent synthetic lethal interactions in yeast. *Molecular Systems Biology* 2005.0026
30. Qi Y, Ye P, **Bader JS**. 2005. Genetic Interaction Motif Finding by Expectation Maximization – a novel statistical model for inferring gene modules from synthetic lethality. *BMC Bioinformatics* 6: 288.
31. Pan X, Ye P, Yuan DS, Wang X, **Bader JS**, Boeke JD. 2005. A DNA integrity network in the yeast *Saccharomyces cerevisiae*. *Cell* 124: 1069-1081.
32. Liu LA, **Bader JS**. 2006. Decoding transcriptional regulatory interactions. *Physica D Nonlinear Phenomena (Special Issue on Dynamics of Complex Networks and Applications)* 224: 174-181.
33. Ooi SL, Pan X, Peyser BD, Ye P, Meluh PB, Yuan DS, Irizarry RA, **Bader JS**, Spencer FA, Boeke JD. 2006. Global synthetic-lethality analysis and yeast functional profiling. *Trends in Genetics* 22:56-63.
34. Gandhi TK, Zhong J, Mathivanan S, Karthick L, Chandrika KN, Mohan SS, Sharma S, Pinkert S, Nagaraju S, Periaswamy B, Mishra G, Nandakumar K, Shen B, Deshpande N, Nayak R, Sarker M, Boeke JD, Parmigiani G, Schultz J, **Bader JS**, Pandey A. 2006.

Analysis of the human protein interactome and comparison with yeast, worm and fly interaction datasets. *Nature Genetics* 38: 285-293.

35. Dorer MS, Kirton D, **Bader JS**, Isberg RR. 2006. RNA Interference Analysis of Legionella in Drosophila Cells: Exploitation of Early Secretory Apparatus Dynamics. *PLoS Pathogens* 2: e34.
36. Bose R, Molina H, Patterson AS, Bitok JK, Periaswamy B, **Bader JS**, Pandey A, Cole PA. 2006. Phosphoproteomic analysis of Her2/neu signaling and inhibition. *Proceedings of the National Academy of Sciences USA* 103: 9773-9778.
37. Liu LA, **Bader JS**. 2007. *Ab initio* prediction of transcription factor binding sites. *Pacific Symposium on Biocomputing* 12: 484-495.
38. Huang H, Zhang LV, Roth FP, **Bader JS**. 2007. Probabilistic paths for protein complex inference. Springer Lecture Notes in Computer Science, Lecture Notes in Bioinformatics: *RECOMB 2006 Satellite Workshops on Systems Biology and Computational Proteomics*. 4532: 14-28.
39. Stuart LM, Boulais J, Charriere GM, Hennessy EJ, Brunet S, Jutras I, Goyette G, Rondeau C, Letarte S, Huang H, Ye P, Morales F, Kocks C, **Bader JS**, Desjardins M, Ezekowitz RA. 2007. A systems biology analysis of the Drosophila phagosome. *Nature* 445: 95-101.
40. Huang H, Jedynak B, **Bader JS**. 2007. Where have all the interactions gone? Estimating the coverage of two-hybrid protein interaction maps. *PLoS Computational Biology* 3: e214.
41. Orchard S, Salwinski L, Kerrien S, Montecchi-Palazzi L, Oesterheld M, Stümpflen V, Ceol A, Chatr-aryamontri A, Armstrong J, Woollard P, Salama JJ, Moore S, Wojcik J, Bader GD, Vidal M, Cusick ME, Gerstein M, Gavin AC, Superti-Furga G, Greenblatt J, **Bader J**, Uetz P, Tyers M, Legrain P, Fields S, Mulder N, Gilson M, Niepmann M, Burgoon L, De Las Rivas J, Prieto C, Perreau VM, Hogue C, Mewes HW, Apweiler R, Xenarios I, Eisenberg D, Cesareni G, Hermjakob H. The minimum information required for reporting a molecular interaction experiment (MIMIx). *Nat Biotechnol.* 2007 Aug;25(8):894-8. PubMed PMID: 17687370.
42. Mathivanan S, Ahmed M, Ahn NG, Alexandre H, Amanchy R, Andrews PC, **Bader JS**, Balgley BM, Bantscheff M, Bennett KL, Björling E, Blagoev B, Bose R, Brahmachari SK, Burlingame AS, Bustelo XR, Cagney G, Cantin GT, Cardasis HL, Celis JE, Chaerkady R, Chu F, Cole PA, Costello CE, Cotter RJ, Crockett D, DeLany JP, De Marzo AM, DeSouza LV, Deutsch EW, Dransfield E, Drewes G, Droit A, Dunn MJ, Elenitoba-Johnson K, Ewing RM, Van Eyk J, Faca V, Falkner J, Fang X, Fenselau C, Figeys D, Gagné P, Gelfi C, Gevaert K, Gimble JM, Gnad F, Goel R, Gromov P, Hanash SM, Hancock WS, Harsha HC, Hart G, Hays F, He F, Hebbar P, Helsens K, Hermeking H, Hide W, Hjernø K, Hochstrasser DF, Hofmann O, Horn DM, Hruban RH, Ibarrola N, James P, Jensen ON, Jensen PH, Jung P, Kandasamy K, Kheterpal I, Kikuno RF, Korf U, Körner R, Kuster B, Kwon MS, Lee HJ, Lee YJ, Lefevre M, Lehvaslaiho M, Lescuyer P, Levander F, Lim MS, Löbke C, Loo JA, Mann M, Martens L, Martinez-Heredia J, McComb M, McRedmond J, Mehrle A, Menon R, Miller CA, Mischak H, Mohan SS, Mohmood R, Molina H, Moran MF, Morgan JD, Moritz R, Morzel M, Muddiman DC, Nalli A, Navarro JD, Neubert TA, Ohara O, Oliva R, Omenn GS, Oyama M, Paik YK, Pennington K, Pepperkok R, Periaswamy B, Petricoin EF, Poirier GG, Prasad TS, Purvine SO, Rahiman BA, Ramachandran P, Ramachandra YL, Rice RH, Rick J, Ronnholm RH, Salonen J, Sanchez JC, Sayd T, Seshi B, Shankari K, Sheng SJ, Shetty V, Shivakumar K, Simpson RJ, Sirdeshmukh R, Siu KW, Smith JC, Smith RD, States DJ, Sugano S, Sullivan M, Superti-Furga G, Takatalo M, Thongboonkerd V, Trinidad JC, Uhlen M, Vandekerckhove J, Vasilescu J, Veenstra TD, Vidal-Taboada JM, Vihinen M, Wait R, Wang X, Wiemann S, Wu B, Xu T, Yates JR, Zhong J, Zhou M, Zhu Y, Zurbig P, Pandey A.

2008. Human Proteinpedia enables sharing of human protein data. *Nature Biotechnology* 26: 164-167.
43. Pan X, Yuan D, Ye P, **Bader J**, Boeke JD. 2008. Response to Dr Stephen Cooper's 'On the use of metaphor to understand, explain, or rationalize redundant genes in yeast'. *FEMS Yeast Research* 8: 349-50.
44. Lin YY, Qi Y, Lu JY, Yuan DS, Zhao Y, **Bader JS**, Boeke JD. 2008. A comprehensive synthetic interaction network governing yeast histone acetylation and deacetylation. *Genes and Development* 22: 2062-2074.
45. Guha U, Chaerkady R, Marimuthu A, Patterson AS, Kashyap MK, Harsha HC, Sato M, **Bader JS**, Lash AE, Minna JD, Pandey A, Varmus HE. 2008. Comparisons of tyrosine phosphorylated proteins in cells expressing lung cancer-specific alleles of EGFR and KRAS. *Proceedings of the National Academy of Sciences USA*. 105: 14112-14117.
46. Dai J, Hyland EM, Yuan DS, Huang H, **Bader JS**, Boeke JD. 2008. Probing nucleosome function: A highly versatile library of synthetic histone H3 and H4 mutants. *Cell*. 134: 1066-1078. (Cover article)
47. Qi Y, Suhail Y, Lin YY, Boeke JD, **Bader JS**. 2008. Finding friends and enemies in an enemies-only network: a graph diffusion kernel for predicting novel genetic interactions and co-complex membership from yeast genetic interactions. *Genome Research*. 18:1991-2004.
48. Huang H, **Bader JS**. 2008. Precision and recall estimates for two-hybrid screens. *Bioinformatics*. 25(3):372-8.
49. Veeramani B, **Bader JS**. 2008. Metabolic flux correlations, genetic interactions and disease. *Journal of Computational Biology*. 16: 291-302. PMID: PMC2909654. Accepted through the 4th Annual Research in Computational Molecular Biology (RECOMB) 2008 Satellite on Systems Biology, Boston, MA.
50. Czar MJ, Anderson JC, **Bader JS**, Peccoud J. 2009. Gene synthesis demystified. *Trends in Biotechnology*. 27:63-72. (Cover article)
51. Dymond JS, Scheifele LZ, Richardson S, Chandrasegaran C, **Bader JS**, Boeke JD. 2009. Teaching synthetic biology, bioinformatics, and engineering to undergraduates: the interdisciplinary Build-a-Genome laboratory. *Genetics*. 181: 13-21.
52. Kut C, Golkhou V, **Bader JS**. 2009. Analytical approximations for the amplitude and period of a relaxation oscillator. *BMC Systems Biology*. 3: 6.
53. Huang H, Maertens AM, Hyland EM, Dai J, Norris A, Boeke JD, **Bader JS**. 2009. HISTONEHITS: a database for histone mutations and their phenotypes. *Genome Research*. 19: 674-681.
54. Lee PA, Dymond JS, Scheifele LZ, Richardson SM, Foelber K, Boeke JD, **Bader JS**. 2010. CloneQC: Lightweight sequence verification for synthetic biology. *Nucleic Acids Res*. May;38(8):2617-23. PMID: 20211841; PMID: PMC2860120.

Associate Professor, Johns Hopkins University (2010–present)

55. Richardson SM, Nunley PW, Yarrington RM, Boeke JD, **Bader JS**. 2010. GeneDesign 3.0 is an updated synthetic biology toolkit. *Nucleic Acids Res.* 2010 May;38(8):2603-6. PMID: 20211837; PMCID: PMC2860129.
56. Park Y, Moore C, **Bader JS**. 2010. Dynamic networks from hierarchical Bayesian graph clustering. *PLoS ONE*. 5(1): e8118. doi:10.1371/journal.pone.0008118. Accepted through the RECOMB 2009 Satellite on Systems Biology, Boston, MA.
57. Rivera CG, Vakhil R, **Bader JS**. 2010. NeMo: Network module identification in Cytoscape. *BMC Bioinformatics*. Jan 18; 11 Suppl. 1:S61. Accepted through the 8th Asia Pacific Bioinformatics Conference (APBC 2010), Bangalore, India.
58. Richardson SM, Olson BS, Dymond JS, Burns R, Chandrasegaran S, Boeke JD, Shehu A, **Bader JS**. 2009. Automated Design of Assemblable, Modular Synthetic Chromosomes. In *Parallel Processing and Applied Mathematics (PPAM)*, 8th International Conference, Revised Selected papers. Wyrzykowski, R., Dongarra, J., Karczewski, K., Wasniewski, J. (Eds.) Springer Lecture Notes in Computer Science 6068: 280-289.
59. Veeramani B, **Bader JS**. Predicting functional associations from metabolism using bi-partite network algorithms. *BMC Syst Biol.* 2010 Jul 14;4:95. PMID: 20630077; PMCID: PMC2919484.
60. Zhong J, Krawczyk SA, Chaerkady R, Huang H, Goel R, **Bader JS**, Wong GW, Corkey BE, Pandey A. Temporal profiling of the secretome during adipogenesis in humans. 2010. *J Proteome Res.* 9(10):5228-38. PubMed PMID: 20707391; PubMed Central PMCID: PMC2948433.
61. Zou B, Yu H, Babcock JJ, Chanda P, **Bader JS**, McManus OB, Li M. Profiling diverse compounds by flux- and electrophysiology-based primary screens for inhibition of human Ether-à-go-go related gene potassium channels. *Assay Drug Dev Technol.* 2010 Dec;8(6):743-54. PubMed PMID: 21158688; PubMed Central PMCID: PMC3002177.
62. Zhong J, Krawczyk SA, Chaerkady R, Huang H, Goel R, **Bader JS**, Wong GW, Corkey BE, Pandey A. Temporal profiling of the secretome during adipogenesis in humans. *J Proteome Res.* 2010 Oct 1;9(10):5228-38. PubMed PMID: 20707391; PubMed Central PMCID: PMC2948433.
63. Park Y, **Bader JS**. Resolving the structure of interactomes with hierarchical agglomerative clustering. *BMC Bioinformatics.* 2011. 12: S44.
64. Huang H, Chanda P, Alonso A, **Bader JS**, Arking DE. Gene-based tests of association. *PLoS Genet.* 2011 Jul;7(7):e1002177. Epub 2011 Jul 28. PubMed PMID: 21829371; PubMed Central PMCID: PMC3145613.
65. Dymond JS, Richardson SM, Coombes CE, Babatz T, Muller H, Annaluru N, Blake WJ, Schwerzmann JW, Dai J, Lindstrom DL, Boeke AC, Gottschling DE, Chandrasegaran S, **Bader JS**, Boeke JD. Synthetic chromosome arms function in yeast and generate phenotypic diversity by design. *Nature.* 2011 Sep 14;477(7365):471-6. doi: 10.1038/nature10403. PubMed PMID: 21918511.
66. Rivera CG, Rosca EV, Pandey NB, Koskimaki JE, **Bader JS**, Popel AS. Novel Peptide-Specific Quantitative Structure-Activity Relationship (QSAR) Analysis Applied to Collagen IV Peptides with Antiangiogenic Activity. *J Med Chem.* 2011 Sep 13. PubMed PMID: 21866962.
67. Lin YY, Kiihl S, Suhail Y, Liu SY, Chou YH, Kuang Z, Lu JY, Khor CN, Lin CL, **Bader JS**, Irizarry R, Boeke JD. Functional dissection of lysine deacetylases reveals that HDAC1 and

- p300 regulate AMPK. *Nature*. 2012 Feb 8;482(7384):251-5. doi: 10.1038/nature10804. PubMed PMID: 22318606; PubMed Central PMCID:PMC3277212.
68. Rivera CG, Mellberg S, Claesson-Welsh L, **Bader JS**, Popel AS. Analysis of VEGF--a regulated gene expression in endothelial cells to identify genes linked to angiogenesis. *PLoS One*. 2011;6(9):e24887. Epub 2011 Sep 13. PubMed PMID: 21931866; PubMed Central PMCID: PMC3172305.
 69. Annaluru N, Muller H, Ramalingam S, Kandavelou K, London V, Richardson SM, Dymond JS, Cooper EM, **Bader JS**, Boeke JD, Chandrasegaran S. Assembling DNA fragments by USER fusion. *Methods Mol Biol*. 2012;852:77-95. PubMed PMID: 22328427.
 70. Muller H, Annaluru N, Schwerzmann JW, Richardson SM, Dymond JS, Cooper EM, **Bader JS**, Boeke JD, Chandrasegaran S. Assembling large DNA segments in yeast. *Methods Mol Biol*. 2012;852:133-50. PubMed PMID: 22328431.
 71. Richardson SM, Liu S, Boeke JD, **Bader JS**. Design-A-Gene with GeneDesign. *Methods Mol Biol*. 2012;852:235-47. PubMed PMID: 22328438.
 72. Cooper EM, Müller H, Chandrasegaran S, **Bader JS**, Boeke JD. The Build-a-Genome course. *Methods Mol Biol*. 2012;852:273-83. PubMed PMID: 22328440.
 73. Chanda P, Yuhki N, Li M, **Bader JS**, Hartz A, Boerwinkle E, Kao WL, Arking DE. Comprehensive evaluation of imputation performance in African Americans. *J Hum Genet*. 2012 Jul;57(7):411-21. doi: 10.1038/jhg.2012.43. Epub 2012 May 31. PubMed PMID: 22648186.
 74. Park Y, **Bader JS**. How networks change with time. *Bioinformatics*. 2012 Jun 15;28(12):i40-8. PubMed PMID: 22689777; PubMed Central PMCID: PMC3371843.
 75. Chanda P, Elhaik E, **Bader JS**. HapZipper: sharing HapMap populations just got easier. *Nucleic Acids Res*. 2012 Jul 27. [Epub ahead of print] PubMed PMID: 22844100.
 76. Chu LH, Rivera CG, Popel AS, **Bader JS**. Constructing the Angiome – a Global Angiogenesis Protein Interaction Network. *Physiol Genomics*. 2012 Aug 21. PubMed PMID: 22911453.
 77. Suhail Y, Kshitiz, Lee J, Walker M, Kim DH, Brennan MD, **Bader JS**, Levchenko A. Modeling Intercellular Transfer of Biomolecules Through Tunneling Nanotubes. *Bull Math Biol*. 2013 Feb 16. [Epub ahead of print] PubMed PMID: 23417627.
 78. Subbian S, O'Brien P, Kushner NL, Yang G, Tsenova L, Peixoto B, Bandyopadhyay N, **Bader JS**, Karakousis PC, Fallows D, Kaplan G. Molecular immunologic correlates of spontaneous latency in a rabbit model of pulmonary tuberculosis. *Cell Commun Signal*. 2013 Feb 28;11(1):16. PubMed PMID: 23448601.
 79. Chanda P, Huang H, Arking DE, **Bader JS**. Fast Association Tests for Genes with FAST. *PLoS One*. 2013 Jul 23;8(7):e68585. doi: 10.1371/journal.pone.0068585. Print 2013. PubMed PMID: 23935874; PubMed Central PMCID: PMC3720833.
 80. Subbian S, Bandyopadhyay N, Tsenova L, O'Brien P, Khetani V, Kushner NL, Peixoto B, Soteropoulos P, **Bader JS**, Karakousis PC, Fallows D, Kaplan G. Early innate immunity determines outcome of Mycobacterium tuberculosis pulmonary infection in rabbits. *Cell Commun Signal*. 2013 Aug 19;11(1):60. [Epub ahead of print] PubMed PMID: 23958185; PubMed Central PMCID: PMC3765177.
 81. Kang TH, Park Y, **Bader JS**, Friedmann T. The Housekeeping Gene Hypoxanthine Guanine Phosphoribosyltransferase (HPRT) Regulates Multiple Developmental and Metabolic

Pathways of Murine Embryonic Stem Cell Neuronal Differentiation. *PLOS ONE*. 2013 Oct 9;8(10):e74967. doi: 10.1371/journal.pone.0074967. PubMed PMID: 24130677; PubMed Central PMCID: PMC3794013.

82. Ellis SE, Gupta S, Ashar FN, **Bader JS**, West AB, Arking DE. RNA-Seq optimization with eQTL gold standards. *BMC Genomics*. 2013 Dec 17;14(1):892. PubMed PMID: 24341889.
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Invited Reviews, Editorials

1. **Bader JS**, Chant J. 2006. When proteomes collide. *Science* 311: 187-188.
2. **Bader JS**. 2008. Systems approaches for pharmacogenetics and pharmacogenomics. *Pharmacogenomics* 9: 257-262.
3. **Bader JS**. 2009. New connections, new components, real dynamics. *Science Signaling* 2: pe48.
4. **Bader JS**. 2011. Meeting report: Grand network convergence, a report of the Systems Biology: Networks meeting, Cold Spring Harbor Laboratory, USA, 22-26 March 2011. *Genome Biology*. 12: 306.
5. Karchin R, Ochs MF, Stuart JM, **Bader JS**. Identification of aberrant pathway and network activity from high-throughput data. *Pac Symp Biocomput*. 2012;17:1-6. PubMed PMID: 22174257.
6. Karchin R, Ochs MF, Stuart JM, Ideker T, **Bader JS**. Identification of aberrant pathway and network activity from high-throughput data. *Pac Symp Biocomput*. 2013;18:103-110. PubMed PMID: 23424116.

Book Chapters

1. **Bader JS**. The *Drosophila* Protein Interaction Network May Be Neither Power-Law nor Scale-Free. In Power Laws, Scale-Free Networks and Genome Biology, Eds. Koonin EV, Wolf YI, Karev GP. Eureka Press, 2005.
2. **Bader JS**. Functional Inference From Probabilistic Protein Interaction Networks. In Encyclopedia of Genetics, Genomics, Proteomics and Bioinformatics. Wiley, 2005. DOI DOI: 10.1002/047001153X.g308202
3. Liu LA, **Bader JS**. Structure-Based Ab Initio Prediction Of Transcription Factor Binding Sites. In Computational Systems Biology (Methods in Molecular Biology vol. 200), Eds. McDermott J, Samudrala R, Bumgarner R, Montgomery K, Ireton R. Humana Press, 2008.

Patents, awarded

1. **Bader JS**, Rothberg JM, Deem MW, Mulhern GT, Went GT. Separation of Charged Particles by a Spatially and Temporally Varying Electric Field. US Patent 5938904 issued Aug 17, 1999.
2. Jarvie TP, **Bader JS**, Went GT. Method for Distance Measurements with Solid-State NMR. US Patent 6027941 issued Feb 22, 2000.
3. **Bader JS**, Rothberg JM, Deem MW, Mulhern GT, Went GT, Simpson J, Henck S. Separation of Charged Particles by a Spatially and Temporally Varying Electric Field. US Patent 6193866 issued Feb 27, 2001.
4. Rothberg JM, **Bader JS**. Method of sequencing a nucleic acid. US Patent 6274320, issued Aug 14, 2001. (Commercialized as the 454 Genome Sequencer 20, subsidiary acquired by Roche for \$155 million on Mar 29, 2007)
5. **Bader JS**, Liu Y, Dziuda DM. Methods for classifying nucleic acids and polypeptides. US Patent 7016788 issued Mar 21, 2006.

6. Rothberg JM, **Bader JS**, Dewell SB, McDade K, Simpson JW, Berka J, Colangelo CM. Method of sequencing a nucleic acid. US Patent 7211390 issued May 1, 2007.
7. Rothberg JM, **Bader JS**, Dewell SB, McDade K, Simpson JW, Berka J, Colangelo CM. Method of sequencing a nucleic acid. US Patent 7244559 issued Jul 17, 2007.
8. Rothberg JM, **Bader JS**, Dewell SB, McDade K, Simpson JW, Berka J, Colangelo CM. Method of sequencing a nucleic acid. US Patent 7264929 issued Sep 4, 2007.
9. Rothberg JM, **Bader JS**, Dewell SB, McDade K, Simpson JW, Berka J, Colangelo CM, Weiner MP. Apparatus and method for sequencing a nucleic acid. US Patent 7335762 issued Feb 26, 2008.

Extramural Funding (completed)

09/01/2005 – 02/28/2006 Mapping Disease-Specific Human Protein Networks
NIH R41GM073492

Role: PI, 20% effort. Analyze disease-relevant genes in a protein interaction network

09/01/2003 – 08/31/2005 Functional Genomic Screen Using RNAi In Drosophila (Complex systems supplement)

NIH 1R01GM067761-01

PI: Norbert Perrimon (Harvard Medical School)

Role: PI, complex systems supplement, 40% effort.

09/01/2006 – 12/31/2007 Comparative systematic genetics for cardiovascular disease gene identification

NIH 1R41HL083571-01

Role: PI, 40% effort. Identify disease-related genes through analysis of high-throughput genetics data in model organisms.

07/01/2006 – 06/30/2009 Yeast Genetic Interaction Map

2 R01 HG002432-04

PI: Jef Boeke

Role: Co-PI, 20% effort. Provide database and algorithms for a complete experimental screen of genetic interactions between non-essential genes in yeast.

01/01/2008 – 12/31/2008 Systems models for toxicity and transport

Center for Alternatives to Animal Testing

PIs: Joel Bader and Joe Bressler (joint mechanism)

Role: PI. Develop unified computational and in vitro models predicting transport across the gut and the blood-brain barrier.

11/01/2004 – 10/30/2009 Networks and Pathways of Lysine Modification Roadmap Center
NIH U54 RR020839

PI: Jef Boeke

Role: Co-Director, Computational Core, 15% effort. Develop technologies for quantitative and time-dependent measurements of lysine modification.

08/01/2007 – 07/31/2010 Synthesis and Restructuring of a Yeast Chromosome

NSF/MCB Genes and Genome Systems PD04-1112

PI: Jef Boeke

Role: Co-PI, 5% effort. Develop software to design, synthesize, and test a synthetic yeast chromosome, and algorithms to analyze genome evolution experiments.

05/01/2006 – 04/31/2011 Mapping Biological Pathways

NSF CAREER 0546446

Role: PI, 20% effort, Develop computational methods for predicting protein-protein and protein-DNA interactions.

09/01/2009 – 09/31/2011 DataNet: The Data Conservancy

NSF OCI 0830976

PI: G. Choudhury

Role: Leader, Biological Data Curation and Analysis

09/01/2010 – 02/28/2012 Genetic Hotspots of Disease Risk
NIH 1R43HG006120

PI: Joel S. Bader, Martin Reese (dual-PI mechanism)
Role: PI, JHU component

07/01/2009 – 06/30/2012 Integrative Genetic Analysis of Autism Brains
Simons Foundation Autism Research Initiative

PI: Dan Arking
Role: Gene-based genetic association tests

01/01/2009 – 12/31/2013 Translational Systems Biology for Human Disease Genetics
Robert J. Kleberg, Jr. and Helen C. Kleberg Foundation

Role: PI, 20% effort. Accelerate the search for disease-related genetic variants by using biological networks and pathways as a framework for analyzing human genetic variation

09/01/2008 – 08/31/2011 Johns Hopkins Ion Channel Screening Center
NIH U54 MH084691

PI: Min Li
Role: Director of Computational Core, 10% effort

04/01/2008 – 03/31/2012 Genetic Analysis of the Nucleosome and RNA Polymerase II: A
Systems Approach

NIH R01 GM084448-01
PI: Nevan Krogan (UCSF)
Role: Co-Investigator, 2% effort. Merge and analyze systematic genetics data.

09/30/2008 – 08/31/2013 Lesch Nyhan Disease Interdisciplinary Studies
NIH R24 DK082840

PI: Theodore Friedmann (UCSD)
Role: Co-I, 5% effort. Understand how defects in purine metabolism pathways lead to the neurobehavioral defects that characterize Lesch Nyhan disease.

DARPA CLIO BAA-11-42 Bader JS (PI) 09/2011 – 12/2014 1.2 calendar
GeneGuard K-plex Integrated Safety Switches

Role: PI (2014, changed from Jef Boeke); Co-PI (2011–2014)
Goal: Design, fabricate, and analyze genetically engineered safety switches for synthetic biology

NIH 1 R01 HL106786-01 Bader JS and Karakousis P (Joint PI/PD)
09/01/10 – 08/31/15 (NCE) 1.2 calendar

A Multidisciplinary Approach to Understanding TB Latency and Reactivation
Role: Joint PI/PD

Goal: Identify host cytokine networks responsible for immunological control of Mtb growth, as well as Mtb regulatory and metabolic pathways required for bacillary growth restriction and reactivation through a systems biology approach including several novel animal models of latent TB infection in combination with transcriptional, proteomic, genetic, imaging, and computational techniques, followed by experimental verification of the data using human samples.

NSF DMS-1228248 Geman D (PI) 09/2012–08/2015 0.5 calendar
Coarse-to-Fine Methods for Genome-Wide Association Studies

Role: Co-PI

Goal: We propose a new framework based on coarse-to-fine sequential testing. We also propose a comprehensive analysis, both empirical and theoretical, of the trade-offs resulting from the introduction of carefully chosen biases about the distribution of active variants within genes and pathways. The top-down strategy we propose is essentially opposite to the static (variant-by-variant) and bottom-up (variants to genes and genes to pathways) methods which dominate the field.

NSF MCB PD04-1112 Boeke J (PI) 09/2007 – 08/2015 0.1 calendar
Synthesis and Restructuring of a Yeast Chromosome

Role: Co-PI

Goal: Design, synthesize, and test a synthetic yeast chromosome, and analyze genome evolution experiments. The Bader lab is responsible for all computational aspects, including design and analysis algorithm development and implementation.

NSF TRMS Kwak J (PI) 10/10 – 09/15 (NCE) 0.5 calendar
Cell-type specific networks: Systems analysis and natural variation in Brassica guard cell responses to drought and ABA

Role: Co-I

Goal: Use a cell-type specific systems approach to build network models enabling researchers to conduct cell-type specific genetics and genomics and to manipulate guard cells towards developing practical strategies for improving water stress tolerance of B. napus and other crop plants.

Extramural Funding (to lab members)

01/01/2005 – 12/31/2005 Postdoctoral Training Fellowship
Institute for Multiscale Modeling of Biological Interactions (IMMBI)
Trainee: Dr. Limin Angela Liu
Role: Research Mentor

01/01/2007– 12/31/2007 IBM Predoctoral Fellowship
Trainee: Ms. Yan Qi
Role: Research Mentor

09/01/2007 – 08/31/2011 DOE Computational Sciences Graduate Fellowship
Trainee: Ms. Sarah Richardson
Role: Research Mentor

09/01/2011 – 12/31/2011 Provost's Undergraduate Research Award (PURA)
Trainee: Mr. Sohail Zahid

06/2014 NSF International Summer School on Biocomplexity, Biodesign and Bioinnovation
Trainee: Mr. William Matern

Extramural Funding (other and non-sponsored)

04/01/2007 – 03/31/2010 Gordon Research Conference: Structural, Functional & Evolutionary Genomics
NIH/NHGRI/NLM/NIEHS 1 R13 HG004283-01

Role: PI, 2% effort. This grant provides funding for the 2007 and 2009 meetings of the GRC on Structural, Functional & Evolutionary Genomics. Vice-Chair (2007)

04/01/2007 – 09/30/2007 Gordon Research Conference: Structural, Functional & Evolutionary Genomics

Pfizer

Role: Conference Vice-Chair, grant from Pfizer for the 2007 meeting

04/01/2007 – 03/31/2008 Genome-Scale Prediction of Transcriptional Regulation
NSF TeraGrid Large Resource Allocation Committee MCA07S006

Role: PI. Grant of CPU cycles.

Microsoft External Research Bader JS (PI) 04/2007 0.1 calendar
Computational Challenges in Synthetic Biology: BioStudio, A Collaborative Editing and Revision
Control Environment for Synthetic Genomes

Role: PI

Goal: Build a synthetic genome design environment.

Internal Funding

Johns Hopkins Discovery Award Dymond J (PI) 09/2015–08/2016 0.3 calendar

High throughput discovery and domestication of bacteriophages for human microbiome engineering

Role: Co-I

Goal: Engineer bacteriophages that will introduce pathogen defense and nutritional support into the human microbiome.

EDUCATIONAL ACTIVITIES

Teaching

Semester	Course	Role	Enrollment
As Assistant Professor (2003–2010)			
2005 Spring	580.688 Introduction to Computational Biology and Bioinformatics (WSE BME)	Sole faculty	1 undergrad, 4 grad
2006 Spring	210.703 Biological Networks and Pathways (ME BME)	Co-taught with Andre Levchenko	20 grad
2006 Spring	260.841 Special Topics in Protein Bioinformatics (SPH Biostats and Molecular Microbiology and Immunology)	1 lecture	20 grad
2007 Spring	187.650 Alternative Methods in Animal Testing (SPH Environmental Health Sciences)	1 lecture	6 grad
2007 Fall	580.420 Build-a-Genome (WSE BME)	Co-taught with Jef Boeke and Srinivasan Chandrasegaran	16 undergrad, 1 postdoc
2007 Fall	580.429 Systems Bioengineering III: Genes to Cells (WSE BME)	Sole faculty	67 undergrad, 8 grad
2008 Spring	580.420 Build-a-Genome (WSE BME)	Co-taught with Jef Boeke and Marc Ostermeier	16 undergrad, 1 grad
2008 Spring	580.492 Build-a-Genome Mentor (WSE BME)	Co-taught with Jef Boeke and Marc Ostermeier	3 undergrad
2008 Fall	580.429 Systems Bioengineering III: Genes to Cells (WSE BME)	Sole faculty	94 undergrad, 2 grad
2008 Fall	580.420 Build-a-Genome (WSE BME)	Co-taught with Jef Boeke and Marc Ostermeier	18 undergrad
2009 Spring	580.420 Build-a-Genome (WSE BME)	Co-taught with Jef Boeke and Marc Ostermeier	16 undergrad,
2009 Fall	580.429 Systems Bioengineering III: Genes to Cells (WSE BME)	Sole faculty	107 undergrad, 7 grad
2009 Fall	580.420 Build-a-Genome (WSE BME)	Co-taught with Jef Boeke	8 undergrad, 1 grad
2009 Fall	580.781 Biomedical Engineering Seminar	Co-organizer with Alexander Popel	30 (anticipated)

2010 Fall	580.429 Systems Bioengineering III: Genes to Cells (WSE BME)	Sole faculty	121 undergrad + grad
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As Associate Professor (2011–2014)

2011 Spring	580.420 Build-a-Genome	Co-taught with Jef Boeke	13 undergrad
2011 Spring	580.492 Build-a-Genome Mentor	Co-taught with Jef Boeke	4 undergrad
2011 Fall	580.429 Systems Bioengineering III: Genes to Cells	Sole faculty	105 undergrad, 6 grad
2011 Fall	580.420 Build-a-Genome	Co-taught with Jef Boeke	10 undergrad
2011 Fall	580.492 Build-a-Genome Mentor	Co-taught with Jef Boeke	1 undergrad
2012 Spring	580.420 Build-a-Genome	Co-taught with Jef Boeke	9 undergrad
2012 Fall	580.429 Systems Bioengineering III: Genes to Cells	Sole faculty	126 undergrad + grad
2013 Spring	580.420 Build-a-Genome	Co-taught with Jef Boeke	9 undergrad
2013 Fall	580.420 Build-a-Genome	Co-taught with Jef Boeke	6 undergrad
2013 Fall	580.429 Systems Bioengineering III: Genes to Cells	Sole faculty	115 undergrad + grad
2014 Spring	580.420 Build-a-Genome	Co-taught with Jef Boeke	8 undergrad
2014 Fall	480.420 Build-a-Genome	Supervising faculty	8 undergrad
2014 Fall	480.429 Systems Bioengineering III: Genes to Cells	Sole faculty	138 undergrad + grad

Teaching Evaluations, Overall Summary (5 = highest, 1 = lowest)

Course	Semester	Response rate	Overall quality	Teaching effectiveness	Intellectual challenge
As Assistant Professor (2003–2010)					
580.688	2005 Spring	62.5%	4.20	4.20	4.40
580.429	2007 Fall	82.2%	4.05	4.22	3.83
580.420	2007 Fall	100.0%	4.89	4.89	4.56
580.420	2008 Spring	100.0%	4.86	4.57	4.14
580.429	2008 Fall	73.0%	4.01	4.32	4.07
580.420	2008 Fall	33%	5.00	5.00	5.00
580.429	2009 Fall	89.4%	4.06	4.19	4.23
580.429	2010 Fall	80.3%	3.79	3.91	4.09
580.429	2010 Fall	80.3%	3.79	3.91	4.09
As Associate Professor (2011–2014)					
580.429	2011 Fall	100.0%	4.23	4.29	4.17
580.420	2012 Spring	100.0%	4.67	4.50	4.00
580.429	2012 Fall	94.4%	3.64	3.47	3.84
580.420	2013 Spring	100.0%	4.67	4.00	4.22
580.420	2013 Fall	100.0%	4.17	4.00	4.00
580.429	2013 Fall	94.8%	3.75	3.58	3.90
580.420	2014 Spring	100.0%	4.75	4.50	4.38

Training Activities

Current Post-doctoral Researchers

Dr. Shlomit Edinger (4/2014–present)
Dr. Kun Yang (6/2012–present)

Current Graduate Students

Mr. Will Matern (Ph.D. student, Biomedical Engineering, 2013–present)
Mr. Yasir Suhail (Ph.D. student, Biomedical Engineering, 2006–present) Passed GBO, 2008.
Passed Thesis Proposal, 2013.
Mr. Jianan Zhan (Ph.D. student, Biomedical Engineering, 2013–present)

Previous Post-Doctoral Researchers

Dr. Faris Alqadah (2010–5/2012) Present position: EBay/Paypal
Dr. Nirmalya Bandyopadhyay (1/2012–9/2015) Present position: Postdoctoral researcher, Harvard Medical School
Dr. Pritam Chanda (2010–8/2013) Present position: Dow AgroSciences
Dr. Guan Shan (2004) Present position: Research Staff, Chinese Academy of Agricultural Science
Dr. Limin Angela Liu (2005–2007) Present position: Senior Software Engineer, OCLC World Libraries, Seattle, WA. Awards: Institute for Multiscale Modeling of Biological Interactions (IMMBI) Postdoctoral Fellowship, 2005.
Dr. Zhiguo Liu (2008–2010)
Dr. Elisa Pappalardo (10/2012–5/2014) Present position: Postdoctoral Researcher, Oxford University
Dr. Ashwin Prakash (1/2013–12/2013)
Dr. Corban Rivera (1/2008–12/2011). Present Position: DuPont
Dr. Giovanni Stracquadanio (8/2010–5/2014) Present Position: Postdoctoral Researcher, Oxford University
Dr. Ping Ye (2003–2008) Present position: Assistant Professor, Biology Department, Washington State University

Previous Ph.D. Students

Hailiang Huang, Ph.D. (Ph.D. student, Biomedical Engineering, 2005–2012) Passed GBO, Mar 2007. Current position: Postdoctoral researcher, Broad Institute.
Yan Qi, Ph.D. (Ph.D. student, Biomedical Engineering, 2005–2010) Passed GBO, 2007. Awarded Ph.D., 2010. Awards: IBM Pre-doctoral Fellowship, 2007. Current position: Associate Consultant (biotech sector), ZS Consultants
Sarah Richardson, Ph.D. (Ph.D. student, Human Genetics, 2006–2012) Passed GBO, 2008. Awards: DOE Computational Sciences Graduate Fellowship, 2007–2011. Current position: Distinguished Postdoctoral Fellow, JGI
Balaji Veeramani, Ph.D. (Ph.D. student, Biomedical Engineering, 2008–2011) GBO passed, 2006. Ph.D. awarded, 2011. Present position: Scientist, Dow AgroSciences.
Yongjin Park, Ph.D. (Ph.D. student, Biomedical Engineering, 2008–2013) Present position: Postdoctoral researcher, Manolis Kellis Lab, MIT.

Previous M.S. Students

Mr. Vahid Golkhou (Ph.D. student, Biomedical Engineering, 2008–2010)
Ms. Alexandra Maertens (Ph.D. student, Toxicology, 2006). Present position:
Mr. A. Scott Patterson (Ph.D. student, Biophysics, 2006–2008). Present position: Counsyl
(personal genetics biotech company)

Additional Rotation Students

Ms. Violeta Beleva (2006)
Mr. Hao Chang (2006)
Mr. David Ellison (2006)
Mr. Srinivas Aripirala (2007)
Mr. Rahul Karnik (2007)
Mr. Eitan Halperin-Stromberg (2008)
Mr. Jason Shirey (2009)

Undergraduate Researchers

Mr. Javed Aman (2007)
Mr. Andy Cheng (2003–2004)
Ms. Linda Gai (2014)
Ms. Carmen Kut (2008)
Mr. Pablo Lee (2008–2010)
Mr. Paul Nunley (2009)
Mr. Ming Jack Po (2003–2004)
Mr. Safi Shareef (2003–2004)
Mr. Somponnat Sompatavanich (2003–2004)
Ms. Reiri Sono (2005–2007)
Mr. Rachit Vakil (2008–2010)
Mr. Johnson Wong (2007)
Mr. Sohail Zahid (2010–2012) Received Provost's Undergraduate Research Award, 2011

High School Researchers

Mr. Jeremy Cohen (2010)
Mr. Adam Gerber (2008)
Mr. Joshua Sloane (2007)
Ms. Vivian Wang (2011)
Mr. Junjie Wu (2008–2009)
Mr. Mitchell Traub (2014)

Thesis Committees, Ph.D.

2008, Robert Prill
2009, Saurabh Paliwal
2009, Raymond Cheong
2011, Anna Silva
2011, Zheng Kuang
2011, Dongwon Lee
2011, Gai Yan
2014, Yun-Chin Cheng

2014, Anna Sliva
2014, Kathryn Winglee
2015, Matthew Brennan

Thesis Committees, M.S.

2008, Harsha Kiran Prabhala
2008, Florence Wu
2015, Jingyi Yu

SERVICE AND ORGANIZATIONAL ACTIVITIES

Departmental

Computational Biology Focus Area, Undergraduate curriculum organizer (2007–present)
Computational Biology Focus Area, Graduate admissions organizer (2007–present)
Departmental seminar series co-organizer (2008–present)
Systems Biology Faculty Search Chair (2013–2014, 2014-2015)

University

Fulbright Mock Interview Committee (2006)
Vredenburg Foundation Scholarship Selection Committee (2007, 2008)
Goldwater Foundation Scholar Selection Committee (2007)
Health Professions Committee (2008–present)
Institute of Genetic Medicine Computational Advisory Board (2008–present)
Computer Science Faculty Search Committee (2007–present, advisor on bioinformatics)
Homewood Library Advisory Committee (2010–present)
Ad Hoc Tenure and Promotion Committee Member (2013)
Director of Human Systems Biology Center Search Co-Chair (2015)

External

Editorial Boards

PLoS Computational Biology, Assistant Editor (2009), Deputy Editor (2010–present)
PLoS ONE, Academic Editor (2009–present)
American Journal of Pharmacogenomics (2006–present)
Biology Direct (2006–present)

Advisory Boards

NIH Workshop on Protein-Protein Interaction Maps for the Mammalian Nervous System (2004)
NIH/NIEHS Working Group on Integrated and Computational Toxicology (2005)
Plant Cell (biostatistics advisor, 2007–present)
Scientific Advisory Board, Canadian Institutes of Health Research, University of Toronto Center for Interactomes and Disease (2008–present)
Scientific Advisory Board, NIH Library of Integrated Network-based Cellular Signatures (LINCS) (2010–2014)

Journal Peer Review

Science, Nature, Cell, PNAS, Journal of Biology, PLoS Biology, Bioinformatics, BMC Bioinformatics, Biology Direct, Biometrics, Drug Discovery, Genetics, Genome Biology, Genome Research, IEEE Transactions, Journal of Theoretical Biology, Molecular Systems Biology, Nature Biotechnology, Nature Medicine, Nucleic Acids Research, PLoS Computational Biology, PLoS Genetics, Plant Cell, PLoS One, Proteins, Proteomics, Statistical Applications in Genetics and Molecular Biology, Trends in Biotechnology, Trends in Microbiology

Study Sections and Review Groups

NIH GGG/GCAT Member (2013–2016)
NIH SSS-Y, Special Emphasis Panel on Biotechnology (ad hoc, 2000–2004)
NIH/NCI Study Section for Integrative Cancer Biology Programs (2004, 2006)
NIH BDMA Biological Data Management and Analysis (ad hoc, 2004–2007)

NIH GCAT (ad hoc, 2005–2008)
NIH GGG (ad hoc, 2005–2008)
NIH NIDDK Data Repository (2008)
NIH Ruth L. Kirschstein NRSA F31 Review Panel (2008)
NIH DMID BAA Systems Biology for Infectious Disease (2008)
NSF Genes and Genomes (2006)
NSF Drug Discovery and Bioinformatics (2007)
NSF Graduate Fellowship Review Panel (2010)
Israel Bi-national Science Foundation (2006)
Israel Science Foundation (2007)
Genome Canada (2004)

Professional Societies

American Association for the Advancement of Science (2003–present)
American Society of Human Genetics (2003–present)
Biomedical Engineering Society (2003–present)
International Society for Computational Biology (2003–present)

Conferences

Faculty, Cold Spring Harbor Genome Informatics Workshop (1999–2000)
Session Chair, Gordon Research Conference on Structural, Functional, and Evolutionary Bioinformatics (2005)
Session Chair, Systems Biology and Bioinformatics, BMES Annual Meeting (2005)
Area Co-Chair, Systems Biology, ISBM Annual Meeting (2006)
Vice-Chair, Gordon Research Conference on Structural, Functional, and Evolutionary Bioinformatics (2007)
Program Committee, 6th IEEE Workshop on High Performance Computational Biology, HiCOMB 2007
Program Committee, RECOMB Satellite Conference on Systems Biology (2007)
Program Committee, Bioinformatics Research and Development (BIRD2007)
Area Co-Chair, Protein Interactions and Molecular Networks, ISMB Annual Meeting (2007)
Program Committee, The Fifth Asia Pacific Bioinformatics Conference, APBC (2007)
Program Committee, Pacific Symposium on Biocomputing (2007)
Area Co-Chair, Protein Interactions and Molecular Networks, ISMB Annual Meeting (2008)
Program Committee, Systems Biology, RECOMB Satellite Meeting (2008)
Program Committee, Pacific Symposium on Biocomputing (2008)
Program Committee, 7th Annual International Conference on Computational Systems Bioinformatics, CSB2008
Program Committee, European Conference on Computational Biology (2008)
Area Co-Chair, Protein Interactions and Molecular Networks, ISMB/ECCB Joint Annual Meeting (2009)
Program Committee Asia Pacific Bioinformatics Conference (2009)
Program Committee, RECOMB Satellite Meeting, Systems Biology (2009)
Proceedings Papers Co-Chair, ISMB Annual Meeting (2010)
Program Committee, RECOMB Annual Meeting (2011)
Program Committee, RECOMB DREAM Meeting (2011)
Program Committee, ISMB Annual Meeting (2011)
Program Committee, Asia Pacific Bioinformatics Conference (2012)
Co-Organizer, Identification of Aberrant Pathway and Network Activity from High-Throughput Data, Pacific Symposium on Biocomputing (2012)
Co-Organizer, Biological Systems Design Special Interest Group, ISMB Annual Meeting (2012)

Co-Organizer, Identification of Aberrant Pathway and Network Activity from High-Throughput Data, Pacific Symposium on Biocomputing (2013)

RECOGNITION

Awards, Honors

Phi Beta Kappa (1986)

Tau Beta Pi (1986)

Class Rank 1 (1986)

NSF Pre-Doctoral Research Fellowship (1986–1989)

Whitaker Biomedical Engineering Foundation New Faculty (2003–2006)

NSF CAREER Award (2006–2011)

Invited Talks

Assistant Professor, Johns Hopkins University (2003–20010)

1. A protein interaction map for *Drosophila melanogaster*. 4th International Georgia Tech Conference on Bioinformatics, Atlanta, GA. Nov 16, 2003.
2. What we've learned from biological networks. Board on Army Science and Technology, Washington, DC. Dec 2, 2003.
3. A protein interaction map for *Drosophila melanogaster*. 3rd Annual Orfeome Meeting, Boston, MA. Dec 3, 2003.
4. A protein interaction map for *Drosophila melanogaster*. Institut Curie, Paris, France. Jan 13, 2004.
5. A protein interaction map for *Drosophila melanogaster*. AAAS Annual Meeting, Seattle, WA. Feb 15, 2004.
6. A protein interaction map for *Drosophila melanogaster*. Gordon Research Conference, Ventura, CA. Feb 16, 2004.
7. A protein interaction map for *Drosophila melanogaster*. Carnegie Institute of Washington, Baltimore, MD, Feb 23, 2004.
8. Biological Networks. Center for Cardiovascular Modeling and Bioinformatics, Johns Hopkins University, Baltimore, MD. Mar 9, 2004.
9. Mapping Biological Networks through Experiment and Computation. Department of Biology, Johns Hopkins University, Baltimore, MD. Apr 22, 2004.
10. Bader Lab Research Summary. Biomedical Engineering Advisory Council, Johns Hopkins University, Baltimore, MD. Apr 27, 2004.
11. Merging Physical and Genetic Interaction Maps. RNAi, Cambridge Healthtech Institute, Boston, MA. Apr 28, 2004.
12. Merging Physical and Genetic Interaction Maps. Harvard Medical School, Boston, MA. Apr 29, 2004.
13. Merging Physical and Genetic Interaction Maps. Mass General Hospital, Boston, MA. Apr 29, 2004.

14. Mapping Biological Networks Through Experiment and Computation. University of Missouri, Kansas City, MO. May 16, 2004.
15. Mapping Biological Networks Through Experiment and Computation. GlaxoSmithKline, King of Prussia, PA. Jun 2, 2004.
16. Mapping Biological Networks. Les Treilles Workshop, Les Treilles, France. 25 Juin 2004.
17. Mapping Biological Networks. IEEE Chapter Talk, Johns Hopkins University, Baltimore, MD. Oct 21, 2004.
18. Mapping Biological Networks. Biomedical Engineering Department, Johns Hopkins University, Baltimore, MD. Oct 22, 2004.
19. Systematic studies of protein networks. Technology Center for Networks and Pathways, Johns Hopkins University School of Medicine, Baltimore, MD. Nov 29, 2004.
20. Some topics about networks. Mathematical Biosciences Institute, Ohio State University, Columbus, OH. Feb 22, 2005.
21. Biological Networks. Biophysics Department, Johns Hopkins University, Baltimore, MD. Apr 4, 2005.
22. Systems Toxicology. NIEHS Workshop, Keystone, CO. Apr 7, 2005.
23. Mapping Biological Networks. Wistar Institute, Philadelphia, PA. Apr 13, 2005.
24. Mapping Biological Networks. DIMACS, Rutgers University, New Brunswick, NJ. May 12, 2005.
25. Introduction to Chemical Genomics. Gordon Research Conference on Structural, Functional and Evolutionary Genomics, Bates College, Lewiston, ME. Jun 23, 2004.
26. A Disease-Centric Draft Map of the Human Interactome. Interactome Networks, Cold Spring Harbor Labs and Wellcome Trust, Hinxton, Great Britain. Sep 2, 2005.
27. A Disease-Centric Draft Map of the Human Interactome. American Institute for Chemical Engineering Annual Meeting, Cincinnati, OH. Nov 1, 2005.
28. Multiscale Modeling of Biological Networks. Institute in Multiscale Modeling of Biological Interactions. Johns Hopkins University, Baltimore, MD. Nov 18, 2005.
29. Mapping Dynamical Biological Networks. Dyonet 2006, Max-Planck Institut, Dresden, Germany. Feb 16, 2006.
30. Reverse and Forward Engineering Networks. New York Academy of Sciences, New York, NY. Mar 23, 2006.
31. Group Testing in Genomics. Department of Applied Mathematics and Statistics, Johns Hopkins University, Baltimore, MD. Apr 27, 2006.
32. Ab Initio Prediction of Transcription Factor Binding. DIMACS, New Brunswick, NJ. May 4, 2006.
33. Group Testing in Genomics. Workshop on Combinatorial and Group Testing, DIMACS, New Brunswick, NJ. May 18, 2006.
34. Ab Initio Prediction of Transcription Factor Binding. Workshop on Systems Biology and Molecular Modeling, Institute of Pure and Applied Mathematics, University of California, Los Angeles, CA. May 23, 2006.

35. Decoding Cellular Wiring Diagrams. Department of Chemical Engineering, Ohio State University, Columbus, OH. Oct 5, 2006.
36. Experimental Gold Standards For Reverse Engineering Network Connections. Dialogue on Reverse Engineering Assessment and Methods (DREAM)/DIMACS. Wave Hill, NY. Sep 8, 2006.
37. Decoding Networks From Genome Sequence. Pfizer, La Jolla, CA. Oct 18, 2006.
38. Decoding Networks From Genome Sequence. Department of Computer Science, University of Southern California, Los Angeles, CA. Oct 19, 2006.
39. Decoding Networks From Genome Sequence. 9th Annual Conference on Computational Genomics, Virginia Bioinformatics Institute and Jackson Labs, Baltimore, MD. Oct 29, 2006.
40. Decoding Networks From Genome Sequence. University of Maryland, Baltimore, MD. Oct 31, 2006.
41. Network Inference And Analysis For Systems Biology. DIMACS Workshop on Complex Networks and Their Applications. Georgia Tech, Atlanta, GA. Jan 24, 2007.
42. Mapping Pathways From The Outside In. NIH Roadmap Center All-Hands Meeting, Technology Centers for Networks and Pathways. NIH, Bethesda, MD. Mar 2, 2007.
43. New Algorithms For Biological Networks. Michigan Genomics Symposium, University of Michigan, Ann Arbor, MI. Apr 16, 2007.
44. New Algorithms For Biological Networks. Department of Computational Biology, University of Pittsburgh, Pittsburgh, PA. May 4, 2007.
45. Technology Center for Networks and Pathways of Lysine Modification, Computational Core, NIH Roadmap Center All-Hands Meeting, Bethesda, MD. May 14, 2007.
46. Pathways at Multiple Resolutions, Systems Biology Consortium Meeting, Pennsylvania State University, Jul 16, 2007.
47. Systems Biology for Genetics, Department of Biophysics Seminar, Johns Hopkins School of Public Health, Oct 15, 2007.
48. Scaling Up to Synthetic Genomics, Microsoft eScience Workshop, Raleigh, NC, Oct 22, 2007.
49. Systems Biology for Genetics, Department of Biology Seminar, University of Maryland, Baltimore County, Nov 8, 2007.
50. Learning from Biological Networks. Department of Biology, University of Pennsylvania Medical School, Nov 13, 2007.
51. Modeling and Remodeling Networks. 6th Georgia Tech – Oak Ridge National Laboratories Conference on Bioinformatics, Atlanta, GA. Nov 15, 2007.
52. Computational Systems Biology, Shanghai Jiao Tong University, Shanghai, China. Jan 10, 2008.
53. Learning from Biological Networks, Duke University Medical Center, Raleigh, NC. Feb 25, 2008.
54. Static Maps to Quantitative Models, Technology Center for Networks and Pathways of Lysine Modification, NIH Roadmap Center All-Hands Meeting, Bethesda, MD. Mar 20, 2008.

55. Decoding and Recoding the Genome, Department of Biomedical Engineering, Boston University, Boston, MA. Mar 27, 2008.
56. Decoding and Recoding the Genome, University of Toronto CIHR Center for Interactomes and Disease, Toronto, Canada. Apr 2, 2008.
57. The prosaic in synthetic biology design. NASA-NSF Joint Workshop Toward a Synthetic Biology, HHMI Janelia Farm, VA. Apr 3, 2008.
58. Systems Biology of the Phagosome, ISMB Annual Meeting, Toronto, Canada. Jul 21, 2008.
59. Finding Meaning in Biological Networks, Santa Fe Institute Workshop, Statistical Inference for Complex Networks, Santa Fe, NM. Dec 4, 2008.
60. Computational Identification of Disease Genes and Pathways, Memorial Sloan Kettering Cancer Center, New York, NY. Feb 12, 2009.
61. The hidden structure of biological networks. Princeton University Genome Center, Princeton, NJ. Mar 5, 2009.
62. Managing complexity in bio-networks. Purdue University, Bioinformatics Seminar, West Lafayette, IN. Mar 31, 2009.
63. Surfing the web of biological interactions. American Society of Plant Biologists, 2009 Annual Meeting, President's Symposium. Honolulu, HI. Jul 22, 2009.
64. Dynamic models for biological networks. UCSD Frontiers in Bioinformatics and Systems Biology Colloquium. San Diego, CA. Jan. 21, 2010.
65. Dynamic community structure in time-varying biological networks. SIAM Conference on Parallel Processing for Scientific Computing (PP10), Seattle, WA. Feb. 24-26, 2010.
66. Statistical physics in systems biology. University of Maryland College Park Statistical Physics Seminar. College Park, MD. Mar. 9, 2010.
67. Statistical mechanics of networks. BioMaPS Institute for Quantitative Biology, Rutgers University, Piscataway, NJ. Apr. 21, 2010.
68. GWiS! They're associated! The gene-wide significance (GWiS) method for gene-based tests of association. Computational Genomics Center, Johns Hopkins University School of Medicine, Baltimore, MD. May 3, 2010.
69. Genes, networks, and disease. Biomedical Engineering Departmental Seminar, Johns Hopkins University, Baltimore, MD. May 12, 2010.
70. Data curation and research. Johns Hopkins University Libraries Assembly, Baltimore, MD. May 21, 2010.

Associate Professor, Johns Hopkins University (2010–present)

71. An inverse problem in biology. 2011 Chandler Mini Statistical Mechanics Meeting. Berkeley, CA. Jan. 7, 2011.
72. Dynamics of heterogeneous networks. Applied Dynamics Seminar, University of Maryland, College Park, MD. Feb. 17, 2011.
73. Network remodeling in development and disease. Systems Biology: Networks, Cold Spring Harbor Laboratory, NY. Mar. 24, 2011.

74. Gene-based tests of association. Computational Biology, Bioinformatics, and Genomics Seminar, University of Maryland, College Park, MD. Apr. 14, 2011.
75. Gene-based tests of association. Systems Biology Workshop, Victorian AgriBiosciences Centre, La Trobe University, Melbourne, Australia. May 18, 2011.
76. Network Dynamics in Development and Disease. Systems Biology Workshop, Victorian AgriBiosciences Centre, La Trobe University, Melbourne, Australia. May 19, 2011.
77. Analysis of Genome-wide Association Studies: methods from the CHARGE consortium of cohort studies. Joint Statistical Meetings, Miami Beach, FL. Aug. 1, 2011.
78. Network Dynamics in Development and Disease. Division of Biostatistics, University of Miami, Miami, FL. Aug 4, 2011.
79. Statistical models for dynamic networks. Tsinghua University, Beijing, China. Nov. 8, 2011.
80. Open source software for synthetic biology. Beijing Genomics Institute, Shenzhen, China. Nov. 14, 2011.
81. Identification of aberrant pathway and network activity from high-throughput data (tutorial). Pacific Symposium on Biocomputing. Big Island, Hawaii. Jan. 3, 2012.
82. Statistical models for dynamic networks. Institute for Mathematics and its Applications. University of Minnesota. Minneapolis, MN. Mar. 1, 2012.
83. Yeast 2.0, or the post-modern Prometheus. New Phytologist. Bristol, UK. Jun. 7, 2012.
84. Designer life. SIAM Discrete Math. Halifax, Canada. Jun. 20, 2012.
85. Yeast 2.0. Concordia University. Montreal, Canada. May 21, 2012.
86. Synthetic biology and Build-a-Genome. Johns Hopkins University Parents' College. Oct. 19, 2012.
87. Dynamics of cell fate. Biomedical Engineering Society Annual Meeting. Atlanta, GA. Oct. 25, 2012.
88. Dynamics of cell fate. Institute of Computational Medicine, Johns Hopkins University. Nov. 6, 2012.
89. Building a synthetic yeast genome. ERA-SynBio Mission to USA. Arlington, VA. Nov. 9, 2012.
90. Genome-scale synthetic biology and *Saccharomyces cerevisiae* 2.0. Genopole Institute of Systems and Synthetic Biology. Evry, France. May 31, 2013.
91. A multidisciplinary approach to understanding TB latency and reactivation. Pasteur Institute, Paris, France. June 26, 2013.
92. Synthetic biology design and analysis tools. Second Annual Sc2.0 Meeting. Imperial College, London, UK. July 12, 2013.
93. Network analysis of bacterial persistence. Los Alamos National Laboratories Workshop on Bacterial Persistence. Los Alamos, NM. August 22, 2013.
94. Protein Capture Reagents Data Working Group. NIH Common Fund Protein Capture Reagents All-Hands Meeting. Rockville, MD. December 16, 2013.
95. Association tests for genes and regions. 2014 Mid-Atlantic Genetic Epidemiology and Statistics (MAGES) Conference: Integrated Systems Biology Analytical Methods for Epidemiological Study of Complex Traits. Philadelphia, PA. May 30, 2014.

96. Genome design and synthesis. International Synthetic and Systems Biology Summer School. Taormina, Sicily, Italy. June 15–19, 2014.
97. Gene and pathway analysis of genome-wide association studies. International Synthetic and Systems Biology Summer School. Taormina, Sicily, Italy. June 15–19, 2014.
98. Genome evolution in synthetic yeast. European Molecular Biology Organization (EMBO) Conference Series, Experimental Approaches to Evolution and Ecology using Yeast & Other Model Systems. Heidelberg, Germany. October 13, 2014.
99. Induced Evolution of Synthetic Yeast Genomes (IESY). ERASynBio Workshop. Brussels, Belgium. November 19, 2014.
100. The agenda for genome-scale research. EU-US Stakeholders Workshop on Standards in Synthetic Biology under the aegis of the SynBio Working Group of the EC-US Task Force in Biotechnology. March 10, 2015.
101. Genome evolution in synthetic yeast. Advances in Systems and Synthetic Biology (ASSB) Summer School, Modeling Complex Biological Systems in the Context of Genomics. Strasbourg, France. March 26, 2015.
102. DNA looping in a synthetic chromosome. University of Catania School of Medicine. Catania, Italy. June 30, 2015.
103. Multi-SCRaMbLE. Fourth Annual Sc2.0 Meeting. New York Genome Center, New York, NY. July 17, 2015.
104. Sc2.0 genome SCRaMbLE-ing and minimization. Center for Advanced Studies Conference Synthetic Biology II. Munich, Germany. July 29, 2015.
105. SCRaMbLE generates combinatorial diversity. BioDesign Megameeting. CUNY Advanced Sciences Research Center. New York, NY. November 13, 2015.
106. Discovering pleiotropy in the genetic basis of disease. The International Symposium on the Frontiers of Precision Medicine and Future Healthcare: The 3rd National Conference on Pharmacogenomics. Shanghai, China. December 9, 2015.