

# Curriculum Vitae

Frederick P. (Fritz) Roth, PhD

Titles: Professor, University of Toronto  
Donnelly Centre for Cellular & Biomolecular Research  
Department of Molecular Genetics  
Department of Computer Science

Senior Scientist, Mt. Sinai Hospital  
Lunenfeld-Tanenbaum Research Institute

Addresses: Donnelly Centre, University of Toronto  
160 College Street  
Toronto, Ontario, M5S 3E1, Canada

Lunenfeld-Tanenbaum Research Institute, Mt. Sinai Hospital  
600 University Avenue, 9th Floor  
Toronto, Ontario, M5G 1X5, Canada

Email : [fritz.roth@utoronto.ca](mailto:fritz.roth@utoronto.ca) Phone: 416-946-5130  
Web : <http://llama.mshri.on.ca/>

Education: BA, Physics and Molecular & Cell Biology, Univ. of California, Berkeley, 1990  
PhD, Biophysics, Harvard University, 1998

Honors: 1993 – 1996 National Science Foundation Graduate Fellowship  
2008 – present Senior Fellow, Canadian Institute for Advanced Research  
2011 – 2017 Canada Excellence Research Chair

Employment:

Summer 1987 Research Assistant, Fly's Eye Cosmic Ray Facility, Physics Dept., U of Utah.

1987 – 1990 Research Assistant, Space Sciences Lab, Berkeley, CA (w/ Dr. Kevin Hurley).

Summer 1989 Research Assistant, U. Calif. Berkeley, Mol. Cell Biol. Dept. (w/ Dr. Jasper Rine).

Summer 1990 Research Fellow, Scripps Inst. of Oceanography, (w/ Dr. Adrianus Kalmijn).

1991 – 1992 Staff Scientist, Operon Technologies, Inc.

1992 – 1998 Graduate Student, Harvard University Program in Biophysics,  
Advisor – Dr. George Church

1998 – 2000 Scientist, Millennium Pharmaceuticals Inc (w/ Dr. Chris Sander).

2000 – 2007 Assistant Professor, Harvard Medical School,  
Department of Biological Chemistry and Molecular Pharmacology

2007 – 2011 Associate Professor, Harvard Medical School,  
Department of Biological Chemistry and Molecular Pharmacology

2011 – 2013 Lecturer, Harvard Medical School,  
Department of Biological Chemistry and Molecular Pharmacology

Frederick P. (Fritz) Roth, PhD

- 2015 – present Co-Director, Genetic Networks Program, Canadian Institute for Advanced Research
- 2011 – present Senior Scientist, Lunenfeld-Tanenbaum Research Institute of Mt. Sinai Hospital, Toronto, ON
- 2011 – present Professor, Donnelly Centre for Cellular and Biomolecular Research, University of Toronto, Toronto ON

Institutional and Program Affiliations:

- 2000 – 2011 Faculty Affiliate, Harvard Graduate Program in Biophysics
- 2000 – 2011 Faculty Affiliate, Biological and Biomedical Science Graduate Program, Harvard Medical School
- 2005 – 2011 Tutor, Harvard Undergraduate Concentration in the Biochemical Sciences
- 2006 – present Member, Center for Cancer Systems Biology, Dana-Farber Cancer Institute
- 2011 – present Cross-appointed to the Dept. of Molecular Genetics, University of Toronto
- 2011 – present Cross-appointed to the Dept. of Computer Science, University of Toronto

Selected Committee Roles:

- 2003 – 2008 Admissions Committee, Harvard Program in Biophysics
- 2006 – 2011 Joint Committee of the Harvard Countway & Boston Medical Libraries
- 2013 – present Donnelly Centre Promotions Committee
- 2014 – present Department of Molecular Genetics Examination Committee

Editorial and Review Experience:

- 2001 – 2004 Associate Editor, **Bioinformatics**
- 2010 – 2013 Associate Editor, **PLoS Computational Biology**
- 2011 – 2015 Associate Editor, **G3: Genes | Genomes | Genetics**
- 2017 – present Advisory Editorial Board Member, **Molecular Systems Biology**
- 2014 – present Member, NIH Genomics, Computational Biology and Technology Study Section
- 2016 – present Chair, NIH , Genomics, Computational Biology and Technology Study Section
- 2017 Member, Canadian Institutes of Health Research Project Review Committee

Teaching Contributions:

- 2000 – 2003 Organizer, Harvard Medical School, Pharmacological Sciences Seminar Series
- 2001 Lecturer, Harvard School of Public Health, Biostatistics 277: Fundamentals of Computational Biology
- 2003 Co-founder & Lecturer, Harvard Medical School, BCMP 370: Computational Genomic Methods for Predicting Gene Function
- 2004 Instructor, Harvard Medical School, MedSci 300: Conduct of Science
- 2005, 2006 Lecturer, Harvard School of Public Health, Biostatistics 280/281: Introduction to Computational Molecular Biology

Frederick P. (Fritz) Roth, PhD

2001 – 2009	Lecturer, Harvard Medical School, BCMP 201: Proteins: Structure, Function and Catalysis
2004 – 2010	Co-founder & Lecturer, Harvard Medical School, Biophysics 205: Computational and Experimental Functional Genomics
2007 – 2009	Lecturer, Neurobiology 300. Tools for Statistical Inference in Experimental Science
2007 – 2009	Lecturer, Harvard Medical School, BCMP 207: Molecular Approaches to Drug Action, Discovery and Design
2008 – 2010	Lecturer, Harvard Medical School, Microbiology 230: Analysis of the Biological Literature.
2011 – 2012	Lecturer, University of Toronto, Topic Course on Functional Genomics & Proteomics: Experimental Approaches
2012	Lecturer, University of Toronto, JTB2010H: Proteomics and Functional Genomics
2013	Co-instructor, University of Toronto, Topic Course on Functional Genomics & Proteomics: Computational Approaches
2013 – 2015	Co-founder & Course Coordinator, MGY360H1: Whole-Genome Sequencing and Analysis Laboratory
2016- present	Co-founder & Head, Computational Biology in Molecular Genetics (CBMG) Track within the Molecular Genetics Graduate Program
2017- present	Founding Co-Instructor, Computational Biology and Bioinformatics (12-week graduate course MMG1012).

Selected Organizational Roles:

2007	Organizer, Special Session on Genetic Interactions, 15 <sup>th</sup> Annual Intelligent Systems for Molecular Biology (ISMB) & 6 <sup>th</sup> European Conference on Computational Biology (ECCB), Austria, Vienna
2008	Co-organizer, Theme on Systems Biology, Experimental Biology 2008 (ASBMB). San Diego, CA Co-organizer, 2nd Annual Conference in Quantitative Genomics: Emerging Quantitative Issues in Parallel Sequencing (EQuIP-Seq), Boston, MA Co-organizer, Session on Model-driven experiment planning, 9th International Conference on Systems Biology, Gothenburg, Sweden
2011 – 2012	Organizing Committee, International Conference on Systems Biology (ICSB) 2012, Toronto, ON
2012 – 2014	Associate Director, Canadian Institute for Advanced Research (CIFAR) Genetic Networks Program.
2014 – present	Co-Director, CIFAR Genetic Networks Program

Peer-Reviewed Publications:

1. *FP Roth\**, JD Hughes\*, PW Estep & GM Church†. Finding DNA regulatory motifs within unaligned noncoding sequences clustered by whole-genome mRNA quantitation. **Nature Biotechnology**, 16: 939-945 (1998).

2. M Damelin, I Simon, TI Moy, B Wilson, S Komili, P Tempst, *FP Roth*, RA Young, BR Cairns & PA Silver†. The Genome-Wide Localization of Rsc9, a Component of the RSC Chromatin-Remodeling Complex, Changes in Response to Stress. **Molecular Cell** 9:563-573 (2002).
3. FD Gibbons & *FP Roth*†. Judging the quality of gene expression-based clustering methods using gene annotation. **Genome Research** 12(10):1574-81 (2002).
4. OD King, RE Foulger, SS Dwight, JV White & *FP Roth*†. Predicting gene function from patterns of annotation. **Genome Research**, 13(5):896-904 (2003).
5. GF Berriz, JV White, OD King & *FP Roth*†. GoFish finds genes with combinations of Gene Ontology attributes. **Bioinformatics** 19(6):788-789 (2003).
6. JR Roth†, E Kofoid, *FP Roth*, OG Berg, J Seger & DI Andersson. Regulating general mutation rates: Examination of the hypermutable state model for Cairnsian adaptive mutation. **Genetics** 163(4):1483-1496 (2003).
7. DS Goldberg & *FP Roth*†. Assessing experimentally derived interactions in a small world. **Proceedings of the National Academy of Sciences** 100(8): 4372-4376 (2003).
8. OD King, JC Lee, AM Dudley, DM Janse, GM Church & *FP Roth*†. Predicting phenotype from patterns of annotation. **Bioinformatics** (Intelligent Systems in Molecular Biology Issue) 19: Suppl 1:I183-I189 (2003).
9. MF Kramer, WJ Cook, *FP Roth*, J Zhu, H Holman, DM Knipe† & DM Coen†. Latent herpes simplex virus infection of sensory neurons alters neuronal gene expression. **Journal of Virology** 77(17):9533-9541 (2003).
10. OD King† & *FP Roth*. A nonparametric model for transcription factor binding sites. **Nucleic Acids Research** 31(19):e116 (2003).
11. GF Berriz, OD King, B Bryant, C Sander & *FP Roth*†. Characterizing gene sets with FuncAssociate. **Bioinformatics** 19(18):2502-2504 (2003).
12. JR Roth†, E Kofoid, *FP Roth*, OG Berg, J Seger & DI Andersson. Adaptive mutation requires no mutagenesis—only growth under selection: A response. **Genetics** 165(4): 2319-2321 (2003).
13. S Li\*, CM Armstrong\*, N Bertin\*, H Ge\*, S Milstein\*, M Boxem\*, P-O Vidalain\*, J-DJ Han\*, A Chesneau\*, T Hao, DS Goldberg, N Li, M Martinez, J-F Rual, P Lamesch, L Xu, M Tewari, SL Wong, LV Zhang, GF Berriz, L Jacotot, P Vaglio, J Reboul, T Hirozane-Kishikawa, Q Li, HW Gabel, A Elewa, B Baumgartner, DJ Rose, H Yu, S Bosak, R Sequerra, A Fraser, SE Mango, WM Saxton, S Strome, S van den Heuvel, F Piano, J Vandenhaute, C Sardet, M Gerstein, L Doucette-Stamm, KC Gunsalus, JW Harper, ME Cusick, *FP Roth*, DE Hill & M Vidal†. A map of the interactome network of the metazoan *C. elegans*. **Science** 303(5657):540-543 (2004).
14. JE Elias, FD Gibbons, OD King, *FP Roth*\*† & SP Gygi\*. Intensity-based protein identification by machine learning from a library of tandem mass spectra. **Nature Biotechnology** 22(2):214-9. (2004).
15. AHY Tong\*, G Lesage\*, GD Bader, H Ding, H Xu, X Xin, J Young, GF Berriz, RL Brost, M Chang, Y Chen, X Cheng, G Chua, H Friesen, DS Goldberg, J Haynes, C Humphries, G He, S Hussein, L Ke, N Krogan, Z Li, JN Levinson, H Lu, P Ménard, C Munyana, AB Parsons, O Ryan, R Tonikian, T Roberts, A-M Sdicu, J Shapiro, B Sheikh, B Suter, SL Wong, LV Zhang, H Zhu, CG Burd, S Munro, C Sander, J Rine, J Greenblatt, M Peter, A Bretscher, G Bell, *FP Roth*, GW Brown, B Andrews†, H Bussey† & C Boone†. Global mapping of the yeast genetic interaction network. **Science** 303: 808-813. (2004).

16. LV Zhang, SL Wong, OD King & *FP Roth*<sup>†</sup>. Predicting co-complexed protein pairs using genomic and proteomic data integration. **BMC Bioinformatics** 5: 38 (2004).
17. FD Gibbons, JE Elias, SP Gygi & *FP Roth*<sup>†</sup>. SILVER helps assign peptides to tandem mass spectra using intensity-based scoring. **Journal of the American Society for Mass Spectrometry** 15(6):910-912 (2004).
18. S Asthana, OD King, FD Gibbons & *FP Roth*<sup>†</sup>. Predicting protein complex membership using probabilistic network reliability. **Genome Research** 14(6):1170-1175 (2004).
19. J-DJ Han, N Bertin, T Hao, DS Goldberg, GF Berriz, LV Zhang, D Dupuy, AJM Walhout, ME Cusick, *FP Roth* & M Vidal<sup>†</sup>. Evidence for dynamically organized modularity in the yeast protein-protein interaction network. **Nature** 430(6995):88-93 (2004).
20. YH Grad, *FP Roth*, MS Halfon & GM Church<sup>†</sup>. Prediction of similarly-acting cis-regulatory modules by subsequence profiling and comparative genomics in *D. melanogaster* and *D. pseudoobscura*. **Bioinformatics** 20(16):2738-2750 (2004).
21. SL Wong, LV Zhang, AHY Tong, Z Li, DS Goldberg, OD King, G Lesage, M Vidal, B Andrews, H Bussey, C Boone & *FP Roth*<sup>†</sup>. Combining biological networks to predict genetic interactions. **Proceedings of the National Academy of Sciences** 101(44): 15682-15687 (2004).
22. LV Zhang, OD King, SL Wong, DS Goldberg, AHY Tong, G Lesage, B Andrews, H Bussey, C Boone & *FP Roth*<sup>†</sup>. Motifs, themes and thematic maps of an integrated *S. cerevisiae* network. **Journal of Biology** 4:6 (2005).
23. SL Wong, LV Zhang & *FP Roth*<sup>†</sup>. Discovering functional relationships: biochemistry versus genetics. **Trends in Genetics** 21(8): 424-427 (2005).
24. KC Gunsalus\*, H Ge\*, AJ Schetter\*, DS Goldberg\*, J-DJ Han, T Hao, N Bertin, N Li, J Huang, L-S Chuang, R Mani, GF Berriz, AA Hyman, B Sönnichsen, CJ Echeverri, *FP Roth*<sup>†</sup>, M Vidal<sup>†</sup> & F Piano<sup>†</sup>. Predictive models of molecular machines involved in *C. elegans* early embryogenesis. **Nature** 436(7052):861-865 (2005).
25. MH Proft, FD Gibbons, M Copeland, *FP Roth* & K Struhl<sup>†</sup>. Genome-wide identification of Sko1 target promoters reveals a regulatory network operated upon osmotic stress in *Saccharomyces cerevisiae*. **Eukaryotic Cell** 4(8):1343-1352 (2005).
26. J-F Rual\*, K Venkatesan\*, T Hao, T Hirozane-Kishikawa, A Dricot, N Li, GF Berriz, FD Gibbons, M Dreze, N Ayivi-Guedehoussou, N Klitgörd, C Simon, M Boxem, S Milstein, J Rosenberg, DS Goldberg, LV Zhang, SL Wong, G Franklin, S Li, JS Albalá, J Lim, C Fraughton, E Llamas, S Cevik, C Bex, P Lamesch, RS Sikorski, J Vandenhoute, HY Zoghbi, A Smolyar, S Bosak, R Sequerra, L Doucette-Stamm, ME Cusick, DE Hill<sup>†</sup>, *FP Roth*<sup>†</sup> & M Vidal<sup>†</sup>. A proteome-scale map of the human interactome network. **Nature** 437:1173-1178 (2005).
27. FD Gibbons, MH Proft, K Struhl & *FP Roth*<sup>†</sup>. Chipper: discovering transcription-factor targets from chromatin immunoprecipitation microarrays using variance stabilization. **Genome Biology** 6(11):R96 (2005).
28. SL Wong & *FP Roth*<sup>†</sup>. Transcriptional compensation for gene loss plays a minor role in maintaining genetic robustness in *Saccharomyces cerevisiae*. **Genetics** 171(2):829-833 (2005).
29. MS Sabatine, E Liu, DA Morrow, E Heller, M Askenazi, R McCarroll, R Weigand, G Berriz, *FP Roth* & RE Gerszten<sup>†</sup>. Metabolomic identification of novel biomarkers of myocardial ischemia. **Circulation** 112(25):3868-3875 Dec 12 (2005).

30. JD Klekota<sup>†</sup>, E Brauner, *FP Roth*<sup>†</sup> & SL Schreiber. Using high-throughput screening data to discriminate compounds with single-target effects from those with side effects. **Journal of Chemical Information and Modeling** 46:1549-1562 (2006).
31. JD Klekota<sup>†</sup>, *FP Roth* & SL Schreiber. Query Chem: A Google-Powered Web Search Combining Text and Chemical Structures. **Bioinformatics** 22(13):1670-1673 (2006).
32. A Derti, *FP Roth*, GM Church & C-T Wu<sup>†</sup>. Mammalian ultraconserved elements are strongly depleted among segmental duplications and copy number variants. **Nature Genetics** 38(10):1216-1220 (2006).
33. RP St.Onge, R Mani, J Oh, M Proctor, E Fung, R Davis, C Nislow, *FP Roth*<sup>†</sup> & G Giaever<sup>†</sup>. Systematic pathway analysis using high-resolution fitness profiling of combinatorial gene deletions. **Nature Genetics** 39(2):199-206 (2007).
34. N Bertin\*, N Simonis\*, D Dupuy\*, ME Cusick, J-DJ Han, HB Fraser<sup>†</sup>, *FP Roth*<sup>†</sup> & M Vidal<sup>†</sup>. Confirmation of organized modularity in the yeast interactome. **PLoS Biology** 5(6) e153 (2007).
35. D Dupuy\*, N Bertin\*, CA Hidalgo R\*, K Venkatesan, D Tu, D Lee, J Rosenberg, N Svrzikapa, A Blanc, A Carnec, A-R Carvunis, R Pulak, J Shingles, J Reece-Hoyes, R Hunt-Newbury, R Viveiros, WA Mohler, M Tasan, *FP Roth*, C Le Peuch, IA Hope, R Johnsen, DG Moerman, A-L Barabási<sup>†</sup>, D Baillie<sup>†</sup> & M Vidal<sup>†</sup>. Genome-scale analysis of *in vivo* spatiotemporal promoter activity in *C. elegans*. **Nature Biotechnology** 25(6):663-668. (2007).
36. H Huang, LV Zhang, *FP Roth* & JS Bader<sup>†</sup>. Probabilistic paths in protein interaction networks. **Proceedings of the RECOMB Conferences on Systems Biology and Computational Proteomics** (2007).
37. S Komili, N Gilks, *FP Roth*<sup>†</sup> & PA Silver<sup>†</sup>. Functional specificity among ribosomal proteins regulates gene expression. **Cell** 131:557-571 (2007).
38. R Mani, RP St. Onge, J Hartman, G Giaever, *FP Roth*<sup>†</sup>. Defining genetic interaction. **Proceedings of the National Academy of Sciences** 105(9):3461-3466 (2008).
39. K Salehi-Ashtiani<sup>†</sup>, X Yang, A Derti, W Tian, T Hao, C Lin, K Makowski, L Shen, RR Murray, D Szeto, N Tusneem, DR Smith, ME Cusick, DE Hill, *FP Roth*<sup>†</sup>, M Vidal<sup>†</sup>. Large-scale coding isoform discovery using targeted cloning, “deep well” pooling, and parallel sequencing. **Nature Methods** 5(7):597-600 (2008).
40. L Peña-Castillo, M Taşan, CL Myers, H Lee, T Joshi, C Zhang, Y Guan, M Leone, A Pagnani, WK Kim, C Krumpelman, W Tian, G Obozinski, Y Qi, S Mostafavi, GN Lin, GF Berriz, FD Gibbons, G Lanckriet, J Qiu, C Grant, Z Barutcuoglu, DP Hill, D Warde-Farley, C Grouios, D Ray, JA Blake, M Deng, M Jordan, WS Noble, Q Morris, J Klein-Seetharaman, Z Bar-Joseph, T Chen, F Sun, OG Troyanskaya, EM Marcotte, D Xu, TR Hughes<sup>†</sup> & *FP Roth*<sup>†</sup>. A critical assessment of *M. musculus* gene function prediction using integrated genomic evidence. **Genome Biology** 9 Suppl 1:S2 (2008).
41. W Tian, LV Zhang, M Taşan, FD Gibbons, OD King, J Park, Z Wunderlich, JM Cherry, *FP Roth*<sup>†</sup>. Combining guilt-by-association and guilt-by-profiling to predict *Saccharomyces cerevisiae* gene function. **Genome Biology** 9 Suppl 1:S7 (2008).
42. M Taşan\*, W Tian\*, DP Hill, FD Gibbons, JA Blake & *FP Roth*<sup>†</sup>. An *en masse* phenotype and function prediction system for *M. musculus*. **Genome Biology** 9 Suppl 1:S8 (2008).
43. M Boxem, Z Maliga, N Klitgord, N Li, I Lemmens, M Mana, L de Lichtervelde, J Mul, D van de Peut, M Devos, N Simonis, MA Yildirim, M Cokol, H-L Kao, H Wang, A-S de Smet, A-L Schläitz, T Hao, S Milstein, C Fan, M Tipsword, K Drew, M Galli, K Rhrissorrakrai, D Drechsel, D Koller, *FP Roth*, LM Iakoucheva, K Dunker, R Bonneau, KC Gunsalus, DE Hill, F Piano, J Tavernier, S van den Heuvel, AA Hyman, M Vidal<sup>†</sup>. A protein domain-based interactome network for *C. elegans* early embryogenesis. **Cell** 134(3):534-545 (2008).

44. NJ Martinez, MC Ow, MI Barrasa, M Hammell, R Sequerra, L Doucette-Stamm, *FP Roth*, V Ambros, AJM Walhout†. Transcription factors and microRNAs function in composite feedback loops in *C. elegans* gene regulatory networks. **Genes & Development** 22(18):2535-49 (2008).
45. GF Berriz & *FP Roth*†. The Synergizer service for translating gene, protein, and other biological identifiers. **Bioinformatics** 24(19):2272-3 (2008).
46. H Yu\*, P Braun\*, MA Yildirim\*, I Lemmens, K Venkatesan, J Sahalie, T Hirozane-Kishikawa, F Gebreab, N Li, N Simonis, T Hao, JF Rual, A Dricot, A Vazquez, RR Murray, C Simon, L Tardivo, S Tam, N Svzikapa, C Fan, AS de Smet, A Motyl, ME Hudson, J Park, X Xin, ME Cusick, T Moore, C Boone, M Snyder, *FP Roth*, AL Barabasi, J Tavernier, DE Hill, M Vidal†. High-quality binary protein interaction map of the yeast interactome network. **Science** 322(5898):104-10 (2008).
47. GD Lewis, R Wei, E Liu, E Yang, X Shi, M Martinovic, L Farrell, A Asnani, M Cyrille, A Ramanathan, O Shaham, GF Berriz, PA Lowry, IF Palacios, M Taşan, *FP Roth*, J Min, C Baumgartner, H Keshishian, T Addona, VK Mootha, A Rosenzweig, SA Carr, MA Fifer, MS Sabatine and RE Gerszten†. Metabolite profiling of blood from individuals undergoing planned heart attack reveals early markers of human myocardial infarction. **Journal of Clinical Investigation** 118(10):3503-3512 (2008).
48. JD Klekota & *FP Roth*†. Chemical substructures that predict biological activity: Exposing the rules of privilege. **Bioinformatics** 24(21):2518-2525 (2008).
49. ME Cusick, A Smolyar, K Venkatesan, J-F Rual, H Yu, H Borick, *FP Roth*, M Vidal†. Literature-curated protein interaction datasets. **Nature Methods** 6(1):39-46 (2009).
50. N Simonis\*, J-F Rual\*, A-R Carvunis\*, M Taşan\*, I Lemmens\*, T Hirozane-Kishikawa, T Hao, JM Sahalie, F Gebreab, S Cevik, N Klitgord, K Venkatesan, C Fan, P Braun, N Li, N Ayivi-Guedehoussou, E Dann, N Bertin, D Szeto, A Dricot, MA Yildirim, C Lin, A-S de Smet, H-L Kao, C Simon, A Smolyar, JS Ahn, M Tewari, M Boxem, S Milstein, H Yu, M Dreze, J Vandenhoute, KC Gunsalus, ME Cusick, DE Hill†, J Tavernier†, *FP Roth*† & Marc Vidal†. Empirically-controlled mapping of the *Caenorhabditis elegans* protein-protein interactome network. **Nature Methods** 6(1):47-54 (2009).
51. K Venkatesan\*, J-F Rual\*, A Vazquez\*, U Stelzl\*, I Lemmens\*, T Hirozane-Kishikawa, T Hao, M Zenkner, X Xin, K-I Goh, MA Yildirim, N Simonis, K Heinzmann, F Gebreab, JM Sahalie, S Cevik, C Simon, A-S de Smet, E Dann, A Smolyar, A Vinayagam, H Yu, D Szeto, H Borick, A Dricot, N Klitgord, RR Murray, C Lin, M Lalowski, J Timm, K Rau, C Boone, P Braun, ME Cusick, *FP Roth*, DE Hill, J Tavernier†, EE Wankert†, A-L Barabási† & M Vidal†. An empirical framework for binary interactome mapping. **Nature Methods** 6(1):83-90 (2009).
52. P Braun\*†, M Taşan\*, M Dreze\*, M Barrios-Rodiles, I Lemmens, H Yu, JM Sahalie, RR Murray, L Roncari, A-S de Smet, K Venkatesan, J-F Rual, ME Cusick, T Pawson, DE Hill, J Tavernier†, JL Wrana†, *FP Roth*† & M Vidal†. An experimentally derived confidence score for binary protein-protein interactions. **Nature Methods** 6(1):91-97 (2009).
53. AM Smith, LE Heisler, J Mellor, F Kaper, MJ Thompson, M Chee, *FP Roth*, G Giaever†, C Nislow†. Quantitative phenotyping via deep barcode sequencing. **Genome Research** 19(10):1836-1842 (2009).
54. GF Berriz, JE Beaver, C Cenik, M Taşan & *FP Roth*†. Next generation software for functional trend analysis. **Bioinformatics** 25(22):3043-3044 (2009).
55. K Salehi-Ashtiani\*†, C Lin\*, T Hao\*, Y Shen, D Szeto, X Yang, L Ghamsari, H Lee, C Fan, RR Murray, S Milstein, N Svzikapa, ME Cusick, *FP Roth*, DE Hill & Marc Vidal†. Large-scale RACE approach for proactive experimental definition of *C. elegans* ORFeome. **Genome Research** 19(12):2334-42 (2009).
56. M Costanzo\*, A Baryshnikova\*, J Bellay, Y Kim, ED Spear, CS Sevier, H Ding, JLY Koh, K Toufighi, S Mostafavi, J Prinz, RP StOnge, B VanderSluis, T Makhnevych, FJ Vizeacoumar, S Alizadeh, S Bahr, RL Brost, Y Chen, M Cokol, R Deshpande, Z Li, Z-Y Lin, W Liang, M Marback, J Paw, B-J San Luis, E Shuteriqi, AHY Tong, N van Dyk, IM Wallace, JA Whitney,

- MT Weirauch, G Zhong, H Zhu, WA Houry, M Brudno, S Ragibizadeh, B Papp, C Pál, *FP Roth*, G Giaever, C Nislow, OG Troyanskaya, H Bussey, GD Bader, A-C Gingras, QD Morris, PM Kim, CA Kaiser, CL Myers†, BJ Andrews†, C Boone†. The Genetic Landscape of a Cell. **Science** 327:425-431 (2010).
57. RC Deo, L Hunter, MS Sabatine, GD Lewis, RS Vasan, TJ Wang, RE Gerszten & *FP Roth*†. Interpreting metabolomic profiles using unbiased pathway models. **PLoS Computational Biology** 6(2):e1000692 (2010).
58. I Jurak, MF Kramer, JC Mellor, AL van Lint, *FP Roth*, DM Knipe, DM Coen†. Numerous conserved and divergent microRNAs expressed by Herpes Simplex Viruses 1 and 2. **J. Virology** 84(9):4659-72 (2010).
59. C Cenik, A Derti, JC Mellor, GF Berriz & *FP Roth*†. Genome-wide functional analysis of human 5' untranslated region introns. **Genome Biology** 11(3):R29 (2010).
60. A Derti, C Cenik, P Kraft, *FP Roth*†. Absence of evidence for MHC-dependent mate selection within HapMap populations. **PLoS Genetics** 6(4):e1000925 (2010).
61. E Kugelberg†, E Kofoid, DI Andersson, Y Lu, J Mellor, *FP Roth*, JR Roth. The tandem inversion-duplication (TID): Selection can stabilize mutations that are common under all conditions. **Genetics** 185(1):65-80. (2010).
62. H Yan, K Venkatesan, JE Beaver, N Klitgord, MA Yildirim, T Hao, DE Hill, ME Cusick, N Perrimon, *FP Roth*†, M Vidal†. Genome-wide gene function prediction resource for *Drosophila melanogaster*. **PLoS One** 5(8) pii: e12139 (2010).
63. GD Lewis, L Farrell, A Souza, E Yang, M Martinovic, X Shi, R Deo, *FP Roth*, A Asnani, DM Systrom, MJ Semigran, MJ Wood, SA Carr, MS Sabatine, CB Clish & RE Gerszten†. Metabolic Signatures of Human Exercise Performance. **Science Translational Medicine** 2(33):33ra37 (2010).
64. JE Beaver, M Tasan, F Gibbons, W Tian, TR Hughes & *FP Roth*†. FuncBase: A resource for quantitative gene function annotation. **Bioinformatics** 26(14):1806-7 (2010).
65. CF Sephton, C Cenik, A Kucukural, E Dammer, B Cenik, Y-H Han, C Dewey, *FP Roth*, J Herz, J Peng, M Moore & G Yu†. Identification of neuronal RNA targets of TDP-43-containing ribonucleoprotein complexes. **Journal of Biological Chemistry** 286(2):1204-15 (2011).
66. Y Suzuki, RP St. Onge, R Mani, OD King, A Heilbut, VM Labunskyy, W Chen, L Pham, LV Zhang, AHY Tong, C Nislow, G Giaever, VN Gladyshev, M Vidal, P Schow, J Lehár & *FP Roth*†. Knocking out multi-gene redundancies via cycles of sexual assortment and fluorescence selection. **Nature Methods** 8(2):159-64 (2011).
67. K Suk, J Choi, Y Suzuki, S Ozturk, J Mellor, KJ Wong, RI Gregory, *FP Roth*†. Reconstitution of human RNA interference in budding yeast. **Nucleic Acids Research** 39(7):e43 (2011).
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\*contributed equally †corresponding author ‡co-senior author

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