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POSITIONS

University of Virginia

Professor, Biomedical Engineering	2015-present
Associate Professor, Biomedical Engineering	2011-2015
Assistant Professor, Biomedical Engineering	2005-2011
Director, Biomedical Engineering Graduate Program	2013-present
Faculty Director, Bioinformatics Core, School of Medicine	2011-present
Non-Resident Faculty Member, Center for Public Health Genomics	2008-present
Faculty Member, Cancer Center	2006-present
Faculty Member, Robert M. Berne Cardiovascular Research Center	2006-present

EDUCATION

University of California, San Diego	Winter 2005
<i>Doctorate of Philosophy</i> , Bioengineering	
Additional Specialization in Bioinformatics	
Advisor: Bernhard Palsson, Ph.D.	
Thesis: Systems Analysis of Cellular Signaling Networks	
University of California, San Diego	Fall 2002
<i>Master of Science</i> , Bioengineering	
Advisor: Bernhard Palsson, Ph.D.	
University of California, San Diego	Spring 2000
<i>Bachelor of Science</i> , Bioengineering	
<i>Magna Cum Laude</i>	

HONORS & RECOGNITION

- Elected Fellow of American Institute of Medical and Biological Engineering (2016)
- Elected Board of Directors, Biomedical Engineering Society (2014-2017)
- Distinguished Career Development Award, U. Virginia Vice President of Research (2014)
- Standing Member, NIH Biodata Management and Analysis (BDMA) study section (2012-2016)
- Award for Excellence in Biomedical Engineering Undergraduate Education, U. Virginia (2012)
- “Most Helpful Mentor”, Biomedical Engineering Undergraduate Program, U. Virginia (2012)
- Participant in U. Virginia Leadership in Academic Matters (LAM) program (2012)
- Member, Academy of Distinguished Educators, U. Virginia (2010)
- National Science Foundation CAREER award (2007-2012)
- Award for Excellence in Biomedical Engineering Undergraduate Education, U. Virginia (2007)
- Whitaker Foundation Graduate Fellowship (2001 – 2004)
- National Science Foundation Graduate Research Fellowship Honorable Mention (2001)

- Award for Excellence as a Teaching Assistant (June 2001)
- *Magna Cum Laude*, University of California, San Diego (June 2000)
- Member of Phi Beta Kappa honor society (June 1999)
- Regents' Scholar, University of California, San Diego (1994-2000)
- Undergraduate Provost's Honor Roll, Every Quarter at University of California, San Diego (1994-2000)
- Eagle Scout (1991)

EDITORIAL BOARDS

- Co-Editor-in-Chief, PLOS Computational Biology (2016 – present)
- Deputy Editor-in-Chief, PLOS Computational Biology (2014 – 2016)
- Editorial Board, Molecular Pharmacology (2014 – present)
- Deputy Editor, PLOS Computational Biology (2012 – 2014)
- Associate Editor, BMC Systems Biology (2010 – present)
- Associate Editor, PLOS Computational Biology (2008 – 2012)

PUBLICATIONS

Corresponding author(s).

% Students, technicians, or post-doctoral fellows under the supervision of J.A. Papin.

* Equal contribution of authors.

1. Bartell JA*, AS Blazier*, P Yen%, JC Thorgensen, L Jelsback, JB Goldberg, JA Papin#. Reconstruction of the metabolic network of *Pseudomonas aeruginosa* to interrogate virulence factor synthesis. 2017. *Nature Communications*. In press.
2. Blais E.M.%, K.D. Rawls%, Z.I. Li%, G.L. Kolling, P. Ye, A. Wallqvist, J.A. Papin#. 2017. Comparative toxicogenomics analyses enabled by reconciled rat and human metabolic networks. *Nature Communications*. In press.
3. Biggs MB%, GL Medlock%, TJ Moutinho Jr.%, HJ Lees, JR Swann, GL Kolling#, JA Papin#. 2017. Systems-level metabolism of the Altered Schaedler Flora, a complete gut microbiota. *The ISME Journal*. In press.
Top Ten Article Downloads, December 2016
4. Mayneris-Perxachs J, DT Bolick, J Leng, GL Medlock%, GL Kolling, JA Papin, JR Swann#, RL Guerrant. 2016. Impact of defined protein and zinc deficiencies on the murine microbiome and metabolic phenotype. *Amer. J. Clinical Nutrition*. 104(5):1253-1262.
List of Most Read Articles, November 2016
5. Nussinov R, JA Papin. 2016. Computing Biology. *PLOS Computational Biology*. 12(7): e1005050.
6. Chaiboonchoe A*, L Ghamsari*, B Dohai, P Ng, B Khraiwesh, A Jaiswal, K Jijakli, J Koussa, DR Nelson, H Cai, X Yang, RL Chang, JA Papin#, H Yu#, S Balaji#, and K Salehi-Ashtiani#. 2016. Systems level analysis of the *Chlamydomonas reinhardtii* metabolic network reveals variability in evolutionary co-conservation. *Molecular BioSystems*. 12(8): 2394-2407.
Cover illustration
7. Biggs M.B.% and J.A. Papin#. 2016. Metabolic network-guided binning of metagenomic sequence fragments. *Bioinformatics*. 32(6): 867-874.
8. Varga J.J*. M. Barbier*, X. Mulet, P. Bielecki, J.A. Bartell%, I. Martinez-Ramos, L.E. Hittle, J.P. Owings, M.R. Davis Jr., F.H. Damron, G.W. Liechti, J. Puchalka, V. Martins dos Santos, R.K. Ernst, J.A. Papin, S. Alberti, A. Oliver, J.B. Goldberg#. 2015. Genotypic and phenotypic analysis of a *Pseudomonas aeruginosa* chronic bronchiectasis isolate reveals differences from cystic fibrosis isolates and laboratory strains. *BMC Genomics*. 16(1):883.

9. Ebrahim A.#, Almaas, E., E. Bauer, A. Bordbar, A.P. Burgard, R.L. Chang, A. Drager, I. Famili, A.M. Feist, R.M. Fleming, S.S. Fong, V. Hatzimanikatis, M.J. Herrgard, A. Holder, M. Hucka, D. Hyduke, N. Jamshidi, S.Y. Lee, N. Le Novere, J.A. Lerman, N.E. Lewis, D. Ma, R. Mahadevan C. Maranas, H. Nagarajan, A. Navid, J. Nielsen, L.K. Nieslen, J. Nogales, A. Noronha, C. Pal, B.O. Palsson, J.A. Papin, K.R. Patil, N.D. Price, J.L. Reed, M. Saunders, R.S. Senger, N. Sonnenschein, Y. Sun, I. Thiele. 2015. Do Genome-scale Models Need Exact Solvers or Clearer Standards? *Molecular Systems Biology*. 11(1):831.
10. Biggs, M.B.%, G.L. Medlock%, G.L. Kolling, J.A. Papin#. 2015. Metabolic network modeling of microbial communities. *WIREs Systems Biology and Medicine*. 7(5): 317-334.
Top 10 most viewed articles in WIREs Systems Biology and Medicine for 2015
<https://goo.gl/OD27M4>
11. Nussinov, R.#, S. Bonhoeffer, J.A. Papin, and O. Sporns. 2015. From "What is" to "What isn't" computational biology. *PLoS Computational Biology*. 11(7):e1004318.
12. Steinway, S.*, M. Biggs*%, T. Loughran, Jr., J.A. Papin#, R. Albert#. 2015. Inference of network dynamics and metabolic interactions in the gut microbiome. *PLoS Computational Biology*. 11(6):e1004338.
Highlighted by PLOS Blogs
<http://goo.gl/ANjF7L>
13. D'Auria, K.M.%, M.J. Bloom%, Y. Reyes, M.C. Gray, E.J. van Opstal, J.A. Papin#, and E.H. Hewlett#. 2015. High temporal resolution of glucosyltransferase dependent and independent effects of *Clostridium difficile* toxins across multiple cell types. *BMC Microbiology*. 15:7.
14. Jensen, P.A.%, B.V. Dougherty%, T.J. Moutinho, Jr.%, and J.A. Papin#. 2015. Miniaturized plate readers for low-cost, high-throughput phenotypic screening. *Journal of Laboratory Automation*. 20(1): 51-55.
15. Newhook, T.E., E.M. Blais%, J.M. Lindberg, S.J. Adair, W. Xin, J.K. Lee, J.A. Papin, J.T. Parsons, and T.W. Bauer#. 2014. A thirteen-gene expression signature predicts survival of patients with pancreatic cancer and identifies new genes of interest. *PLoS One*. 9(9):e105631.
16. Jensen, P.A.%, and J.A. Papin#. 2014. MetDraw: automated visualization of genome-scale metabolic network reconstructions and high-throughput data. *Bioinformatics*. 30(9):1327-1328.
17. Bartell, J.A.% *, P. Yen%*, J. Varga, J.B. Goldberg, and J.A. Papin#. 2014. Comparative metabolic network analysis of *Burkholderia* pathogens. *Journal of Bacteriology*. 196: 210-226.
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Top 20 "Most-Read Articles during January 2014" in Journal of Bacteriology.
UVAToday (<http://news.virginia.edu/content/virtual-bacteria-shed-light-cystic-fibrosis-infections>)
18. Biggs, M.B.%, and J.A. Papin#. 2013. Novel multiscale modeling tool applied to *Pseudomonas aeruginosa* biofilm formation. *PLoS One*. 8(10): e78011.
19. Walters, D.M., J.B. Stokes, S.J. Adair, E.B. Stelow, C.A. Borgman, B.T. Lowrey, W. Xin, E.M. Blais%, J.K. Lee, J.A. Papin, J.T. Parsons, T.W. Bauer#. 2013. Clinical, molecular and genetic validation of a murine orthotopic xenograft model of pancreatic adenocarcinoma using fresh human specimens. *PLoS One*. 8(1): e77065.
20. Wagenseller, A.G., A. Shada, K.M. D'Auria%, C. Murphy, D. Sun, K.R. Molhoek, J.A. Papin, A. Dutta, C.L. Slingluff, Jr.#. 2013. MicroRNAs induced in melanoma treated with combination targeted therapy of Temeisrolimus and Bevacizumab. *Journal of Translational Medicine*. 11(1): 218.
21. D'Auria, K.M.%*, G. Kolling*, G. Donato, C. Warren, E. Hewlett#, and J.A. Papin#. 2013. *In vivo* physiological and transcriptional profiling reveals host responses to *Clostridium difficile* Toxin A and Toxin B. *Infection & Immunity*. 81: 3814-3824.
22. Koskimaki, J., A.S. Blazier, A. Clarens, and J.A. Papin. 2013. Computational models of algae metabolism for industrial applications. *Industrial Biotechnology*. 9: 185-195.
23. Walpole, J., J.A. Papin, and S.M. Peirce#. 2013. Multiscale computational models of complex biological systems. *Annual Review of Biomedical Engineering*. 15:137-154.
24. Thiele, I. #*, N. Swainston*.,..., A.K. Chavali%.,...J.A. Papin,.,..., D.B. Kell, P. Mendes, B.O. Palsson. 2013. A community-driven global reconstruction of human metabolism. *Nature Biotechnology*. 31(5): 419-425.

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Popular Science (<http://www.popsci.com/technology/article/2013-03/researchers-create-google-map-human-metabolism>)

Redorbit (<http://www.redorbit.com/news/health/1112795467/recon-metabolism-map-created-by-researchers-030413/>)

NIGMS, NIH homepage, NIGMS Director's Featured Research Advance (<http://nigms.nih.gov>)

25. Schmidt, B.J., J.A. Papin, and C.J. Musante#. 2013. Mechanistic systems modeling to guide drug discovery and development. *Drug Discovery Today*. 18:116-127.
26. Blais, E.M%, A.K. Chavali%, and J.A. Papin#. 2013. Linking genome-scale metabolic modeling and genome-annotation. *Methods in Molecular Biology*. 985:61-83.
27. Blazier, A.S. %, and J.A. Papin#. 2012. Integration of expression data in genome-scale metabolic network reconstructions. *Frontiers in Physiology*. 3:299. doi: 10.3389/fphys.2012.00299.
28. Chavali, A.K.%, A.S. Blazier%, J.L. Tlaxca, P.A. Jensen%, R.D. Pearson, and J.A. Papin#. 2012. Metabolic network analysis predicts efficacy of FDA-approved drugs targeting the causative agent of a neglected tropical disease. *BMC Systems Biology*. 6(1):27.
Top 10 BMC Systems Biology viewed article for May 2012.
Featured as a "Hot Topic" on BMC Systems Biology homepage May 2012.
29. Tilgman, R.W.#, E.M. Blais%, C.R. Cowan, N.E. Sherman, P.R. Grigera, E.D. Jeffery, J.W. Fox, B.R. Blackman, D.J. Tschumperlin, J.A. Papin, J.T. Parsons. 2012. Matrix rigidity regulates cancer cell growth by modulating cellular metabolism and protein synthesis. *PLoS One*. 7(5): e37231.
30. Chavali, A.K.%, K.M. D'Auria%, E.L. Hewlett, R.D. Pearson, and J.A. Papin#. 2012. A metabolic network approach for the identification and prioritization of antimicrobial drug targets. *Trends in Microbiology*. 20: 113-123.
31. D'Auria, K.M.%, G.M. Donato, M.C. Gray, G.L. Kolling, C.A. Warren, L.M. Cave, M.D. Solga, J.A. Lannigan, J.A. Papin#, E. Hewlett#. 2012. Systems analysis of the transcriptional response of human ileocecal epithelial cells to *Clostridium difficile* toxins and effects on cell cycle control. *BMC Systems Biology*. 6:2.
Top 10 BMC Systems Biology viewed article for January 2012.
"Highly Accessed" article for BMC Systems Biology.
32. Haggart, C., J. Bartell, and J.A. Papin. 2011. Whole-genome metabolic network reconstruction and constraint-based modeling. *Methods in Enzymology*. 500:411-433.
33. Jensen, P.A.%, K. Lutz%, and J.A. Papin#. 2011. TIGER: Toolbox for integrating genome-scale metabolic models, expression data, and transcriptional regulatory networks. *BMC Systems Biology*. 5:147.
Top 10 BMC Systems Biology viewed article for September 2011, October 2011.
"Highly Accessed" article for BMC Systems Biology.
34. Chang, R.L., L. Ghamsari, A. Manichaikul%, E. Hom, B. Santhanam, W. Fu, Y. Shen, B.O. Palsson, K. Salehi-Ashtiani#, J.A. Papin#. 2011. Metabolic network reconstruction of *Chlamydomonas* offers insight into light-driven algal metabolism. *Molecular Systems Biology*. 7:518. doi: 10.1038/msb.2011.52.
Featured as an Editor's Choice in the journal Science (August 12, 2011).
Top 10 MSB downloaded article for August 2011, September 2011, October 2011.
Featured in:
Biofuels Digest (<http://biofuelsdigest.com/bdigest/2011/08/05/metabolic-pathway-of-model-algae-mapped-at-genome-scale/>),
The National (<http://www.thenational.ae/news/uae-news/science/nyu-abu-dhabi-researcher-pitches-in-on-algae-based-fuel-research>),
New York University (<http://nyuad.nyu.edu/news.events/press-release-algal-research-08-11.html>),
Nature Middle East (<http://www.nature.com/nmiddleeast/2011/110914/full/nmiddleeast.2011.122.html>),
UVAToday (<http://www.virginia.edu/uvatoday/newsRelease.php?id=16042>)
WINA Morning News (1070 AM) in Charlottesville, Virginia on September 24, 2011.
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35. Molhoek, K.R., A.L. Shada, M. Smolkin, S. Chowbina%, J.A. Papin, D.L. Brautigan, and C.L. Slingluff#. 2011. Comprehensive analysis of RTK activation in human melanomas reveals novel autocrine signaling through IGF-1R. *Melanoma Research*. 21(4): 274-284.
36. Ghamsari, L.*, S. Balaji*, Y. Shen, X. Yang, D. Balcha, C. Fan, T. Hao, H. Yu#, J.A. Papin#, and K. Salehi-Ashtiani#. 2011. Genome-wide functional annotation and structural verification of metabolic ORFeome of *Chlamydomonas reinhardtii*. *BMC Genomics*. 12(Suppl 1): S4.
37. Oberhardt, M.A.%*, J. Puchalka*, V.M. dos Santos#, and J.A. Papin#. 2011. Reconciliation of genome-scale metabolic reconstructions for comparative systems analysis. *PLoS Computational Biology*. 7(3): e1001116. doi:10.1371/journal.pcbi.1001116.
Highlighted in the journal BioTechniques, May 2011.
Featured on PLoS Computational Biology homepage as well as on UVAToday and other media outlets (<http://www.virginia.edu/uvatoday/newsRelease.php?id=14641>).
38. Jensen, P.A.%, and J.A. Papin#. 2011. Functional integration of a metabolic network model and expression data without arbitrary thresholding. *Bioinformatics*. 27(4): 541-547.
39. Benedict, K.F., F. MacGabhann, R.K. Amanfu, A.K. Chavali%, E.P. Gianchandani%, L.S. Glaw, M.A. Oberhardt%, B.C. Thorne, J.H. Yang, J.A. Papin, S.M. Peirce, J.J. Saucerman, and T.C. Skalak#. 2011. Systems analysis of small signaling modules relevant to eight human diseases. *Annals of Biomedical Engineering*. 39(2): 621-635.
40. Oberhardt, M.A.%, J.B. Goldberg, M. Hogardt, and J.A. Papin#. 2010. Metabolic network analysis of *Pseudomonas aeruginosa* during chronic cystic fibrosis lung infection. *Journal of Bacteriology*. 192(20): 5534-5548.
41. Ruppin, E., J.A. Papin, L.F. de Figueiredo, and S. Schuster#. 2010. Metabolic reconstruction, constraint-based analysis and game theory to probe genome-scale metabolic networks. *Current Opinion in Biotechnology*. 21(4): 502-510.
42. Schmidt, B.J.%, X. Lin-Schmidt, A. Chamberlin%, K. Salehi-Ashtiani#, and J.A. Papin#. 2010. Metabolic systems analysis to advance algal biotechnology. *Biotechnology Journal*. 5: 660-670.
43. Sefcik LS, J.L. Wilson, J.A. Papin, E.A. Botchwey#. 2010. Harnessing systems biology approaches to engineer functional microvascular networks. *Tissue Engineering, Part B Reviews*. 16(3):361-370.
44. Gianchandani, E.P.%, A.K. Chavali%, and J.A. Papin#. 2010. The application of flux balance analysis in systems biology. *Wiley Interdisciplinary Reviews: Systems Biology and Medicine*. doi:10.1002/wsbm.60.
Top 10 cited paper for inaugural Impact Factor calculations (2012) for WIREs Systems Biology and Medicine.
45. Schmidt, B.J., J.A. Papin, and M.B. Lawrence#. 2009. Nano-motion dynamics are determined by surface-tethered selectin mechanokinetics and bond formation. *PLoS Computational Biology*. 5(12): e1000612.
46. Oberhardt, M.A.%, B.O. Palsson, and J.A. Papin#. 2009. Applications of genome-scale metabolic reconstructions. *Nature/EMBO Molecular Systems Biology*. 5: 320.
Top 10 downloaded article for February 2010 and March 2010.
47. Manichaikul, A.%, L. Ghamsari, E.F.Y. Hom, C. Lin, R.R. Murray, R.L. Chang, T. Hao, Y. Shen, A.K. Chavali%, I. Thiele, X. Yang, E. Mello, D.E. Hill, M. Vidal, K. Salehi-Ashtiani#, and J.A. Papin#. 2009. Metabolic network analysis integrated with transcript verification for sequenced genomes. *Nature Methods*. 6(8): 589-592.
48. Allen, T.E.#, Saucerman, J.J., Papin, J.A., and Peirce, S.M. 2009. Development and assessment of a novel systems bioengineering course integrating modeling and experimentation, *Proceedings for the 2009 American Society for Engineering Education (ASEE) Annual Conference and Exposition*.
49. Glass G.%, J.A. Papin, J.W. Mandell#. 2009. SIMPLE: A Sequential Immunoperoxidase Labeling and Erasing Method. *Journal of Histochemistry & Cytochemistry*. 57(10):899-905.
October 2009 Issue's Article of the Month.
50. Roberts, S.B., J.L. Robichaux%, A.K. Chavali%, P.A. Manque, V. Lee, A.M. Lara, J.A. Papin#, and G.A. Buck#. 2009. Proteomic and network analysis characterize stage-specific metabolism in *Trypanosoma cruzi*. *BMC Systems Biology*. 3:53.
"Highly Accessed" article for BMC Systems Biology.

51. Gianchandani E.P. %, A.R. Joyce, B.O. Palsson, and J.A. Papin#. 2009. Functional states of the genome-scale *Escherichia coli* transcriptional regulatory system. *PLoS Computational Biology*. 5(6): e1000403. doi:10.1371/journal.pcbi.1000403.
52. Wieghaus, K.A.*, E.P. Gianchandani*%, R.A. Neal, M.A. Paige, M.L. Brown, J.A. Papin#, and E.A. Botchwey#. 2009. Phthalimide neovascular factor 1 (PNF1) modulates MT1-MMP activity in human microvascular endothelial cells. *Biotechnology and Bioengineering*. 103: 796-807.
53. Oberhardt M.A.%, A.K. Chavali%, and J.A. Papin#. 2009. Flux balance analysis: interrogating genome-scale metabolic networks. *Methods in Molecular Biology*. 500:61-80.
54. Mandell, J.W. #, C.N. Locke%, G. Glass%, E.P. Gianchandani%, T.D. Bourne, D. Schiff, S. Amos, and J.A. Papin. 2009. Dephosphorylation of β -arrestin 1 in high grade gliomas. *Journal of Neuropathology and Experimental Neurology*. 68(5):535-541.
55. Puchalka, J. *, M.A. Oberhardt*%, M. Godinho, A. Bielecka, D. Regenhardt, K. Timmis, J.A. Papin#, and V.M. dos Santos#. 2008. Genome-scale reconstruction and analysis of the *Pseudomonas putida* KT2440 metabolic network facilitates applications in biotechnology. *PLoS Computational Biology*, 4: e1000210.
56. Chavali, A.K. *%, E.P. Gianchandani*%, K.S. Tung, M.B. Lawrence, S.M. Peirce, and J.A. Papin#. 2008. Characterizing emergent properties of immunological systems with multi-cellular rule-based computational modeling. *Trends in Immunology*, 29: 589-599.
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57. Wieghaus, K.A. *, E.P. Gianchandani*, M.A. Paige, M.L. Brown, E.A. Botchwey, and J.A. Papin#. 2008. Novel pathway compendium analysis elucidates mechanism of pro-angiogenic synthetic small molecule. *Bioinformatics*, 24(20): 2384-2390.
58. Lee, J.M. *%, E.P. Gianchandani*%, J. Eddy%, and J.A. Papin#. 2008. Dynamic analysis of integrated signaling, metabolic, and regulatory networks. *PLoS Computational Biology*. 4(5): e1000086. doi:10.1371/journal.pcbi.1000086.
59. Chavali, A.K.%, J. Eddy%, J. Whittemore%, K. Williams%, and J.A. Papin#. 2008. Systems analysis of metabolism in the pathogenic trypanosomatid *Leishmania major*. *Nature/EMBO Molecular Systems Biology*. 4:177.
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60. Gianchandani, E.P. *%, M.A. Oberhardt*%, A. P. Burgard, C.D. Maranas, and J.A. Papin#. 2008. Predicting biological system objectives de novo from internal state measurements. *BMC Bioinformatics*. 9:43.
61. Oberhardt, M.A.*%, J. Puchalka*, K. Fryer%, V.M. dos Santos#, and J.A. Papin#. 2008. Genome-scale metabolic network analysis of the opportunistic pathogen *Pseudomonas aeruginosa* PAO1. *Journal of Bacteriology*. 190(8):2790-803.
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Featured in conference artwork and promotional materials for the ASM meeting Pseudomonas 2009 in Hannover, Germany (see <http://genomics1.mh-hannover.de/pseudomonas2009/>)
62. Robertson, S.H. %, C.K. Smith%, A.L. Langhans%, S.E. McLinden%, M.A. Oberhardt%, K.R. Jakab, B. Dzamba, D.W. DeSimone, J.A. Papin#, and S.M. Peirce#. 2007. Multiscale computational analysis of *Xenopus laevis* morphogenesis reveals key insights of systems-level behavior. *BMC Systems Biology*. 1:46.
63. Wieghaus, K.A., E.P. Gianchandani%, M.L. Brown, J.A. Papin, and E.A. Botchwey#. 2007. Mechanistic Interrogation of Phthalimide Neovascular Factor 1 (PNF1) using Network Analysis Tools. *Tissue Engineering*. 13(10): 2561-2575.
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64. Gianchandani, E.P.*%, J.A. Papin*#, N.D. Price, A.R. Joyce, and B.O. Palsson. 2006. Matrix formalism for transcriptional regulatory systems. *PLoS Computational Biology*, 2: 902-917.

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65. Lee, J.M. %, E.P. Gianchandani%, and J.A. Papin#. 2006. Flux Balance Analysis in the Era of Metabolomics. *Briefings in Bioinformatics*, 7: 140-150.
66. Gianchandani, E.P. %, D.L. Brautigan, and J.A. Papin#. 2006. Systems Analyses Characterize Integrated Functions of Biochemical Networks. *Trends in Biochemical Sciences*, 31: 284-291.
67. Peirce-Cottler, S.M., T.S. Skalak, and J.A. Papin. 2006. Multi-scale systems integration from cells to tissues: coupling intracellular network analysis with tissue-patterning simulations. *IBM Journal of Research and Development*, 50(6): 601-615.
68. Papin, J.A., T. Hunter, B.O. Palsson, and S. Subramaniam. 2005. Reconstruction of large-scale cellular signaling networks and analysis of their properties. *Nature Reviews Molecular Cell Biology*, 6: 99-111.

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69. Papin, J.A., J.L. Reed, and B.O. Palsson. 2004. Hierarchical thinking in network biology: the unbiased modularization of biochemical networks. *Trends in Biochemical Sciences*, 29: 641-647.

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70. Papin, J.A., J. Stelling, N.D. Price, S. Klamt, S. Schuster, and B.O. Palsson. 2004. Comparison of network-based pathway analysis methods. *Trends in Biotechnology*, 22: 400-405.
71. Papin, J.A., and B.O. Palsson. 2004. The JAK-STAT signaling network in the human B-cell: an extreme signaling pathway analysis. *Biophysical Journal*, 87: 37-46.
72. Papin, J.A., and B.O. Palsson. 2004. Topological analysis of signaling networks: a scalable framework to obtain emergent properties including crosstalk. *Journal of Theoretical Biology*, 227: 283-297.
73. Papin, J.A., and S. Subramaniam. 2004. Bioinformatics and cellular signaling. *Current Opinion in Biotechnology*, 15: 78-81.
74. Price, N.D.*, J.L. Reed*, J.A. Papin*, S. J. Wiback, and B.O. Palsson. 2003. Network-based analysis of metabolic regulation in the human red blood cell. *Journal of Theoretical Biology*, 225: 1985-1994.
75. Papin, J.A., N.D. Price, S.J. Wiback, D.A. Fell, and B.O. Palsson. 2003. Metabolic pathways in the post-genome era. *Trends in Biochemical Sciences*, 28: 250-258.
76. Palsson, B.O., N.D. Price, and J.A. Papin. 2003. Development of network-based pathway definitions: the need to analyze real metabolic networks. Letter to the Editor, *Trends in Biotechnology*, 21: 195-198.
77. Price, N.D., J.A. Papin, C.H. Schilling, and B.O. Palsson. 2003. Genome-scale microbial *in silico* models: the constraints-based approach. *Trends in Biotechnology*, 21: 162-169.
78. Price, N.D.*, J.L. Reed*, J.A. Papin*, I. Famili, and B.O. Palsson. 2003. Analysis of metabolic capabilities using singular value decomposition of extreme pathway matrices. *Biophysical Journal*, 84: 794-804.
79. Papin, J.A.*, N.D. Price*, and B.O. Palsson. 2002. Extreme pathway lengths and reaction participation in genome-scale metabolic networks. *Genome Research*, 12: 1889-1900.
80. Price, N.D.*, J.A. Papin*, and B.O. Palsson. 2002. Determination of redundancy and systems properties of *Helicobacter pylori*'s metabolic network using genome-scale extreme pathway analysis. *Genome Research*, 12: 760-769.

Highlighted by Current Opinions in Microbiology as one of six articles of "special interest" in genomics for May-June 2002.

81. Papin, J.A.*, N.D. Price*, J.S. Edwards, and B.O. Palsson. 2002. The genome-scale metabolic extreme pathway structure in *Haemophilus influenzae* shows significant network redundancy. *Journal of Theoretical Biology*, 215: 67-82.

BOOK CHAPTERS

1. Dougherty, B.*, T. Moutinho*, J.A. Papin. 2016. Accelerating the Drug Development Pipeline with Genome-Scale Metabolic Network Reconstructions, in *Systems Biology*, ed. Stefan Hohmann, Jens Nielsen. Wiley Biotechnology.

2. Hayenga, H. , B. Thorne, P. Yen, J.A. Papin, S. M. Peirce, and J. Humphrey. 2012. Multi-Scale Computational Modeling in Vascular Biology: from Molecular Mechanisms to Tissue-Level Structure and Function, in *Multiscale Computer Modeling in Biomechanics and Biomedical Engineering*, ed. Amit Gefen. Springer.
3. Jensen, P.A. and J.A. Papin. 2012. Linear Algebra, in *Encyclopedia of Systems Biology*, eds. Olaf Wolkenhauer.
4. Chowbina, S., K.A. Janes, S.M. Peirce, and J.A. Papin. 2011. Mathematical and computational models in cancer, in: *Targeted Therapies: Mechanisms of Resistance*, ed. Dan Gioeli. Springer.
5. Papin, J.A. #, E.P. Gianchandani%, and S. Subramaniam#. 2006. Mapping the genotype-phenotype relationship in cellular signaling networks: building bridges over the unknown, in: *Systems Biology*, eds. Isidore Rigoutsos and Gregory Stephanopoulos. Oxford University Press.
6. Papin, J.A., N.D. Price, and B.O. Palsson. 2004. *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.

OTHER PUBLICATIONS

1. PLOS Blog Post: The Ethics of Big Data. <http://blogs.plos.org/biologue/2015/02/09/ethics-big-data-focus-feature/>

ISSUED PATENTS

“Serial Multiple Antigen Colocalization in Paraffin-Embedded Tissue”

US Patent No. 8,753,824 B2

Issued Date: June 17, 2014

Inventors: James Mandell, Jason Papin, George Glass

INTERNATIONAL PATENT APPLICATIONS

“Miniaturized multiwell plate reader for phenotypic screening and related method thereof”

International Patent Application Serial No. PCT/US2013/063867

Filed: October 8, 2013

Inventors: Paul Jensen, Jason Papin

“Flask-based continuous optical density monitor”

U.S. Provisional Patent Application Serial No. 62/154,332

Filed: April 29, 2015

Inventors: Jason Papin, Bonnie Dougherty, Kevin Seitter, Alisha Geldert

PROVISIONAL PATENT APPLICATIONS

“Coculture chamber plate device and related method thereof”

U.S. Provisional Patent Application Serial No. 62/405,604

Filed: October 7, 2016

Inventors: Thomas Moutinho Jr., John Christopher Panagides, Matthew Biggs, Jason Papin

“Metabolic network analysis-directed assessment of FDA-approved drugs for a neglected tropical disease”

U.S. Provisional Patent Application Serial No. 61/438,331

Filed: February 1, 2011

Inventors: Jason Papin, Arvind Chavali

“Predicting biological system objectives from internal state measurements”

U.S. Provisional Patent Application Serial No. 60/959,221
Filed: July 12, 2007
Inventors: Jason Papin, Erwin Gianchandani, Matthew Oberhardt

“Compositions and methods of neovascular functions”
U.S. Provisional Patent Application Serial No. 60/958,031
Filed: July 2, 2007
Inventors: Edward Botchwey, Jason Papin, Erwin Gianchandani, Kristen Wieghaus

CONSULTING

Hemoshear, LLC
June 2015 - present

CURRENT FUNDING

Project: REU Site: Multi-Scale Systems Bioengineering
Dates: 12/2016 – 11/2019
Role: Faculty Mentor
% effort: 0%
Collaborators: PI: Timothy Allen, PhD; University of Virginia
Amount: \$361,861
Organization: National Science Foundation

Project: Tackling malaria resistance with an integrated modeling/experimental approach
Dates: 08/2016 – 07/2018
Role: MPI
% effort: 10%
Collaborators: MPI: Jennifer Guler, PhD; University of Virginia
Amount: \$434,586
Organization: National Institutes of Health, NIAID
Grant Number:

Project: Center for Systems Bioengineering – Team Planning Grant
Dates: 06/2016 – 05/2017
Role: Co-PI
% effort: 5%
Collaborators: Co-PIs: Kevin Janes, PhD; Shayn Peirce-Cottler, PhD; Jeffrey Saucerman, PhD; Matthew Lazarra, PhD; Roseanne Ford, PhD; University of Virginia
Amount: \$120,000
Organization: University of Virginia School of Engineering and Applied Sciences

Project: Transdisciplinary big data science training at UVa
Dates: 04/2016 – 03/2021
Role: PI (Contact)
% effort: 5%
Collaborators: Co-PIs: Don Brown, PhD; Thomas Loughran, MD; Kevin Skadron, PhD; University of Virginia
Amount: \$1,430,160
Organization: National Institutes of Health, NLM
Grant Number: T32-LM012416

Project: Design of context-aware surveillance system for nosocomial outbreaks involving non-patient reservoirs.

Dates: 07/2015 – 06/2017

Role: Co-PI

% effort: 2.5%

Collaborators: Amy Mathers, MD; Don Brown, PhD; Jennifer Mason Lobo, PhD; Laura Barnes, PhD, University of Virginia

Amount: \$200,000

Organization: Wallace H. Coulter Foundation – University of Virginia partnership

Project: BMEs GO Pro: a professional development internship program for BME PhD students.

Dates: 07/2015 – 06/2016

Role: PI

% effort: 0%

Amount: \$32,900

Organization: Wallace H. Coulter Foundation – University of Virginia partnership

Project: Metabolism of Microbial Persister Cells.

Dates: 04/2015 – 04/2018

Role: PI

% effort: 8%

Amount: \$580,363

Organization: Unilever, Inc.

Project: Tissue-specific metabolic networks for toxicology predictions.

Dates: 02/2014 – 02/2019

Role: PI

% effort: 20%

Collaborators: Shayn Peirce-Cottler, PhD, University of Virginia; Salman Khetani, PhD, Colorado State University; Ping Li, PhD, and Anders Wallqvist, PhD, DoD Biotechnology HPC Software Applications Institute (BHSI)

Amount: \$1.25 million

Organization: Department of Defense

Grant Number: W81XWH-14-C-0054

Project: R01: Mapping and predicting metabolic fluxes between the ileal microbiome and host.

Dates: 01/2014 – 12/2017

Role: PI

% effort: 20%

Collaborators: Martin Wu, PhD, Glynis Kolling, PhD, Richard Guerrant, MD, University of Virginia; Jonathan Swann, University of Reading (UK)

Amount: \$1.4 million

Organization: National Institutes of Health, NIGMS

Grant Number: GM108501

PAST FUNDING

Project: Harnessing systems biology to tackle drug resistance.

Dates: 4/2014 – 3/2016

Role: PI

% effort: 0%

Amount: \$50,000

Organization: Distinguished Career Development Award, U. Virginia Vice President of Research

Project: R01: Network analysis of pathogenicity in *Pseudomonas aeruginosa*

Dates: 08/2010 – 06/2015 (no cost extension to 12/31/2015)

Role: PI

% effort: 35%

Collaborator: Joanna Goldberg, PhD, University of Virginia

Amount: \$1.4 million

Organization: National Institutes of Health, NIGMS

Grant Number: GM088244

Project: Development of a gene-signature-based prognostic test for pancreatic cancer

Dates: 12/2013 – 11/2014

Role: Co-PI

% effort: 2.4%

Collaborators: Todd Bauer, MD; J. Thomas Parsons, PhD; Jae Lee, PhD, University of Virginia

Amount: \$100,000

Organization: Ivy Foundation; University of Virginia

Project: Profiling antibiotic resistance and microbial growth with a novel plate reader

Dates: 07/2013 – 08/2015

Role: PI (with Erik Hewlett, MD, University of Virginia)

% effort: 10%

Amount: \$150,000

Organization: Wallace H. Coulter Foundation – University of Virginia partnership

Project: Mapping and predicting metabolic fluxes in the gut microbiome.

Dates: 06/2013 – 05/2014

Role: PI

% effort: 0%

Collaborators: Martin Wu, PhD, Glynis Kolling, PhD, Richard Guerrant, MD, University of Virginia

Amount: \$50,000

Organization: University of Virginia, Vice President of Research

Project: Integrated analysis of cellular responses to toxins from *Clostridium difficile*.

Dates: 03/2009 – 02/2014

Role: Faculty

% effort: 10%

Collaborator: PI - Erik Hewlett, MD, University of Virginia

Amount: \$1.1 million (~\$250,000 under supervision of J.A. Papin)

Organization: National Institutes of Health – MARCE-2 (PI: M.M. Levine, U. Maryland)

Project: Systems analysis of *Burkholderia cenocepacia* in polymicrobial disease.

Dates: 04/2010 – 03/2013

Role: PI

% effort: 8%

Collaborator: Joanna Goldberg, PhD, University of Virginia

Amount: \$194,400

Organization: Cystic Fibrosis Foundation

Project: CAREER: Interrogating Pathogen-Host Relationships with Genome-Scale Network Analysis

Dates: 05/2007 – 04/2012

Role: PI

% effort: 5%

Amount: \$400,000

Organization: National Science Foundation

Project: Experimental definition and validation of protein coding transcripts in *Chlamydomonas reinhardtii*

Dates: 09/2007 – 08/2011

Role: PI of subcontract

% effort: 10%

Collaborators: Harvard Medical School, Dana-Farber Cancer Institute – PI – Kourosch Salehi-Ashtiani, PhD; Co-PI – David Hill, PhD; Co-PI – Marc Vidal, PhD

Amount: \$1.4 million (~\$300,000 in subcontract to J. Papin)

Organization: Department of Energy

Project: A Novel Systems Bioengineering Course for Engineering Curricula: Integrating Computational Systems Modeling with High-Throughput Experimentation

Dates: 01/2008 – 12/2010

Role: Co-PI

% effort: 4%

Collaborators: PI – Timothy Allen, PhD, University of Virginia; Co-PI – Shayn Peirce-Cottler, PhD, University of Virginia; Co-PI – Jeffrey Saucerman, PhD, University of Virginia.

Amount: \$150,000

Organization: National Science Foundation

Project: Systems biology approaches for adenoid cystic carcinoma.

Dates: 09/2009 – 12/2011

Role: PI

% effort: 2%

Collaborator: Chris Moskaluk, MD, PhD, University of Virginia

Amount: \$82,500

Organization: Adenoid Cystic Carcinoma Research Foundation

Project: *Research Experience for Undergraduates (REU) Supplement*. CAREER: Interrogating Pathogen-Host Relationships with Genome-Scale Network Analysis

Dates: 05/2010 – 08/2010

Role: PI

% effort: 0%

Amount: \$10,000

Organization: National Science Foundation

Project: Quantitative Unbiased Immunohistochemical Signaling Pathway Analysis (QUISPA): Development and Application to Therapy-Directed Classification of Malignant Gliomas

Dates: 04/2006 – 12/2009

Role: Co-PI

% effort: 10%

Collaborators: Co-PI – James Mandell, MD, PhD, University of Virginia; Consultant – David Schiff, MD, University of Virginia

Amount: \$170,000

Organization: Wallace H. Coulter Foundation – University of Virginia partnership

Project: Application of Immunohistochemical Signaling Network Analysis Platform (I-SNAP) to Multiple Cancer Types

Dates: 04/2007 – 12/2008

Role: Co-PI

% effort: 0%

Collaborators: Co-PI – James Mandell, MD, PhD, University of Virginia

Amount: \$50,000

Organization: Rebecca T. and James P. Craig Foundation and from the University of Virginia Cancer Center
NCI P30 CA44570