

YANA BROMBERG

Assistant Professor

Department of Biochemistry and Microbiology

Rutgers University, School of Environmental and Biological Sciences

76 Lipman Drive, Suite 218, New Brunswick, NJ 08901

Phone: +1.848.932.5638 / E-mail: yanab@rci.rutgers.edu

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 (Biomedical Informatics), Andrey Rzhetsky (Biomedical Informatics), Lawrence Shapiro (Biochemistry/Molecular 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

2001

Magna Cum Laude

Brooklyn Technical High School, Brooklyn, NY

Biomedical Track

1997

Honor roll, third in class of 1200

APPOINTMENTS

Institute of Advanced Studies, Technical University of Munich, Germany

**Hans Fischer Fellow, Dept. of Bioinformatics and
Computational Biology**

2014-Present

Rutgers University, New Brunswick, NJ

Adjunct Assistant Professor, Dept. of Genetics

2013-Present

Rutgers University, New Brunswick, NJ

Assistant Professor, Dept. of Biochemistry and Microbiology

2010-Present

BioSof, LLC, New York, NY

Chief Scientific Officer (Bioinformatics Tool Development)

2008-Present

JPM Global, New York, NY

Software Developer (Natural Language Processing Tools)

2007-2008

Columbia University, New York, NY

**Post-doctoral Research Scientist, Dept. of Biochemistry and
Molecular Biophysics**

2006-2010

HONORS

ISCB Board member nomination (<i>Voting In Progress</i>)	2015
Hans Fischer Fellowship for Outstanding Early Career Scientists, Institute of Advanced Studies at Technical University of Munich	2014-2017
Brooklyn Tech Younger Alumni Recognition Award for Career Progress	2014
ISCB Travel Fellowship Award	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 Scholarship recipient	1997

ABBREVIATIONS USED: *AACR* = American Association for Cancer Research; *AMIA* = American Medical Informatics Association; *ASHG* = American Society for Human Genetics; *BSB* = Brazilian Symposium on Biocomputing; *CAGI* = Critical Assessment of Genome Interpretation; *ECCB* = European Conference on Computational Biology, biannually joint with ISMB; *ISCB* = International Society for Computational Biology; *ISMB* = Intelligent Systems in Molecular Biology, flagship conference of ISCB; *PSB* = Pacific Symposium on Biocomputing; *TUM* = Technische Universität München; *VarI-SIG* = Variation Satellite Interest Group Meeting at ISMB/ECBB

SCHOLARSHIP

PUBLICATIONS (33 total, in reverse publication order, *corresponding author, advises, [OR] = Original Research, [RW] = Review, [MS] = Meeting Summary)

1. **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]
 2. Hecht, M.*, **Bromberg, Y.**, Rost, B. (2015) Better prediction of functional effects for sequence variants. *BMC Genomics*, **16**(Suppl 8):S1. [OR]
 3. **Bromberg, Y.*** and Capriotti E.* (2015) SNP-SIG 2013: the state of the art of genomic variant interpretation. *Bioinformatics* **31** (3): 449-450. [MS]
 4. 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]
 5. **Bromberg, Y.*** and Capriotti, E.* (2014) SNP-SIG 2013: from coding to non-coding - new approaches for genomic variant interpretation. *BMC Genomics* 2014, **15**(Suppl 4):S1 [MS]
 6. 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 AB. (2014) PredictProtein--an open resource for online prediction of protein structural and functional features. *Nucleic Acids Res.* 2014:gku366 [OR]
 7. 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]
 8. 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]
 9. **Bromberg, Y.*** (2013). Building a genome analysis pipeline to predict disease risk and prevent disease. *J Mol Biol* **425**, 3993-4005. [RW]
-

-
10. **Bromberg, Y.***, Kahn, P. C., and Rost, B. (2013) Neutral and weakly nonneutral sequence variants may define individuality. *Proc Natl Acad Sci U S A* 110, 14255-14260 [OR]
 11. 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]
 12. **Hecht, M.***, **Bromberg, Y.**, Rost, B. (2013). News from the protein mutability landscape. *J Mol Biol* 425, 3937-3948. [OR]
 13. **Bromberg, Y.*** and Capriotti, E.* (2013) Thoughts from SNP-SIG 2012: future challenges in the annotation of genetic variations. *BMC Genomics* 14 Suppl 3, S1 [MS]
 14. Capriotti, E.* , Altman, R. B., and **Bromberg, Y.*** (2013) Collective judgment predicts disease-associated single nucleotide variants. *BMC Genomics* 14 Suppl 3, S2 [OR]
 15. **Bromberg Y.*** (2013) Chapter 15: Disease Gene Prioritization. *PLoS Comput Biol* 9(4): e1002902. [Book Chapter]
 16. 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., Annese, 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]
 17. **Bromberg, Y.*** and 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]
 18. **Schaefer, C.***, Meier, A., Rost, B., **Bromberg, Y.** (2012) SNPdbe: constructing an nsSNP functional impacts database. *Bioinformatics* 28, 601-602 [OR]
 19. **Schaefer, C.***, **Bromberg, Y.**, Achten, D., and Rost, B. (2012) Disease-related mutations predicted to impact protein function. *BMC Genomics* 13 Suppl 4, S11 [OR]
 20. Rawat, S. R., Mannisto, M. K., **Bromberg, Y.**, and 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]
 21. **Harel, A.***, Falkowski, P., and **Bromberg, Y.*** (2012) TrAnsFuSE refines the search for protein function: oxidoreductases. *Integr Biol (Camb)* 4, 765-777 [OR]
 22. Capriotti, E.* , Nehrt, N. L.* , Kann, M. G.* , **Bromberg, Y.*** (2012) Bioinformatics for personal genome interpretation. *Brief Bioinform* 13, 495-512 [RW]
 23. 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]
 24. 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]
 25. Sester, M., Kobernick, 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]
-

-
26. **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]
 27. 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 Melanocortin-3 receptor mutations with severe adult obesity in a large North American case-control study. *Hum Mol Genet* 18, 1140-1147 [OR]
 28. **Bromberg, Y.***, and Rost, B. (2009) Correlating protein function and stability through the analysis of single amino acid substitutions. *BMC Bioinformatics* 10 Suppl 8, S8 [OR]
 29. **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]
 30. 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., and 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]
 31. **Bromberg, Y.***, Yachdav, G., Rost, B. (2008) SNAP predicts effect of mutations on protein function. *Bioinformatics* 24, 2397-2398 [OR]
 32. **Bromberg, Y.*** and Rost, B. (2008) Comprehensive in silico mutagenesis highlights functionally important residues in proteins. *Bioinformatics* 24, i207-212 [OR]
 33. **Bromberg, Y.*** and Rost, B. (2007) SNAP: predict effect of non-synonymous polymorphisms on function. *Nucleic Acids Res* 35, 3823-3835 [OR]
-

INVITED TALKS (51 total, in reverse order)

Keynotes

1. 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*. September 9, 2015.
 2. MidSouth Computational Biology and Bioinformatics Society (MCBIOS) annual conference. Little Rock, AR. *Interpreting genomic data to inform pathogenesis pathways*. March 13, 2015.
-

Conference presentations

1. Basel Computational Biology Conference ([BC]2 2015). Basel, Switzerland. *Functional basis of microorganism classification*. June 8, 2015.
 2. Great Lakes Bioinformatics Conference (GLBio 2015). *Functional basis of microorganism classification*. May 19, 2015.
 3. Great Lakes Bioinformatics Conference (GLBio 2015). *Personalized Medicine Tutorial*. May 18, 2015.
 4. 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*. December 16, 2014.
 5. 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*. October 2, 2014.
 6. Gordon Research Conference on Human Single Nucleotide Polymorphisms & Disease, Personalized Medicine and Rare Diseases session, *Discussion leader*, Stonehill College, Easton, MA. *Genetics of Personalized Medicine and Rare diseases*. August 7, 2014
-

-
7. ISMB'2014 conference, Career Development for Women in Science meeting, Boston, MA. *What makes a job candidate stand out: Perspectives from young group leaders and the people who hire them.* July 15, 2014
 8. BioIT conference, Clinical Genomics Track, Boston, MA. *Mapping Disease Risk to The Human Variome.* April 30, 2014.
 9. 2013 Summit on Translational Bioinformatics, San Francisco, CA. *Future challenges in the annotation of genetic variation.* March 18, 2013
 10. VarI-SIG 2012 Meeting, Long Beach, CA. *Noise in Biology.* July 14, 2012.
 11. 107 Statistical Mechanics Conference, Rutgers, NJ. *Differentiating SNP-mediated function disruption from disease.* May 6, 2012.
 12. Critical Assessment of Genome Interpretation (CAGI 2011) meeting, Berkeley, CA. *Evaluating (Crohn's) Disease Predisposition From Exome Data.* December 9, 2011
 13. CAGI 2011 meeting, Berkeley, CA. *Divining P53 recovery mutants.* December 9, 2011.
 14. Meeting of the Society for Bioinformatics in the Nordic Countries, Helsinki, Finland. *Identifying protein functional sites using in silico mutagenesis.* May 5, 2011
 15. High Performance Computing Symposium, Lehigh University, Bethlehem, PA. *Identifying protein functional sites using in silico mutagenesis.* April 15, 2011
 16. Symposium on Microbiology, Rutgers, New Brunswick, NJ. *Identifying protein functional sites using in silico mutagenesis.* February 4, 2011
 17. CAGI 2010 meeting, Berkeley, CA. *Evaluating SNPs using SNAP.* December 10, 2010.
 18. Humboldt Technische Universitat Munchen Institute for Advanced Study (TUM-IAS) General Assembly, Lake Starnberg, Germany. *Annotating protein function via mutation analysis: a SNAPpy approach.* April 12, 2010.
 19. ECCB 2008 conference, Cagliari, Italy. *Comprehensive in silico mutagenesis highlights functionally important residues in proteins.* September 25, 2008
 20. NLM trainee meeting, Bethesda, MD. *Predicting functional effects of nsSNPs: a Neural Network approach.* July 11, 2005.
-

Invited talks

-
1. Dept. of Biomedical Informatics, Columbia University, New York, NY. *Interpreting genomic data to inform pathogenesis pathways.* April 21, 2015.
 2. Dept. of Biomedical and Health Informatics, The Children's Hospital of Pennsylvania, Philadelphia, PA. *Interpreting genomic data to inform pathogenesis pathways.* April 8, 2015.
 3. Dept. of Biological Sciences, Seton Hall University, South Orange, NJ. *Functional Bases of Microorganism Classification.* March 26, 2015
 4. 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.* October 31, 2014.
 5. 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.* October 6, 2014.
 6. Fermentation Club Seminar, Rutgers, New Brunswick, NJ. *Functional Bases of Microorganism Classification.* September 12, 2014
 7. Interactive Group on Human Genetics, UMDNJ, Piscataway, NJ. *Exome analysis for disease gene prioritization.* March 11, 2014.
 8. Computing Seminar Series, Oklahoma Medical Research Foundation, Oklahoma City, OK. *Functional basis of microorganism classification.* October 3, 2013
 9. Research Seminar Series, Oklahoma Medical Research Foundation, Oklahoma City, OK. *Noise in the (human) machine: functionally neutral variants, individuality, and disease.* October 3, 2013
-

-
10. Dept. of Biomedical Informatics retreat, *Invited presentation and panel discussion*, Columbia University, NY. **Adventures in Bioinformatics**. September 10, 2013
 11. Dept. of Genetics Adjunct Professor Seminar, Rutgers, NJ. *Noise in biology or how neutral variants define individuality*. February 25, 2013
 12. Ecology and Evolution Membership Seminar, Rutgers, NJ. *Computing prokaryotic diversity using functional similarity*. October 25, 2012
 13. Environmental Microbial Genomics Group, Ecole Centrale de Lyon, Université de Lyon, France. *Computing prokaryotic diversity using functional similarity*. October 1, 2012
 14. Buck Institute for Research on Aging, Novato, CA. *Noise in Biology*. July 6, 2012.
 15. Institute of Clinical Molecular Biology, Christian-Albrechts-University, Kiel, Germany. *CAGI 2011: Critical Assessment of Genome Interpretation: SNAP results*. March 9, 2012.
 16. 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*. July 21, 2011
 17. Center for Biotechnology and Medicine, Rutgers, New Brunswick, NJ. *Defining "functional effects" in mutation databases*. June 9, 2011.
 18. EMBL / TUM retreat, Schliersee, Germany. *Identifying protein functional sites using in silico mutagenesis*. April 2, 2011
 19. Buck Institute for Research on Aging, Novato, CA. *Identifying protein functional sites using in silico mutagenesis*. March 18, 2011
 20. Environmental and Occupational Health Sciences Institute, Rutgers, New Brunswick, NJ. *Identifying protein functional sites using in silico mutagenesis*. February 17, 2011
 21. Center for Computational and Integrative Biology, Rutgers, Camden, NJ. *Annotating protein function via mutation analysis: a SNAPpy approach*. November 22, 2010
 22. Genentech, San Francisco, CA. *Predicting functional effects of nsSNPs using SNAP: Screening for Non-Acceptable Polymorphisms*. February 17, 2010
 23. Fermentation Club seminar, Rutgers, NJ. *Annotating protein function via mutation analysis: a SNAPpy approach*. January 29, 2010.
 24. Monsanto, St. Louis, MO. *Predicting functional effects of nsSNPs using SNAP: Screening for Non-Acceptable Polymorphisms*. April 21, 2009
 25. European Molecular Biology Laboratories (EMBL), Heidelberg, Germany. *Protein function in terms of mutation*. March 11, 2009.
 26. Basel University Biozentrum / Swiss Institute for Bioinformatics, Basel, Switzerland. *Protein function in terms of mutation*. March 9, 2009.
 27. Dept. of Structural & Molecular Biology, United College of London, London, UK. *Protein function in terms of mutation*. December 19, 2008
 28. GeneCards meeting, Crown Human Genome Center, Weizmann Institute, Rehovot, Israel. *Comprehensive in silico mutagenesis highlights functionally important residues in proteins*. September 10, 2008.
 29. Dissertation Defense, Columbia University, NY. *SNAP: Screening for Non-Acceptable Polymorphisms*. December 5, 2006.
-

POSTERS (17 total, in reverse order of presentation, advisees)

1. Zhu, C., Delmont, T.O., Vogel, T., **Bromberg Y.** Functional basis of microorganism classification. *IAS Spring General Assembly 2015, Garching, Germany*
 2. Zhu, C., Delmont, T.O., Vogel, T., **Bromberg Y.** Functional basis of microorganism classification. *PSB 2015, Kona, HI*
 3. Cook, L., Karkar, S., **Bromberg Y.** Tracing evolution of electron transfer. Aresty Summer Science Program for Undergraduates. *Research Poster Session 2014. New Brunswick, NJ*
-

-
4. Zhu, C., **Bromberg, Y.** GenSpec, genome-based species identification tool for archaea. *ISMB 2014, Boston, MA*
 5. Xing, J., Bruse, S., Moreau, M., **Bromberg Y.**, Jang, J., Wang, N., Picchi, M., Klensney-Tait, J., Zabner, J., Mao, J., Belinsky, S., Nyunoya, T. Whole Exome Sequencing in Severe Chronic Obstructive Pulmonary Disease. *ASHG 2014, San Diego, CA*
 6. **Bromberg Y.** Variome-based Identification of Crohn's Disease Predisposition. *ASHG 2013, Boston, MA*
 7. Goldberg T., Rost B., **Bromberg Y.** Sequence-Based Prediction of Bacterial Type III Effector Proteins. *ISMB/ECCB 2013, Berlin, Germany*
 8. Hecht M., Bromberg Y., Rost B. SNAP2 a method and server for predicting functional effects. *ISMB/ECCB 2013, Berlin, Germany*
 9. Jelen, B.I., Zhu, C., **Bromberg, Y.**, Falkowski, P. G. The Number of Pathway Genes Limits the Diffusion of Biogeochemical Pathways Across the Network of Life. *GRC Geobiology, Ventura, CA.*
 10. Goldberg T., Hamp T., **Bromberg Y.**, Vicedo E., Rost B. Sub-cellular localization: high-throughput annotation of entire genomes and a source for novel phylogenetic insights. *ISCB Asia 2012, Shenzhen, China*
 11. Goldberg T., Hamp T., **Bromberg Y.**, Vicedo E., Rost B. Sub-cellular localization: high-throughput annotation of entire genomes and a source for novel phylogenetic insights. *ECCB 2012, Basel, Switzerland*
 12. Senn S., Falkowski P.G., **Bromberg Y.** Structural Relationships of Oxidoreductases. *ISMB 2012, Long Beach, CA*
 13. Harel, A., Chan, C.X., Bhattacharya, D., Falkowski, P.G., **Bromberg, Y.** Evolution of transition metal binding domains. *ISMB/ECCB 2011, Vienna, Austria*
 14. **Bromberg, Y.**, Rost B. Improved manuscript search through PubSeq. *PSB 2011, Kona, HI*
 15. Rosman, D.S., **Bromberg, Y.**, Weinstein, A., Reiss, M. Phenotypic Diversity of Disease-associated Transforming Growth Factor- β (TGF- β) Type I Receptor Gene (TGFB1) Mutants. *AACR 2011 meeting, Washington, DC*
 16. **Bromberg, Y.**, Rost B. Annotating functionally important residues of the Melanocortin-4 receptor. *ISMB/ECCB 2009, Stockholm, Sweden*
 17. **Bromberg, Y.**, Rost B. SNPfun: correlating variation and function. *ISMB 2008, Toronto, Canada*
-

COURSES (primary audience and level of involvement indicated in parenthesis)

Rutgers University, New Brunswick, NJ

11:126:485/16:765:585 <i>Bioinformatics</i> (Grad/Undergrad, 100%)	2011-Present
A 13-lecture and 13-computational lab series newly developed by Dr. Bromberg. It is currently a curriculum requirement for the Biotechnology major, and a well-attended elective for other majors, <i>e.g.</i> Biochemistry, Genetics, and Computer Science.	
11:115:201 <i>Contemporary issues in Biochemistry</i> (Undergrad, 1/26 lectures)	2014-Present
Douglas Project SUPER <i>Introduction to Scientific Research</i> (Undergrad, 1/14 seminars)	2014-Present
16:215:601 <i>Seminar in Ecology</i> (Grad, 1/14 seminars)	2014-Present
11:115:404/504 <i>General Biochemistry</i> (Undergrad, 1/26 lectures)	2013-Present
11:115:301 <i>Introduction to Biochemistry</i> (Undergrad, 2/26 lectures)	2012-2013
16:682:521 <i>Seminars in Microbiology</i> (Grad, 1/13 seminars)	2010-Present
11:115:428/16:115:616 <i>Homology Modeling of Proteins</i> (Grad/Undergrad, 2/26 lectures)	2011-2012

University of Bologna, Italy

<i>Mapping genomes to disease</i> (Intensive graduate course, 100%)	May 2015
A 20-hour lecture and practical applications series newly developed by Dr. Bromberg for students in University of Bologna International Masters Bioinformatics program. It will be transformed into a special topics graduate course in personalized medicine at Rutgers.	

SERVICE

Professional Activities

Co-chair, Computational Approaches to Study Microbes and Microbiomes workshop, PSB	2016
Chair, Disease Theme, ISMB/ECCB main conference	2015-Present
Guest Associate Editor, PLoS Computational Biology	2013-Present
Co-Organizer, Junior PI Meeting, ISMB/ECCB	2013-Present
Discussion leader, CAGI 2012/2013 meeting , Berlin, Germany. <i>Structure vs. evolution for variant interpretation.</i>	July 2013
Co-Chair, VarI-SIG	2011-Present
Editor, VarI-SIG Proceedings, BMC Genomics	2011-Present
Organizer, Grant Writing Workshop and Tutorial, ISMB/ECCB	2011-2012
Chair, ISMB/ECCB Poster and Short Talks Sessions	2010-Present

Ad hoc Grant Proposal Reviews

National Scientific Foundation (US NSF), 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

Conference Review Committees

BioOntologies Proceedings	2014
AMIA Translational Bioinformatics Proceedings	2012
BSB Proceedings	2012

VarI-SIG Proceedings	2011-Present
ISMB Killer App Award	2010-2012
ISMB/ECCB/PSB Proceedings	2005-Present

Journal Review

Bioinformatics, Biomedical Informatics, BMC Bioinformatics, BMC Genomics, Current Opinion in Molecular Therapeutics, Current Protein & Peptide Science, DATABASE: Journal of Biological Databases and Curation, Journal of Molecular Biology, European Journal of Drug Metabolism and Pharmacokinetics, Integrative Biology, Human Molecular Genetics, Human Mutation, IEEE ACM Transactions on Computational Biology & Bioinformatics, PLoS Computational Biology, PLoS One, PLoS Genetics, Proteins, Protein Science, The FASEB Journal

Membership and affiliations

Member of the Eveleigh Fenton endowed chair faculty search committee	2015
Member of the Rutgers Discovery Informatics Institute (RDI2) Internal Advisory Board	2014-present
Chair of Admissions and Academic Standards Committee of the Microbial Biology Graduate Program, Rutgers	2014
Member of the ASM, American Society for Microbiology	2014-Present
Member of the Theobald Smith Society	2014-Present
Member of the Human Genetics Institute of NJ	2012-Present
Member of the Ecology and Evolution Graduate Program, Rutgers	2012-Present
Member of the Physical Facilities and Space Committee	2012-2013
Member of Admissions and Academic Standards Committee of the Microbial Biology Graduate Program, Rutgers	09/2011-08/2014
Research Experience for Undergraduates (REU) Mentor	
Member of Microbiology and Molecular Genetics Program, Rutgers	2011-Present
Associate Clinical Member, the Cancer Institute of New Jersey (CINJ)	2011-Present
Member of Microbial Biology Program, Rutgers	2010-Present
Member of Interview Committee, SEBS General Honors Program	2010-Present
Member of International Society for Computational Biology (ISCB)	2010-Present
Member of Phi Beta Kappa Society	2003-Present
