Curriculum Vitae

Frederick P. (Fritz) Roth, PhD

Titles: Professor, University of Toronto
Donnelly Centre for Cellular & Biomolecular Research
Department of Molecular Genetics
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Citizenship: Dual US and Canadian

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

Honors:

2011 – 2017	Canada Excellence Research Chair
2008 – 2020	Senior Fellow, Canadian Institute for Advanced Research
1993 – 1996	National Science Foundation Graduate Fellowship

Employment:

2011 – present	Professor, Donnelly Centre for Cellular and Biomolecular Research, University of Toronto, Toronto ON
2011 – present	Senior Investigator, Lunenfeld-Tanenbaum Research Institute of Mt. Sinai Hospital, Toronto, ON
2014 – 2020	Co-Director, Genetic Networks Program, Canadian Institute for Advanced Research (CIFAR)
2012 – 2014	Associate Director, Genetic Networks Program, Canadian Institute for Advanced Research (CIFAR)
2007 – 2010	Associate Professor, Harvard Medical School, Department of Biological Chemistry and Molecular Pharmacology
2000 – 2007	Assistant Professor, Harvard Medical School, Department of Biological Chemistry and Molecular Pharmacology
1998 – 2000	Scientist, Millennium Pharmaceuticals Inc (w/ Dr. Chris Sander).
1992 – 1998	Graduate Student, Harvard University Program in Biophysics, (w/ Dr. George Church).
1991 – 1992	Staff Scientist, Operon Technologies, Inc.
Summer 1990	Research Fellow, Scripps Inst. of Oceanography, (w/ Dr. Adrianus Kalmijn).
Summer 1989	Research Assistant, UC Berkeley, Mol. Cell Biol. Dept. (w/ Dr. Jasper Rine).
1987 – 1990	Research Assistant, Space Sciences Lab, Berkeley, CA (w/ Dr. Kevin Hurley).
Summer 1987	Research Assistant, Fly's Eye Cosmic Ray Facility, Physics Dept., U. of Utah.

Academic Institutional Roles

2020 – present	Executive Committee, Atlas of Variant Effects Alliance
2020 – 2022	Director, Computational Biology in Molecular Genetics (CBMG) Track within the Molecular Genetics Graduate Program
2019 – present	Scientific Advisory Board, Mouse Genome Database, Jackson Laboratory, Bar Harbor, ME
2018 – 2019	Faculty of Medicine Decanal Promotions Committee
2017 – present	Department of Molecular Genetics Admissions Committee
2016	Co-founder, Computational Biology in Molecular Genetics (CBMG) Track within the Molecular Genetics Graduate Program
2014 – present	Department of Molecular Genetics Examination Committee
2013 – 2017	Donnelly Centre Promotions Committee
2011 – present	Cross-appointed to the Dept. of Computer Science, University of Toronto
2011 – present	Cross-appointed to the Dept. of Molecular Genetics, University of Toronto
2006 – present	Member, Center for Cancer Systems Biology, Dana-Farber Cancer Institute
2006 – 2011	Member, Joint Committee of the Harvard Countway & Boston Medical Libraries
2005 – 2011	Tutor, Harvard Undergraduate Concentration in the Biochemical Sciences
2003 – 2008	Admissions Committee, Harvard Program in Biophysics
2000 – 2011	Faculty, Biological & Biomedical Sciences Grad Program, Harvard Med School
2000 – 2011	Faculty, Harvard Graduate Program in Biophysics

Industry Roles

2021 – present	Strategic Advisory Board Member, BioSymetrics, Inc.
2021 – present	Scientific Advisory Board Member, Constantiam Biosciences, Inc.
2015 – present	Scientific Advisory Board Member, SeqWell, Inc.
2015 – 2017	Scientific Advisory Board Member, Ranomics, Inc.

Selected Editorial and Review Experience

2017 – present	Advisory Editorial Board Member, Molecular Systems Biology
2017 – 2019	Chair, NIH Genomics, Computational Biology and Technology Study Section
2014 – 2019	Member, NIH Genomics, Computational Biology and Technology Study Section
2011 – 2015	Associate Editor, G3: Genes|Genomes|Genetics
2010 – 2013	Associate Editor, PLoS Computational Biology
2001 – 2004	Associate Editor, Bioinformatics

Selected Teaching Contributions

2022 – present	Lecturer, MMG3204H: Practical Applications of Genome Interpretation (6-week graduate course)
2022 – present	Lecturer, MMG1001: Foundational Genetics Approaches (12-week graduate course)
2019 – present	Founding Co-Instructor/Co-Coordinator, Foundational Computational Biology I and II (2 6-week graduate topic courses).
2017- 2019	Founding Instructor, Computational Biology and Bioinformatics (12-week graduate course).
2016 – present	Lecturer, MGY360H1: Whole-Genome Sequencing and Analysis Laboratory
2013 – 2015	Co-founder & Course Coordinator, MGY360H1: Whole-Genome Sequencing and Analysis Laboratory
2011 – 2013	Lecturer, University of Toronto, Topic Course on Functional Genomics & Proteomics: Experimental Approaches

2008 – 2010	Lecturer, Harvard Medical School, Microbiology 230: Analysis of the Biological Literature.
2007 – 2009	Lecturer, Harvard Medical School, BCMP 207: Molecular Approaches to Drug Action, Discovery and Design
2007 – 2009	Lecturer, Neurobiology 300. Tools for Statistical Inference in Experimental Science
2004 – 2010	Co-founder & Lecturer, Harvard Medical School, Biophysics 205: Computational and Experimental Functional Genomics
2001 – 2009	Lecturer, Harvard Medical School, BCMP 201: Proteins: Structure, Function and Catalysis

Selected Conference Organizing Roles (within past 5 years)

2023	Organizing Committee, Cold Spring Harbor Laboratories Meeting on Network Biology, New York, United States
2022	Lead Organizer, Mutational Scanning Symposium, Toronto, ON
2020	Program Committee, Yeast Genetics Meeting (YGM) and The Allied Genetics Conference (TAGC).
2020	Organizer, Atlas of Variant Effects Planning Workshop, Seattle, WA

Selected Speaking Roles (international events within past 5 years)

2023	Invited Speaker, Society for Inherited Metabolic Disorders (SIMD), Salt Lake City, UT
2023	Speaker, Quantitative Biology Meeting, Puerto Rico, US
2023	Speaker, Invitae, Inc., San Francisco, CA
2023	Speaker, Genentech, San Francisco, CA
2023	Speaker, Helix, Inc.
2022	Speaker, Ambry Genetics, Inc.
2022	Speaker, NIH/NHGRI Center for Multiplexed Analysis of Phenotypes Retreat
2022	Speaker, BridgeBio Inc.
2022	Invited Speaker, Workshop on Functional Analysis of Sequence Variants in Hereditary Breast and Ovarian Cancer Genes, Leiden, NL
2021	Speaker, Alexion Pharmaceuticals, Inc.
2021	Speaker, Amicus Therapeutics, Inc.
2021	Speaker, Beam Therapeutics, Inc.
2021	Speaker, Dynacure, Inc.,
2021	Seminar Speaker, Boston Children's Hospital, Boston, MA
2021	Invited Speaker, Belgrade Bioinformatics Conference, Belgrade, Croatia
2021	Speaker, NIH/NHGRI Center for Multiplexed Analysis of Phenotypes Retreat
2021	Speaker, Deep Genomics, Inc.
2021	Invited Speaker, NIH/NHGRI&NCATS Meeting on Acidemias and Homocysteinuria
2021	Invited Speaker, Cold Spring Harbor Asia Meeting on Yeast and Life Sciences
2021	Speaker, HTG Therapeutics, Inc.
2021	Speaker, Mutational Scanning Symposium
2021	Seminar Speaker, Weizmann Institute (Rehovot, Israel) [canceled due to pandemic]
2021	Seminar Speaker, Alnylam Pharmaceuticals, Inc. Boston, MA
2020	Speaker, Atlas of Variant Effects Alliance Kickoff Workshop
2020	Speaker, NIH/NHGRI Center for Multiplexed Analysis of Phenotype Retreat
2020	Speaker, U Washington, Seattle Genome Sciences Summer Program Seminar
2020	Keynote speaker, 28th Intelligent Systems in Molecular Biology Variant Interpretation Community of Special Interest (VarI-COSI)

2020 Invited Speaker, Hereditary Breast and Ovarian Cancer Variants of Uncertain Significance Workshop, Leiden, Netherlands [canceled due to pandemic]
2020 Invited Speaker, From Basic to Life Sciences X, Cavtat, Croatia [canceled due to pandemic]
2020 Invited Speaker/Panelist, NIH/ NCI SeqSPACE, "Sequencing Strategies for Population and Cancer Epidemiology studies" Webinar and Panel Discussion
2019 Participant, Illumina Workshop on Variants of Functional Significance, Seattle WA
2019 Speaker, One Brave Idea Foundation Meeting, Boston, MA, USA
2019 Seminar Speaker, Molecular Biosciences Department, U Texas, Austin, TX
2019 DFCI Center for Cancer Systems Biology/UMassMed Program in Systems Biology Retreat, Gloucester, MA
2019 Seminar Speaker, Univ. of Copenhagen, Copenhagen, Denmark
2019 Keynote speaker, 29th International Conference on Yeast Genetics and Molecular Biology (ICYGMB), Goteborg, Sweden
2019 Seminar Speaker, European Bioinformatics Institute, Hinxton, UK
2019 Invited Speaker, Myriad Genetics, Salt Lake City, UT
2019 Ambry Genetics Webinar
2019 American College of Medical Genetics and Genomics Annual Meeting, Seattle, WA
2019 Speaker, CIFAR Workshop on Personalized Genomics, Santa Cruz, CA
2019 Speaker, CIFAR Genetic Networks Program Meeting, Santa Cruz, CA
2019 Keynote Speaker, Cold Spring Harbor Laboratory Meeting on Network Biology, Cold Spring Harbor, NY
2019 Seminar Speaker, UCSF Dept of Bioengineering & Therapeutic Sciences, CA
2019 Speaker, Invitae, Inc., San Francisco, CA
2019 18th Annual Workshop at Bellairs - Single Cell and Massively Parallel Approaches, Holetown, Barbados
2018 NIH/NHGRI Centers of Excellence in Genomic Science Grantee Meeting
2018 CIFAR Genetic Networks Program Meeting, Toronto, ON
2018 Invited Speaker, Mt Sinai Icahn School of Medicine, New York City, NY
2018 CIFAR Molecular Architecture of Life workshop, Toronto, ON
2018 NIH Centers of Excellence in Genome Sciences Meeting, Chicago, IL
2018 Invited speaker, Dana Farber Cancer Institute Center for Cancer Systems Biology/ UMassMedical Program in Systems Biology Retreat, Gloucester, MA
2018 Jasper Rine Symposium, Berkeley, CA
2018 One Brave Idea Webinar
2018 Speaker and Lecturer, CSHL Yeast Genetics and Genomics Course
2018 CIFAR-GETx Conference, Toronto ON
2018 Seminar Speaker, University of Ljubljana, Ljubljana, Slovenia
2018 Invited Seminar, University of Michigan, Ann Arbor, MI
2018 Invited Seminar, Department of Human Genetics, Univ. of Utah, UT
2018 Invited Speaker, Recursion Pharmaceuticals Systems Biology Minisymposium, UT

Peer-Reviewed Research Publications

1. B Floyd[*], J Weile[*], P Kannankeril, A Glazer, C Reuter, C MacRae, E Ashley*, D Roden*, *FP Roth*[*], V Parikh[*,†]. Proactive variant effect mapping aids diagnosis in pediatric cardiac arrest. **Circulation: Genomic and Precision Medicine** (in press).
2. DK Kim*, B Weller*, CW Lin*, D Sheykhkarimli*, JJ Knapp*, G Dugied, A Zanzoni, C Pons, MJ Tofaute, SB Maseko, K Spirohn, F Laval, L Lambourne, N Kishore, A Rayhan, M Sauer, V Young, H Halder, N Marin-de la Rosa, O Pogoutse, A Strobel, P Schwehn, R Li, S Rothballer, M Altmann, P

Cassonnet, G Dugied, AG Cote, LE Vergara, I Hazelwood, BB Liu, M Nguyen, R Pandiarajan, B Dohai, PAR Coloma, J Poirson, P Giuliana, L Willems, M Taipale, Yves Jacob, Tong Hao, DE Hill, C Brun, JC Twizere, D Krapmann, M Heinig, C Falter, P Aloy, C Demeret†, M Vidal†, MA Calderwood†, *FP Roth*†, P Falter-Braun†. A proteome-scale map of the SARS-CoV-2 human contactome. **Nature Biotechnology** 41(1):140-149 (2023).

3. D Choi, N Khan, L Monterminib, N Tawil, B Meehan, D-K Kim, *FP Roth*, M Divangahi, J Rak†. Quantitative proteomics and biological activity of extracellular vesicles engineered to express SARS-CoV-2 spike protein. **Journal of Extracellular Biology** 2022;1:e58 (2022).
4. D Kuang, J Weile, N Kishore, AF Rubin, S Fields, DM Fowler, *FP Roth*†. MaveRegistry: a collaboration platform for multiplexed assays of variant effect. 37(19):3382-3383 **Bioinformatics** (2021).
5. D Kuang, R Truty, J Weile, B Johnson, K Nykamp, C Araya, RL Nussbaum, *FP Roth*†. Prioritizing genes for systematic variant effect mapping. **Bioinformatics** 36(22-23):5448-5455 (2021).
6. J-H Kim, Y Seo, M Jo, H Jeon, Y-S Kim, E-J Kim, D Seo, W-H Lee, SR Kim, N Yachie, Q Zhong, M Vidal, *FP Roth*, K Suk†. A genetic interaction screen in yeast identifies genes relevant to human PAK1 function in glioma. **Journal of Biological Chemistry** 295(50):16906-16919 (2020).
7. J van Leeuwen†, C Pons, G Tan, JZ Wang, J Hou, J Weile, M Gebbia, W Liang, E Shuteriqi, Z Li, M Lopes, M Ušaj, A Dos Santos Lopes, N van Lieshout, CL Myers, *FP Roth*, P Aloy, BJ Andrews† & C Boone†. Systematic analysis of bypass suppression of essential genes. **Molecular Systems Biology** 16(9):e9828 (2020).
8. MA Chiasson, NJ Rollins, JJ Stephany, KA Sitko, KA Matreyek, M Verby, S Sun, *FP Roth*, D DeSloover, D Marks, AE Rettie, DM Fowler†. Multiplexed measurement of variant abundance and activity reveals VKOR topology, active site and human variant impact. **eLife** 2020;9:e58026 (2020).
9. D-K Kim, JJ Knapp, D Kuang, A Chawla, P Cassonnet, H Lee, D Sheykhkarimli, P Samavarchi-Tehrani, H Abdouni, A Rayhan, Li R, Pogoutse O, E Coyaud, S van der Werf, C Demeret, A-C Gingras, B Raught, Y Jacob†, *FP Roth*†. A flexible genome-scale resource of SARS-CoV-2 coding sequence clones. **G3: Genes|Genomes|Genetics** 10(9):3399-3402 (2020).
10. D Kuang, J Weile, R Li, TW Ouellette, JA Barber, *FP Roth*†. MaveQuest: a web resource for planning experimental tests of human variant effects. **Bioinformatics** 36(12):3938-3940 (2020).
11. K Luck*, D-K Kim*, L Lambourne*, K Spirohn*, BE Begg, W Bian, R Brignall, T Cafarelli, FJ Campos-Laborie, B Charloteaux, D Choi, AG Cote, M Daley, S Deimling, A Desbuleux, A Dricot, M Gebbia, MF Hardy, N Kishore, JJ Knapp, IA Kovács, I Lemmens, MW Mee, JC Mellor, C Pollis, C Pons, AD Richardson, S Schlabach, B Teeking, A Yadav, M Babor, D Balcha, O Basha, S-F Chin, SG Choi, C Colabella, G Coppin, C D'Amata, D De Ridder, S De Rouck, M Duran-Frigola, H Ennajdaoui, F Goebels, A Gopal, G Haddad, M Helmy, Y Jacob, Y Kassa, R Li, N van Lieshout, A MacWilliams, D Markey, JN Paulson, S Rangarajan, J Rasla, A Rayhan, T Rolland, A San Miguel, Y Shen, D Sheykhkarimli, GM Sheynkman, E Simonovsky, M Tasan, A Tejeda, J-C Twizere, Y Wang, R Weatheritt, J Weile, Y Xia, X Yang, E Yeger-Lotem, Q Zhong, P Aloy, GD Bader, J De Las Rivas, S Gaudet, T Hao, J Rak, J Tavernier, V Tropepe, DE Hill†, M Vidal†, *FP Roth*†, MA Calderwood†. A reference map of the human protein interactome. **Nature** 580(7803):402-408 (2020).
12. PM Muller*, J Rademacher*, RD Bagshaw*, C Wortmann, C Barth, J van Unen, KM Alp, G Giudice, RL Eccles, LE Heinrich, P Pascual-Vargas, M Sanchez-Castro, L Brandenburg, G Mbamalu, M Tucholska, L Spatt, MT Czajkowski, RW Welke, S Zhang, V Nguyen, T Rrustemi, P Trnka, K Freitag, B Larsen, O Popp, P Mertins, A-C Gingras, *FP Roth*, K Colwill, C Bakal, O Pertz, T Pawson, E Petsalaki†, O Rocks†. Systems-analysis of RhoGEF/RhoGAP regulatory proteins reveals spatially organized Rac1 signaling from integrin adhesions. **Nature Cell Biology** 22(4):498-511 (2020).
13. S Sun*, J Weile*,†, M Verby, Y Wu, Wang, Y, AG Cote, I Fotiadou, J Kitaygorodsky, M Vidal, J Rine, P Ješina, V Kozich†, *FP Roth*†. A proactive genotype-to-patient-phenotype map for cystathionine beta-synthase. **Genome Medicine** 12(1):13 (2020).
14. JH Kim, Y Seo, M Jo, H Jeon, WH Lee, N Yachie, Q Zhong, M Vidal, *FP Roth*, K Suk. Yeast-based genetic interaction analysis of human kinome. **Cells**. 9(5):1156 (2020).

15. A Celaj, M Gebbia, L Musa, AG Cote, J Snider, V Wong, M Ko, T Fong, P Bansal, JC Mellor, G Seesankar, M Nguyen, S Zhou, L Wang, N Kishore, I Stagljar, Y Suzuki, N Yachie† & *FP Roth*†. Highly combinatorial genetic interaction analysis reveals a multi-drug transporter influence network. **Cell Systems** 9:1-14 (2020).
16. D Esposito*, J Weile*, J Shendure, LM Starita, AT Papenfuss, *FP Roth*†, DM Fowler† & AF Rubin†. MaveDB: an open-source platform to distribute and interpret data from multiplexed assays of variant effect. **Genome Biology** 20(1):223 (2019).
17. J Zhang, LN Kinch, Q Cong, P Katsonis, O Lichtarge, C Savojardo, G Babbi, PL Martelli, E Capriotti, R Casadio, A Garg, D Pal, J Weile, S Sun, M Verby, *FP Roth* & NV Grishin†. Assessing predictions on fitness effects of missense variants in calmodulin. **Human Mutation** 40(9):1463-1473 (2019).
18. F Yang, D-K Kim, H Nakagawa, S Hayashi, S Imoto, L Stein, *FP Roth*†. Quantifying immune-based counterselection of somatic mutations. **PLoS Genetics** 15(7):e1008227 (2019).
19. Y Wu, J Weile, AG Cote, S Sun, J Knapp, M Verby, *FP Roth*†. A web application and service for imputing and visualizing missense variant effect maps. **Bioinformatics** 35(17):3191-3193 (2019).
20. E Deneault, M Faheem, SH White, DC Rodrigues, S Sun, W Wei, A Piekna, T Thompson, JL Howe, L Chalil, V Kwan, S Walker, P Pasceri. *FP Roth*, RKC Yuen, KK Singh, J Ellis† & SW Scherer†. CNTN5-/+ or EHMT2-/+ iPSC-derived neurons from individuals with autism develop hyperactive neuronal networks. **eLife** 8:e40092 (2019).
21. A Sokolov, S Ashenden, N Sahin, R Lewis, N Erdem, E Ozaltan, A Bender, *FP Roth*, M Cokol†. Characterizing ABC-transporter substrate-likeness using a clean-slate genetic background. **Frontiers in Pharmacology** 10:448 (2019).
22. ZB Weinstein, N Kuru, S Kiriakov, AC Palmer, AS Khalil, PA Clemons, MH Zaman, *FP Roth*, M Cokol†. Modeling the impact of drug interactions on therapeutic selectivity. **Nature Communications** 9(1):3452 (2018).
23. D Choi, L Montermini, DK Kim, B Meehan, *FP Roth*, J Rak†. The impact of oncogenic EGFRvIII on the proteome of extracellular vesicles released from glioblastoma cells. **Molecular and Cellular Proteomics**. 17(10):1948-1964 (2018).
24. JJ Diaz-Mejia, A Celaj, JC Mellor, A Cote, A Balint, B Ho, P Bansal, F Shaeri, M Gebbia, J Weile, M Verby, A Karkhanina, Y Zhang, C Wong, J Rich, D Prendergast, G Gupta, S Ozturk, D Durocher, GW Brown, *FP Roth*†. Mapping DNA-damage-dependent genetic interactions in yeast via party mating and barcode fusion genetics. **Molecular Systems Biology** (2018).
25. J Weile, S Sun, AG Cote, J Knapp, M Verby, JC Mellor, Y Wu, C Pons, C Wong, N van Lieshout, F Yang, M Tasan, G Tan, S Yang, DM Fowler, R Nussbaum, JD Bloom, M Vidal, DE Hill, P Aloy & *FP Roth*†. A framework for exhaustively mapping functional missense variants. **Molecular Systems Biology** 13(12):957 (2017).
26. I Vigentini†, M Gebbia, A Belotti, R Foschino, *FP Roth*. CRISPR/Cas9 system as a valuable genome editing tool for wine yeasts with application to decrease urea production. **Frontiers in Microbiology** 8(2194):1-11 (2017).
27. M Jo, AY Chung, N Yachie, M Seo, H Jeon, Y Nam, Y Seo, E Kim, Q Zhong, M Vidal, HC Park†, *FP Roth*†, K Suk†. Yeast genetic interaction screen of human genes associated with amyotrophic lateral sclerosis: identification of MAP2K5 kinase as a potential drug target. **Genome Research** 27(9):1487-1500 (2017).
28. J Zhang, LN Kinch, Q Cong, J Weile, S Sun, AG Cote, *FP Roth*, NV Grishin†. Assessing predictions of fitness effects of missense mutations in SUMO-conjugating enzyme UBE2I. **Human Mutation**. 38(9):1051-1063 (2017).
29. A Celaj, U Schlecht, J Smith, W Xu, S Suresh, M Miranda, AM Aparicio, M Proctor, RW Davis, *FP Roth*† & RP St.Onge†. Quantitative analysis of protein interaction network dynamics in yeast. **Molecular Systems Biology** 13(7):934 (2017)**.**

30. F Yang, S Sun, G Tan, M Costanzo, DE Hill, M Vidal, BJ Andrews, C Boone & *FP Roth*[†]. Identifying pathogenicity of human variants via paralog-based yeast complementation. **PLOS Genetics** 13(5):e1006779 (2017).

31. MJ Betts, O Wichmann, M Utz, T Andre, E Petsalaki, P Minguez, L Parca, *FP Roth*, A-C Gavin, P Bork & RB Russell[†]. Systematic identification of phosphorylation-mediated protein interaction switches. **PLOS Computational Biology** 13(3):e1005462 (2017).

32. C Cenik, HN Chua, G Singh, A Akef, MP Snyder, AF Palazzo, MJ Moore[†] & *FP Roth*[†]. A common class of transcripts with 5'-intron depletion, distinct early coding sequence features, and N1-methyladenosine modification. **RNA** 23(3):270-283 (2017).

33. J van Leeuwen[*], C Pons**[*]**, JC Mellor, TN Yamaguchi, H Friesen, J Koschwanez, MM Ušaj, M Pechlaner, M Takar, M Ušaj, B VanderSluis, K Andrusiak, P Bansal, A Baryshnikova, C Boone, J Cao, A Cote, M Gebbia, G Horecka, I Horecka, E Kuzmin, N Legro, W Liang, N van Lieshout, M McNee, B-J San Luis, F Shaeri, E Shuteriqi, S Sun, Lu Yang, J-Y Youn, M Yuen, M Costanzo, A-C Gingras, P Aloy, C Oostenbrink, A Murray, TR Graham, CL Myers[†], BJ Andrews[†], *FP Roth*[†] & C Boone[†]. Exploring genetic suppression interactions on a global scale. **Science** 354(6312):pii:aag0839 (2016).

34. T Shekhar-Guturja, GM Gunaherath, EM Wijeratne, JP Lambert, AF Averette, SC Lee, T Kim, YS Bahn, F Tripodi, R Ammar, K Döhl, K Niewola-Staszkowska, L Schmitt, RJ Loewith, *FP Roth*, D Sanglard, D Andes, C Nislow, P Coccetti, AC Gingras, J Heitman, AA Gunatilaka & LE Cowen[†]. Dual action antifungal small molecule modulates multidrug efflux and TOR signaling. **Nature Chemical Biology** 12(10):867-875 (2016).

35. *FP Roth*[†] & J Wakeley[†]**.** Taking exception to human eugenics. (Letter to the Editor) **Genetics** 206(2):821-823 (2016).

36. Q Zhong[*,†], SJ Pevzner[*], T Hao, Y Wang, R Mosca, J Menche, M Taipale, M Taşan, C Fan, X Yang, P Haley, RR Murray, F Mer, F Gebreab, S Tam, A MacWilliams, A Dricot, P Reichert, B Santhanam, L Ghamsari, MA Calderwood, T Rolland, B Charloteaux, S Lindquist, AL Barabási, DE Hill, P Aloy, ME Cusick, Y Xia, *FP Roth*[†] & M Vidal[†]. An inter-species protein–protein interaction network across vast evolutionary distance. **Molecular Systems Biology** 12(4):865 (2016).

37. N Yachie[*,†], E Petsalaki[*], JC Mellor, J Weile, Y Jacob, M Verby, SB Ozturk, S Li, AG Cote, R Mosca, JJ Knapp, M Ko, A Yu, M Gebbia, N Sahni, S Yi, T Tyagi, D Sheykhkarimli, JF Roth, C Wong, L Musa, J Snider, Y-C Liu, H Yu, P Braun, I Stagljar, T Hao, MA Calderwood, L Pelletier, P Aloy, DE Hill, M Vidal & *FP Roth*[†]. Pooled-matrix protein interaction screens using Barcode Fusion Genetics. **Molecular Systems Biology** 12(4):863 (2016).

38. S Sun, F Yang, G Tan, M Costanzo, R Oughtred, J Hirschman, C Theesfeld, P Bansal, N Sahni, S Yi, A Yu, T Tyagi, C Tie, DE Hill, M Vidal, BJ Andrews, C Boone, K Dolinski & *FP Roth*[†]. An extended set of yeast-based functional assays accurately identifies human disease mutations. **Genome Research** 26(5):670-80 (2016).

39. X Yang, J Coulombe-Huntington, S Kang, GM Sheynkman, T Hao, A Richardson, S Sun, F Yang, YA Shen, RR Murray, K Spirohn, BE Begg, M Duran-Frigola, A MacWilliams, SJ Pevzner, Q Zhong, SA Trigg, S Tam, L Ghamsari, N Sahni, S Yi, MD Rodriguez, D Balcha, G Tan, M Costanzo, B Andrews, C Boone, XJ Zhou, K SalehiAshtiani, B Charloteaux, AA Chen, MA Calderwood, P Aloy, *FP Roth*[‡], DE Hill[‡], LM Iakoucheva[†], Y Xia[†] & Marc Vidal[†]. Widespread expansion of protein interaction capabilities by alternative splicing. **Cell** 164(4):805-817 (2016).

40. TV Vo, J Das, MJ Meyer, NA Cordero, N Akturk, X Wei, BJ Fair, AG Degatano, R Fragoza, LG. Liu, A Matsuyama, M Trickey, S Horibata, A Grimson, H Yamano, M Yoshida, *FP Roth*, JA Pleiss, Y Xia & H Yu[†]. A proteome-wide fission yeast interactome reveals network evolution principles from yeasts to human. **Cell** 164(1-2):310-23 (2016).

41. T Hart[*], MC Chandrashekhar[*], M Aregger[*], Z Steinhart, KR Brown, G MacLeod, M Mis, M Zimmermann, A Fradet-Turcotte, S Sun, P Mero, P Dirks, S Sidhu, *FP Roth*, OS Rissland, D Durocher, S Angers & J Moffat[†]. High-resolution CRISPR screens reveal fitness genes and genotype-specific cancer liabilities. **Cell** 163(6):1515-26 (2015).

42. E Petsalaki†, AO Helbig, A Gopal, A Pasculescu, *FP Roth*† & T Pawson. SELPHI: Correlation-based identification of kinase-associated networks from global phospho-proteomics datasets. **Nucleic Acids Research** 43(W1):W276-82 (2015).

43. N Sahni, S Yi, M Taipale, JI Fuxman Bass, J Coulombe-Huntington, F Yang, J Peng, J Weile, GI Karras, Y Wang, IA Kovács, A Kamburov, I Krykbaeva, MH Lam, G Tucker, V Khurana, A Sharma, Y-Y Liu, N Yachie, Q Zhong, Y Shen, A Palagi, A San-Miguel, C Fan, D Balcha, A Dricot, DM Jordan, JM Walsh, AA Shah, X Yang, A Stoyanova, A Leighton, MA Calderwood, Y Jacob, ME Cusick, K Salehi-Ashtiani, LJ Whitesell, S Sunyaev, B Berger, A-L Barabási, B Charloteaux, DE Hill, T Hao, *FP Roth*‡, Y Xia‡, AJM Walhout‡, S Lindquist†‡ & M Vidal†‡. Widespread macromolecular interaction perturbations in human genetic disorders. **Cell** 161(3):647-660 (2015).

44. F Yang, E Petsalaki, T Rolland, DE Hill, M Vidal & *FP Roth*†. Protein domain-level landscape of cancer-type-specific somatic mutations. **PLoS Computational Biology** 11(3):e1004147 (2015).

45. M Taşan*, G Musso*, T Hao, M Vidal, CA MacRae, *FP Roth*†. Selecting causal genes from genome-wide association studies via functionally coherent subnetworks. **Nature Methods** 12(2):154-159 (2015).

46. M Irimia, RJ Weatheritt, JD Ellis, NN Parikshak, T Gonatopoulos-Pournatzis, M Babor, M Quesnel-Vallières, J Tapial, B Raj, D O'Hanlon, M Barrios-Rodiles, MJE Sternberg, SP Cordes, *FP Roth*, JL Wrana, DH Geschwind & BJ Blencowe†. A highly conserved program of neuronal microexons is misregulated in autistic brains. **Cell** 159(7): 1511-1523 (2014).

47. RC Deo†, G Musso, M Tasan, P Tang, A Poon, C Yuan, JF Felix, RS Vasan, R Beroukhim, T De Marco, P-Y Kwok, CA MacRae & *FP Roth*†. Prioritizing causal disease genes using unbiased genomic features. **Genome Biology** 15(12):534 (2014).

48. T Rolland*, M Tasan*, B Charloteaux*, SJ Pevzner*, Q Zhong*, N Sahni*, S Yi*, I Lemmens, C Fontanillo, R Mosca, A Kamburov, SD Ghiassian, X Yang, L Ghamsari, D Balcha, BE Begg, P Braun, M Brehme, MP Broly, A-R Carvunis, D Convery-Zupan, R Corominas, J Coulombe-Huntington, E Dann, M Dreze, A Dricot, C Fan, E Franzosa, F Gebreab, BJ Gutierrez, MF Hardy, M Jin, S Kang, R Kiros, GN Lin, K Luck, A MacWilliams, J Menche, RR Murray, A Palagi, MM Poulin, X Rambout, J Rasla, P Reichert, V Romero, E Ruyssinck, JM Sahalie, A Scholz, AA Shah, A Sharma, Y Shen, K Spirohn, S Tam, AO Tejeda, SA Trigg, J-C Twizere, K Vega, J Walsh, ME Cusick, Y Xia, A-L Barabasi, L Iakoucheva, P Aloy, J De Las Rivas, J Tavernier, MA Calderwood, DE Hill, T Hao, *FP Roth*† & M Vidal†. A proteome-scale map of the human interactome network. **Cell** 159(5):1212-1226 (2014).

49. K Yilancioglu, ZB Weinstein, C Meydan, A Akhmetov, I Toprak, A Durmaz, I Iossifov, H Kazan, *FP Roth* & M Cokol†. Target-independent prediction of drug synergies using only drug lipophilicity. **Journal of Chemical Information and Modeling** 54(8):2286-93 (2014).

50. VM Labunskyy, Y Suzuki, TJ Hanly, A Murao, *FP Roth*† & VN Gladyshev†. The Insertion Green Monster (iGM) method for expression of multiple exogenous genes in yeast. **G3: Genes|Genomes|Genetics** 4(7):1183-91 (2014).

51. M Cokol†, ZB Weinstein, K Yilancioglu, M Tasan, A Doak, D Cansever, B Mutlu, S Li, R Rodriguez-Esteban, M Akhmedov, A Guvenek, M Cokol, S Cetiner, G Giaever, I Iossifov, C Nislow, B Shoichet & *FP Roth*†. Large-scale identification and analysis of suppressive drug interactions. **Chemistry & Biology** 21:541-551 (2014).

52. R. Corominas, X Yang, GN Lin, S Kang, Y Shen, L Ghamsari, M Broly, M Rodriguez, S Tam, SA Trigg, C Fan, S Yi, M Tasan, I Lemmens, X Kuang, N Zhao, D Malhotra, J Michaelson, V Vacic, MA Calderwood, *FP Roth*, J Tavernier, S Horvath, K Salehi-Ashtiani, D Korkin, J Sebat, D Hill, T Hao, M Vidal & L Iakoucheva. A protein interaction network of alternatively spliced isoforms from brain links genetic risk factors for autism. **Nature Communications** 5:3650 (2014).

53. G Musso, M Tasan, C Mosimann, JE Beaver, E Plovie, LA Carr, HN Chua, J Dunham, K Zuberi, H Rodriguez, Q Morris, L Zon, *FP Roth*† & CA MacRae†. Novel cardiovascular gene functions revealed via systematic phenotype prediction in zebrafish. **Development** 141:224-235 (2014).

54. J Das, TV Vo, X Wei, JC Mellor, V Tong, AG Degatano, X Wang, L Wang, NA Cordero, N Kruer-Zerhusen, A Matsuyama, JA Pleiss, SM Lipkin, M Yoshida, *FP Roth* & H Yu†. Cross-species protein interactome mapping reveals species-specific wiring of stress-response pathways. **Science Signalling** 6(276):ra38 (2013).

55. K Mahadevan, H Zhang, A Akef, XA Cui, S Gueroussov, C Cenik, *FP Roth* & AF Palazzo†. RanBP2/Nup358 potentiates the translation of a subset of mRNAs encoding secretory proteins. **PLoS Biology** 11(4):e1001545. (2013).

56. TR Pak & *FP Roth*†. ChromoZoom: a flexible, fluid, web-based genome browser. **Bioinformatics** 29(3):384-6 (2013).

57. O Rozenblatt-Rosen*, RC Deo*, M Padi*, G Adelmant*, MA Calderwood, T Rolland, M Grace, A Dricot, M Askenazi, M Tavares, S Pevzner, F Abderazzaq, D Byrdsong, A-R Carvunis, AA Chen, J Cheng, M Correll, M Duarte, C Fan, SB Ficarro, R Franchi, B Garg, N Gulbahce, T Hao, AM Holthaus, R James, A Korkhin, L Litovchick, JC Mar, TR Pak, S Rabello, R Rubio, Y Shen, S Singh, JM Spangle, M Tasan, S Wanamaker, JT Webber, J Roecklein-Canfield, E Johannsen, A-L Barabási, R Beroukhim, E Kieff, ME Cusick, Hill DE†, K Münger†, JA Marto†, J Quackenbush†, *FP Roth*†, JA DeCaprio†, & M Vidal†. Interpreting cancer genomes using systematic host perturbations by tumour virus proteins. **Nature** 487(7408):491-495 (2012).

58. E Cheng, JA Vaisica, J Ou, A Baryshnikova, Y Lu, *FP Roth* and GW Brown†. Genome rearrangements caused by depletion of essential DNA replication proteins in *Saccharomyces cerevisiae*. **Genetics** 192(1):147-60 (2012).

59. A Derti & *FP Roth*†. Response to "MHC-dependent mate choice in humans: Why genomic patterns from the HapMap European American data set support the hypothesis": HapMap genotypes do not confidently support a role for the MHC locus in human mate selection. **Bioessays** 34(7):576-577 (2012).

60. N Gulbahce*, H Yan*, A Dricot, M Padi, D Byrdsong, R Franchi, D-S Lee, O Rozenblatt-Rosen, JC Mar, MA Calderwood, A Baldwin, B Zhao, B Santhanam, P Braun, N Simonis, K-W Huh, K Hellner, M Grace, A Chen, R Rubio, JA Marto, NA Christakis, E Kieff, *FP Roth*, Jennifer Roecklein-Canfield, JA DeCaprio, ME Cusick, J Quackenbush, DE Hill, K Münger, M Vidal† & A-L Barabási†. Viral perturbations of host networks reflect disease etiology. **PLoS Computational Biology** 8(6):e1002531 (2012).

61. M Tasan, HJ Drabkin, JE Beaver, W Tian, JA Blake & *FP Roth*†. A resource of quantitative functional annotation for *H. sapiens* genes. **G3: Genes|Genomes|Genetics** 2(2):223-233 (2012).

62. M Cokol, HN Chua, M Tasan, B Mutlu, ZB Weinstein, Y Suzuki, ME Nergiz, M Costanzo, A Baryshnikova, G Giaever, C Nislow, CL Myers, BJ Andrews, C Boone, *FP Roth*†. Systematic exploration of synergistic drug pairs. **Molecular Systems Biology** 7(544):1-9 (2011).

63. Arabidopsis Interactome Mapping Consortium [*FP Roth* was a member of the Bioinformatics & Analysis Group and the Steering Group]. Evidence for network evolution in an *Arabidopsis* interactome map. **Science** 333(6042):601-7 (2011).

64. MS Mukhtar, A-R Carvunis, M Dreze, P Epple, J Steinbrenner, J Moore, M Tasan, M Galli, T Hao, MT Nishimura, SJ Pevzner, SE Donovan, L Ghamsari, B Santhanam, V Romero, MM Poulin, F Gebreab, BJ Gutierrez, S Tam, D Monachello, M Boxem, CJ Harbort, N McDonald, L Gai, H Chen, Y He, EU Effectoromics Consortium, J Vandenhaute, *FP Roth*, DE Hill, JR Ecker, M Vidal†, J Beynon†, P Braun†, JL Dangl†. Independently evolved virulence effectors converge onto cellular hubs in a plant immune system network. **Science** 333(6042):596-601 (2011).

65. H Yu, L Tardivo, S Tam, E Weiner, F Gebreab, C Fan, N Svrzikapa, T Hirozane-Kishikawa, E Rietman, X Yang, J Sahalie, K Salehi-Ashtiani, T Hao, ME Cusick, DE Hill, *FP Roth*, P Braun & M Vidal†. Next-generation sequencing to generate interactome datasets. **Nature Methods** 8(6):478-80 (2011).

66. C Cenik, HN Chua, H Zhang, S Tarnawsky, A Akef, A Derti, M Tasan, MJ Moore, AF Palazzo†, *FP Roth*†. Genome analysis reveals interplay between 5'UTR introns and nuclear mRNA export for secretory and mitochondrial genes. **PLoS Genetics** 7(4):e1001366 (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).

68. 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).

69. 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).

70. 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).

71. 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).

72. 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).

73. 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).

74. 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).

75. 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).

76. 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).

77. 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).

78. 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).

79. K Salehi-Ashtiani*†, C Lin*, T Hao*, Y Shen, D Szeto, X Yang, L Ghamsari, H Lee, C Fan, RR Murray, S Milstein, N Svrzikapa, 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).

80. GF Berriz, JE Beaver, C Cenik, M Taşan & *FP Roth*†. Next generation software for functional trend analysis. **Bioinformatics** 25(22):3043-3044 (2009).

81. 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).

82. 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).

83. 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 Wanker[†], A-L Barabási[†] & M Vidal[†]. An empirical framework for binary interactome mapping. **Nature Methods** 6(1):83-90 (2009).

84. 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 Vandenhaute, 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).

85. 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).

86. JD Klekota & *FP Roth*[†]. Chemical substructures that predict biological activity: Exposing the rules of privilege. **Bioinformatics** 24(21):2518-2525 (2008).

87. 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).

88. 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 Svrzikapa, 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).

89. GF Berriz & *FP Roth*[†]. The Synergizer service for translating gene, protein, and other biological identifiers. **Bioinformatics** 24(19):2272-3 (2008).

90. 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).

91. 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 Schlaitz, 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[†]. A protein domain-based interactome network for *C. elegans* early embryogenesis. **Cell** 134(3):534-545 (2008).

92. M Taşan[*], W Tian[*], DP Hill, FD Gibbons, JA Blake & *FP Roth*[†]. An *en masse* phenotype and function prediction system for *M. musculus*. **Genome Biology** 9 Suppl 1:S8 (2008).

93. W Tian, LV Zhang, M Taşan, FD Gibbons, OD King, J Park, Z Wunderlich, JM Cherry, *FP Roth*[†]. Combining guilt-by-association and guilt-by-profiling to predict *Saccharomyces cerevisiae* gene function. **Genome Biology** 9 Suppl 1:S7 (2008).

94. 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[†] & *FP Roth*[†]. A critical assessment of *M. musculus* gene function prediction using integrated genomic evidence. **Genome Biology** 9 Suppl 1:S2 (2008).

95. K Salehi-Ashtiani[†], 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*[†], M Vidal[†]. Large-scale coding isoform discovery using targeted cloning, "deep well" pooling, and parallel sequencing. **Nature Methods** 5(7):597-600 (2008).

96. R Mani, RP St. Onge, J Hartman, G Giaever, *FP Roth*[†]. Defining genetic interaction. **Proceedings of the National Academy of Sciences** 105(9):3461-3466 (2008).

97. S Komili, N Gilks, *FP Roth*[†] & PA Silver[†]. Functional specificity among ribosomal proteins regulates gene expression. **Cell** 131:557-571 (2007).

98. H Huang, LV Zhang, *FP Roth* & JS Bader[†]. Probabilistic paths in protein interaction networks. **Proceedings of the RECOMB Conferences on Systems Biology and Computational Proteomics** (2007).

99. 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[†], D Baillie[†] & M Vidal[†]. Genome-scale analysis of *in vivo* spatiotemporal promoter activity in *C. elegans*. **Nature Biotechnology** 25(6):663-668. (2007).

100. N Bertin[*], N Simonis[*], D Dupuy[*], ME Cusick, J-DJ Han, HB Fraser[†], *FP Roth*[†] & M Vidal[†]. Confirmation of organized modularity in the yeast interactome. **PLoS Biology** 5(6) e153 (2007).

101. RP St.Onge, R Mani, J Oh, M Proctor, E Fung, R Davis, C Nislow, *FP Roth*[†] & G Giaever[†]. Systematic pathway analysis using high-resolution fitness profiling of combinatorial gene deletions. **Nature Genetics** 39(2):199-206 (2007).

102. A Derti, *FP Roth*, GM Church & C-T Wu[†]. Mammalian ultraconserved elements are strongly depleted among segmental duplications and copy number variants. **Nature Genetics** 38(10):1216-1220 (2006).

103. JD Klekota[†], *FP Roth* & SL Schreiber. Query Chem: A Google-Powered Web Search Combining Text and Chemical Structures. **Bioinformatics** 22(13):1670-1673 (2006).

104. JD Klekota[†], E Brauner, *FP Roth*[†] & 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).

105. MS Sabatine, E Liu, DA Morrow, E Heller, M Askenazi, R McCarroll, R Weigand, G Berriz, *FP Roth* & RE Gerszten[†]. Metabolomic identification of novel biomarkers of myocardial ischemia. **Circulation** 112(25):3868-3875 Dec 12 (2005).

106. SL Wong & *FP Roth*[†]. Transcriptional compensation for gene loss plays a minor role in maintaining genetic robustness in *Saccharomyces cerevisiae*. **Genetics** 171(2):829-833 (2005).

107. FD Gibbons, MH Proft, K Struhl & *FP Roth*[†]. Chipper: discovering transcription-factor targets from chromatin immunoprecipitation microarrays using variance stabilization. **Genome Biology** 6(11):R96 (2005).

108. 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 Albala, J Lim, C Fraughton, E Llamosas, S Cevik, C Bex, P Lamesch, RS Sikorski, J Vandenhaute, HY Zoghbi, A Smolyar, S Bosak, R Sequerra, L Doucette-Stamm, ME Cusick, DE Hill[†], *FP Roth*[†] & M Vidal[†]. A proteome-scale map of the human interactome network. **Nature** 437:1173-1178 (2005).

109. MH Proft, FD Gibbons, M Copeland, *FP Roth* & K Struhl[†]. 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).

110. 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*[†], M Vidal[†] & F Piano[†]. Predictive models of molecular machines involved in *C. elegans* early embryogenesis. **Nature** 436(7052):861-865 (2005).

111. SL Wong, LV Zhang & *FP Roth*†. Discovering functional relationships: biochemistry versus genetics. **Trends in Genetics** 21(8): 424-427 (2005).

112. LV Zhang, OD King, SL Wong, DS Goldberg, AHY Tong, G Lesage, B Andrews, H Bussey, C Boone & *FP Roth*†. Motifs, themes and thematic maps of an integrated *S. cerevisiae* network. **Journal of Biology** 4:6 (2005).

113. SL Wong, LV Zhang, AHY Tong, Z Li, DS Goldberg, OD King, G Lesage, M Vidal, B Andrews, H Bussey, C Boone & *FP Roth*†. Combining biological networks to predict genetic interactions. **Proceedings of the National Academy of Sciences** 101(44): 15682-15687 (2004).

114. YH Grad, *FP Roth*, MS Halfon & GM Church†. 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).

115. J-DJ Han, N Bertin, T Hao, DS Goldberg, GF Berriz, LV Zhang, D Dupuy, AJM Walhout, ME Cusick, *FP Roth* & M Vidal†. Evidence for dynamically organized modularity in the yeast protein-protein interaction network. **Nature** 430(6995):88-93 (2004).

116. S Asthana, OD King, FD Gibbons & *FP Roth*†. Predicting protein complex membership using probabilistic network reliability. **Genome Research** 14(6):1170-1175 (2004).

117. FD Gibbons, JE Elias, SP Gygi & *FP Roth*†. 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).

118. LV Zhang, SL Wong, OD King & *FP Roth*†. Predicting co-complexed protein pairs using genomic and proteomic data integration. **BMC Bioinformatics** 5: 38 (2004).

119. 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).

120. 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).

121. 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).

122. 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).

123. GF Berriz, OD King, B Bryant, C Sander & *FP Roth*†. Characterizing gene sets with FuncAssociate. **Bioinformatics** 19(18):2502-2504 (2003).

124. OD King† & *FP Roth*. A nonparametric model for transcription factor binding sites. **Nucleic Acids Research** 31(19):e116 (2003).

125. 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).

126. 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).

127. DS Goldberg & *FP Roth*†. Assessing experimentally derived interactions in a small world. **Proceedings of the National Academy of Sciences** 100(8): 4372-4376 (2003).

128. 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).

129. GF Berriz, JV White, OD King & *FP Roth*†. GoFish finds genes with combinations of Gene Ontology attributes. **Bioinformatics** 19(6):788-789 (2003).

130. OD King, RE Foulger, SS Dwight, JV White & *FP Roth*†. Predicting gene function from patterns of annotation. **Genome Research**, 13(5):896-904 (2003).

131. FD Gibbons & *FP Roth*†. Judging the quality of gene expression-based clustering methods using gene annotation. **Genome Research** 12(10):1574-81 (2002).

132. 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).

133. *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).

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Preprints not yet available via peer-reviewed journal

134. W van Loggerenberg*, S Sowlati-Hashjin*, J Weile, R Hamilton, A Chawla, M Gebbia, N Kishore, L Fresard, S Mustajoki, E Pischik, E Di Pierro, M Barbaro, Y Floderus, C Schmitt, L Gouya, A Colavin, R Nussbaum, ECH Friesema, R Kauppinen, J To-Figueras, AK Aarsand, RJ Desnick‡, M Garton†‡, *FP Roth*†‡. Systematically testing human HMBS missense variants to reveal mechanism and pathogenic variation. **bioRxiv** https://doi.org/10.1101/2023.02.06.527353 (2023).

135. Y Zhao, D Tabet, DR Contreras, AN Kousholt, J Weile, H Melo, L Hoeg, AG Coté, ZY Lin, D Setiaputra, J Jonkers, AC Gingras, FG Herreros, *FP Roth*, D Durocher†. Genome-scale mapping of DNA damage suppressors identifies GNB1L as essential for ATM and ATR biogenesis. **bioRxiv** https://doi.org/10.1101/2022.09.23.508845 (2022).

136. H-W Tang*, K Spirohn*, Y Hu, T Hao, IA Kovacs, Y Gao, R Binari, D Yang-Zhou, KH Wan, JS Bader, D Balcha, W Bian, BW Booth, AG Cote, S De Rouck, A Desbuleux, D-K Kim, JJ Knapp, WX Lee, I Lemmens, C Li, M Li, R Li, H Lim, K Luck, D Markey, C Pollis, S Rangarajan, J Rodiger, S Schlabach, Y Shen, B TeeKing, *FP Roth*, J Tavernier, M Calderwood, DE Hill, SE Celniker†, M Vidal†, N Perrimon†, S Mohr†. Next-generation large-scale binary protein interaction network for Drosophila. **bioRxiv** https://doi.org/10.1101/2022.08.02.502359 (2022).

137. S Gersing, M Cagiada, M Gebbia, AP Gjesing, G Seesankar, A Stein, AL Gloyn, T Hansen, *FP Roth*†, K Lindorff-Larsen†, R Hartmann-Petersen†**.** A multiplexed assay of human glucokinase reveals thousands of potential disease variants with both decreased and increased activity. **bioRxiv** https://doi.org/10.1101/2022.05.04.490571 (2022).

138. I Hoskins, S Sun, A Cote, *FP Roth*, C Cenik†. satmut_utils: a simulation and variant calling package for multiplexed assays of variant effect. **bioRxiv** https://doi.org/10.1101/2022.04.25.489390 (2022).

139. RA Silverstein, S Sun, M Verby, J Weile, Y Wu, M Gebbia, I Fotiadou, J Kitaygorodsky, *FP Roth*†. A systematic genotype-phenotype map for missense variants in the human intellectual disability-associated gene GDI1. **bioRxiv** https://doi.org/10.1101/2021.10.06.463360 (2022).

140. D Kuang, R Li, Y Wu, J Weile, RA Hegele, *FP Roth*†. Empowering rare variant burden-based gene-trait association studies via optimized computational predictor choice. **bioRxiv** https://doi.org/10.1101/2021.09.20.459182 (2022).

141. L Lambourne*, A Yadav*, Y Wang*, A Desbuleux*, D Kim, T Cafarelli, C Pons, IA Kovács, N Jailkhani, S Schlabach, D De Ridder, K Luck, W Bian, Y Shen, Z Yang, M Mee, M Helmy, Y Jacob, I

Lemmens, T Rolland, AG Coté, M Gebbia, N Kishore, JJ Knapp, JC Mellor, J Reimand, J Tavernier, ME Cusick, P Falter-Braun, K Spirohn, Q Zhong, P Aloy, T Hao, B Charloteaux, *FP Roth*†, DE Hill†, MA Calderwood†, JC Twizere†, M Vidal†. Binary interactome models of inner- versus outer-complexome organization. **bioRxiv** https://doi.org/10.1101/2021.03.16.435663 (2021).

142. JR. St-Germain, A Astori, P Samavarchi-Tehrani, H Abdouni, V Macwan, D-K Kim, JJ Knapp, *FP Roth*, A-C Gingras†, B Raught†. A SARS-CoV-2 BioID-based virus-host membrane protein interactome and virus peptide compendium: new proteomics resources for COVID-19 research. **bioRxiv** https://doi.org/10.1101/2020.08.28.269175 (2020).

143. EMN Laurent, Y Sofianatos, A Komarova, J-P Gimeno, P Samavarchi-Tehrani, D-K Kim, H Abdouni, M Duhamel, P Cassonnet, JJ Knapp, D Kuang, A Chawla, D Sheykhkarimli, A Rayhan, R Li, O Pogoutse, DE Hill, MA Calderwood, P Falter-Braun, P Aloy, U Stelzl, M Vidal, A-C Gingras, GA Pavlopoulos, S Van Der Werf, I Fournier, *FP Roth*, M Salzet†, C Demeret†, Y Jacob†, E Coyaud†. Global BioID-based SARS-CoV-2 proteins proximal interactome unveils novel ties between viral polypeptides and host factors involved in multiple COVID19-associated mechanisms. **bioRxiv** https://doi.org/10.1101/2020.08.28.272955 (2020).

144. P Samavarchi-Tehrani, H Abdouni, JDR Knight, A Astori, R Samson, Z-Y Lin, D-K Kim, JJ Knapp, J St-Germain, CD Go, B Larsen, CJ Wong, P Cassonnet, C Demeret, Y Jacob, *FP Roth*, B Raught†, A-C Gingras†. A SARS-CoV-2-host proximity interactome. **bioRxiv** https://doi.org/10.1101/2020.09.03.282103 (2020).

145. AO Helbig†, M Kofler, G Gish, K Lorenzen, M Tucholska, C Zhang, *FP Roth*, T Pawson, K Colwill†, E Petsalaki†. Decoding the functional Fes kinase signaling network topology in a lymphocyte model. **bioRxiv** https://doi.org/10.1101/125088 (2020).

146. TR Pak, M Rodriguez, *FP Roth*†**.** Why clinical trials are terminated. **bioRxiv** http://dx.doi.org/10.1101/021543 (2015).

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Reviews, Perspectives, and Other Publications

147. D Tabet, V Parikh, P Mali, *FP Roth*†, M Claussnitzer†. Scalable functional assays for the interpretation of human genetic variation. **Annual Review of Genetics** 56:441-465 (2022)**.**

148. A Savinov†, *FP Roth*†. Seeds of their own destruction: dominant-negative peptide screening yields functional insight and therapeutic leads. **Cell Systems**. 12(7):691-693 (2021).

149. J Weile†, *FP Roth*†. Multiplexed assays of variant effects contribute to a growing genotype-phenotype atlas. **Human Genetics**.137(9):665-678 (2018).

150. LM Starita†, N Ahituv, MJ Dunham, JO Kitzman, *FP Roth*, G Seelig, J Shendure, DM Fowler†. Variant interpretation: functional assays to the rescue. **American Journal of Human Genetics** 101(3):315-325 (2017).

151. *FP Roth*. Doctors' Notes: Don't put too much faith in home-based gene testing. **Toronto Star**. April 7 2015 issue: p.E5 (2015).

152. *FP Roth* interviewed by Erica Johnson for "Gene Genie" episode. **CBC Marketplace**. CBC, Toronto, ON. Broadcast April 3 2015.

153. SR Sunyaev† & *FP Roth*†. Systems biology and the analysis of genetic variation. *Current Opinion in Genetics & Development* 23(6):599-601 (2013).

154. Y Suzuki, J Stam, M Novotny, N Yachie, RS Lasken & *FP Roth*†. The Green Monster process for the generation of yeast strains carrying multiple gene deletions. **Journal of Visualized Experiments** 70, e4072 (2012).

155. AA Bicknell, C Cenik, HN Chua, *FP Roth* & MJ Moore†. Introns in UTRs: Why we should stop ignoring them. **Bioessays** 34(12):1025-34 (2012).

156. A-R Carvunis, *FP Roth*, MA Calderwood, ME Cusick, G Superti-Furga & M Vidal. Interactome Networks. Chapter 3 in **Handbook of Systems Biology**, 1st Edition. Ed. M. Walhout, M. Vidal & J. Dekker, Academic Press, Amsterdam, The Netherlands (2012).
157. O Stegle, *FP Roth*, Q Morris & J Listgarten. Personalized medicine: from genotypes and molecular phenotypes towards computed therapy. **Proceedings of the Pacific Symposium on Biocomputing** 323-6 (2012).
158. HN Chua & *FP Roth*†. Discovering the targets of drugs via computational systems biology. **Journal of Biological Chemistry** 286(27):23653-23658 (2011).
159. RC Deo† & *FP Roth*. Pathways of the heart. **Circulation***: Cardiovascular Genetics* 2(4): 303-305 (2009).
160. *FP Roth*, HD Lipshitz & BJ Andrews. Q&A: Epistasis. **Journal of Biology** 8:35 (2009).
161. LV Zhang & *FP Roth*†. Biomolecular network structure and function, in **Encyclopedia of Complexity and Systems Science**. Ed. RA Meyers, Springer, New York, USA (2009).
162. TR Hughes & *FP Roth*†. A race through the maze of genomics evidence. (Introduction to a Special Issue on Quantitative Inference of Gene Function) **Genome Biology** 9 Suppl 1:S1 (2008).
163. RE Gerszten, F Accurso, GR Bernard, RM Caprioli, EW Klee, GG Klee, I Kullo, TA Laguna, *FP Roth*, M Sabatine, P Srinivas, TJ Wang, LB Ware†. Challenges in translating plasma proteomics from bench to bedside: Update from the NHLBI Clinical Proteomics Programs. Lung Cellular & Molecular Physiology. **Am J Physiol Lung Cell Mol Physiology** (Review) 295(1):L16-22 (2008).
164. *FP Roth* & B Andrews. Systems Biology: a shared goal with diverse views. (Perspective) **ASBMB Today** (2007).
165. S Komili & *FP Roth*†. Genetic interaction screens advance in reverse. **Genes and Development** (Perspective) 21(2):137-42 (2007).
166. Y Suzuki & *FP Roth*†**.** Systematic genetics swims forward elegantly. **Molecular Systems Biology** (News & Views) 2:48 (2006).
167. GD Bader, AH Tong, LV Zhang, *FP Roth*, B Andrews & C Boone. Exploiting synthetic genetic interactions to predict pathways and complexes, Chapter 40 in **Protein-Protein Interactions: A Molecular Cloning Manual**, 2nd Edition. Ed. Erica Golemis, Cold Spring Harbor Laboratory Press, New York, USA (2005).
168. *FP Roth*†. Bringing out the best features of expression data. **Genome Research** (Insight/Outlook) 11(11):1801-1802 (2001).
169. *FP Roth*. Regulons revealed with gene expression data and studies on DNA sequencing via ion conductance. **Doctoral Thesis, Harvard University Graduate Biophysics Program** (1998).

*contributed equally †corresponding author ‡co-senior author

Patents

FP Roth, J Mellor, Y Lu. Entangled Mate Sequencing. 13/497069. U.S. patent application no. 20120245039) (published Nov 1, 2012).

FP Roth, M Cokol, K Chua. Synergistic Combination Therapy. 13/497272. U.S. patent application no. 20120277193 (published Sept 27 2012).

FP Roth, J Mellor, Y Suzuki. Methods and applications for stitched DNA barcodes. U.S.S.N. 12/236,912. U.S. patent no. 20090098555. (published Sept 18 2012).

FP Roth, OD King, LV Zhang; Method for constructing eukaryotic cells having multiple genomic deletions and/or insertions. U.S.S.N. 11/780,132 (U.S. patent publication no. 20080032404; corresponds to international patent application no. PCT/US06/03626, published as WO2006/083995).

FP Roth, C Van Huffel, JV White, AW Shyjan. Methods and compositions for the identification, assessment, prevention and therapy of human cancers. USPTO applications 20020051978, 20020120004, and 20030129629; international (PCT) applications WO/2001/061048 and WO/2001/061050.

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2022 – 2026 NIH/NHLBI R01HL164675 (Roden, Roth, Ashley). "Generating missense variant effect maps for cardiovascular disease genes"

2021 – 2026 NIH/NHGRI UM1 HG011989 (Vidal). "Molecular phenotyping of ~100,000 coding variants across Mendelian disease genes"

2021 – 2023 Beam Therapeutics (Roth). "Variant effect maps to enable alpha-1 antitrypsin therapy"

2021 – 2023 NIH R21 HG011523 (Roth). "Technology for ten-minute resolution protein interaction mapping at proteome scale"

2021 – 2023 Biogen, Inc. (Roth). "Systematically and proactively testing variant effects for SOD1"

2019 – 2024 NIH/NIGMS R01 GM133185 (Vidal, Roth, Calderwood) "Incomplete penetrance via edgetic suppression"

2019 – 2023 NIH/NHGRI RM1 HG010461 Center for Excellence in Genomic Sciences (Fowler). "Center for the multiplexed assessment of phenotype"

2018 – 2025 CIHR Foundation Grant (Roth). "Systematically mapping context-dependent protein interactions and functional human sequence variation"

Past funding:

2020 – 2022 Deep Genomics, Inc. (Roth). "A proactive variant effect map for ATP7B"

2020 – 2020 Thistledown Foundation (Raught, Gingras, Roth). "Mapping and disrupting the SARS-CoV-2 protein interactome"

2019 – 2020 One Brave Idea Foundation (Roth). "Systematic exploration of coronary heart disease genetics"

2019 – 2020 Alnylam Pharmaceuticals, Inc. (Roth). "A comprehensive variant effect map for HMBS"

2017 – 2018 One Brave Idea (Roth). "Establishing efficient assays for functional variation in coronary heart disease-relevant genes"

2015 – 2018 NIH/NHGRI U41 HG001715 (Vidal, Hill, Roth). "A human binary interactome reference map by 2020"

2012 – 2015 NIH/NHGRI U01 HG001715 (Vidal, Hill, Roth). "Mapping the first half of the REFERENCE human binary protein interactome"

2011 – 2017 CERC Secretariat (Roth). Canada Excellence Research Chair in Integrative Biology

2009 – 2011 NIH/NIMH R21 MH087394 (Harlow). "How genetic variation in protein kinases affects drug response

2008 – 2011 NIH/NHGRI R01 HG0017115 (Vidal, Hill, Roth). "Mapping the human binary interactome network"

2008 – 2010 NIH/NHGRI R21 HG004756 (Roth). "Technology for large-scale genetic interaction discovery in *S. cerevisiae*"

2007 – 2009 NIH/NCI R21 CA130266 (Roth). "Methods for engineering *S. cerevisiae* strains with multiple precise deletions"

2007 – 2009 NIH/NINDS R01NS054052/P01NS035611 (Moskowitz). "Migraine drug prophylaxis"

2007 Taplin Funds for Discovery (equipment award). "A next-generation DNA sequencer enabling diverse large-scale studies"

2005 – 2009	NIH/NHLBI U01 HL81341 (Gerzten). "Establishing proteomic biomarkers of myocardial injury.
2005 – 2007	W. M. Keck Foundation (Vidal). "The first version of the Human Interactome Map"
2005 – 2008	NIH/NHGRI R01HG0017115 (Vidal). "*C. elegans* and Human Interactome Project"
2005 – 2011	NIH/NHGRI R01 HG003224 (Roth). "Computational methods for directed functional genomics"
2003	The Milton Fund of Harvard University (Roth). "A computational search for pre-mRNA sequence elements that regulate alternative splicing"
2002 – 2005	NIH/NCI P20 CA96470-01 (Wong). "Center for Computational Study of Biological Systems"
2001 – 2003	Harvard Medical School/Aventis Collaborative Research Award (Roth). "Computational methods for probabilistic drug target selection"