

YANA BROMBERG

Professor

Department of Biochemistry and Microbiology

Rutgers University, School of Environmental and Biological Sciences

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EDUCATION

Columbia University, New York, NY

Ph.D., Biomedical Informatics (Bioinformatics Track)

2007

Dissertation Title: Prediction and Analysis of Effects of Non-Synonymous Single Nucleotide Polymorphisms on (Product) Protein Function

Advisors: Burkhard Rost (Biochemistry/Molecular Biophysics), Rudolph L. Leibel (Pediatrics and Medicine/Molecular Genetics)

Thesis Committee: David E. Shaw (Biomed. Informatics), Andrey Rzhetsky (Biomed. Informatics), Lawrence Shapiro (Biochem/Mol. Biophysics)

Columbia University, New York, NY

M.Phil. Biomedical Informatics

2004

State University of NY (SUNY) at Stony Brook, Stony Brook, NY

B.A. Biology / B.Eng. Computer Science (Magna Cum Laude)

2001

APPOINTMENTS

Emory University, Atlanta, GA

Acting Professor, Depts. of Biology and Computer Science

2022-

Rutgers University, New Brunswick, NJ

Full Professor with Tenure, Dept. of Biochemistry and Microbiology

2021-2022

International Society for Computational Biology (ISMB)

Vice President, Board of Directors

2020-2023

Institute of Advanced Studies, University of Bologna, Italy

Visiting Fellow

2020

Rutgers University, New Brunswick, NJ

Associate Professor with Tenure, Dept. of Biochemistry and Microbiology

2016-2021

Institute for Advanced Study, Technical University of Munich, Germany

Hans Fischer Fellow, Dept. of Bioinformatics and Comp. Biology

2014-Present

Rutgers University, New Brunswick, NJ

Adjunct Professor, Dept. of Genetics

2013-Present

Rutgers University, New Brunswick, NJ

Assistant Professor, Dept. of Biochemistry and Microbiology

2010-2016

BioSof, LLC, New York, NY

Chief Scientific Officer (Bioinformatics Tool Development)

2008-Present

Columbia University, New York, NY

Postdoc, Dept. of Biochemistry and Molecular Biophysics

2006-2010

HONORS

Tech Times highlight: 50 years of women at Tech	2020
Stony Brook University 40 under Forty	2020
Visiting Fellowship at the Institute for Advanced Studies at the Alma Mater Studiorum, University of Bologna, Italy	2020
Research Excellence Award, School of Environmental and Biological Sciences, Rutgers	2017
Hans Fischer Fellowship for Outstanding Early Career Scientists, Institute of Advanced Studies at Technical University of Munich	2014-2016
NSF CAREER Award	2016
Rutgers Board of Trustees Research Fellowship for Scholarly Excellence	2016
Theobald Smith Society Young Investigator Award	2016
PhRMA Foundation Research Starter Award	2015
Brooklyn Tech Younger Alumni Recognition Award for Career Progress	2014
International Society for Computational Biology Travel Fellowship	2008
NLM Biomedical Informatics research training fellow	2001-2005
Weizmann Institute of Science, Karyn Kupcinec International Science School Scholar	2000
SUNY at Stony Brook Honors Scholar	1997-2001
National Merit Scholar	1997
Guideposts Scholar	1997

SCHOLARSHIP

PEER REVIEWED SCIENTIFIC PUBLICATIONS (69 total, in reverse publication order, advisees underlined, [OR] = Original Research, [RW] = Review)

1. Aptekmann, A.A., Buongiorno, J., Giovannelli, D., Glamoclija, M., Ferreiro, D.U., **Bromberg, Y.** (2022) mebipred: identifying metal-binding potential in protein sequence, *Bioinformatics* in review. *Bioinformatics* 38(14), 3532–3540[OR]
 2. Hoarfrost A, Aptekmann A, Farfanuk G, Bromberg Y. (2022) Shedding Light on Microbial Dark Matter with A Universal Language of Life. *Nature Communications*. 13(1), 1-12 [OR]
 3. Zeng, Z., Bromberg, Y. (2022). Inferring potential cancer driving synonymous variants. *Genes* 13 (5), 778 [OR]
 4. **Bromberg, Y., Aptekmann, A., Mahlich, Y., Cook, L., Senn, S., Miller, M., Nanda, V., Ferreiro, D.U., Falkowski, P.G.** (2022) Quantifying Structural Relationships of Metal Binding Sites Suggests Origins of Biological Electron Transfer. *Science Advances*. 14, 8(2):eabj3984 [OR].
 5. Sun, S., Miller, M., Wang, Y., Tyc, K.M., Cao, X., Scott, R.T., Tao, X., **Bromberg, Y.**, Schindler, K., Xing, J. (2022). Predicting embryonic aneuploidy rate in IVF patients using whole-exome sequencing. *Human Genetics*, 1-13.
 6. Lubin JH, Zardecki C, Dolan EM, Lu C, Shen Z, Dutta S, Westbrook JD, Hudson BP, Goodsell DS, Williams JK, Voigt M, Sarma V, Xie L, Venkatachalam T, Arnold S, Alvarado LHA, Catalfano K, Khan A, McCarthy E, Staggers S, Tinsley B, Trudeau A, Singh J, Whitmore L, Zheng H, Benedek M, Currier J, Dresel M, Duvvuru A, Dyszel B, Fingar E, Hennen EM, Kirsch M, Khan AA, Labrie-Cleary C, Laporte S, Lenkeit E, Martin K, Orellana M, de la Campa MO, Paredes I, Wheeler B, Rupert A, Sam A, See K, Zapata SS, Craig PA,
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- Hall BL, Jiang J, Koeppe JR, Mills SA, Pikaart MJ, Roberts R, **Bromberg Y**, Hoyer JS, Duffy S, Tischfield J, Ruiz FX, Arnold E, Baum J, Sandberg J, Brannigan G, Khare SD, Burley SK. (2022) Evolution of the SARS-CoV-2 proteome in three dimensions (3D) during the first six months of the COVID-19 pandemic. *Proteins: Structure, Function, and Bioinformatics* [OR]
7. Zeng, Z., Aptekmann, A.A., Bromberg, Y. (2021) Decoding the effects of synonymous variants. *Nucleic acids research*. 16;49(22):12673-91 [OR].
 8. Mahlich Y, Miller M, Zeng Z, Bromberg Y. (2021) Low Diversity of Human Variation Despite Mostly Mild Functional Impact of De Novo Variants. *Frontiers in Molecular Biosciences*. 8(74). [OR]
 9. Honarbakhsh M, Ericsson A, Zhong G, Isoherranen N, Zhu C, Bromberg Y, Van Buiten C, Malta K, Joseph L, Sampath H, Lackey AI, Storch J, Vetriani C, Chikindas ML, Breslin P, Quadro L. (2021) Impact of vitamin A transport and storage on intestinal retinoid homeostasis and functions. *J Lipid Res*. 62:100046. [OR]
 10. Bernhofer, M., Dallago, C., Karl, T., Satagopam, V., Heinzinger, M., Littmann, M., Olenyi, T., Qiu, J., Schütze, K., Yachdav, G., Ashkenazy, H., Ben-Tal, N., **Bromberg, Y.**, Goldberg, T., Kajan, L., O'Donoghue, S., Sander, C., Schafferhans, A., Schlessinger, A., Vriend, G., Mirdita, M., Gawron, P., Gu, W., Jarosz, Y., Trefois, C., Steinegger, M., Schneider, R., Rost, B. (2021) PredictProtein - Predicting Protein Structure and Function for 29 Years, *Nucleic Acids Research*, gkab354 [OR]
 11. Zhu, C., M. Miller, N. Lusskin, B.B. Pinto, L. Maccario, M. Haggblom, T. Vogel, C. Larose, Bromberg, Y. (2020) Snow Microbiome Functional Analyses Reveal Novel Aspects of Microbial Metabolism of Complex Organic Compounds. *Microbiology Open*, e1100 [OR]
 12. Zhu, C., Miller, M., Zeng, Z., Wang, Y., Mahlich, Y., Aptekmann, A., Bromberg, Y. (2020) Computational approaches for unraveling the effects of variation in the human genome and microbiome. *Annual Review of Biomedical Data Science*. 3 [RW]
 13. ElAbd, H., **Bromberg, Y.**, Hoarfrost, A., Lenz, T., Franke, A., Wendorff, M. (2020) Amino Acid Encoding for Deep Learning Applications. *BMC Bioinformatics*. 21(1): p. 235. [OR]
 14. Zhu, C., Miller, M., Lusskin, N., Mahlich, Y., Wang, Y., Zeng, Z., Bromberg, Y. (2019) Fingerprinting cities: differentiating subway microbiome functionality. *Biology Direct*. 14(1):19. [OR]
 15. Miller, M., Vitale, D., Rost, B., **Bromberg, Y.** (2019) fuNTRp: Identifying protein positions for variation driven functional tuning. *Nucleic Acids Res*. pii: gkz818. [OR]
 16. Wang, Y., Astrakhan, Y., Petersen, B.S., Franke, A., Bromberg, Y. (2019) Identifying Crohn's disease signal from variome analysis. *Genome Med* 11(1), 59 [OR]
 17. Zeng, Z., Bromberg, Y. (2019) Predicting the Effects of Synonymous Variants: Systematic Review and Perspectives. *Frontiers in Genetics*. 10(914) [RW/OR]
 18. Wang, Y., Miller, M., Bromberg, Y. (2019) Identifying mutation-driven changes in gene functionality that lead to venous thromboembolism. *Hum Mutat.*, 40(9):1321-1329 [OR]
 19. Miller, M., Wang, Y., Bromberg, Y. (2019). What went wrong with variant effect predictor performance for the PCM1 challenge. *Hum mutat*, 40(9):1486-1494. [OR]
 20. Clark WT, Kasak L, Bakolitsa C, Hu Z, Andreoletti G, Babbi G, **Bromberg Y**, Casadio R, Dunbrack R, Folkman L, Ford CT. Assessment of predicted enzymatic activity of alpha-N-acetylglucosaminidase (NAGLU) variants of unknown significance for CAGI 2016 (2019). *Hum mutat*. 40(9):1519-1529. [PR]
 21. Kasak, L., Bakolitsa, C., Hu, Z., Yu, C., Rine, J., Dimster-Denk, D.F., Pandey, G., De Baets, G., **Bromberg, Y.**, Cao, C., Capriotti, E., Casadio, R., Van Durme, J., Giollo, M., Karchin, R., Katsonis, P., Leonardi, E., Lichtarge, O., Martelli, P.L., Masica, D., Mooney, S.D., Olatubosun, A., Radivojac, P., Rousseau, F., Pal, L.R., Savojardo, C., Schymkowitz, J., Thusberg, J., Tosatto, S.C.E., Vihinen, M., Valiaho, J., Repo, S., Moul, J., Brenner, S.E., and Friedberg, I. (2019) Assessing Computational Predictions of the Phenotypic Effect of Cystathionine-beta-Synthase Variants. *Hum Mutat*, 40(9):1530-1545. [PR]
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22. Monzon, A.M., Carraro, M., Chiricosta, L., Reggiani, F., Han, J., Ozturk, K., Wang, Y., Miller, M., **Bromberg, Y.**, Capriotti, E., Savojardo, C., Babbi, G., Martelli, P.L., Casadio, R., Katsonis, P., Lichtarge, O., Carter, H., Kousi, M., Katsanis, N., Andreoletti, G., Moulton, J., Brenner, S.E., Ferrari, C., Leonardi, E., Tosatto, S.C.E. (2019). Performance of computational methods for the evaluation of Pericentriolar Material 1 missense variants in CAGI-5. *Hum Mutat.*, 40(9):1474-1485. [PR].
 23. Voskanian, A., Katsonis, P., Lichtarge, O., Pejaver, V., Radivojac, P., Mooney, S.D., Capriotti, E., **Bromberg, Y.**, Wang, Y., Miller, M., Martelli, P.L., Savojardo, C., Babbi, G., Casadio, R., Cao, Y., Sun, Y., Shen, Y., Garg, A., Pal, D., Yu, Y., Huff, C.D., Tavtigian, S.V., Young, E., Neuhausen, S.L., Ziv, E., Pal, L.R., Andreoletti, G., Brenner, S.E., Kann, M.G. (2019) Assessing the performance of in-silico methods for predicting the pathogenicity of variants in the gene CHEK2, among Hispanic females with breast cancer. *Hum Mutat.*, 40(9):1612-1622 [PR]
 24. Pejaver, V., Babbi, G., Casadio, R., Folkman, L., Katsonis, P., Kundu, K., Lichtarge, O., Martelli, P.L., Miller, M., Moulton, J., Pal, L.R., Savojardo, C., Yin, Y., Zhou, Y., Radivojac, P., **Bromberg, Y.** (2019) Assessment of methods for predicting the effects of PTEN and TPMT protein variants. *Hum Mutat.*, 40(9):1495-1506 [PR]
 25. McInnes, G., Daneshjou, R., (Wang, Y., **Bromberg, Y.**, as part of CAGI thromboembolism risk challenge participants) Moulton, J., Brenner, S., Altman, R. (2019) Predicting venous thromboembolism risk from exomes in the Critical Assessment of Genome Interpretation (CAGI) challenges. *Hum Mutat.*, 29 May 2019 [PR]
 26. Honarbakhsh, M., Malta, K., Erricson, A., Zhu, C., **Bromberg, Y.**, Zhong, G., Isoherranen, N., Van Buiten, C., Raskin, I., Chikindas, M., Breslin, P., and Quadro, L. (2019). Interaction between dietary vitamin A, gut microbes, and host vitamin A status. *The FASEB Journal*, 33(1_supplement), pp.484-7. [OR]
 27. Mahlich, Y., Steinegger, M., Rost, B., **Bromberg, Y.** (2018) HFSP: High speed homology-driven function annotation of proteins. *Bioinformatics* 34 (13), i304-i312 [OR]
 28. McDermott, J., **Bromberg, Y.**, Partridge, M. (2018) Ten Simple Rules for Drawing Scientific Comics. *PLoS computational biology*, 14(1), e1005845. [OR]
 29. Zhu, C., Miller, M., Marpaka, S., Vaysberg, P., Rühlemann, M.C., Wu, G., Heinsen, F.A., Tempel, M., Zhao, L., Lieb, W., Franke, A., **Bromberg, Y.** (2018) Functional sequencing read annotation for high precision microbiome analysis. *Nucleic Acids Research*, gkx1209. [OR]
 30. Zhu, C., Mahlich, Y., Miller, M., **Bromberg, Y.** (2018) fusionDB: assessing microbial diversity and environmental preferences via functional similarity networks. *Nucleic Acids Research*, 46(D1), D535-D541 [OR]
 31. Wang, S., Mandell, J.D., Kumar, Y., Sun, N., Morris, M.T., Arbelaez, J., Nasello, C., (**Bromberg, Y.** as part of) Tourette International Genetics Study (TIC Genetics), Tourette Syndrome Genetics Southern and Eastern Europe (TSGENESEE), Tourette Association of America International Consortium for Genetics (TAAICG), Fernandez, T.V., Buxbaum, J.D., De Rubeis, S., Grice, D.E., Xing, J., Heiman, G.A., Tischfield, J.A., Paschou, P., Willsey, A.J., State, M.W. (2018) *De novo* sequence and copy number variants are strongly associated with Tourette Disorder and implicate cell polarity in pathogenesis. *Cell reports*, 24(13), pp.3441-3454 [OR]
 32. Miller, M., Zhu, C., Mahlich, Y., **Bromberg, Y.** (2017) CLuBBer: removing the bioinformatics bottleneck in big data analyses. *Journal of Integrative Bioinformatics*. [OR]
 33. Daneshjou, R., Wang, Y., **Bromberg, Y.**, Bovo, S., Martelli, P.L., Babbi, G., Lena, P.D., Casadio, R., Edwards, M., Gifford, D., Jones, D.T., Sundaram, L., Bhat, R.R., Li, X., Pal, L.R., Kundu, K., Yin, Y., Moulton, J., Jiang, Y., Pejaver, V., Pagel, K.A., Li, B., Mooney, S.D., Radivojac, P., Shah, S., Carraro, M., Gasparini, A., Leonardi, E., Giollo, M., Ferrari, C., Tosatto, S.C.E., Bachar, E., Azaria, J.R., Ofra, Y., Unger, R., Niroula, A., Vihinen, M., Chang, B., Wang, M.H., Franke, A., Petersen, B.S., Pirooznia, M., Zandi, P., McCombie, R., Potash, J.B., Altman, R.B., Klein, T.E., Hoskins, R.A., Repo, S., Brenner, S.E., and Morgan,
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- A.A. (2017) Working toward precision medicine: Predicting phenotypes from exomes in the Critical Assessment of Genome Interpretation (CAGI) challenges. *Hum Mutat.* **38**(9): p. 1182-1192. [PR]
34. Liu, J., Lopez, N., Ahn, Y. B., Goldberg, T., **Bromberg, Y.**, Kerkhof, L. J., Häggblom, M. M. (2017). Novel Reductive Dehalogenases from the Marine Sponge Associated Bacterium *Desulfoluna spongiiphila*. *Environmental Microbiology Reports*, **9**(5):537-49 [OR]
 35. Willsey, A. J., Abdulkadir, M., Barr, C. L. (**Bromberg, Y.** as part of) Tourette Genomics Consortium, Tischfield, J.A., State, M.W., Heiman, G.A. (2017) De Novo Coding Variants Are Strongly Associated with Tourette Disorder. *Neuron*, **94**(3): 486 - 499.e9 [OR]
 36. Mahlich, Y., Hecht, M., De Beer, T.A.P., **Bromberg, Y.**, Rost, B. (2017) Common sequence variants affect molecular function more than rare variants? *Sci Rep.* **7**(1): p. 1608. [OR]
 37. Carraro, M., Minervini, G., Giollo, M., **Bromberg, Y.**, Capriotti, E., Casadio, R., Dunbrack, R., Elefanti, L., Fariselli, P., Ferrari, C., Gough, J., Katsonis, P., Leonardi, E., Lichtarge, O., Menin, C., Martelli, P. L., Niroula, A., Pal, L. R., Repo, S., Scaini, M. C., Vihinen, M., Wei, Q., Xu, Q., Yang, Y., Yin, Y., Zaucha, J., Zhao, H., Zhou, Y., Brenner, S. E., Moul, J., Tosatto, S. C.E. (2017), Performance of in silico tools for the evaluation of p16INK4a (CDKN2A) variants in CAGI. *Hum Mutat.* **2017**;00:1-9 [PR]
 38. Miller, M., **Bromberg, Y.**, Swint-Kruse, L. (2017) Computational predictors fail to identify amino acid substitution effects at rheostat positions. *Sci Rep.* **7**: p. 41329. [OR]
 39. Goldberg, T., Rost, B., **Bromberg, Y.** (2016). Computational prediction shines light on type III secretion origins. *Sci Rep.* **6**: 34516. [OR]
 40. Reeb, J., Hecht, M., Mahlich, Y., **Bromberg, Y.**, Rost, B. (2016) Predicted molecular effects link to system level of disease. *PLoS Comput Biol.* **12**(8): p. e1005047. [OR]
 41. Rost, B., Radivojac, P., **Bromberg, Y.** (2016) Protein function in precision medicine: deep understanding with machine learning. *FEBS Lett.* **590**(15): p. 2327-41 [RW]
 42. Bruse, S., Xing, J., Moreau, M., **Bromberg, Y.**, Jang, J., Wang, N., Picchi, M., Lin, Y., Langley, R., Qualls, C., Klensney-Tait, J., Zabner, J., Mao, J., Belinsky, S., Tesfaigzi, Y., Nyunoya T. (2016) Whole exome sequencing identifies novel candidate genes that modify chronic obstructive pulmonary disease susceptibility. *Hum Genomics.* **10**: p. 1. [OR]
 43. Zhu, C., Delmont, T.O., Vogel, T.M., **Bromberg, Y.** (2015) Functional basis of microorganism classification. *PLoS Comput Biol.* **11**(8): e1004472. [OR]
 44. Hecht, M., **Bromberg, Y.**, Rost, B. (2015) Better prediction of functional effects for sequence variants. *BMC Genomics.* **16**(Suppl 8):S1. [OR]
 45. Yachdav, G., Kloppmann, E., Kajan, L., Hecht, M., Goldberg T., Hamp, T., Hönigschmid, P., Schafferhans, A., Roos, M., Bernhofer, M., Richter, L., Ashkenazy, H., Punta, M., Schlessinger, A., **Bromberg, Y.**, Schneider, R., Vriend, G., Sander, C., Ben-Tal, N., Rost, B. (2014) PredictProtein--an open resource for online prediction of protein structural and functional features. *Nucleic Acids Res.* **W1**: W337-W343 [OR]
 46. Harel, A., **Bromberg, Y.**, Falkowski, P.G., Bhattacharya, D. (2014) Evolutionary history of redox metal-binding domains across the tree of life. *Proc Natl Acad Sci U S A.* **111**(19):7042-7047. [OR]
 47. Senn, S., Nanda, V., Falkowski, P.G., **Bromberg, Y.** (2014). Function-based assessment of structural similarity measurements using metal co-factor orientation. *Proteins.* **82**:648-656 [OR]
 48. **Bromberg, Y.** (2013). Building a genome analysis pipeline to predict disease risk and prevent disease. *J Mol Biol.* **425**: 3993-4005. [RW]
 49. Ren, X., Graham, J.C., Jing, L., Mikheev, A.M., Gao, Y., Lew, J.P., Xie, H., Kim, A.S., Shang, X., Friedman, C., Vail, G., Fang, M.Z., **Bromberg, Y.**, Zarbl, H. (2013). Mapping of Mcs30, a new mammary carcinoma susceptibility quantitative trait locus (QTL30) on rat chromosome 12: identification of fry as a candidate Mcs gene. *PLoS One.* **8**: e70930. [OR]
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50. **Bromberg, Y.**, Kahn, P. C., Rost, B. (2013) Neutral and weakly nonneutral sequence variants may define individuality. *Proc Natl Acad Sci U S A.* **110**: 14255-14260 [OR]
 51. Ellinghaus, D., Zhang, H., Zeissig, S., Lipinski, S., Till, A., Jiang, T., Stade, B., **Bromberg, Y.**, Ellinghaus, E., Keller, A., Rivas, M.A., Skieceviciene, J., Doncheva, N.T., Liu, X., Liu, Q., Jiang, F., Forster, M., Mayr, G., Albrecht, M., Hasler, R., Boehm, B.O., Goodall, J., Berzuini, C.R., Lee, J., Andersen, V., Vogel, U., Kupcinskis, L., Kayser, M., Krawczak, M., Nikolaus, S., Weersma, R.K., Ponsioen, C.Y., Sans, M., Wijmenga, C., Strachan, D.P., McArdle, W.L., Vermeire, S., Rutgeerts, P., Sanderson, J.D., Mathew, C.G., Vatn, M.H., Wang, J., Nothen, M.M., Duerr, R.H., Buning, C., Brand, S., Glas, J., Winkelmann, J., Illig, T., Latiano, A., Annesse, V., Halfvarson, J., D'Amato, M., Daly, M.J., Nothnagel, M., Karlsen, T.H., Subramani, S., Rosenstiel, P., Schreiber, S., Parkes, M., Franke, A. (2013) Association Between Variants of PRDM1 and NDP52 and Crohn's Disease, Based on Exome Sequencing and Functional Studies. *Gastroenterology.* **145**: 339-347 [OR]
 52. **Hecht, M., Bromberg, Y.**, Rost, B. (2013). News from the protein mutability landscape. *J Mol Biol.* **425**: 3937-3948. [OR]
 53. Capriotti, E., Altman, R. B., **Bromberg, Y.** (2013) Collective judgment predicts disease-associated single nucleotide variants. *BMC Genomics.* **14**(Suppl 3): S2 [OR]
 54. **Schaefer, C.**, Meier, A., Rost, B., **Bromberg, Y.** (2012) SNPdbe: constructing an nsSNP functional impacts database. *Bioinformatics.* **28**: 601-602 [OR]
 55. **Schaefer, C., Bromberg, Y.**, Achten, D., Rost, B. (2012) Disease-related mutations predicted to impact protein function. *BMC Genomics.* **13** (Suppl 4): S11 [OR]
 56. Rawat, S. R., Mannisto, M. K., **Bromberg, Y.**, Haggblom, M. M. (2012) Comparative genomic and physiological analysis provides insights into the role of Acidobacteria in organic carbon utilization in Arctic tundra soils. *FEMS Microbiol Ecol.* **82**: 341-355 [OR]
 57. **Harel, A.**, Falkowski, P., **Bromberg, Y.** (2012) TrAnsFuSE refines the search for protein function: oxidoreductases. *Integr Biol (Camb).* **4**: 765-777 [OR]
 58. Capriotti, E., Nehrt, N. L., Kann, M. G., **Bromberg, Y.** (2012) Bioinformatics for personal genome interpretation. *Brief Bioinform.* **13**: 495-512 [RW]
 59. Wainreb, G., Ashkenazy, H., **Bromberg, Y.**, Starovolsky-Shitrit, A., Haliloglu, T., Ruppin, E., Avraham, K. B., Rost, B., Ben-Tal, N. (2010) MuD: an interactive web server for the prediction of non-neutral substitutions using protein structural data. *Nucleic Acids Res* **38**: W523-528[OR]
 60. Zaghoul, N. A., Liu, Y., Gerdes, J. M., Gascue, C., Oh, E. C., Leitch, C. C., **Bromberg, Y.**, Binkley, J., Leibel, R. L., Sidow, A., Badano, J. L., Katsanis, N. (2010) Functional analyses of variants reveal a significant role for dominant negative and common alleles in oligogenic Bardet-Biedl syndrome. *Proc Natl Acad Sci U S A.* **107**: 10602-10607 [OR]
 61. Sester, M., Koebernick, K., Owen, D., Ao, M., **Bromberg, Y.**, May, E., Stock, E., Andrews, L., Groh, V., Spies, T., Steinle, A., Menz, B., Burgert, H. G. (2010) Conserved amino acids within the adenovirus 2 E3/19K protein differentially affect downregulation of MHC class I and MICA/B proteins. *J Immunol.* **184**: 255-267 [OR]
 62. **Bromberg, Y.**, Yachdav, G., Ofran, Y., Schneider, R., Rost, B. (2009) New in protein structure and function annotation: hotspots, single nucleotide polymorphisms and the 'Deep Web'. *Curr Opin Drug Discov Devel.* **12**: 408-419 [RW]
 63. **Bromberg, Y.**, Overton, J., Vaisse, C., Leibel, R. L., Rost, B. (2009) In silico mutagenesis: a case study of the melanocortin 4 receptor. *Faseb J.* **23**: 3059-3069 [OR]
 64. **Bromberg, Y.**, Rost, B. (2009) Correlating protein function and stability through the analysis of single amino acid substitutions. *BMC Bioinformatics.* **10**(Suppl 8): S8 [OR]
 65. Calton, M. A., Ersoy, B. A., Zhang, S., Kane, J. P., Malloy, M. J., Pullinger, C. R., **Bromberg, Y.**, Pennacchio, L. A., Dent, R., McPherson, R., Ahituv, N., Vaisse, C. (2009) Association of functionally significant Melanocortin-4 but not MC-3 receptor mutations with severe adult obesity in a large North American case-control study. *Hum Mol Genet.* **18**: 1140-1147 [OR]
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66. **Bromberg, Y.**, Yachdav, G., Rost, B. (2008) SNAP predicts effect of mutations on protein function. *Bioinformatics*. **24**, 2397-2398 [OR]
 67. **Bromberg, Y.**, Rost, B. (2008) Comprehensive in silico mutagenesis highlights functionally important residues in proteins. *Bioinformatics*. **24**: i207-212 [OR]
 68. Dokmanovic-Chouinard, M., Chung, W. K., Chevre, J. C., Watson, E., Yonan, J., Wiegand, B., **Bromberg, Y.**, Wakae, N., Wright, C. V., Overton, J., Ghosh, S., Sathe, G. M., Ammala, C. E., Brown, K. K., Ito, R., LeDuc, C., Solomon, K., Fischer, S. G., Leibel, R. L. (2008) Positional cloning of "Lisch-Like", a candidate modifier of susceptibility to type 2 diabetes in mice. *PLoS Genet*. **4**: e1000137 [OR]
 69. **Bromberg, Y.**, Rost, B. (2007) SNAP: predict effect of non-synonymous polymorphisms on function. *Nucleic Acids Res*. **35**: 3823-3835 [OR]
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PRE-PRINTS (unpublished only, advisees underlined)

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70. [**Bromberg, Y.** as part of] Genome Interpretation Consortium (2022). CAGI, the Critical Assessment of Genome Interpretation, establishes progress and prospects for computational genetic variant interpretation methods. *arXiv e-prints*, pp.arXiv-2205.
 71. Mason-Buck, G., Graf, A., Elhaik, E., Robinson, J., Pospiech, E., Oliveira, M., Moser, J., Lee, P.K.H., Githae, D., Ballard, D., **Bromberg, Y.**, Casimiro-Soriguer, C.S., Dhungel, E., Ahn, T., Kawulok, J., Loucera, C., Ryan, F., Walker, A.R., Zhu, C., Mason, C.E., Amorim, A., Syndercombe Court, D., Branicki, W., Labaj, P. (2020) DNA Based Methods in Intelligence - Moving Towards Metagenomics. *Preprints*, 2020020158 [RW]
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INVITED PUBLICATIONS (18 total, in reverse publication order, [SO] = scientific opinion, [BC] = book chapter, [MS] = Meeting Summary)

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72. **Bromberg, Y.**, P. Radivojac (2022). Computational interpretation of human genetic variation. *Human Genetics* [SO].
 73. **Bromberg, Y.** (2022). Tightening the (neural) net for protein structure prediction. *Nature Reviews Genetics*, pp.1-1 [SO].
 74. Burley, S. K., **Bromberg, Y.**, Craig, P., Duffy, S., Dutta, S., Hall, B.L., Hudson, B.P., Jiang, J., Khare, S.D., Koeppe, J.R., Lubin, J.H., et.al (2020). "Virtual Boot Camp: COVID-19 evolution and structural biology." *Biochemistry and molecular biology education: a bimonthly publication of the International Union of Biochemistry and Molecular Biology*. [MS]
 75. Hazen, R.M., **Bromberg, Y.**, Downs, R.T., Eleish, A., Falkowski, P.G., Fox, P., Giovannelli, D., Hummer, D.R., Hystad, G., Golden, J.J., Knoll, A.H., Li, C., Liu, C., Moore, E.K., Morrison, S.M., Muscente, A.D., Prabhu, A., Ralph, J., Rucker, M.Y., Runyon, S.E., Warden, L.A., Zhong, H. (2019) Deep Carbon through Deep Time: Data-Driven Insights, in *Deep Carbon: Past to Present*, B.N. Orcutt, I. Daniel, and R. Dasgupta. Cambridge University Press: Cambridge. p. 620-652. <https://deepcarbon.net/project/whole-earth-carbon> [BC]
 76. **Bromberg, Y.**, El-Mabrouk, N., & Radivojac, P. (2019). ISMB/ECCB 2019 Proceedings. *Bioinformatics*, **35**(14), i1-i2. [MS]
 77. **Bromberg, Y.**, Capriotti, E., Carter, H. (2019) VarI-COSI 2018: a forum for research advances in variant interpretation and diagnostics. *BMC Genomics*. **20**(Suppl 8): p.550 [MS]
 78. **Bromberg, Y.**, Radivojac, P. (2018) ISMB 2018 proceedings, *Bioinformatics* **34** (13), i2. [MS]
 79. **Bromberg, Y.**, Capriotti, E., Carter, H. (2016) VarI-SIG 2015: methods for personalized medicine - the role of variant interpretation in research and diagnostics. *BMC Genomics*. **17** Suppl 2: p. 425. [MS]
 80. Beerenwinkel, N., **Bromberg, Y.** (2017) **Ismb/Eccb 2017 Proceedings Papers Committee**. *Bioinformatics*. **33**(14): p. i3-i4. [MS]
 81. **Bromberg, Y.**, Hahn, M.W., Radivojac, P. (2016) Computational approaches to the understanding of evolution of molecular function. *Pac Symp Biocomput*. **22**:1-2 [MS]
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82. Greene, C.S., Foster, J.A., Stanon, B.A., Hogan, D.A., **Bromberg, Y.** (2016) Computational approaches to study microbes and microbiomes. *Pac Symp Biocomput 2016*. :557-567 [MS]
 83. **Bromberg, Y.** and Capriotti, E. (2015) VarI-SIG 2014: from SNPs to variants: interpreting different types of genetic variants. *BMC Genomics*. **16**(Suppl 8):I1. [MS]
 84. **Bromberg, Y.** and Capriotti E. (2015) SNP-SIG 2013: the state of the art of genomic variant interpretation. *Bioinformatics*. **31**(3): 449-450. [MS]
 85. **Bromberg, Y.**, Capriotti, E. (2014) SNP-SIG 2013: from coding to non-coding - new approaches for genomic variant interpretation. *BMC Genomics*. **15**(Suppl 4):S1 [MS]
 86. **Bromberg, Y.**, Capriotti, E. (2013) Thoughts from SNP-SIG 2012: future challenges in the annotation of genetic variations. *BMC Genomics*. **14**(Suppl 3): S1 [MS]
 87. **Bromberg Y.** (2013) Disease Gene Prioritization. *PLoS Comput Biol*. **9**(4): e1002902. [BC]
 88. de Ridder, J., **Bromberg, Y.**, Michaut, M., Satagopam, V.P., Corpas, M., MacIntyre, G., Alexandrov, T. (2013). The young PI buzz: learning from the organizers of the Junior Principal Investigator Meeting at ISMB-ECCB 2013. *PLoS Comput Biol*. **9**: e1003350. [MS]
 89. **Bromberg, Y.**, Capriotti, E. (2012). SNP-SIG Meeting 2011: identification and annotation of SNPs in the context of structure, function, and disease. *BMC Genomics* **13** Suppl 4, S1. [MS]
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INVITED TALKS (144 total, in reverse order)

Keynotes and Plenary

1. 8th IBSE (Integrative Biology and Systems medicine) Colloquium at IIT Madras, India (online). **Are DNA variants bugs or features?** Sep 15, 2021
https://www.youtube.com/watch?v=5FHjyUD36_A
 2. NSF Predicting Pandemic Emergence workshop. Online. *Teaching an old dog new tricks: ideas for preventing pandemics using existing techniques*. Feb 25, 2021
 3. Rutgers Annual ENIGMA Astrobiology Symposium, New Brunswick, NJ. *Increasing Complexity of Nanomachines in Microbial Ancestors / Part 2*. June 16, 2020
 4. Rutgers Annual ENIGMA Astrobiology Symposium, New Brunswick, NJ. *Increasing Complexity of Nanomachines in Microbial Ancestors*. May 8, 2019.
 5. 4D-Workshop (Deep-time Data Driven Discovery), Washington, DC. *Deep learning from deep time: computational techniques for mapping protein structure-function relationships to evolutionary time-scales*. Jun 4, 2018
 6. VIB Applied Bioinformatics in Life Sciences Conference 2018, Leuven, Belgium. *Deeper understanding of microbiomes as a benefit of forgetting microbial names*. Mar 8, 2018.
 7. International Symposium on Molecular Evolution and Medicine. Philadelphia, PA. *Improving variant effect prediction: function, disease, and evolution of "normal."* Sep 16, 2017
 8. Goldschmidt Conference 2017, Geobiology in the Time of Big Data session, Paris, France. *Food and Dating Proteins: Assessing Origins of Biological Electron Transfer*. Aug 14, 2017.
 9. Joint Genome Informatics Workshop (GIW) and International Conference on Bioinformatics (InCoB), GIW/INCOB 2015 conference, Tokyo, Japan. *Cracking the disease code: large-scale genomic data analysis unveils pathogenesis pathways*. Sep 9, 2015.
Post conference interview: <https://www.youtube.com/watch?v=0C3b1tEBP34s>
 10. MidSouth Computational Biology and Bioinformatics Society (MCBIOS) annual conference. Little Rock, AR. *Interpreting genomic data to inform pathogenesis pathways*. Mar 13, 2015.
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General Interest and Outreach

11. Middle School STEM Explorers. *Do computers dream of electronic sheep?* Aug 2, 2022
 12. ISMB Student Council meeting 2021. *Decoding the DNA Blueprints of molecular functionality: the "how did you do this?" version*. Jul 24, 2021
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13. Night Science episode 8. *Yana Bromberg on getting creative with machine learning*. Jun 28, 2021 <http://tinyurl.com/9symbys>
 14. Tools of Science Series. *Case Study: ENIGMA*. Oct 21, 2020 <https://www.youtube.com/watch?v=DGTPPy2fNyc>
 15. I am Brooklyn Tech, Brooklyn Technical High School Alumni Event, *Translational Bioinformatics and computational Biomedicine Think Tank*. Feb 3, 2021
 16. Women in Computer Science Seminar, University of Auckland, Auckland, New Zealand. *Women in Science: strategic decisions for promotion*. Dec 8, 2019
 17. Meaning of Life Symposium. MIT, Cambridge, MA. *42, or if I HAD TO formalize my thoughts*. Mar 13, 2019. <https://www.youtube.com/watch?v=jLeSvhd364o>
 18. TedX Rutgers "Pale Blue Dot" conference, New Brunswick, NJ. *What makes us human? People, microbes, and the "stuff" of life*. Feb 23, 2019. <https://www.youtube.com/watch?v=h8DnekuuaU8>
 19. Green Brook Middle School, Teen Talk club, Greenbrook, NJ. *Adventures in science and life*. Apr 20, 2018
 20. ISMB Junior Principal Investigator Meeting, Orlando, FL. *Climbing the tenure ladder: strategic decisions for promotion*. Jul 10, 2016 <https://www.slideshare.net/secret/nuUow4umoqGYQQ>
 21. Brooklyn Technical High School Invited speaker series, New York, NY. *Curiouser and curiouser: getting involved in bioinformatics research*. Oct 21, 2015.
 22. Career Development for Women in Science meeting, ISMB'2014, Boston, MA. *What makes a job candidate stand out: Perspectives from young group leaders and the people who hire them*. Jul 15, 2014
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Conference presentations

23. UK-Conference of Bioinformatics and Computational Biology 2022, Structural Bioinformatics session. Online. *Protein fossils: metal binding then and now*. Sep 28, 2022
 24. Japanese Geoscience Union conference (JpGU2022), Astrobiology session. Online. *Metallic signatures of the origins of life*. May 24, 2022
 25. Rutgers Microbiology Symposium. New Brunswick, NJ. *Metallic signatures of the origins of life*. May 5, 2022
 26. Representation learning in Biology special session of ISMB2021. Online. **Short DNA sequence embeddings uncover metagenome function**. July 25, 2021
 27. RUMP (Rutgers University Microbiome Program) Seminar. Online. *Microbiome functional annotation informs host phenotypes and environmental changes*. May 14, 2021
 28. DoD Tri-Service Microbiome Consortium Bioinformatics meeting. Online. *Microbiome functional annotation informs host phenotypes and environmental changes*. Apr 14, 2021.
 29. Cell Press and Patterns webinar on Applying Machine Learning to Multi-Omics Data. *Predicting the effects of "invisible" variants*. Dec 9, 2020
 30. Second Workshop on Microbiomics, Metagenomics, and Metabolomics @ ACM-BCB'2019. Niagara Falls, NY. *Importance of functional fitness: microb(iom)ial functional distances describe environmental preferences*. Sep 8, 2019
 31. US-Serbia/West Balkan Data Science Workshop, Belgrade, Serbia. *Deeper understanding of microbiomes as a benefit of forgetting microbial names*. Aug 28, 2018
 32. CAGI'18 meeting, Chicago, IL. *CAGI 2018: PTEN and TPMT challenges, the state of the art in evaluating variant effects*. Jul 5, 2018.
 33. Microbiology at Rutgers Symposium, Rutgers University, New Brunswick, NJ. *Deeper understanding of microbiomes as a benefit of forgetting microbial names*. Feb 2, 2018
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34. i3D retreat, Rutgers University, Newark, NJ. *Understanding molecular function and malfunction*. Oct 25, 2017
 35. Principles of gene circuit design workshop. Oaxaca, Mexico. *Predicting modifiable protein residues for more effective analysis of exonic variation*. Sep 11, 2017
<http://www.birs.ca/events/2017/5-day-workshops/17w5143/videos/watch/201709111648-Bromberg.html>
 36. American Chemical Society (ACS) Symposium Fall meeting, Washington, DC. *Don't forget to set the function to low: predicting modifiable protein residues and effects of their variation*. Aug 21, 2017.
 37. LabRoots Genetics and Genomics Virtual Event. *Not all variants are created equal: what went wrong in the prediction of functional effects of exomic variation*. May 10, 2017
<https://www.youtube.com/watch?v=IPTWtV7b758>
 38. Computational BioMedicine - From genes to networks to biomarkers. University of Southern Denmark (SDU), Odense, Denmark. *Not all variants are created equal: what went wrong in the prediction of functional effects of exomic variation*. April 18, 2017.
 39. The Theobald Smith Society (NJ American Society for Microbiology) meeting. Rutgers University, New Brunswick, NJ. *Tell me what you do and I'll tell you who you are: functional basis of microorganism and microbiome annotation*. Nov 14, 2016
 40. Gordon Research Conference on Human SNPs & Disease, Understanding the Mechanisms of Variant Effects in the Era of Genome Sequencing, Mount Holyoke College, South Hadley, MA. *Interpreting genomics data to infer pathogenesis pathways*. Jun 14, 2016
 41. Keck-RPI Science Day Meeting. Rensselaer Polytechnic Institute, Troy, NY. *Food and Dating Proteins: Assessing Origins of Biological Electron Transfer*. Jun 8, 2016.
 42. Humboldt Technische Universitat Munchen Institute for Advanced Study (TUM-IAS) General Assembly, Garching, Germany. *Functional Basis of Microorganism Classification*. Apr 28, 2016
 43. Pacific Symposium on Biocomputing (PSB 2016) "Computational approaches to study microbes and microbiomes" workshop, Kona, HI. *Functional basis of microorganism classification*. Jan 5, 2016.
 44. Basel Computational Biology Conference ([BC]2 2015), Basel, Switzerland. *Functional basis of microorganism classification*. Jun 8, 2015.
 45. Great Lakes Bioinformatics Conference (GLBio 2015) conference, West Lafayette, IN. *Functional basis of microorganism classification*. May 19, 2015.
 46. Great Lakes Bioinformatics Conference (GLBio 2015) conference, West Lafayette, IN. *Personalized Medicine Tutorial*. May 18, 2015.
 47. GIW/ISCB-Asia 2014 conference, Tokyo, Japan. *The last straw did not break the camel's back: searching for causative variants of polygenic disease disregards individual predisposing genomic differences*. Dec 16, 2014.
 48. IAS Fellows Meeting. Technical University of Munich, Garching, Germany. *Tell me what you do and I'll tell you who you are: exploring functional basis of microorganism classification*. Oct 2, 2014.
 49. Gordon Research Conference on Human SNPs & Disease, Discussion leader, Easton, MA. *Genetics of personalized medicine and rare diseases*. Aug 7th, 2014
 50. BioIT conference, Clinical Genomics Track, Boston, MA. *Mapping Disease Risk to The Human Variome*. Apr 30, 2014.
 51. Critical Assessment of Genome Interpretation (CAGI 2013) meeting, Discussion leader, Berlin, Germany. *Structure vs. evolution for variant interpretation*. Jul 18, 2013
 52. 2013 Summit on Translational Bioinformatics, San Francisco, CA. *Future challenges in the annotation of genetic variation*. Mar 18, 2013
 53. VarI-SIG 2012 Meeting, Long Beach, CA. *Noise in Biology*. Jul 14, 2012.
 54. 107 Statistical Mechanics Conference, Rutgers, NJ. *Differentiating SNP-mediated function disruption from disease*. May 6, 2012.
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55. Critical Assessment of Genome Interpretation (CAGI 2011) meeting, Berkeley, CA. *Evaluating (Crohn's) Disease Predisposition From Exome Data*. Dec 9, 2011
 56. Critical Assessment of Genome Interpretation (CAGI 2011) meeting, Berkeley, CA. *Divining P53 recovery mutants*. Dec 9, 2011.
 57. Meeting of the Society for Bioinformatics in the Nordic Countries, Helsinki, Finland. *Identifying protein functional sites using in silico mutagenesis*. May 5, 2011
 58. High Performance Computing Symposium, Lehigh University, Bethlehem, PA. *Identifying protein functional sites using in silico mutagenesis*. Apr 15, 2011
 59. Symposium on Microbiology, Rutgers, New Brunswick, NJ. *Identifying protein functional sites using in silico mutagenesis*. Feb 4, 2011
 60. Critical Assessment of Genome Interpretation (CAGI 2010) meeting, Berkeley, CA. *Evaluating SNPs using SNAP*. Dec 10, 2010.
 61. Humboldt Technische Universität München Institute for Advanced Study (TUM-IAS) General Assembly, Lake Starnberg, Germany. *Annotating protein function via mutation analysis: a SNAPpy approach*. Apr 12, 2010.
 62. European Conference on Computational Biology, Cagliari, Italy. *Comprehensive in silico mutagenesis highlights functionally important residues in proteins*. Sep 25, 2008
 63. NLM trainee meeting, Bethesda, MD. *Predicting functional effects of nsSNPs: a Neural Network approach*. Jul 11, 2005.
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Special course seminars

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64. FEMS Summer School for Postdocs, Microbiology for a Sustainable Future, Split, Croatia. *Beyond Taxonomy: what can we learn from microbiome function?* Sep 8, 2022
 65. Institute for Quantitative Biomedicine Boot Camp, Rutgers, New Brunswick, NJ. *Evolution and sequence similarity: why are whales more related to cows than to fish?* Jun 23, 2020
<https://www.youtube.com/watch?v=1lC9bwvTrVM>
 66. Microbiome Analysis Workshop, Penn State University, University Park, PA. *Functional basis of microb[iom]e annotation: theory to practice*. Mar 5-6, 2020
 67. Strategies and Techniques for Analyzing Microbial Population Structures (STAMPS) course, Marine Biological Laboratory. *Functional basis of microb[iom]e annotation: theory to practice*. Woods Hole, MA. Jul 31, 2019
 68. The molecular basis of diseases: can we infer phenotypes from protein variant analysis? FEBS 2018 Advanced Course, Bologna, Italy. *Labeling tune-able protein positions for evaluating variation effects*. May 24, 2018
 69. Protein Prediction for Computer Scientists, Undergrad Guest Lectures, Technical University of Munich, Munich, Germany. *Predicting effects of exomic variation*. July 9, 2017
<https://www.youtube.com/watch?v=CQCdiSbGbz0>
<https://www.youtube.com/watch?v=Cs14ZZdjU8U>
 70. Protein Prediction for Computer Scientists, Undergrad Guest Lectures, Technical University of Munich, Munich, Germany. *Functional basis of microorganism classification*. June 25, 2015
<https://www.youtube.com/watch?v=sIypYuJdgEM>
<https://www.youtube.com/watch?v=KNr0Urfu8ns>
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Invited talks

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71. College of Information Sciences and Technology and Penn State Microbiome Center, Joint Seminar, State College, PA. *Learning DNA-ish: Understanding the language of molecular functionality encoded in the genome and the metagenome*. Oct 14, 2021
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72. Dept. of Biology Seminar Series, Emory University, Atlanta, GA. *Learning DNA-ish: Understanding the language of molecular functionality encoded in the genome and the metagenome.* Oct 7, 2021
 73. Westchester Chemical Society Chapter of ACS, Westchester, NY. *Finding Origins of Life in Ancient Biological Electric Wiring.* Oct 6, 2021
 74. Center for Computational Biology and Bioinformatics, Indiana University School of Medicine, Virtual Seminar. *Are DNA variants bugs or features?* Sep 27, 2021
 75. Department of Chemistry and Chemical Biology, Stevens Institute of Technology, Hoboken, NJ. *Microbiome Functionality as a Signature of the Environmental Conditions.* Sep. 24, 2021.
 76. Genome Science Institute Seminar Series, Boston University School of Medicine, Boston, MA. *Decoding the DNA blueprints of human and microbiome molecular functionality.* Feb 17, 2021
 77. Dept. of Computer Science. Johns Hopkins University, Baltimore, MD. *Computational methods for decoding the DNA blueprints of molecular functionality.* Feb 12, 2021
 78. Dept. of Biology, University of North Carolina, Chapel Hill, NC. *Decoding the DNA blueprints of human and microbiome molecular functionality.* Feb 5, 2021
 79. Genomics@Columbia seminar series, Columbia University, New York, NY. *Predicting the effects of "invisible" variants.* Dec 10, 2020
 80. Dept. of Biochemistry and Biophysics, University of Pennsylvania, Philadelphia, PA. *Beyond conservation: defining ranges of protein residue mutability.* Jan 27, 2020.
 81. Knowledge Management Student Group Seminar, University of Auckland, Auckland, New Zealand. *Machine learning and medicine: are the rules the same or is the bar higher?* Dec 19, 2019.
 82. Dept. of Computer Science, Machine Learning Group Seminar, University of Waikato, Hamilton, New Zealand. *Protein function in health and disease.* December 16, 2019
 83. Medical School Seminar, University of Auckland, Auckland, New Zealand. *Protein function in health and disease.* Dec 12, 2019
 84. School of Computer Science Seminar, University of Auckland, Auckland, New Zealand. *Machine learning questions in protein structure and function analysis of healthy and disease genomes and microbiomes.* Dec 10, 2019
 85. Dept. of Computer Science Colloquium, Tufts University, Medford, MA. *Protein structure and function in healthy and disease genomes and microbiomes.* Nov 21, 2019
 86. Dept. of Computer Science Colloquium, Northeastern University, Boston, MA. *Protein function in health and disease.* Nov 20, 2019
 87. Bioinformatics and Computational Biology Program Seminar, Worcester polytechnic Institute, Worcester, MA. *Protein structure and function in healthy and disease genomes and microbiomes.* Oct 3, 2019
 88. Penn Bioinformatics Forum, University of Pennsylvania, Philadelphia, PA. *Protein structure and function in healthy and disease (gen- and microbiom-) omes.* Sep 18, 2019.
 89. Microbiome Center Seminar Series, Penn State University, University Park, PA. *Forget their names: understanding the microbiome without focusing on individual microbes.* Mar 15, 2019.
<https://www.youtube.com/watch?v=7IfFt6H975o>
 90. Dept. of Biology, Emory University, Atlanta, GA. *Forget their names: understanding the microbiome without focusing on individual microbes.* Nov 8, 2018.
 91. Computational Genomics seminar series, Icahn School of Medicine at Mount Sinai, New York, NY. *Cracking the disease code: analyzing genomic variation to identify pathogenesis pathways and predict disease.* Oct 22, 2018
 92. NAI Kickoff Meeting, Rutgers University, New Brunswick, NJ. *Evolution of Nanomachines.* May 21, 2018
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93. School of Informatics, Computing, & Engineering Research Seminar, Indiana University, Bloomington, IN. *Hiding in plain sight: finding new knowledge at the intersection of big data and precision medicine*. Apr 6, 2018
 94. MIT Math & CSAIL Bioinformatics seminar, Cambridge, MA. *Deeper understanding of microbiomes as a benefit of forgetting microbial names*. Apr 4, 2018
 95. Nature International Journal of Science Research seminar, New York, NY. *Cracking the disease code: analyzing genomic variation to identify pathogenesis pathways and predict disease*. Apr 3, 2018
 96. Carnegie Institution Geophysical Laboratory seminar series, Washington, DC. *Timing evolution of biological redox via structural similarity network analysis*. Mar 25, 2018
<https://www.youtube.com/watch?v=ewoO1lbuyjE>
 97. Center for Bioinformatics Research series, Indiana University, Bloomington, IN. *Functional basis of microbiome annotation: theory to practice*. Dec 7, 2017
 98. IBD Genetics Consortium Cycle IV meeting, Bethesda, MD. *Functional basis of microbiome annotation in disease: theory to practice*. Nov 30, 2017
 99. Genomic Instability & Cancer Genetics Research Program Meeting, Rutgers Cancer Institute, New Brunswick, NJ. *Hiding in plain sight: finding new knowledge at the intersection of big data and precision medicine*. Nov 9, 2017
 100. Epidemiology colloquium, Medical center of the university of Munich, LMU, Munich, Germany. *Functional basis of microbiome annotation: theory to practice*. Jul 11, 2017
 101. Peking Union Medical College Hospital and Chinese Academy of Medical Sciences joint seminar, Beijing, China. *Functional basis of microbiome analysis*. May 16, 2017
 102. State Key Laboratory of Microbial Metabolism seminar, Shanghai Jiao Tong University, Shanghai, China. *Functional basis of microbiome analysis*. May 15, 2017
 103. Henan Provincial People's Hospital Seminar, Zhengzhou, China. *Functional basis of microbiome analysis*. May 13, 2017
 104. Systems Biology seminar at Boston University, Boston, MA. *Functional basis of microorganism and microbiome annotation*. Apr 14, 2017.
 105. Department of Computer Science Seminar Series, NJIT, Newark, NJ. *Not all variants are created equal: what went wrong in the prediction of functional effects of exomic variation*. Feb 21, 2017.
 106. Department of Computational Biology Seminar Series, University of Lausanne, Switzerland. *Functional basis of microbiome annotation*. Jan 26, 2017.
 107. Computational Biology Group, Department of Computational Biology, University of Lausanne, Switzerland. *Not all variants are created equal: what went wrong in the prediction of functional effects of exomic variation*. Jan 23, 2017.
 108. Helmholtz Zentrum Seminar. Munich, Germany. *Functional Bases of Microorganism Classification*. May 23, 2016.
 109. European Bioinformatics Institute (EBI), European Molecular Biology Laboratory (EMBL), Hinxton, England. *Extracting molecular function patterns from microbial genomes and metagenomes*. Apr 10, 2016
 110. University College London, Department of Structural & Molecular Biology, London, England. *Extracting molecular function patterns from microbial genomes and metagenomes*. Apr 5, 2016
 111. Randall Seminar Series, Dept. of Biological Sciences, University of Idaho, Moscow, ID. *Functional Bases of Microorganism Classification*. Mar 11, 2016.
 112. How Proteins Became the Catalysts of Life Workshop, Rutgers, Piscataway, NJ. *Food and Dating Proteins: Assessing Origins of Biological Electron Transfer*. Jan 28th, 2016
 113. Frontiers in Bioinformatics and Systems Biology Colloquium. UCSD, Sand Diego, CA. *Mapping genomic variation to complex diseases*. Jan 14, 2016.
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114. New York Genome Center Five Points Lecture. New York Genome Center, New York, NY. *Mapping genomic variation to complex diseases*. Dec 2, 2015.
 115. Rutgers University Center for Proteomics Research (CIPR) workshop on Advances in Computational and Data Science for Investigative Discovery in Biology and Medicine. New Brunswick, NJ. *Does a computer dream of sheep genes, proteins, and functions?* Oct 22, 2015.
 116. Joint research retreat of the Rutgers School of Environmental and Biological Sciences (SEBS, New Brunswick) and the Rutgers Center for Computational and Integrative Biology (CCIB), Camden, NJ. *"Function" in biology: a computational analysis*. Oct 9, 2015.
 117. Rutgers Child Health Institute (CHI) Science Seminar Series meeting, New Brunswick, NJ. *Interpreting genomic data to inform pathogenesis pathways*. Sep 28, 2015.
 118. Microbiome Working Group meeting, Columbia University Medical Center (CUMC), New York, NY. *Tell me what you do and I'll tell you who you are: functional basis of microorganism classification*. Sep 14, 2015
 119. Dept. of Biomedical Informatics, Columbia University, New York, NY. *Interpreting genomic data to inform pathogenesis pathways*. Apr 21, 2015.
 120. Dept. of Biomedical and Health Informatics, The Children's Hospital of Pennsylvania, Philadelphia, PA. *Interpreting genomic data to inform pathogenesis pathways*. Apr 8, 2015.
 121. Dept. of Biological Sciences, Seton Hall University, South Orange, NJ. *Functional Bases of Microorganism Classification*. Mar 26, 2015
 122. Dept. of Biochemistry and Molecular Biology, University of Kansas Medical Center, Kansas City, KS. *The last straw did not break the camel's back: searching for causative variants of polygenic disease disregards individual predisposing genomic differences*. Oct 31, 2014.
 123. Basel Computational Biology Center (BC2), Basel University Biozentrum / Swiss Institute for Bioinformatics, Basel, Switzerland. *The last straw did not break the camel's back: searching for causative variants of polygenic disease disregards individual predisposing genomic*. Oct 6, 2014.
 124. Fermentation Club Seminar, Rutgers, New Brunswick, NJ. *Functional Bases of Microorganism Classification*. Sep 12, 2014
 125. Interactive Group on Human Genetics, UMDNJ, Piscataway, NJ. *Exome analysis for disease gene prioritization*. Mar 11, 2014.
 126. Computing Seminar Series, Oklahoma Medical Research Foundation, Oklahoma City, OK. *Functional basis of microorganism classification*. Oct 3, 2013
 127. Research Seminar Series, Oklahoma Medical Research Foundation, Oklahoma City, OK. *Noise in the (human) machine: functionally neutral variants, individuality, and disease*. Oct 3, 2013
 128. Dept. of Biomedical Informatics retreat, *Invited presentation and panel discussion*, Columbia University, NY. **Adventures in Bioinformatics**. Sep 10, 2013
 129. Dept. of Genetics Adjunct Professor Seminar, Rutgers, NJ. *Noise in biology or how neutral variants define individuality*. Feb 25, 2013
 130. Ecology and Evolution Membership Seminar, Rutgers, NJ. *Computing prokaryotic diversity using functional similarity*. Oct 25, 2012
 131. Environmental Microbial Genomics Group, Ecole Centrale de Lyon, Université de Lyon, France. *Computing prokaryotic diversity using functional similarity*. Oct 1, 2012
 132. Buck Institute for Research on Aging, Novato, CA. *Noise in Biology*. Jul 6, 2012.
 133. Institute of Clinical Molecular Biology, Christian-Albrechts-University, Kiel, Germany. *CAGI 2011: Critical Assessment of Genome Interpretation: SNAP results*. Mar 9, 2012.
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134. Dept. of Biochemistry and Molecular Biology, The George S Wise Faculty of Life Sciences, Tel Aviv University, Tel Aviv, Israel. *Identifying protein functional sites using in silico mutagenesis*. Jul 21, 2011
 135. Center for Biotechnology and Medicine, Rutgers, New Brunswick, NJ. *Defining "functional effects" in mutation databases*. Jun 9, 2011.
 136. Joint European Molecular Biology Laboratory (EMBL) and Technische Universitat Munchen (TUM) retreat, Schliersee, Germany. *Identifying protein functional sites using in silico mutagenesis*. Apr 2, 2011
 137. Buck Institute for Research on Aging, Novato, CA. *Identifying protein functional sites using in silico mutagenesis*. Mar 18, 2011
 138. Environmental and Occupational Health Sciences Institute, Rutgers, New Brunswick, NJ. *Identifying protein functional sites using in silico mutagenesis*. Feb 17, 2011
 139. Center for Computational and Integrative Biology, Rutgers, Camden, NJ. *Annotating protein function via mutation analysis: a SNAPpy approach*. Nov 22, 2010
 140. Genentech, San Francisco, CA. *Predicting functional effects of nsSNPs using SNAP: Screening for Non-Acceptable Polymorphisms*. Feb 17, 2010
 141. Fermentation Club seminar, Rutgers, NJ. *Annotating protein function via mutation analysis: a SNAPpy approach*. Jan 29, 2010.
 142. Monsanto, St. Louis, MO. *Predicting functional effects of nsSNPs using SNAP: Screening for Non-Acceptable Polymorphisms*. Apr 21, 2009
 143. European Molecular Biology Laboratories (EMBL), Heidelberg, Germany. *Protein function in terms of mutation*. Mar 11, 2009.
 144. Basel University Biozentrum / Swiss Institute for Bioinformatics, Basel, Switzerland. *Protein function in terms of mutation*. Mar 9, 2009.
 145. Dept. of Structural & Molecular Biology, United College of London, London, UK. *Protein function in terms of mutation*. Dec 19, 2008
 146. GeneCards meeting, Crown Human Genome Center, Weizmann Institute, Rehovot, Israel. *Comprehensive in silico mutagenesis highlights functionally important residues in proteins*. Sep 10, 2008.
 147. Dissertation Defense, Columbia University, NY. *SNAP: Screening for Non-Acceptable Polymorphisms*. Dec 5, 2006.
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FUNDING

ACTIVE

NASA CAN8 Astrobiology Institute (Falkowski, PI) National Aeronautics and Space Administration (NASA) <i>ENIGMA: Evolution of Nanomachines in Geospheres and Microbial Ancestors</i> Building computational tools to understand the (early life on Earth) evolution of protein structures necessary for biological electron transfer.	04/2018 – 04/2023 \$1,216,147 to lab
NIH 1 R01 MH115958 (Heiman, PI) National Institutes of Mental Health (NIMH) <i>1/7 Collaborative Genomic Studies of Tourette Disorder</i> Optimizing computational pipeline (AVA,Dx) for identifying Tourette genes from genome variation data.	06/2018 – 03/2023 \$102,532 to lab

NSF CAREER Award: 1553289 (Bromberg, PI) NSF Advances in Biological Informatics (ABI) <i>Molecular functional diversity of microbes and microbiomes</i> Developing tools for functional analysis and classification of bacteria, with applications to microbiome (community) analysis.	04/2016 – 04/2023 \$1,091,177 total
NIH 1 R01 DE032216 (Coker, PI) NIH National Institute of Dental and Craniofacial Research (NIDCR) <i>HPV, HIV and Oral Microbiota Interplay in Nigerian Youth</i> Developing deep learning methods for mining microbiome data from children with persistent HPV infections.	07/2022 – 08/2026 \$498,076 to lab
NSF Predictive Intelligence for Pandemic Prevention Phase I: Development Grants (Fefferman, PI) NSF Division of Computing and Communication Foundations (CCF) <i>Predicting Emergence in Multidisciplinary Pandemic Tipping-Points (PREEMPT)</i>	08/2022 – 08/2023 \$35,465 to lab
PENDING	
NSF Collaborative Research (Nanda, PI) NSF Molecular Foundations for Biotechnology (MFB) <i>Building Molecular Circuits with a Protein Electronics Kit</i>	09/2022 – 08/2025
COMPLETED	
NIH 1 R[U]01 GM115486 01 (Bromberg, PI) National Institutes of General Medical Sciences (NIGMS) <i>AVA,Dx: Analysis of Variation for Association with Disease</i>	09/2015 – 05/2022
Alfred P. Sloan Foundation workshop grant (Hazen, PI) <i>4-D Workshop: Deep-Time Data-Driven Discovery and Evolution of Earth</i>	11/2017 – 06/2018
Hans Fischer Fellowship (Bromberg, PI) Institute of Advanced Studies at the Technische Universitat Munchen <i>FuSiON: Functional Basis of Microorganism Classification.</i>	07/2014 – 10/2018
NIH 5 U24 MH068457 12 (Tischfield, PI) National Institutes of Mental Health (NIMH) <i>Center for Genomic Studies on Mental Disorders</i>	06/2013 – 05/2018
Informatics Research Starter Grant (Bromberg, PI) PhRMA Foundation <i>Analysis of Variation for Association with Disease.</i>	01/2015 – 12/2015
GBMF2807 (Falkowski, PI) Gordon and Betty Moore Foundation <i>Evolutionary map of life's electron transfer reactions.</i>	04/2011 – 04/2014
NIH R43-LM010156-01 (Bromberg, PI) National Library of Medicine (NLM), SBIR Phase 1 <i>Improved Manuscript Search Through PubSeq</i>	06/2009 – 03/2011

TEACHING

COURSES (primary audience and % responsibility)

Rutgers University, New Brunswick, NJ

11:126:485/16:765:585 <i>Bioinformatics</i> (Grad/U-grad, 100%)	2011-Present
A 13-week lecture/computational lab series developed by Dr. Bromberg. Curriculum requirement for the Biotechnology major, and a well-attended elective for other majors.	
01:460:225 <i>Astrobiology</i> (U-grad, 8%)	2019-Present
16:681:530 <i>Introduction to Molecular Medicine</i> (Grad, 8%)	2017
16:682:550 <i>Special Topics in Microbial Biology: Bioinformatics Journal Club</i> (Grad, 50%)	2015
11:115:201 <i>Contemporary issues in Biochemistry</i> (U-grad, 5%)	2014-Present
Douglas Project SUPER <i>Introduction to Scientific Research</i> (U-grad, 8%)	2014-2018
16:215:601 <i>Seminar in Ecology</i> (Grad, 8%)	2014-2016
11:115:404/504 <i>General Biochemistry</i> (U-grad, 5%)	2013-Present
11:115:301 <i>Introduction to Biochemistry</i> (U-grad, 10%)	2012-2013
16:682:521 <i>Seminars in Microbiology</i> (Grad, 8%)	2010-Present
11:115:428/16:115:616 <i>Homology Modeling of Proteins</i> (Grad/U-grad, 10%)	2011-2012

Technical University of Munich, Munich, Germany

<i>Protein Prediction for Computer Scientists</i> (Undergrad, Guest Lectures)	2015-2019
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University of Bologna, Italy

<i>Mapping genomes to disease</i> (Intensive graduate course, 100%)	2015, '17, '18
A 20-hour lecture and practical applications series newly developed by Dr. Bromberg for students in University of Bologna International Masters Bioinformatics program.	

STUDENTS AND POST-DOCS (Rutgers, unless otherwise specified; IAS=Institute for Advanced Study, TUM=Technische Universitat Munchen, SDU=U of Southern Denmark)

Post-Docs (2 current of 11 total)

1. Dr. Prabakaran Ram	06/2022 – present
2. Dr. Yannick Mahlich	09/2019 – present
3. Dr. Ariel Aptekmann	04/2019 – 03/2022
4. Dr. Adrienne Hoarfrost	04/2019 – 06/2020
5. Dr. Kenneth McGuinness	09/2018 – 09/2019
6. Dr. Maximillian Miller	03/2018 – 01/2021
7. Dr. Chengsheng Zhu	04/2017 – 03/2020
8. Dr. Anton Molyboha	02/2017 – 02/2018
9. Dr. Wenfeng Kang	05/2014 – 09/2014
10. Dr. Stefan Senn	03/2012 – 03/2014
11. Dr. Arye Harel	09/2010 – 04/2014

Ph.D. Students (2 current of 8 total)

1. Maria De Paolis Kaluza	Northeastern University, Computer Science, , co-advisor	08/2022 – Present
2. Henri Chung	U Iowa, Bioinformatics and Computational Biology, co-advisor	09/2021 – Present
3. Zishou Zeng	Rutgers, Quantitative Biomedicine	09/2017 – 05/2022
4. Carl Maximilian Miller	TUM Bioinformatics and Computational Biology	11/2015 – 03/2017
5. Yanran Wang	Rutgers, Microbiology and Molecular Genetics	04/2015 – 04/2020
6. Yannick Mahlich	TUM Bioinformatics and Computational Biology, IAS student	11/2014 – 07/2019
7. Tatyana Goldberg	TUM Bioinformatics and Computational Biology, co-advisor	01/2012 – 05/2016
8. Chengsheng Zhu	Rutgers, Microbial Biology	04/2011 – 04/2017

Graduate Students, non-PhD thesis advisement (17 total)

1. Silvia Benevenuto	Computer Science, University of Padova. Visiting Scientist	02/2022 – 08/2022
2. Pavan Kumar Velaga	Computer Science, Master's work	06/2021 – 02/2022
3. Margot Shumaker	Microbial Biology, Rotation	09/2021 – 12/2021
4. Justin Koestrich	Molecular Biosciences, Rotation	02/2021 – 04/2021
5. Kyle Flannery	Molecular Biosciences, Rotation	02/2021 – 04/2021
6. Alyssa Carillo	Molecular Biosciences, Rotation	12/2020 – 02/2021
7. Mikhail Bass	Quantitative Biomedicine, Rotation	02/2020 – 05/2020
8. Dan Liu	Quantitative Biomedicine, Rotation	02/2020 – 05/2020
9. Yanick Spreen	TUM Bioinformatics and Computational Biology, Masters student	10/2019 – 06/2020
10. Jan Siess	Quantitative Biomedicine, Rotation	09/2018 – 12/2018
11. Arnav Pondicherry	Rutgers-RWJMS medical school, Independent Research	10/2017 – 01/2018
12. Alexandra Pushkar	Quantitative Biomedicine, Rotation	09/2016 – 07/2017
13. Nidia Obscura Acosta	University of Helsinki, Mathematics and Computer Science. Master thesis	05/2016 – 05/2017
14. Lisheng Zhou	Microbiology and Molecular Genetics, Rotation	01/2012 – 03/2012
15. Ben Jelen	Environmental Sciences, Rotation	08/2011 – 12/2013
16. Maximilian Hecht	TUM Bioinformatics and Computational Biology, Project supervisor	01/2011 – 05/2015
17. Christian Schaefer	TUM Bioinformatics and Computational Biology, Project supervisor	01/2010 – 11/2012

Thesis Committees (advisor, 11 total)

1. Tongji Xing	Molecular Biosciences	Present
2. Nora Lopez	Microbial Biology	09/2021

3.	Yuanchao Zhang	<i>Microbiology and Molecular Genetics</i>	01/2020
4.	Juan Miguel Cejuela Perez	<i>TUM Bioinformatics and Computational Biology</i>	03/2018
5.	Nicole Koribanics	<i>Environmental Microbiology</i>	06/2017
6.	Christian Wiwie	<i>SDU Dept. of Mathematics and Computer Science</i>	01/2017
7.	Nora Lopez	<i>Environmental Microbiology</i>	12/2016
8.	Ashley DeNegre	<i>Ecology and Evolution</i>	11/2015
9.	Guy Yachdav	<i>TUM Bioinformatics and Computational Biology</i>	07/2015
10.	Omar Haq	<i>Molecular Biophysics and Computational Biology</i>	05/2012
11.	Mauro Lapelosa	<i>Molecular Biophysics and Computational Biology</i>	10/2011

Undergraduate Students (IR = Independent Research; 22 total)

1.	Andrew Sam (<i>Biotechnology</i>) <i>Evolution of Synuclein</i>	Honors Thesis: S'22
2.	Daniel Liu (<i>Biotechnology</i>) <i>Deep learning the viral language</i>	IR: S'21, F'21
3.	Michael Gleyzer (<i>Statistics / Mathematics</i>) <i>Predicting variant functional effects using machine learning</i>	IR: Sum'20
4.	Darin Mak (<i>Biomedical Engineering</i>) <i>Linking metagenome data to the human genome</i>	IR: F'19, S'20
5.	Shon Shmushkevich (<i>Molecular Biology, Hunter College</i>) <i>Microbial functionality in marine sediments</i>	IR: Sum'19, F'19, S'20
6.	Anusha Siddaramanna (<i>Computer Science</i>) <i>Optimizing scoring of variation-disrupted genes</i>	IR: Sum'19, F'19
7.	Alexis Faulborn (<i>Plant Biotechnology and Biochemistry</i>) <i>Predicting position-driven non-synonymous variant functional effects</i>	IR: S'19, Sum'19
8.	Revanth Korrapolu (<i>Computer Science</i>) <i>Optimizing large-scale sequence alignments</i>	IR: F'18, S'19
9.	Chahna Patel (<i>Biomedical Engineering</i>) <i>Differentiating eukaryotic and prokaryotic origins of sequencing reads</i>	IR: S'18, Sum'18, F'18, S'19
10.	Nicholas Lusskin (<i>Biotechnology</i>) <i>Differentiating microbiome environments by read functional analysis</i>	IR: F'17, S'18, F'18, S'19
11.	Daniel Vitale (<i>Biology</i>) <i>Differentiating toggles and rheostats in variant effect predictions</i>	IR: S'17
12.	Riva Patel (<i>Biochemistry</i>) <i>Annotating oxygen requirements of oxidoreductases</i>	IR: F'15, S'16
13.	Srinayani Marpaka (<i>Genetics, Computer Science</i>)	IR: S'15, F'15

Extracting metagenome function from read data

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|--|---|
| 14. Akash Mitra (<i>Genetics, Biotechnology</i>)
<i>Analysis of functional effect of synonymous variants</i> | IR: S'15 |
| 15. Linda Cook (<i>Computer Science</i>)
<i>Evolution of metal-binding folds for electron transfer</i> | Aresty Summer Science program,
Sum'14, IR: S'15 |
| 16. Manfred Roos (<i>Computational Biology and Bioinformatics, TUM</i>)
<i>Prediction of active sites from protein sequence</i> | Bachelor Thesis,
2012-2014 |
| 17. Pavel Vaysberg (<i>Biotechnology</i>)
<i>Extracting metagenome function from read data.</i> | IR: S'14, F'14 |
| 18. Remy Koch (<i>Biotechnology</i>)
<i>Automated annotation of protein catalytic sites</i> | IR: S'14 |
| 19. Catherine Plotts (<i>Nutritional Sciences</i>)
<i>MeSH term-based identification of disease-related publications</i> | IR: F'12, S'13 |
| 20. Sean Bryan (<i>Biotechnology</i>)
<i>Automated annotation of protein sequence sites of importance.</i> | IR: Sum'12, F'12,
S'13 |
| 21. Steven Yen (<i>Biotechnology</i>)
<i>Disease-gene identification using NLP</i> | IR: Sum'12 |
| 22. Chris Rusnak (<i>Mathematics, Biology</i>)
<i>Sequence analysis for active site identification in proteins.</i> | DIMACS REU
Sum'11, IR: from
F'11 to S'13 |

High School Students (4 total)

1. Jeffrey Yang	Westfield High School	05/2018-01/2019
2. Alexander Chong	Brooklyn Technical High School	06/2013-09/2013
3. Eva Justo	Brooklyn Technical High School	06/2013-09/2013
4. Brian Okonski	Brooklyn Technical High School	06/2013-09/2013

SERVICE

ABBREVIATIONS: *CAGI* = Critical Assessment of Genome Interpretation, *ECCB* = European Conference on Computational Biology, biannually joint with ISMB; *GRC* = Gordon Research Conference, *IEEE* = Institute of Electrical and Electronics Engineers, *ISCB* = International Society for Computational Biology; *ISMB* = Intelligent Systems in Molecular Biology, flagship conference of ISCB; *PSB* = Pacific Symposium on Biocomputing; *VarI - COSI/-SIG* = Variation Interpretation Community of Special Interest / Satellite Interest Group Meeting

Professional Activities

Member, Technical Advisory Board, IIT Madras, India	2021-Present
Member, CAGI Scientific Council	2020-Present
Member, Brooklyn Technical High School Advisory Board	2020-Present
Member, ISCB COVID-19 Taskforce	2020-2021
Vice President, ISCB Board of Directors	2020-Present

Chair , GRC Human Single Nucleotide Polymorphisms & Disease	2020-2022
Vice-Chair , GRC Human Single Nucleotide Polymorphisms & Disease	2018
Organizer , Computational and Translational Methods for Cancer Genomics Workshop	2018
Chair , Proceedings, ISCB-Latin America conference	2018
Chair , 4-D Workshop for Deep-Time Data Driven Discovery	2018
Member , Editorial Board, Journal of Bacteriology	2018-Present
Member , Informatics Advisory Committee for the PhRMA Foundation	2018-2020
Member , ISMB Awards and Keynote Selection Committee	2017-2019
Program Chair , IEEE International Conference on Bioinformatics and Biomedicine (BIBM)	2017
Chair , Computational Approaches to Understanding the Evolution of Molecular Function, PSB	2017
Chair , Proceedings track, joint ISMB/ECCB conference	2017-2019
Chair , Computational Approaches to Study Microbes and Microbiomes workshop, PSB	2016
Director , ISCB Board of Directors	2016-Present
Chair , Proteins Theme, ISCB-Latin America conference	2016
Organizer , GRC Power Hour (women in science)	2016
Chair , Disease Theme, joint ISMB/ECCB conference	2015-2016
Guest Associate Editor , PLoS Computational Biology	2013-Present
Organizer , Junior PI Meeting, ISMB/ECCB	2013-2015
Editor , BMC Genomics, Proceedings of the VarI-SIG special issue	2011-2019
Chair (and VarI-COSI representative since 2014), VarI-SIG	2011-2019
Organizer , Grant Writing Workshop and Tutorial, ISMB/ECCB	2011-2012
Chair , ISMB/ECCB Poster and Short Talks Sessions	2010-2015

Grant Proposal Review

Panels: PhRMA foundation, NIH BDMA (National Institutes of Health Biodata Management and Analysis), NIH *ad hoc* panels, NSF BIO and CISE (National Science Foundation Biological Sciences AND Computer and Information Science and Engineering) directorate panels, DOE *ad hoc* panels

External: European Research Council (ERC), Swiss National Science Foundation (SNSF), Polish National Academy of Sciences (NCN), French National Institute of Health and Medical Research (INSERM), KU Leuven (University of Leuven, Belgium) Research Council

University service and membership

Member, Rutgers advancement and Promotions Committee	2021-Present
Chair, Dept. of Biochemistry and Microbiology and Dept. of Marine and Coastal Sciences joint faculty search committee	2017
Founding Member, IQB (Institute for Quantitative Biomedicine) Graduate program, Rutgers	2015-Present
Member, Eveleigh Fenton endowed chair Biochemistry and Microbiology faculty search committee	2015
Member, Center for Digestive Health in the New Jersey Institute for Food, Nutrition, and Health (IFNH) faculty search committee	2015

Member, Rutgers Discovery Informatics Institute Internal Advisory Board	2014-Present
Member, Human Genetics Institute of NJ	2012-Present
Member, Ecology and Evolution Graduate Program, Rutgers	2012-Present
Member, University Physical Facilities and Space Committee	2012-2013
Associate Clinical Member, the Cancer Institute of New Jersey (CINJ)	2011-Present
Member, Microbiology and Molecular Genetics Program, Rutgers	2011-Present
Member (and 2014 Chair), Admissions and Academic Standards Committee of the Microbial Biology Graduate Program, Rutgers	2011-2014
Research Experience for Undergraduates (REU) Mentor	2011-2013
Member, Microbial Biology Program, Rutgers	2010-Present
Member, Interview Committee, SEBS General Honors Program	2010-Present

Affiliations

Member, ISCB Representative, FASEB Science Research Conferences Advisory Committee	2016-2017
Member, ASM: American Society for Microbiology	2014-2017
Member, Theobald Smith Society	2014-2017
Member, American Medical Informatics Association (AMIA)	2003-2007
Member, ISCB	2003-Present
Member, Phi Beta Kappa Society	2001-Present
