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EDUCATION

2005 Ph.D., Bioengineering, University of California, San Diego
2000 B.S. (with University Honors), Chemical Engineering, Brigham Young University

PROFESSIONAL EXPERIENCE

2009- Affiliate, Department of Computer Science, University of Illinois
2009- Faculty Member, Neuroscience Program, University of Illinois
2008- Faculty Member, Center for Biophysics and Computational Biology
2007- Faculty Member, Center for Advanced BioEnergy Research, University of Illinois
2007- Faculty Member, Roy J. Carver Biotechnology Center, University of Illinois
2007- Affiliate, Department of Bioengineering, University of Illinois
2007- Faculty Member, Institute for Genomic Biology, University of Illinois
2007- Assistant Professor of Chemical and Biomolecular Engineering, University of Illinois
2006- Investigator, Pacific Northwest Brain Tumor Alliance
2006-2007 Investigator, Pacific Ovarian Cancer Research Consortium
2006-2007 Research Scientist, Lee Hood Lab, Institute for Systems Biology
2005-2006 Postdoctoral Fellow, Lee Hood Lab, Institute for Systems Biology
2001-2005 Graduate Research Assistant, Bernhard Palsson Lab, University of California, San Diego

HONORS & ACTIVITIES

2010-2013 Young Investigator Award, Roy J. Carver Charitable Trust
2010- Deputy Editor-in-Chief, *PLoS Computational Biology*
2009-2010 Associate Editor, *PLoS Computational Biology*
2009- Associate Editor, *BMC Systems Biology*
2009-2014 NSF CAREER Award
2008-2012 NIH Howard Temin Pathway to Independence Award in Cancer Research
2006 Tomorrow's PIs, *Genome Technology*
2006-2007 Sam E. and Kathleen Henry Postdoctoral Fellowship, American Cancer Society

PEER-REVIEWED PUBLICATIONS

h-index = 20 (Google scholar)

45. Chandrasekaran, S., and **Price, N.D.**, Probabilistic integrative modeling of genome-scale metabolic and regulatory networks in *Escherichia coli* and *Mycobacterium tuberculosis*, Submitted (2010)

44. Yan, X., Ma, L., Yi, D., Yoon, J.G., Diercks, A., **Price, N.D.**, Hood, L., Foltz, G., and Tian, Q., A CD133-related gene expression signature identifies an aggressive glioblastoma subtype with excessive mutations, Submitted (2010)
43. Ghosh, A., Zhao, H., and **Price, N.D.**, Genome-scale consequences of cofactor balancing in engineered pentose utilization pathways in *Saccharomyces cerevisiae*," Submitted (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*, Epub ahead of print, (2010)
41. Shi, L., et al., 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)
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, In press (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, 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*, eds. Hans Westerhoff and Boris Kholodenko, (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*, 225:1985-1994 (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)

GRANTS

- K99/R00 (Price) 9/1/2008 – 8/31/2012
NIH/NCI
Howard Temin Pathway to Independence Award in Cancer Research: Identifying network perturbations using secreted protein profiles in glioblastoma
To develop a novel means to track network perturbations via the secreted proteome, and to apply this to the study of glioblastoma, the most common and devastating form of brain cancer, in order to identify potential blood markers to guide diagnosis and therapy choice.
(Role: PI)
- Subcontract (Price) 6/1/2008-5/30/2010
Department of Defense (Hood)
Brain-Region and Cell-Type Specific Transcripts for Informative Diagnostics
To identify mRNA transcripts that are uniquely (or mostly) expressed only in particular regions of the brain or in specific cell types for use as specific molecular markers for brain diseases.
(Role: Subcontract PI)
- Grant (Zhao) 4/1/2008 – 3/30/2011
Energy Biosciences Institute-Beyond Petroleum (BP)
Engineering a Yeast Strain that Efficiently Utilizes C5/C6 Sugars
To engineer a strain of *Saccharomyces cerevisiae* that can efficiently metabolize C5/C6 sugars for the production of ethanol, optimizing at the level of both the pathway and genome-scale network
(Role: Co-I)
- Subcontract (Price) 4/1/2009-3/31/2014
Department of Defense (Federoff)
Discovery and Validation of Peripheral Biomarkers of Traumatic Brain Injury
(Role: Subcontract PI)
- CAREER (Price) 2/1/2009-1/31/2013
National Science Foundation
CAREER: Systems biology and engineering of *Clostridium beijerinckii* for enhanced butanol production
(Role: PI)
- Grant (Fouke) 11/1/2008 – 10/30/2011
Energy Biosciences Institute
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)
- Subcontract (Price) 7/1/2009 – 6/30/2010
Luxembourg (Hood, Galas)
Computational analysis of blood diagnostics linked to in vivo biological networks for systems medicine consortium
(Role: PI of subcontract)

Young Investigator Award (Price) Roy J. Carver Charitable Trust Integrated metabolic and regulatory network analysis of glioblastoma (Role: PI)	2/1/2010-1/31/2013
Grant (Metcalf, Price) Energy Biosciences Institute (BP) Metabolic engineering of methanogenic Archaea (Role: Co-I)	3/1/2010-2/28/2012
GTL (Metcalf, Price, Whitaker, Ma) DOE Methanogenic archaea and the global carbon cycle: a systems biology approach to the study of <i>Methanosarcina</i> species (Role: Co-I)	4/1/2010-3/31/2015
Grant (Schulten, Price) DOE	
Developmental Research Grant (Price) NIH/NCI P50 CA083636 (Urban) Pacific Ovarian Cancer Research Consortium Network-based gene expression analysis for enhanced target identification in ovarian cancer (Role: PI of the Developmental Research Project)	7/1/2006 – 11/1/2008

PRESENTATIONS

INVITED TALKS

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. Human disease diagnosis and prognosis using relative expression analysis, IEEE Engineering in Medicine and Biology Meeting, Minneapolis, MN, Sept 5, 2009
32. Systems approaches to disease stratification, Institute for Systems Biology, Seattle, WA, August 3, 2009
31. 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. 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. 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. 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. 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. Towards the engineering of *Clostridium beijerinckii* for improved bio-butanol production, Governmental Forum, Chinese Academy of Sciences, Shanghai, China, April 17, 2008
25. Model-guided Cellular Engineering, Partner Institute for Computational Biology, Chinese Academy of Sciences, Shanghai, China, April 16, 2008
24. Systems biology in medicine: applications to anemia, diabetes, and cancer, John Hopkins University, Institute for Computational Medicine, Baltimore, MD, February 8, 2008
23. Systems biology in medicine: applications to anemia, diabetes, and cancer, Purdue University Department of Statistics Seminar, West Lafayette, IN, February 5, 2008
22. Relative expression analysis for cancer diagnosis and prognosis, Information Theory and Applications Meeting, University of California, San Diego, January 31, 2008
21. Systems biology in medicine: applications to anemia, diabetes, and cancer, University of Illinois Department of Statistics Seminar, December 6, 2007

20. Computational challenges for systems biology and personalized medicine, DOE Frontiers in Extreme Computing Workshop, Santa Cruz, October 22, 2007
19. Relative expression classifiers for cancer diagnosis and prognosis, National Cancer Institute Nanotechnology Alliance Investigators Meeting, October 18, 2007
18. Relative expression molecular signatures of cancer diagnosis and prognosis, Biomedical Engineering Society Annual Meeting, Los Angeles, CA, Sept. 27, 2007
17. 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. Marker pairs for highly-accurate cancer diagnosis, Institute for Systems Biology Board of Directors Meeting, Seattle, WA, May 16, 2007
15. 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. Systems biology in medicine: applications to anemia, diabetes, and cancer, Chemical Engineering Department Seminar, Brigham Young University, Mar 22, 2007
12. Molecular signatures to diagnose cancer and inform treatment choice, Nanosystems Biology Cancer Center Retreat, Ventura, CA, Feb. 24, 2006
11. Molecular signatures to identify causal network perturbations: a case study in *Halobacterium*, Nanosystems Biology Cancer Center Retreat, Ventura, CA, Feb. 23, 2006
10. Molecular signatures for cancer diagnosis and target identification, Aegean Conferences: Pathways, Networks, and Systems IV, Mykonos, Greece, Oct. 2006
9. 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. 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. 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. Comprehensive assessment of genome-scale metabolic network states under physico-chemical constraints, Institute for Systems Biology, Oct. 2005, Seattle, WA
5. Assessing the capabilities of genome-scale metabolic networks, University of Virginia, Department of Chemical Engineering, Mar. 2005, Charlottesville, VA
4. Assessing the capabilities of genome-scale metabolic networks, Georgia Institute of Technology, Department of Chemical and Biomolecular Engineering, Feb. 2005, Atlanta, GA

3. Assessing the capabilities of genome-scale metabolic networks, Cornell University, Department of Biomedical Engineering, Feb. 2005, Ithaca, NY
2. 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. Genome-scale models of metabolism: evaluating the consequences of constraints, Institute for Systems Biology, Jan. 2005, Seattle, WA

NATIONAL AND INTERNATIONAL MEETINGS (Accepted Abstracts)

15. Nathan D. Price, Relative Expression Analysis for Cancer Diagnosis and Perturbed Network Identification, International Conference on Biomolecular Engineering, Santa Barbara, CA, Jan. 21, 2009
14. Caroline Milne, Ravali Raju, and Nathan D. Price, Metabolic network reconstruction and analysis of butanol producing strain *Clostridium beijerinckii*, Annual Meeting of Biomedical Engineering Society, Oct. 4, 2008
13. Swati Gupta, James Eddy, and Nathan D. Price, Gene Set Expression Reversal Analysis, Annual Meeting of Biomedical Engineering Society, Oct. 3, 2008
12. James Eddy and Nathan D. Price, Pathway Expression Rank Analysis (p-XRAY): A novel method for gene set expression analysis, Annual Meeting of Biomedical Engineering Society, Oct 3, 2008
11. Nathan D. Price, Relative Expression Reversals For Disease Diagnosis And Biological Discovery, American Institute for Chemical Engineers Annual Meeting, Los Angeles, CA, Nov. 8, 2007
10. Nathan D. Price, Molecular signatures to inform cancer diagnosis and treatment choice, American Institute for Chemical Engineers Annual Meeting, San Francisco, CA, 2006
9. Nathan D. Price, Molecular signatures for cancer diagnosis, Biomedical Engineering Society Annual Meeting, Chicago, IL, 2006
8. Nathan D. Price, Multi-dimensional annotation of genomes, Center for Non-Linear Studies Workshop on Collective Formation and Specialization in Biological and Social Systems, 2005, Santa Fe, NM
7. Nathan D. Price, Uniform random sampling of candidate metabolic phenotypes: application to enzymopathies, disease states, and adaptive evolution, American Institute of Chemical Engineers Annual Meeting, 2004, Austin, TX
6. Nathan D. Price, Identifying constraints that govern cell behavior: a key to converting conceptual to computational models in biology, Biomedical Engineering Society Annual Meeting, 2004, Philadelphia, PA
5. Nathan D. Price, Monte Carlo simulation of metabolic networks: implications for interpreting experimental data, American Institute of Chemical Engineers Annual Meeting, 2003, San Francisco, CA

4. Nathan D. Price, Characterizing the phenotypic potential of cell-scale metabolic networks using uniform random sampling, Biomedical Engineering Society Annual Meeting, 2003, Nashville, TN
3. Nathan D. Price, Bringing genomes to life: the use of whole-cell *in silico* models, Networks in Plant Biology, First European Plant Science Organization Meeting, 2002, Brunnen, Switzerland
2. Nathan D. Price, Genome-scale metabolic pathway analysis of *Haemophilus Influenzae* and *Helicobacter pylori*, American Institute of Chemical Engineers Annual Meeting, 2002, Indianapolis, IN
1. Nathan D. Price, Metabolic Extreme Pathway Analysis of *Haemophilus influenzae* and *Helicobacter pylori*, American Institute of Chemical Engineers Annual Meeting, 2001, Reno, NV

SERVICE ACTIVITIES

Editorships of Journals or Other Learned Publications

Deputy Editor-in-Chief, *PLoS Computational Biology*, 2010-present

Associate Editor, *PLoS Computational Biology*, 2009-2010

Associate Editor, *BMC Systems Biology*, 2009-present

Lead Guest Editor, Special Issue of *Biotechnology Journal*, focus area: Systems biology for Biotech Applications, 2009

Guest Editor, *Advances in Bioinformatics*, 2009

Guest Editor, Special issue of *IEEE Transactions in Information Theory*, focus area: Genomics and Neuroscience, 2009

Thesis Committees:

Michael Bednarz, Physics

Matthew Benedict, Chemical & Biomolecular Engineering (chair)

Sriram Chandrasekaran, Biophysics & Computational Biology (chair)

James Eddy, Bioengineering (chair)

Matthew Gonnerman, Chemical & Biomolecular Engineering (chair)

Swati Gupta, Biophysics & Computational Biology (chair)

Jerrold Henderson, Chemical & Biomolecular Engineering

Shu-Wen Huang, Bioinformatics Program of GSLIS, (chair)

Younhee Ko, Computer Science (co-chair)

Shuyi Ma, Chemical & Biomolecular Engineering (chair)

Caroline Milne, Chemical & Biomolecular Engineering (chair)

Chelsea Monty, Chemical & Biomolecular Engineering

Ravali Raju, Chemical & Biomolecular Engineering (chair)

Elijah Roberts, Biophysics and Computational Biology

Ryan Sullivan, Chemical & Biomolecular Engineering

Jaeyun Sung, Chemical & Biomolecular Engineering (chair)

Weng Lin Tang, NUS-Illinois Chemical & Biomolecular Engineering

Chunjing Wang, Chemical & Biomolecular Engineering (chair)

Yuliang Wang, Chemical & Biomolecular Engineering (chair)

Selected awards won by my students:

Lucas Edelman, Harvey Jordan Award as best student in College of Engineering, Univ. of Illinois, 2009

James Eddy, 2nd Place, Chemical & Biomolecular Engineering Graduate Research Symposium, 2009

Caroline Milne, Chemistry-Biology Training Grant Fellow, 2009-2010

Lucas Edelman, 2nd Place, Chemical & Biomolecular Engineering Department Undergraduate Poster Competition, 2009

James Eddy, Graduate Student Research Award (1 of 8 nationally), Annual Meeting of Biomedical Engineering Society, 2008 & 2009 (won twice)

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

Service in Chemical and Biomolecular Engineering Department:

- Graduate Admissions Coordinator, 2007-date
- Department Representative for Campus Bioinformatics Program
- Faculty Recruiting Committee, 2008-2009
- Self-study Committee for Departmental External Review, 2009

Reviewer for Journals: *PNAS*, *Molecular Systems Biology*, *Cancer Research*, *Nucleic Acids Research*, *PLoS Biology*, *PLoS Computational Biology*, *PLoS Genetics*, *Bioinformatics*, *Biophysical Journal*, *Genome Biology*, *PLoS ONE*, *Biotechnology Progress*, *BMC Bioinformatics*, *BMC Systems Biology*, *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* and *IET Systems Biology*

Reviewer for funding agencies:

- *Department of Energy, Advanced Scientific Computing Research (ASCR), Unsolicited Proposals Panel, Biology Panel, 2008*
- *Nederlands Instituut voor Zuivelonderzoek Voeding (Dutch Science Academy), 2008*
- *National Science Foundation, Energy for Sustainability Panel, 2010*