

- 2012–present Scientific Advisory Committee, DOE ENIGMA (Ecosystems and Networks Integrated with Genes and Molecular Assemblies) Program; *Chair of committee in 2013*
- 2011–2014 Board of Directors, P4 Medicine Institute
- 2010–2012 Invited Member, Institute of Medicine (IOM) Committee to Review Omics-Based Tests to Predict Clinical Outcomes
- 2010–2011 Steering Committee, Mayo Clinic-University of Illinois Alliance for Technology-Driven Medicine
- 2008–2011 Scientific Advisory Board, TetraVitae Biosciences, Inc. (sold to Eastman in 2011)

Editorial Boards

- 2016-present Executive Advisory Board, *Advanced Biosystems*
- 2015-present Founding Editorial Board, *Cell Systems* (*Cell* family journal)
- 2012-present Editorial Advisory Board, *Science Translational Medicine* (*Science* family journal)
- 2014-present Associate Editor, *IEEE Life Science Letters*
- 2012–present Editorial Board, *Industrial Biotechnology*
- 2009–present Associate Editor, *Biotechnology Journal*
- 2009–present Deputy Section Editor, *BMC Systems Biology* (Associate Editor, 2009-2011)
- 2009–2014 Deputy Editor-in-Chief, *PLOS Computational Biology* (Associate Editor, 2009-2010)

Honors

- 2016 Grace A. Goldsmith Award, American College of Nutrition
- 2011 Camille Dreyfus Teacher-Scholar
- 2010 Young Investigator Award, Roy J Carver Charitable Trust
- 2009 National Science Foundation CAREER Award
- 2008 Howard Temin Pathway to Independence Award in Cancer Research, National Cancer Institute
- 2007 Tomorrow's PIs, *Genome Technology*
- 2006–2007 Sam E. and Kathleen Henry Postdoctoral Fellowship, American Cancer Society

PEER-REVIEWED PUBLICATIONS

h-index = 39 (Google Scholar)

122. Sagner, M., McNeil, A., Puska, P., Auffray, C., **Price, N.D.**, Hood, L., Lavie, C.J., Han, Z., Chen, Z., Brahmachari, S.K., McEwen, B.S., Soares, M.B., Balling, R., Epel, E., and Arena, R. The P4 Health Continuum – a novel framework to prevent and treat chronic diseases, Epub ahead of print. *Progress in Cardiovascular Diseases* (2016)
121. Allen, M., Burgess, J.D., Ballard, T., Serie, D., Wang, X., Younkin, C.S., Sun, Z., Kouri, N., Baheti, S., Wang, C., Carrasquillo, M.M., Nguyen, T., Lincoln, S., Malphrus, K., Murray, M., Golde, T., **Price, N.D.**, Younkin, S.G., Schellenberg, G.D., Asmann, Y., Ordog, T., Crook, J., Dickson, D., Ertekin-Taner, N., Gene expression, methylation and neuropathology correlations at progressive supranuclear palsy risk loci, *Acta Neuropathologica* 132:197-211(2016).
120. Carrasquillo, M.M., Allen, M., Burgess, J., Strickland, S.L., Aryal, S., Siuda, J., Kachadoorian, M.L., Medway, C., Younkin, C.S., Nair, A., Wang, C., Chanana, P., Wang, X., Serie, D., Nguyen, T., Lincoln, S., Malphrus, K.G., Morgan, K., Golde, T.E., **Price, N.D.**, White, C.C., De Jager, P.L., Bennett, D.A., Asmann, Y.W., Crook, J.E., Petersen, R.C., Graff-Radford, N.R., Dickson, D.W., Younkin, S.G., Ertekin-Taner, N., A regulatory variant at the TREM gene cluster associates with decreased Alzheimer's

disease risk, and increased TREML1 and TREM2 brain gene expression, *Alzheimer's & Dementia*, (Submitted, 2016)

119. Allen, M. *, Burgess, J. *, Wang, X. *, Serie, D., Chai, H-S, Younkin, C.S., Nguyen, T., Malphrus, K.G., Lincoln, S., Golde, T.E., **Price, N.D.**, Petersen, R.C., Graff-Radford, N.R., Younkin, S.G., Dickson, D.W., Crook, J.R., Asmann, Y.W., and Ertekin-Taner, N., Brain transcriptome analyses reveal conserved networks in human neurodegenerative diseases, *Nature Neuroscience* (Submitted, 2016)

118. Dinov, I.D., Heavner, B., Tang, M., Glusman, G., Chard, K., Darcy, M., Madduri, R., Pa, J., Spino, C., Kesselman, C., Foster, I., Deutsch, E.W., Price, N.D., Van Horn, J.D., Ames, J., Clark, K., Hood, L., Hampstead, B.M., Dauer, W., Toga, A.W., Predictive big data analytics: A study of Parkinson's disease using large, complex, heterogeneous, incongruent, multi-source, and incomplete observations, *PLOS ONE* 11:e0157077 (2016)

117. Allen, M. *, Carrasquillo, M.M. *, Funk, C.C., Heavner, B.D., Zou F., Younkin, C.S., Burgess J.D., Chai, H.S., Crook, J., Eddy, J.A., Li, H., Logsdon, B., Wang, X., Serie, D., Wang, C., Nguyen, T., Lincoln S., Malphrus, K., Bisceglia, G., Li, M., Golde, T.E., Mangravite, L., Asmann, Y., **Price, N.D.**, Petersen, R.C., Graff-Radford, N.R., Dickson, D.W., Younkin, S.G., Ertekin-Taner, N., Human whole genome genotype and transcriptome data for Alzheimer's and other neurodegenerative diseases, *Scientific Data* (Accepted, 2016)

116. Ghosh, D., Funk, C.C., Caballero, J., Shah, N., Rouleau, K., Earls, J.C., Soroceanu, L., Foltz, G., Cobbs, C.S., **Price, N.D.**, Hood, L., Identification and characterization of invasion-mediating cell-surface proteins in the blood of glioblastoma multiforme patients, *Cell Systems* (In revision, 2016)

114. McDonald, D.T., Glusman, G., and **Price, N.D.**, Personalized nutrition through big data, *Nature Biotechnology*, (2016).

113. Pestal, K., Funk, C.C., Snyder, J.M., **Price, N.D.**, Treuting, P.M., Stetson, D., Independent control of MDA5-driven autoimmunity and multi-organ development by ADAR1, *Immunity*, (2015)

112. Garcia de Lomana, A.L., Schäuble, S., Valenzuela, J., Imam, S., Carter, W., Bilgin, D.D., Yohn, C.B., Turkarslan, S., Reiss, D., Orellana, M.V., **Price, N.D.**, and Baliga, N.S., Transcriptional program for nitrogen starvation-induced lipid accumulation in *Chlamydomonas reinhardtii*, *BMC Biotechnology for Biofuels*, Epub ahead of print (2015)

111. Zhou, J.X. *, Samal, A. *, Fouquier d'Hérouël, A., **Price, N.D.**, Sui Huang, Relative stability of network states in Boolean network models of gene regulation in development, *Biosystems* 142-143:15-24 (2016)

110. Imam, S., Schäuble, S., Valenzuela, J., García de Lomana, A.L., Carter, W., **Price, N.D.**, and Baliga, N.S., A refined genome-scale reconstruction of *Chlamydomonas* metabolism: A platform for systems-level analyses, Epub ahead of print, *The Plant Journal*, (2015)

109. Tian, Q., Sangar, V., and **Price, N.D.**, Emerging proteomic technologies provide enormous and underutilized potential for brain cancer research, *Molecular & Cellular Proteomics* Epub ahead of print, (2015)

108. Almaas, E., Bauer, E., Bordbar, A., Burgard, A.P., Chang, R.L., Dräger, A., Ebrahim, A., Famili, I., Feist, A.M., Fleming, R.M.T., Fong, S.S., Hatzimanikatis, V., Herrgård, M.J., Holder, A., Hyde, D., Jamshidi, N., Lee, S.Y., Lerman, J.A., Lewis, N.E., Ma, D., Mahadevan, R., Maranas, C., Nagarajan, H.,

- Navid, A., Nielsen, J., Nielsen, L.K., Nogales, J., Noronha, A., Pal, C., Palsson, B. Ø, Papin, J.A., Patil, K.R., **Price, N.D.**, Reed, J.L., Saunders, M., Senger, R.S., Sonnenschein, N., Sun, Y., and Thiele, I. (author order alphabetical), Do Genome-scale Models Need Exact Solvers or Clearer Standards?, *Molecular Systems Biology* (Accepted, 2015)
107. Heavner, B.D., and **Price, N.D.**, Comparative analysis of yeast metabolic network models highlights progress, opportunities for metabolic reconstruction, *PLOS Computational Biology*, (Accepted, 2015)
106. Ma, S., Minch, K.J., Rustad, T.R., Hobbs, S., Zhou, S.L., Sherman, D.R., and **Price, N.D.**, Integrated modeling of gene regulatory and metabolic networks in *Mycobacterium tuberculosis*, *PLOS Computational Biology*, (2015)
105. Magis, A.T., Funk, C.C., and **Price, N.D.**, SNAPR: a bioinformatics pipeline for efficient and accurate RNA-seq alignment and analysis, *IEEE Life Science Letters*, 1: 22-35 (2015)
104. Toga, A.W., Foster, I., Kesselman, C., Madduri, R., Chard, K., Deutsch, E.W., **Price, N.D.**, Glusman, G., Heavner, B.D., Dinov, I.D., Ames, J., Van Horn, J., Kramer, R., and Hood, L., Big biomedical data as the key resource for discovery science, *Journal of the American Medical Informatics Association* (JAMIA). Epub ahead of print (2015)
103. Hood, L., Brogaard, K., and **Price, N.D.**, A Vision for 21st Century Healthcare, *Cancer Medicine* (Eds. Kufe, D.W., Pollock, R.E., Weichselbaum, R.R., Bast, R.C., Gansler, T.S., Holland, J.F., and Frei, E), Ninth Edition, (2015)
102. Imam, S., Schauble, S., Brooks, A.N., Baliga, N.S., and **Price, N.D.**, Data-driven integration of genome-scale regulatory and metabolic network models, 6:409, *Frontiers in Microbiology* (2015)
101. Turkarlan, S., Peterson, E., Rustad, T., Minch, K., Reiss, D.J., Morrison, B., Ma, S., **Price, N.D.**, Sherman, D.R., and Baliga, N.S., A comprehensive map of genome-wide regulation in *Mycobacterium tuberculosis*, *Scientific Data* 2:150010 (2015)
100. Eddy, J.A., Funk, C.C., and **Price, N.D.**, Systems biology contributions to cell biology, *Trends in Cell Biology*, (2015)
99. Ament, S.A., Szelinger, S., Glusman, G., Detera-Wadleigh, S., Ashworth, J., Hou, L., Akula, N., Shekhtman, T., Badner, J.A., Brunkow, M.E., Mauldin, D.E., Stittrich, A.B., Rouleau, K., Nurnberger, J.I., Edenberg, H.J., Gershon, E.S., Schork, N.J., The Bipolar Genome Study, **Price, N.D.**, Gelinias, R., Hood, L., Craig, D.W., McMahon, F.J., Kelsoe, J.R., Roach, J.C., Rare variants in neuronal excitability genes influence risk for bipolar disorder, *Proc. Natl. Acad. Sci. USA*, 112:3576-81 (2015)
98. Simeonidis, E., and **Price, N.D.**, *Journal of Industrial Microbiology and Biotechnology*, 42: 327-338 (2015)
97. Heavner, B., and **Price, N.D.**, Transparency in metabolic network reconstruction enables scalable biological discovery, *Current Opinion in Biotechnology*, 34C:105-109 (2015)
96. Chandrasekaran, S., Rittschof, C., Djukovic, D., Gu, H., Raftery, D., **Price, N.D.***, and Robinson, G.* Aggression is Associated with Aerobic Glycolysis in the Honey Bee Brain, *Genes, Brain, and Behavior* (2015). *Corresponding authors

95. Chakrabarty, P., Li, A., Ceballos-Diaz, C., Funk, C.C., Eddy, J.A., Moore, B., Rosario, A.M., Verbeeck, C., Sacino, A., Nix, S., Janus, C., **Price, N.D.**, Das, P., Golde, T.E., IL-10 Alters Immunoproteostasis in APP mice, Increasing Plaque Burden and Worsening Cognitive Behavior, *Neuron*, (2015)
94. Minch, K.J., Rustad, T.R., Peterson, E. Winkler, J., Reiss, D.J., Ma, S., Hickey, M., Brabant, B., Morrison, B., Turkarslan, S., Mawhinney, C., Galagan, J., **Price, N.D.**, Baliga, N.S., and Sherman, D.R., The DNA binding network of *Mycobacterium tuberculosis*, *Nature Communications* 6:5829 (2015)
93. Hood, L., Lovejoy, J., and **Price, N.D.**, Integrating big data and actionable health coaching to optimize wellness, *BMC Medicine*, 13:4 (2015). **Highly Accessed** (special distinction given to the most downloaded papers in the journal)
92. Geman, D., Ochs, M., **Price, N.D.**, Tomasetti, C., and Younes, L., An Argument for Mechanism-Based Statistical Inference in Cancer, *Human Genetics*, 134(5):479-95 (2015)
91. Rustad, T.R., Minch, K.J., Winkler, J., Hobbs, S., Hickey, M, Brabant, W., Turkarslan, S., **Price, N.D.**, Baliga, N.S., and Sherman, D.R., Mapping and manipulating the *M. tuberculosis* transcriptome using a transcription factor overexpression-derived regulatory network, *Genome Biology*, 15(11):502 (2014). **Highly Accessed** (special distinction given to the most downloaded papers in the journal)
90. Ma, S., Sung, J., Magis, A.T., Wang, Y., Geman, D., and **Price, N.D.**, Assessing inter-study variability and diversity sufficiency for robust molecular signatures, *PLOS ONE*, 9:e110840, (2014)
89. Benedict, M.N., Mundy, M.B., Henry, C.S., Chia, N., and **Price, N.D.**, Likelihood-based gene annotations for gap filling and quality assessment in genome-scale metabolic models, *PLOS Computational Biology*, 10:e1003882 (2014)
88. Sangar, V., Funk, C.C., Kusebauch, U., Campbell, D.S., Moritz, R.L., and **Price, N.D.**, Quantitative proteomic analysis reveals effects of EGFR on invasion promoting proteins secreted by glioblastoma cells, *Molecular and Cellular Proteomics* (2014)
87. Hood, L., and **Price, N.D.**, Promoting Wellness and Demystifying Disease: The 100K Project, *Clinical Omics*, May Issue: 20-24 (2014). Featured in *Genetic Engineering & Biotechnology News*.
86. Ma, S., Earls, J., Eddy, J.A., and **Price, N.D.**, Integrative Omics Approaches in Network Medicine, *Network Medicine*, Eds. E. Silverman and J. Loscalzo (2014)
85. Hood, L., and **Price, N.D.**, Demystifying Disease, Democratizing Health Care, *Science Translational Medicine*, 6, 225ed5 (2014)
84. Richards, M.A., Cassen, V., Heavner, B.D., Ajami, N., Herrmann, A., and **Price, N.D.**, MediaDB: a database of growth conditions in defined media, *PLOS ONE*, (Accepted, 2014)
83. Craig, T.A., Zhang, Y., Magis, A.T., Funk, C.C., **Price, N.D.**, Ekker, S.C., and Kumar, R., Detection of 1,25-Dihydroxyvitamin D-Regulated miRNAs in Zebrafish by Whole Transcriptome Sequencing, *Zebrafish*. Epub ahead of print. (2014)
82. Wang, Y., Geman, D., **Price, N.D.**, Relative mRNA levels of functionally interacting proteins are consistent disease molecular signatures, *PLOS ONE*, (In revision, 2014)

81. Benedict, M.N., Henriksen, J.R., Metcalf, W.W., Whitaker, R.J., and **Price, N.D.**, ITEP: An integrated toolkit for exploration of pan-genomes, *BMC Genomics*, 15:8 (2014)
80. Chandrasekaran, S., and **Price, N.D.**, Metabolic constraint-based refinement of transcriptional regulatory networks, *PLOS Computational Biology*, 9:e1003370 (2013). Highlighted in *Nature Reviews Genetics*.
79. Dong, Y., Kumar, C.G., Kim, P.J., Chia, N.L.P., Flynn, T., Miller, P., Cann, I.K.O., Mackie, R.M., **Price, N.D.**, Sanford, R., ... Friend, G., Yannarell, A.C., Shilts, W.W., Finley, R.J., and Fouke, B.W., Microbial life inhabits 1.8 km-deep saline sandstone reservoirs in the North American midcontinent, *Environmental Microbiology* (2013)
78. Lausted, C., Lee, I., Zhou, Y., Qin, S., Sung, J., **Price, N.D.**, Hood, L. and Wang, K., Systems approach to neurodegenerative disease biomarker discovery, *Annual Review of Pharmacology and Toxicology* (2013)
77. Bai, J., Abernethy, D.R., **Price, N.D.**, Sangar, V., Systems pharmacology modeling: An approach to improving drug safety, *Biopharmaceutics & Drug Disposition* (2013)
76. Wang, C., Funk, C.C., Eddy, J.A., **Price, N.D.**, Transcriptional analysis of aggressiveness and heterogeneity across astrocytoma grades, *PLOS ONE*, 8:e76694 (2013)
75. Flores, M., Glusman, G., Brogaard, K., **Price, N.D.**, and Hood, L., P4 Medicine: How Systems Medicine Will Transform the Healthcare Sector and Society, *Personalized Medicine*, 10: 565-576 (2013)
74. Li, X.J., Hayward, C., Fong, P.Y., Dominguez, M., Hunsucker, S.W., Lee, L.W., McLean, M., Law, S., Butler, H., Schirm, M., Gingras, O., Lamontagne, J., Allard, R., Chelsky, D., **Price, N.D.**, Lam, S., Massion, P.P., Pass, H., Rom, W.N., Vachani, A., Fang, K.C., Hood, L., and Kearney, P., A systems biology derived proteomic classifier in blood for the molecular characterization of pulmonary nodules, *Science Translational Medicine* (2013)
73. Georgatos, F., Ballereau, S., Pellet, J., Ghanem, M., **Price, N.D.**, Hood, L., Guo, Y.K., Boutigny, D., Auffray, C., Balling R., and Schneider, R., Computational infrastructures for data and knowledge management in systems biology, *Systems Biology: Integrative Biology and Simulation Tools*, Editors: Prokop, A. and Csukas, B., Springer (2013)
72. **Price, N.D.**, Genome-scale models for microbial factories, *Industrial Biotechnology*, 9: 177-178 (2013)
71. Wang, Y., Li, X. Milne, C.B., Jansson, H., Lin, W., Phan, G., Jin, Y.S., **Price, N.D.**, and Blaschek, H.P., Development of a gene knockout system using mobile group II introns (Targetron) and genetic disruption of acid production pathways in *Clostridium beijerinckii*, *Applied and Environmental Microbiology*, Epub ahead of print. (2013)
70. Labhsetwar, P., Cole, J., Roberts, E., **Price, N.D.**, and Luthey-Schulten, Z., Heterogeneity in protein expression induces metabolic variability in a modeled *Escherichia coli* population, *Proceedings of the National Academy of Sciences USA*, 110:14006-11 (2013)
69. Heavner, B.D., Smallbone, K., **Price, N.D.**, and Walker, L.P., Version 6 of the Consensus Yeast Metabolic Network Refines Biochemical Coverage and Improves Model Performance, *Database*, (2013)

68. Sung, J., Kim, P.J., Ma, S., Funk, C.C., Magis, A.T., Wang, Y., Hood, L., Geman, D., and **Price, N.D.**, Multi-study integration of brain cancer transcriptomes reveals organ-level molecular signatures, *PLOS Computational Biology*, 9:e1003148 (2013)
67. Thiele, I., Swainston, N., Fleming, R.M.T., Hoppe, A., Sahoo, S., ... **Price, N.D.**, ... , Goryanin, I., Nielsen, J., Westerhoff, H.V., Kell, D.B., Mendes, P., and Palsson, B.O., A community-driven global reconstruction of human metabolism, *Nature Biotechnology*, 31:419-25 (2013)
66. Earls, J.C., Eddy, J.A., Funk, C., Ko, Y., Magis, A., and **Price, N.D.**, AUREA: An open-source software system for accurate and user-friendly identification of relative expression molecular signatures, *BMC Bioinformatics*, (2013). **Highly Accessed** (special distinction given to the most downloaded papers in the journal)
65. Gonnerman, M.C., Benedict, M.N., Feist, A.M., Metcalf, W.W., **Price, N.D.**, Genomically and biochemically accurate metabolic reconstruction of *Methanosarcina barkeri* iMG746, *Biotechnology Journal* (2013)
65. Ko, Y. *, Ament, S.A. *, Eddy, J.A., Caballero, J., Earls, J.C., Hood, L., and **Price, N.D.**, Cell type-specific genes show striking and distinct patterns of spatial expression in the mouse brain, *Proceedings of the National Academy of Sciences USA*, 110:3095-3100 (2013).
64. Simeonidis, E., Chandrasekaran, S., and **Price, N.D.**, A guide to integrating transcriptional regulatory and metabolic networks using Probabilistic Regulation of Metabolism (PROM), *Methods in Molecular Biology*, 985:103-12 (2013)
63. Wang, Y., Eddy, J.A., and **Price, N.D.**, Reconstruction of genome-scale metabolic models for 126 human tissues using mCADRE, *BMC Systems Biology*, 6:153 (2012). **Highly Accessed** (special distinction given to the most downloaded papers in the journal)
62. Yang, J.L., Cogdell, D., Eddy, J.A., Trent, J., Price, N.D., and Zhang, W., Expression of PRUNE2 mRNA and its positive correlation with non-coding RNA PCA3 in leiomyosarcoma, *Chinese journal of oncology*, 34: 497 (2012)
61. Simcha, D., **Price, N.D.**, and Geman, D., The limits of *de novo* DNA motif discovery, *PLOS ONE*, 7:e47836 (2012)
60. Sangar, V., Eddy, J.A., Simeonidis, E., and **Price, N.D.**, Understanding aberrant energy metabolism in disease through mechanistic modeling, *Frontiers in Computational Physiology and Medicine*, 3:404 (2012)
59. Magis, A.T., and **Price, N.D.**, The top-scoring ‘N’ algorithm: A generalized relative expression classification method from small numbers of biomolecules, *BMC Bioinformatics*, 13:227 (2012)
58. Craig, T.A., Zhang, Y. McNulty, M.S., Middha, S., Magis, A.T., Funk, C.C., **Price, N.D.**, Ekker, S.C., and R., Whole Transcriptome RNA Sequencing Detects Multiple $1\alpha,25$ -Dihydroxyvitamin D3-Sensitive Metabolic Pathways in Zebrafish Embryos, *Molecular Endocrinology*, 26:1630-42 (2012)
57. Committee for the Review of Omics-Based Tests for Predicting Patient Outcomes in Clinical Trials (including **Price, N.D.**); Christine M. Micheel, Sharyl J. Nass, Gilbert S. Omenn, Editors; Evolution of Translational Omics: Lessons Learned and the Path Forward. Institute of Medicine (2012) *National Academy of Sciences Press*. 300 pages.

56. Hood, L., Flores, M.A., Brogaard, K.R., and **Price, N.D.**, Systems medicine and the emergence of proactive P4 medicine: predictive, preventive, personalized, and participatory, *Handbook of Systems Biology* (A. J. Marian Walhout, Marc Vidal, and Job Dekker, editors), Elsevier, San Diego, CA. (In press, 2012)
55. Sung, J., Wang, Y., Chandrasekaran, S., Witten, D.M., and **Price, N.D.**, Molecular signatures from omics data: from chaos to consensus, *Biotechnology Journal*, 7:946-57 (2012)
54. Bebek, G., Koyuturk, M., **Price, N.D.**, and Chance, M.R., Network biology methods integrating biological data for translational science, *Briefings in Bioinformatics*, 13:446-59 (2012)
53. Benedict, M.N., Gonnerman, M.C., Metcalf, W.W., and **Price, N.D.**, Genome-scale metabolic reconstruction and hypothesis testing in the methanogenic archaeon *Methanosarcina acetivorans* C2A, *Journal of Bacteriology*, 194:855-65 (2012)
52. Tian, Q., **Price, N.D.**, and Hood, L., Systems cancer medicine: Towards realization of personalized, predictive, preventive, and personalized (P4) medicine, *Journal of Internal Medicine*, 271:111-21 (2012)
51. Kim, P.-J., and **Price, N.D.**, Genetic co-occurrence network across all sequenced microbes, *PLoS Computational Biology*, 7:e1002340 (2011)
50. Chandrasekaran, S., Ament, S.A., Eddy, J.A., Rodriguez-Zas, S., Schatz, B.R., **Price, N.D.*** and Robinson, G.E.* , Behavior-Specific Changes In Transcriptional Modules Lead To Distinct And Predictable Neurogenomic States, *Proceedings of the National Academy of Sciences USA*, 108:18020-5 (2011). *Co-corresponding authors
49. Ghosh, A., Zhao, H., and **Price, N.D.**, Genome-scale consequences of cofactor balancing in engineered pentose utilization pathways in *Saccharomyces cerevisiae*, *PLoS ONE* 6(11): e27316 (2011)
48. Milne, C.B., Eddy, J.A., Raju, R., Ardekani, S., Kim, P.-J., Senger, R.S., Jin, Y.-S., Blaschek, H.P., and **Price, N.D.**, Metabolic network reconstruction and genome-scale model of butanol-producing strain *Clostridium beijerinckii* NCIMB 8052, *BMC Systems Biology*, 5:130 (2011). **Highly Accessed** (special distinction given to the most downloaded papers in the journal)
47. Li, Q., Singh, C.R., Ma, S., **Price, N.D.**, and Jagannath, C., Label-free proteomics and systems biology analysis of mycobacterial phagosomes in dendritic cells and macrophages, *Journal of Proteome Research*, 10:2425-39 (2011)
46. Magis, A.T., Earls, J.C., Ko, Y.,-H, Eddy, J.A., and **Price, N.D.**, Graphics processing unit implementations of relative expression analysis algorithms enable dramatic computational speedup, *Bioinformatics*, 27:872-3 (2011)
45. Yan, X., Ma, L., Yi, D., Yoon, J.G., Diercks, A., Foltz, G., **Price, N.D.**, Hood, L., and Tian, Q., A CD133-related gene expression signature identifies an aggressive glioblastoma subtype with excessive mutations, *Proceedings of the National Academy of Sciences USA*, 108:1591-1596 (2011)
44. Ma, S., Funk, C., and **Price, N.D.**, Systems approaches to molecular cancer diagnostics, *Discovery Medicine*, 10:531-42 (2010)

43. Chandrasekaran, S., and **Price, N.D.**, Probabilistic integrative modeling of genome-scale metabolic and regulatory networks in *Escherichia coli* and *Mycobacterium tuberculosis*, *Proceedings of the National Academy of Sciences USA*, 107:17845-50 (2010)
42. Yang, J., Eddy, J.A., Pan, Y., Hategan, A., Tabus, I., Wang, Y., Cogdell, D., **Price, N.D.**, Pollock, R.E., Lazar, A.J.F, Hunt, K.K., Trent, J.C., and Zhang, W., Mesenchymal to epithelial reverting transition in leiomyosarcoma through regulation of slug, *Molecular and Cellular Proteomics*, 9:2405-13 (2010)
41. Shi, L., et al. (MAQC-II Consortium), The MicroArray Quality Control (MAQC)-II study of common practices for the development and validation of microarray-based predictive models, *Nature Biotechnology*, 28: 827-838 (2010)
40. **Price, N.D.**, and Lee, S.Y., Editorial: Systems biology for biotech applications, *Biotechnology Journal*, 5:636-637 (2010)
39. Kim, P.J., and **Price, N.D.**, Macroscopic kinetic effects of cell-to-cell variation in biochemical reactions, *Physical Review Letters*, 104:148103 (2010). Highlighted by *Science News* (“Enzymes Exposed”, 2010).
38. Edelman, L.B., Eddy, J.A., and **Price, N.D.**, *In silico* models of cancer, *Wiley Interdisciplinary Reviews: Systems Biology and Medicine*, 2: 438–459 (2010)
37. Eddy, J.A., Hood, L., **Price, N.D.***, and Geman, D., Identifying tightly regulated and variably expressed networks by Differential Rank Conservation (DIRAC), *PLoS Computational Biology*, 6:e1000792 (2010)
*Corresponding author
36. Eddy, J.A., Sung, J., Geman, D., and **Price, N.D.**, Relative expression analysis for molecular cancer diagnosis and prognosis, *Technology in Cancer Research and Treatment*, 9:149-159 (2010)
35. Ezeji, T., Milne, C.B., **Price, N.D.**, and Blaschek, H.P., Achievements and perspectives to overcome the poor solvent resistance in acetone and butanol producing microorganisms, *Applied Microbiology and Biotechnology*, 85:1697-1712 (2010)
34. Galas, D.J., Nykter, M., Carter, G.W., **Price, N.D.**, and Shmulevich, I., Biological information and the complexity of sets: Information measures and metrics for complex systems, *IEEE Transactions on Information Theory*, 56: 667 - 677 (2010)
33. Milne, C.B., Kim, P.J., Eddy, J.A., and **Price, N.D.**, Accomplishments of genome-scale *in silico* modeling in industrial and medical biotechnology, *Biotechnology Journal*, 4:1653-1670 (2009)
32. Edelman, L.B., Toia, G., Geman, D., Zhang, W., and **Price, N.D.**, Two-transcript gene expression classifiers in the diagnosis and prognosis of human diseases, *BMC Genomics*, 10:e583 (2009). **Highly Accessed** (special distinction given to the most downloaded papers in the journal)
31. Edelman, L.B., Chandrasekaran, S., **Price, N.D.**, Systems biology of embryogenesis, *Reproduction, Fertility, and Development*, 22:98-105 (2009).
30. Blaschek, H.P., Ezeji, T., and **Price, N.D.**, Present and future possibilities for the deconstruction and utilization of lignocellulosic biomass, *Handbook of Bioenergy* (2009)

29. Hwang, D., Lee, I.Y., Yoo, H., Gehlenborg, N., Cho, J.H., Petritis, B., Baxter, D., Pitstick, R., Young, R., Spicer, D., **Price, N.D.**, Hohmann, J., DeArmond, S.J., Carlson, G.A., Hood, L., A Systems Approach to Prion Disease, *Molecular Systems Biology*, 5:252 (2009)
28. Eddy, J.A., and **Price, N.D.**, "Biological data integration and model building," *Encyclopedia of Complexity and Systems Science*, (Meyers, R.A., editor) Springer (2009)
27. **Price, N.D.**, Edelman, L.B., Lee, I., Yoo, H., Hwang, D., Carlson, G., Galas, D.J., Heath, J.R., and Hood, L., Systems biology and systems medicine, *Genomic and Personalized Medicine: From Principles to Practice* (Ginsburg, G. and Willard, H., editors). Vol.1, pp. 131-141, Elsevier, (2009)
26. Nykter, M., **Price, N.D.**, Larjo, A., Aho, T., Kauffman, S.A., Yli-Harja, O., and Shmulevich, I., Critical Boolean networks exhibit maximal information diversity in structure-dynamics relationships, *Physical Review Letters*, 100:058702 (2008)
25. Nykter, M., **Price, N.D.**, Aldana, M., Ramsey, S., Kauffman, S.A., Hood, L., Yli-Harja, O., and Shmulevich, I., Gene expression dynamics in the macrophage exhibit criticality, *Proceedings of the National Academy of Sciences USA*, 105:1897-1900 (2008)
24. **Price, N.D.**, Foltz, G., Madan, A., Hood, L., and Tian, Q., Systems biology and cancer stem cells, *Journal of Cellular and Molecular Medicine*, 12:97-110 (2008)
23. **Price, N.D.**, and Shmulevich, I., Biochemical and statistical network models for systems biology, *Current Opinion in Biotechnology*, 18:365-370 (2007)
22. **Price, N.D.**, Trent, J., El-Naggar, A.K., Cogdell, D., Taylor, E., Hunt, K.K., Pollock, R.E., Hood, L., Shmulevich, I., and Zhang, W., Highly accurate two-gene classifier for differentiating gastrointestinal stromal tumors and leiomyosarcomas, *Proceedings of the National Academy of Sciences USA*, 104:3414-3419 (2007)
21. Gianchandani, E.J., Papin, J.A., **Price, N.D.**, Joyce, A., and Palsson, B.O., Matrix formalism for representing functional states of transcriptional regulatory networks, *PLoS Computational Biology*, 2: e101 (2006)
20. **Price, N.D.**, Thiele, I., and Palsson, B.O., Candidate states of *Helicobacter pylori*'s genome-scale metabolic network upon application of loop law thermodynamic constraints, *Biophysical Journal*, 90:3919-3928 (2006)
19. Barrett, C., **Price, N.D.**, and Palsson, B.O., Network-based analysis of metabolic regulation using uniform random sampling and singular value decomposition, *BMC Bioinformatics*, 7:132 (2006)
18. Becker, S.A., **Price, N.D.**, and Palsson, B.O., Metabolite coupling in genome-scale metabolic networks, *BMC Bioinformatics*, 7:111 (2006)
17. Allen, T.E., **Price, N.D.**, Joyce, A., and Palsson, B.O., Long-range patterns in microbial genome sequences indicate significant chromosomal organization, *PLoS Computational Biology*, 2(1): e2 (2006)
16. Thiele, I., Vo, T., **Price, N.D.**, and Palsson, B.O., Genome-scale metabolic model of *Helicobacter pylori*, iIT338: an *in silico* genome-scale characterization of single and double deletion mutants, *Journal of Bacteriology*, 187:5818-5830 (2005)

15. Thiele, I., **Price, N.D.**, Vo, T. and Palsson, B.O., Candidate steady-state flux distributions in human mitochondria metabolism: impact of diabetes, ischemia, and diet, *Journal of Biological Chemistry*, 280:11683-11695 (2005)
14. **Price, N.D.**, Reed, J.L., and Palsson, B.O., Genome-scale models of microbial cells: evaluating the consequences of constraints, *Nature Reviews Microbiology*, 2: 886-897 (2004)
13. **Price, N.D.**, Schellenberger, J., and Palsson, B.O., Uniform sampling of steady state flux spaces: Means to design experiments and interpret enzymopathies, *Biophysical Journal*, 87:2172-2186 (2004)
12. Papin, J.A., Stelling, J., **Price, N.D.**, Klamt, S., Schuster, S., Palsson, B.O., Comparison of network-based pathway analysis methods, *Trends in Biotechnology*, 22:400-405 (2004)
11. Raghunathan, A., **Price, N.D.**, . . . and Kolker, E., *In silico* metabolic model and protein expression of *Haemophilus influenzae* strain Rd KW20 in rich medium, *OMICS: A Journal of Integrative Biology*, 8:25-42 (2004)
10. Papin, J.A., **Price, N.D.**, and Palsson, B.O., *In silico* cells: studying genotype-phenotype relationships using constraints-based models, in: Metabolic Engineering in the Post-Genomic Era (Westerhoff, H., and Kholodenko, B., editors) (2004)
9. **Price, N.D.**, Reed, J.L., Papin, J.A., Wiback, S.J., and Palsson, B.O., Network-based analysis of regulation in the human red blood cell, *Journal of Theoretical Biology*, 225:1985-194 (2003)
8. **Price, N.D.**, Papin, J.A., Schilling, C.H., and Palsson, B.O., Genome-scale microbial *in silico* models: The constraints-based approach, *Trends in Biotechnology*, 21:162-169 (2003)
7. Papin, J.A., **Price, N.D.**, Wiback, S.J., Fell, D.A., and Palsson, B.O., Metabolic pathways in the post-genome era, *Trends in Biochemical Sciences*, 28:250-258 (2003)
6. **Price, N.D.**, Reed, J.L., Papin, J.A., Famili, I. and Palsson, B.O., Analysis of metabolic capabilities using singular value decomposition of extreme pathway matrices, *Biophysical Journal*, 84:794-804 (2003)
5. Palsson, B.O., **Price, N.D.**, Papin, J.A., Development of network-based pathway definitions: the need to analyze real metabolic networks, *Trends in Biotechnology*, 21:195-198 (2003)
4. **Price, N.D.**, Famili, I., Beard, D.A. and Palsson, B.O., Extreme pathways and Kirchhoff's second law, *Biophysical Journal*, 83:2879-2882 (2002)
3. Papin, J.A., **Price, N.D.**, and Palsson, B.O., Extreme pathway lengths and reaction participation in genome-scale metabolic networks, *Genome Research*, 12:1889-1900 (2002)
2. Papin, J.A., **Price, N.D.**, Edwards, J.S., and Palsson, B.O., The genome-scale metabolic extreme pathway structure in *Haemophilus influenzae* shows significant network redundancy, *Journal of Theoretical Biology*, 215:67-82 (2002)
1. **Price, N.D.**, Papin, J.A., Palsson, B.O., Determination of redundancy and systems properties of the metabolic network of *Helicobacter pylori* using genome-scale extreme pathway analysis, *Genome Research*, 12:760-769 (2002)

GRANTSCurrent

NIA: 1U01AG046139-01 (Golde, Price Ertekin-Taner, Younkin) A Systems Approach to Targeting Innate Immunity in AD (Role: Multiple PI)	9/20/13 - 08/31/18 \$1,541,305 (my portion)
DOE: ARPA-E (Price, Ragsdale, Leigh, Smith) Anaerobic bioconversion of methane to methanol (Role: Multiple PI)	1/01/14 – 12/31/16 \$752,000 (my portion)
Grant (Price) CHDI Foundation Connecting transcriptional regulation to metabolic networks in HD (Role: PI)	5/15/2014-4/14/2016 \$675,188
Grant (Price, Muglia) Bill & Melinda Gates Foundation Systems Biology Approaches to Birth Timing and Preterm Birth Risk (Role: Co-PI)	12/15/2014-12/14/2016 \$505,320 (my portion)
Camille Dreyfus Teacher-Scholar Award (Price) Camille and Henry Dreyfus Foundation Integrative Reconstruction, Modeling, Design, and Experimental Modifications of Complex Biochemical Reaction Networks for Systems Biology and Medicine (Role: PI)	6/15/2011-6/14/2016 \$75,000
Grant (Hood, Price) Robert Wood Johnson Foundation Initial scale up for the 100K Project (Role: Co-PI)	12/1/2014-8/1/2015 \$648,950
Grant (Hood, Price) M. J. Murdock Charitable Trust Enhanced data analysis of the 100 Pioneers and initial scale up of 100K project (Role: Co-PI)	1/1/2015-12/31/2017 \$700,000
Subcontract (Price) NSF Brain Metabolic Plasticity and Aggression (Role: PI)	7/01/13 - 06/30/14 \$202,302
BD2K Center (Toga) NIH Big Data for Discovery Science (Role: Co-I)	12/15/2014-12/14/2019 \$1,500,000
Grant (Hood, Price) GAPPS and Bill & Melinda Gates Foundation Systems Biology of Preterm Birth: A Pilot Study	2/01/13 - 01/31/15 \$246,177

(Role: Co-I)

NIGMS: P50GM076547 (Aitchison) 9/01/12-08/31/17
 Center for Quantitative Systems Biology \$18M
 (Role: Co-I)

Completed

K99/R00 (Price) 9/1/2008 – 8/31/2012
 NIH/NCI \$889,245
 Howard Temin Pathway to Independence Award in Cancer Research: Identifying network perturbations using secreted protein profiles in glioblastoma
 (Role: PI)

CAREER (Price) 2/1/2009-1/31/2014
 NSF \$400,000
 Systems biology and engineering of *Clostridium beijerinckii* for enhanced butanol production
 (Role: PI)

Young Investigator Award (Price) 2/1/2010-12/31/2013
 Roy J. Carver Charitable Trust \$345,000
 Integrated metabolic and regulatory network analysis of glioblastoma
 (Role: PI)

Subcontract (Price) 7/01/13 - 06/30/14
 Huntington Society of Canada \$27,490
 Mapping Hepatic Dysfunction in Huntington's Disease
 (Role: Subcontract PI)

Grant (Schulten, Price, Woese) 7/1/2010-6/30/2013
 DOE \$1,500,000
 Computational Modeling of Fluctuations in Energy and Metabolic Pathways of Methanogenic Archaea
 (Role: Co-I)

Developmental Research Grant (Price) 7/1/2006 – 11/1/2009
 NIH/NCI P50 CA083636 (Urban) \$45,000
 Pacific Ovarian Cancer Research Consortium
 Network-based gene expression analysis for enhanced target identification in ovarian cancer
 (Role: PI of Subcontract)

Grant (Fouke, Price, DeVille, Liu) 11/1/2008 – 8/1/2011
 Energy Biosciences Institute \$1,129,700 (total amount)
 Distribution and Diversity of Metabolic Processes in Subsurface Microbial Communities Integrated with Reservoir Environmental Conditions and Geological History: A Universal Template for Microbially Enhanced Hydrocarbon Recovery
 (Role: Co-I)

Grant (Zhao, Price, Li) 6/1/2008 – 5/31/2011
 Energy Biosciences Institute (BP) \$1,100,000 (total amount)

Engineering a yeast strain that efficiently utilizes C5/C6 sugars
(Role: Co-I)

Subcontract (Price) 6/16/2008-6/15/2011
Department of Defense - TATRC (Hood) \$145,000 (subcontract)
Brain-Region and Cell-Type Specific Transcripts for Informative Diagnostics
(Role: PI of subcontract)

GTL (Blaschek, Price, Jin) 7/16/2011-7/15/2013
DOE \$1,250,000
Understanding Fundamental Aspects of Butanol Production by *Clostridium beijerinckii*
(Role: Co-I)

Subcontract (Price) 7/1/2009-6/30/2013
DoD (Federoff many others) \$707,000 (subcontract) \$15.3 M (total grant)
Discovery and Validation of Peripheral Biomarkers of Traumatic Brain Injury
(Role: PI of Subcontract)

GTL (Metcalf, Price, Whitaker) 7/16/2010-7/15/2013
DOE \$2,500,000
Methanogenic archaea and the global carbon cycle: a systems biology approach to the study of
Methanosarcina species
(Role: Co-I)

PRESENTATIONS

INVITED TALKS

141. Panel talk, Optimizing health and reducing disease through scientific wellness, Stanford Medicine X, Palo Alto, CA, September 18, 2016

140. Widely broadcast panel, Why personalized nutrition will revolutionize the way we approach health, MindBodyGreen Revitalize Meeting, Phoenix, AZ, September 17, 2017

139. Plenary talk, Genome-scale analysis of mRNA and miRNA regulation in preterm birth, Bioinformatics and Systems Biology Symposium, International Federation of Placental Associations, Portland, OR, September 14, 2016

138. Invited talk, A scientific wellness approach to improving pregnancy outcomes, Bioinformatics and Systems Biology Symposium, International Federation of Placental Associations, Portland, OR, September 14, 2016

137. Invited talk, Systems biology approaches to human wellness and disease, Earle A. Chiles Research Institute at Providence Cancer Center, Portland, OR, September 13, 2016

136. Plenary talk, The 100K Wellness Project: A data-rich longitudinal study for the digital age, 2nd International Summer Symposium on Systems Biology, INMEGEN, Mexico City, Mexico, August 2, 2016

135. Invited talk, Integrating longitudinal multi-omics data for personalized health, Intelligent Systems in Molecular Biology Annual Meeting, Orlando, FL, July 10, 2016
134. Keynote, Metabolic analyses in microbes and humans, Systems Modeling Meeting at the Intelligent Systems in Molecular Biology Annual Meeting, Orlando, FL, July 9, 2016
133. Seminar, Integrating longitudinal multi-omics data for personalized health, West Virginia University School of Medicine, Blacksburg, WV, June 21, 2016
132. Distinguished Seminar Series, The 100K Wellness Project: A data-rich longitudinal study for the digital age, Institute for Computational Medicine, Johns Hopkins University, Baltimore, MD, May 3, 2016
131. Invited talk, The 100K Wellness Project: Enhancing health via actionable big data, Takeda Pharmaceuticals meeting on Precision Medicine, Boston, MA, May 2, 2016
130. Plenary talk, The 100K Wellness Project: An integrative longitudinal study for the digital age, Presidential Symposium, American College of Nutrition, San Diego, CA, April 4, 2016
129. Invited talk, The 100K Wellness Project: Enhancing health via actionable big data, Molecular Medicine Tri-Con, San Francisco, CA, March 7, 2016
128. Seminar, The 100K Wellness Project: A data-rich longitudinal study for the digital age, 50th Anniversary of the UCSD Bioengineering Department lecture, La Jolla, CA, January 29, 2016
127. Seminar, Harnessing longitudinal data to optimize wellness and reduce disease, Indian Institute of Science, Bangaluru, India, December 11, 2015
126. Invited lecture, Integrated mechanistic and statistical network analysis for metabolic engineering, Quantitative Systems Biology School, Bangaluru, India, December 10, 2015
125. Invited lecture, Integrated modeling of metabolic and gene regulatory networks: Introduction to methods, Quantitative Systems Biology School, Bangaluru, India, December 9, 2015
124. Invited lecture, Introduction to metabolic network reconstruction and modeling, Quantitative Systems Biology School, Bangaluru, India, December 8, 2015
123. R.A. Mashelkar Endowment Lecture, Harnessing longitudinal data to optimize wellness and reduce disease, National Chemical Laboratory, Pune, India, December 7, 2015
122. Plenary talk, A 360-degree view of you: Scientific Wellness and Precision Food, Panel on Revolutions in Healthcare: Impacts on the Future of the Food Industry, MIT Media Lab and Culinary Institute of America's ReTHINK Food conference, Napa Valley, CA, November 7, 2015
121. Invited talk, Panel Discussion on Precision Medicine, SINAIInnovations meeting, Mt. Sinai Hospital, New York City, NY October 27, 2015, New York City, NY
120. Plenary talk, Genomics, Big Data, Informatics, and the Future of Medicine, Personalized Lifestyle Medicine Institute Thought Leaders Consortium, Chicago, IL, October 23, 2015

119. *Keynote*, Predicting and preventing disease: Lessons from the 100K Wellness Project, Gordon Research Conference, on Toxicity Andover, NH, August 10, 2015
118. Invited talk, Integrating multi-omic data analytics and health coaching to optimize wellness and minimize disease, 11th International Conference on Pathways, Networks, and Systems Medicine, Chania, Crete, Greece
117. *Keynote*, Integrating the principles of preventive and personalized medicine to advance wellness, The Clinical Genome Conference, San Francisco, CA, June, 22, 2015
116. Plenary talk, The 100K person wellness project: A data-rich longitudinal study for the digital age, Institute for Functional Medicine Annual Conference, Austin, TX, May 30, 2015
115. Invited talk, Integrated mechanistic and statistical network modeling for metabolic engineering, Cell Factories and Biosustainability Conference, Copenhagen, Denmark, May 18, 2015
114. Invited talk, The 100K person wellness project: A data-rich longitudinal study for the digital age, Technology Alliance Symposium on Big Data in Washington State, Seattle, WA, March 3, 2015
113. Invited talk, From genomics to health actionability: the 100(K) person wellness project, Public Health Genomics Symposium, Seattle, WA, January 28, 2015
112. Session *Keynote*, The 100K Person Wellness Project: A Data-rich Longitudinal Study for the Digital Age, Pacific Symposium on Biocomputing – Personalized Medicine Session, Kona, Hawaii, January 7, 2015
111. Seminar, Integrative data analysis for biology, medicine, and wellness, Columbia University, December 10, 2014
110. Invited talk, The 100K Person Wellness Project: A Data-rich Longitudinal Study for the Digital Age, Association of Academic Health Centers Annual Meeting, December 4, 2014
109. Seminar, Integrative data analysis for biology, medicine, and wellness, Washington University, St. Louis, MO, December 2, 2014
108. *Keynote*, Systems approaches to diagnostics, Amgen Biomarker Symposium, Thousand Oaks, CA, September 19, 2014
107. *Keynote*, Integrating the Principles of Preventative and Personalized Medicine to Advance Wellness, Leaders in BioBanking Congress, Seattle, WA, September 15, 2014
106. Invited talk, Metabolic Reconstruction of Methanogenic Archaea, Gordon Research Conference on Molecular Basis of Microbial One-Carbon Metabolism, South Hadley, MA, August 12, 2014
105. *Keynote*, Generating Tailored Solutions from Big Data: In Silico Modeling of Biological Networks, Annual Meeting of Health and Environmental Sciences Initiative, Washington, D.C., June 11, 2014
104. Seminar, Harnessing omics data for biological and medical discovery, Department of Molecular and Cellular Biology, Dartmouth College, Hanover, NH, June 3, 2014

103. Invited talk, Integrated analytics for health and omics analysis of astronauts before, during, and after extended space travel, NASA-CASIS Biomedical Research Symposium, Columbia University, May 28, 2014
102. Invited talk, Reconstruction, refinement, and relevance of metabolic networks, 3rd Constraint-based Reconstruction and Analysis (COBRA) Meeting, Charlottesville, VA, May 23, 2014
101. *Keynote*, Systems approaches to P4 Medicine across multiple diseases, Sleep Apnea Genetics International Consortium Annual Meeting, San Diego, CA, May 16, 2014
100. Invited talk, Computational biology and *in silico* modeling, Bill & Melinda Gates Foundation-Global Alliance to Prevent Prematurity and Stillbirth Workshop, April 28, 2014
99. Plenary talk, Harnessing omics data for biological and medical discovery, UT-KBRIN Bioinformatics Summit, Lake Barkley State Park, KY
98. Seminar, Multi-Omic Interrogation of Perturbed Networks in Cancer, Dana Farber Cancer Institute, Harvard Medical School, April 2, 2014
97. Invited talk, Modeling and simulating cellular networks, MITRE Corporation Meeting, McLean, VA, March 26, 2014
96. Invited talk, Integrative modeling of metabolic and regulatory networks, Advanced Lecture Course on Systems Biology, Innsbruck, Austria, March 4, 2014
95. Invited talk, Challenges in Translational Omics: Strategies for Success, Personalized Medicine World Congress, Palo Alto, CA, January 21, 2014
94. Seminar, Biomolecular network analysis of biological and medical discovery, Duke Center for Systems Biology & Duke Institute for Genome Sciences and Policy, Duke University, Durham, NC, November 18, 2013
93. Seminar, Harnessing big data for biological and medical discovery, Department of Biochemistry, Baylor College of Medicine, Houston, TX, November 7, 2013
92. Seminar, Integrated statistical and mechanistic modeling for systems biology, Department of Chemical Engineering, Princeton University, Princeton, NJ, October 23, 2013
91. Invited talk, New computational technologies for RNA sequencing and multi-network integration, 2nd Annual Systems Biomedicine Symposium, Luxembourg, Oct 22, 2013
90. Invited talk, Biomolecular networks in the brain, International Workshop on Bioinformatics and Systems Biology, Kyoto, Japan, July 20, 2013
89. Invited talk, Biomolecular networks in the brain, Luxembourg-ISB Partnership Symposium, Luxembourg, June 10, 2013
88. *Keynote*, Harnessing Big Data to Drive Innovation in Biology and Medicine, Amgen Innovation Summit, Seattle, WA, (video broadcast also to Thousand Oaks, CA campus), May 16, 2013

87. *Keynote*, Harnessing Big Data for Biological and Medical Discovery, 1st Annual Big Data in Biology Symposium, University of Texas, Austin, TX, May 10, 2013
86. Invited talk, Challenges in Translational Omics: Strategies for Success, American Association of Clinical Chemists, April 19, 2013
85. Seminar, Integrated statistical and mechanistic models for biological and medical discovery, Food and Drug Administration, Washington, D.C., February 26, 2013
84. Invited talk, Integrated statistical and mechanistic models for biological and medical discovery, Symposium on Quantitative Approach to Biological Complexity, Pohang, Korea, February 18, 2013
83. Invited talk, Molecular Medicine Tri-Con, Feb. 14, 2013, San Francisco, CA
82. *Session keynote*, Identification of perturbed networks from high-throughput data, Pacific Symposium on Biocomputing, January 6, 2013
81. Invited talk, Systems approaches to molecular diagnostics, Zing Conference on Mathematical and Computational Medicine, December 4, 2012
80. *Theodore L. Badger Lecture in Network Medicine*, Network medicine approaches to disease, Channing Division of Network Medicine, Harvard Medical School, November 13, 2012
79. Invited talk, Educational experiences provided via the Illinois iGEM team, Camille Dreyfus Teacher-Scholars Symposium: "Research Frontiers in the Chemical Sciences," October 26, 2012
78. Seminar, Integrated network modeling for human health and disease, Mayo Clinic, Rochester, MN, October 19, 2012
77. Invited talk, Reproducibility of inter-lab studies with omics data, NCI Director's Workshop of Data Reproducibility, Bethesda, MD, September 14, 2012
76. Invited panelist, The Coming Future of Precision Medicine, Milken Institute-Sponsored Celebration of Science, Washington, D.C., September 9, 2012
75. Seminar, Integrated analysis of genome-scale biomolecular networks, Vancouver Bioinformatics User Group, University of British Columbia, Vancouver, Canada, September 20, 2012
74. Seminar, Integrated analysis of genome-scale biomolecular networks, Vancouver Bioinformatics User Group, University of British Columbia, Vancouver, Canada, September 20, 2012
73. Invited talk, Systems approaches to disease diagnosis, Short Course Introduction to Systems Biology, Seattle, WA, August 10, 2012
72. Invited talk, Integrated modeling of genome-scale metabolic and transcriptional regulatory networks, National Centers for Systems Biology Annual Meeting, Chicago, IL, July 20, 2012
71. Invited talk, Integrated modeling of genome-scale metabolic and transcriptional regulatory networks, Canadian Society of Microbiology annual meeting, Vancouver, Canada, June 23, 2012

70. Seminar, Integrated analysis of genome-scale biomolecular networks, Simon Fraser University, Vancouver, Canada, June 22, 2012
69. Invited talk, Integrated modeling of genome-scale metabolic and transcriptional regulatory networks, Aegean Pathways, Networks, and Systems Medicine Meeting, Rhodes, Greece, June 13, 2012
68. Invited talk, Systems approaches to disease diagnostics, Center for Clinical and Translational Science Annual Scientific Meeting, Ohio State University, May 18, 2012
67. Seminar, Integrated analysis of genome-scale biomolecular networks, Seattle BioMed, Seattle, WA April 9, 2012
66. Seminar, Systems analysis of gene expression in the brain, Center for Sleep and Circadian Neurobiology, University of Pennsylvania Medical School, January 13, 2012
65. Seminar, Integrated analysis of genome-scale biomolecular networks, Department of Chemical Engineering, Rice University, TX, September 20, 2011
64. Invited talk, Integrated modeling of metabolic and transcriptional regulatory networks, Energy Biosciences Institute Symposium, Urbana, IL, October 1, 2011
63. Seminar, Integrated analysis of genome-scale biomolecular networks, Department of Chemical Engineering, University of Texas, Austin, TX, September 20, 2011
62. Invited Talk, Probabilistic modeling of integrated biomolecular networks, Metabolic Pathways Workshop, International Conference on Systems Biology, September 3, 2011
61. Invited Talk, Integrative modeling of regulatory and metabolic networks, DOE workshop on Genomics Driving Modeling in Biology, Park City, UT, July 27, 2011
60. Invited Talk, Systems and network-based approaches to genomic medicine, NHLBI Genomic Medicine and Lung Diseases Workshop, Bethesda, MD, July 18, 2011
59. Seminar, Systems approaches for glioma research, Neuro-Oncology Group, Mayo Clinic, Rochester, MN, June 20, 2011
58. Keynote talk, Genomics-enable science for medicine, energy, and the environment, University of Illinois Alumni Event, Seattle, WA, May 18, 2011
57. Seminar, Model-guided discovery for systems biology and medicine, Department of Bioengineering, University of Washington, Seattle, WA, May 17, 2011
56. Seminar, Integrated network models to link genotype and phenotype, Department of Chemical Engineering, University of California, Santa Barbara, May 12, 2011
55. Seminar, Integrated network models to link genotype and phenotype, Department of Physiology & Biophysics, Case Western Reserve University, Cleveland, OH, May 9, 2011
54. Invited Talk, Integrated modeling of metabolic and regulatory networks, Metabolic Pathways Workshop, University of Edinburgh, Edinburgh, Scotland, UK, April 7, 2011

53. Seminar, Microbial systems biology for energy and the environment, Institute for Systems Biology, Seattle, WA, March 14, 2011
52. Seminar, Systems approaches to disease diagnostics and perturbed network identification, School of Informatics, Indiana University, IN, Apr 22, 2011
51. Seminar, Systems approaches to disease diagnostics and perturbed network identification, SomaLogic, Inc., Boulder, CO, Feb 28, 2011
50. Invited talk, Automated approaches to building integrated regulatory and metabolic models, Workshop on Environmental Systems Biology, Seattle, WA, January 10, 2011
49. Tutorial, Integrative –omics for translational science, Pacific Symposium on Biocomputing, Hawaii, January 3, 2011
48. Seminar, Argonne National Laboratory, Integrated modeling of genome-scale biomolecular networks, December 2, 2010
48. Invited Talk, International Conference on Systems Biology, Metabolic Pathways Workshop, Edinburgh, Scotland, UK, October 15, 2010
47. Invited Talk, NSF Workshop on Marine Microbiology, Washington, D.C., October 11, 2010
46. Seminar, Center for Pharmaceutical Biotechnology, University of Illinois, Chicago, September 23, 2010
45. Seminar, Department of Bioengineering, University of Illinois, Urbana-Champaign, IL, September 2, 2010
44. Department of Defense Microbial Data Integration Workshop, Lawrence-Berkeley National Labs, Berkeley, CA, August 12, 2010
43. Systems Biology Short Course, Systems approaches to disease stratification, Institute for Systems Biology, Seattle, WA, August 6, 2010
42. 8th International Aegean Conference on Pathways, Networks, and Systems Medicine, Rhodes, Greece, July 12, 2010
41. Institute for Systems Biology Retreat, Spatial expression patterns of cell-type specific genes in the brain, June 19, 2010
40. Panelist Speaker, Personalized Medicine Symposium, Research Triangle Park, Durham, NC, June 15, 2010
39. Translation Biomedical Research Seminar, University of Illinois, Systems approaches to disease diagnosis and prognosis, April 5, 2010
38. Seminar, Genome Institute of Singapore, Systems approaches to disease stratification, Jan. 21, 2010
37. Seminar, Institute of Chemical and Engineering Sciences, Singapore, Model-guided cellular engineering for biotechnology and bioenergy, Jan. 20, 2010.

36. *Keynote address*, Systems biology approaches to embryogenesis, International Embryo Transfer Society Annual Meeting, Cordoba, Argentina, January 11, 2010
35. Seminar, Systems medicine approaches to disease diagnosis and prognosis, Department of Genetics, Case Western Medical School, Dec. 9, 2009
34. *Keynote address*, Genome-scale *in silico* models: applications in biotechnology and biomedicine, Metabolic Pathway Analysis Workshop, Leiden, Netherlands, Oct 29, 2009
33. Invited talk, Human disease diagnosis and prognosis using relative expression analysis, IEEE Engineering in Medicine and Biology Meeting, Minneapolis, MN, Sept 5, 2009
32. Invited talk, Systems approaches to disease stratification, Institute for Systems Biology, Seattle, WA, August 3, 2009
31. Seminar, Relative expression analysis for cancer diagnosis and perturbed network identification, Mathematical Biology Seminar, Department of Mathematics, University of Illinois, Urbana, IL, April 2, 2009
30. Invited talk, Relative expression analysis for cancer diagnosis and perturbed network identification, International Conference on Biomedical Engineering (special Systems Biology session sponsored by Eli Lilly), Singapore, December 5, 2008
29. Seminar, Relative expression analysis for cancer diagnosis and perturbed network identification, Physics of Living Cells Seminar, Department of Physics, University of Illinois, Urbana, IL, October 31, 2008
28. Invited talk, Relative expression analysis for cancer diagnosis and perturbed network identification, Institute for Operations Research and The Management Sciences (INFORMS) Annual Meeting, Washington, D.C., October 14, 2008
27. Invited talk, Tutorial on Constraint-based Reconstruction and Analysis of Genome-Scale Biochemical Networks, IEEE Genomics and Signal Processing (GENSIPS) meeting, Phoenix, AZ, June 8, 2008
26. Invited talk, Towards the engineering of *Clostridium beijerinckii* for improved bio-butanol production, Governmental Forum, Chinese Academy of Sciences, Shanghai, China, April 17, 2008
25. Invited talk, Model-guided Cellular Engineering, Partner Institute for Computational Biology, Chinese Academy of Sciences, Shanghai, China, April 16, 2008
24. Seminar, Systems biology in medicine: applications to anemia, diabetes, and cancer, John Hopkins University, Institute for Computational Medicine, Baltimore, MD, February 8, 2008
23. Seminar, Systems biology in medicine: applications to anemia, diabetes, and cancer, Purdue University Department of Statistics Seminar, West Lafayette, IN, February 5, 2008
22. Seminar, Relative expression analysis for cancer diagnosis and prognosis, Information Theory and Applications Meeting, University of California, San Diego, January 31, 2008
21. Seminar, Systems biology in medicine: applications to anemia, diabetes, and cancer, University of Illinois Department of Statistics Seminar, December 6, 2007

20. Invited talk, Computational challenges for systems biology and personalized medicine, DOE Frontiers in Extreme Computing Workshop, Santa Cruz, October 22, 2007
19. Invited talk, Relative expression classifiers for cancer diagnosis and prognosis, National Cancer Institute Nanotechnology Alliance Investigators Meeting, October 18, 2007
18. Invited talk, Relative expression molecular signatures of cancer diagnosis and prognosis, Biomedical Engineering Society Annual Meeting, Los Angeles, CA, Sept. 27, 2007
17. Invited talk, Computational challenges in systems biology, Argonne National Lab Town Hall Meeting: Simulation and Modeling at the Exascale for Energy, Ecological Sustainability and Global Security, Argonne, IL, May 31, 2007
16. Invited talk, Marker pairs for highly-accurate cancer diagnosis, Institute for Systems Biology Board of Directors Meeting, Seattle, WA, May 16, 2007
15. Invited talk, Simple two-gene test to accurately differentiate gastrointestinal stromal tumor and leiomyosarcoma, National Cancer Institute Site Visit for the Nanosystems Biology Cancer Center, California Institute of Technology, Pasadena, CA, Mar. 28, 2007
13. Seminar, Systems biology in medicine: applications to anemia, diabetes, and cancer, Chemical Engineering Department Seminar, Brigham Young University, Mar 22, 2007
12. Invited talk, Molecular signatures to diagnose cancer and inform treatment choice, Nanosystems Biology Cancer Center Retreat, Ventura, CA, Feb. 24, 2006
11. Invited talk, Molecular signatures to identify causal network perturbations: a case study in *Halobacterium*, Nanosystems Biology Cancer Center Retreat, Ventura, CA, Feb. 23, 2006
10. Invited talk, Molecular signatures for cancer diagnosis and target identification, Aegean Conferences: Pathways, Networks, and Systems IV, Mykonos, Greece, Oct. 2006
9. Invited talk, Glioblastoma diagnosis and drug target identification using systems analysis of blood: A vision for the future, Pacific Northwest Brain Tumor Alliance VC Meeting, Seattle, WA, Apr. 2006
8. Invited talk, Gene expression markers to predict outcome of chemotherapy in ovarian cancer, Pacific Ovarian Cancer Research Consortium External and Internal Advisory Meeting, Seattle, WA, Apr. 2006
7. Invited talk, Glioblastoma diagnosis and drug target identification using systems analysis of blood: A vision for the future, Nanosystems Biology Cancer Center Retreat, Ventura, CA, Apr. 2006
6. Invited talk, Comprehensive assessment of genome-scale metabolic network states under physico-chemical constraints, Institute for Systems Biology, Oct. 2005, Seattle, WA
5. Seminar, Assessing the capabilities of genome-scale metabolic networks, University of Virginia, Department of Chemical Engineering, Mar. 2005, Charlottesville, VA
4. Seminar, Assessing the capabilities of genome-scale metabolic networks, Georgia Institute of Technology, Department of Chemical and Biomolecular Engineering, Feb. 2005, Atlanta, GA

3. Seminar, Assessing the capabilities of genome-scale metabolic networks, Cornell University, Department of Biomedical Engineering, Feb. 2005, Ithaca, NY
2. Seminar, Assessing the capabilities of genome-scale metabolic networks, University of Illinois at Urbana-Champaign, Department of Chemical and Biomolecular Engineering, Jan. 2005, Urbana, IL
1. Seminar, Genome-scale models of metabolism: evaluating the consequences of constraints, Institute for Systems Biology, Jan. 2005, Seattle, WA

SERVICE ACTIVITIES

Graduate Students and Postdoctoral Researchers Supervised:

Graduate Students (all in PhD programs unless otherwise noted)

Daniel Baker, Biophysics and Computational Biology (MS), 2010-2013
Matthew Benedict, Chemical & Biomolecular Engineering, Supervised 2009-2014
Sriram Chandrasekaran, Biophysics, Supervised 12/2008 – 2013
John Earls, Computer Science, 8/2010-date
James Eddy, Bioengineering, Supervised 8/2007-2012
Matthew Gonnerman, Chemical & Biomolecular Eng., Supervised 10/2008-2012
Swati Gupta, Biophysics and Computational Biology, Supervised 8/2007-12/2010
MS: “Meta-analysis of gene expression in honey bee brains”
Shu-Wen Huang, Bioinformatics Program of GSLIS, Supervised 5/2008-8/2009
MS: “Comparative analysis of molecular networks in gastrointestinal stromal tumor and leiomyosarcoma”
Younhee Ko, Computer Science, Supervised 6/2009-12/2010
Piyush Labhsetwar, Biophysics & Computational Biology, Supervised 12/2009-date
Shuyi Ma, Chemical & Biomolecular Engineering, Supervised 10/2009-2015
Andrew Magis, Biophysics & Computational Biology, 2010-2014
Caroline Milne, Chemical & Biomolecular Engineering, Supervised 10/2007-2012
Jocelynn Pearl, Molecular & Cellular Biology, Supervised 4/2014-date
Ravali Raju, Chemical & Biomolecular Engineering, Supervised 10/2007-12/2009
M.S.: “Coupled computational and experimental analysis of genome-scale metabolism in *Clostridium beijerinckii*”
Matthew Richards, Chemical & Biomolecular Engineering, Supervised 10/2010-2016
Bozena Sawicka, Chemical & Biomolecular Engineering (MS), Supervised 2010-2011
Jaeyun Sung, Chemical & Biomolecular Engineering, Supervised 2007-2012
Chunjing Wang, Chemical & Biomolecular Engineering, Supervised 2007-2013
Yuliang Wang, Chemical & Biomolecular Engineering, Supervised 10/2009-2014

Postdoctoral Researchers

Seth Ament, Supervised 2012-date
Ben Heavner, Supervised 2012-date
Evangelos Simeonidis, Supervised 2011-date
Areejit Samal, Supervised 2012-2013
Vineet Sangar, Supervised 2011-date
Nicholas Chia, Supervised 2010-2012
Cory Funk, Supervised 2010-date

Ramkumar Hariharan, Supervised 2012-2013
Saheed Imam, Supervised 2014-date
Alexey Kolodkin, Supervised 2012-2013
Charu Gupta Kumar, Supervised 2010-2012
Younhee Ko, Supervised 2011
Adai Vellaichamy, Supervised 2010
Amit Ghosh, Supervised 2009-2011
Pan Jun Kim, Supervised 2008-2011

Selected awards won by my students:

Seth Ament, NARSAD Young Investigator Award from the Brain and Behavior Research Society, 2014
Seth Ament, World Congress of Psychiatric Genetics Travel Award, 2014
Sriram Chandrasekaran, Harvard Junior Fellow, 2013
Sofie Bluvstein, HHMI Summer Research Fellowship, 2013
Sriram Chandrasekaran, Finalist, Lemelson MIT-Illinois Student Prize, 2012
Sriram Chandrasekaran, HHMI Graduate Fellowship, 2011-2014
Sriram Chandrasekaran, Best Presentation Award, Cell and Molecular Biology Symposium, University of Illinois, 2010 (across all biology related departments in the college)
Shuyi Ma, NSF Graduate Research Fellowship, 2009-2012
Lucas Edelman, Harvey Jordan Award as most outstanding undergraduate student in College of Engineering graduating class, Univ. of Illinois, 2009
Caroline Milne, Chemistry-Biology Training Grant Fellow, 2009-2010
James Eddy, Graduate Student Research Award (1 of 8 nationally), Annual Meeting of Biomedical Engineering Society, 2008 & 2009 (won twice in a row)
Lucas Edelman, Thomas J. Bardos Undergraduate Research Award, American Association for Cancer Research, 2008-2009
Jaeyun Sung and Seth Hanson, 3rd Place, 2nd Annual Midwest Symposium on Computational Biology and Bioinformatics Poster Competition (over 40 entrants), 2008

Trainees in independent academic positions:

Seth Ament, Assistant Professor, University of Maryland (starting 2016)
Sriram Chandrasekaran, Assistant Professor, University of Michigan (starting 2016)
Nicholas Chia, Assistant Professor, Mayo Clinic, Rochester, MN
Pan-Jun Kim, Assistant Professor, POSTECH & Asia Pacific Institute for Theoretical Physics
Adai Vellaichamy, Associate Professor, Anna University, India
Areejit Samal, Assistant Professor, Institute of Mathematical Sciences, Chennai, India
Yuliang Wang, Research Assistant Professor, University of Washington (starting 2016)

Reviewer for Journals: *Science*, *New England Journal of Medicine*, *Nature Biotechnology*, *Nature Genetics*, *Nature Methods*, *Nature Communications*, *PNAS*, *Science Translational Medicine*, *Cell Metabolism*, *Molecular Systems Biology*, *Molecular and Cellular Biology*, *Cancer Research*, *Clinical Cancer Research*, *Nucleic Acids Research*, *PLOS Computational Biology*, *PLOS Genetics*, *Bioinformatics*, *Biophysical Journal*, *Genome Biology*, *PLoS ONE*, *Biotechnology Progress*, *BMC Systems Biology*, *BMC Medicine*, *BMC Bioinformatics*, *BMC Genomics*, *Biotechnology and Bioengineering*, *AIChE Journal*, *Interface: A Journal of the Royal Society*, *Technology in Cancer Research and Treatment*, *Journal of Biological Systems*, *Journal of Theoretical Biology*, *Computer Methods and Programs in Biomedicine*, *FEBS Journal*, *Microbial Biotechnology*, *IET Systems Biology* and others.

Reviewer for funding agencies (incomplete list):

- National Institutes of Health, Permanent Study Section Member, Modeling and Analysis of Biological Systems (MABS), 2015-date
- National Institutes of Health, Ad hoc reviewer, 2012-date (many panels)
- Department of Energy, Advanced Scientific Computing Research (ASCR), Unsolicited Proposals Panel, Biology Panel, 2008; Early Career Awards Panel, 2012
- Nederlands Instituut voor Zuivelonderzoek Voeding (Dutch Science Academy), 2008
- National Science Foundation, Energy for Sustainability Panel, 2010; Biotechnology, Biochemical and Biomass Engineering Panel, 2010
- Ad hoc reviews for panels in Israel and Canada