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Positions

Associate professor and director, Bioinformatics Core, Buck Institute for Research on Aging, 2014-present.
Adjunct associate professor, University of California, Berkeley, Department of Plant and Microbial Biology, 2015-present.
Adjunct associate professor, University of Southern California Davis School of Gerontology, 2014-present.
Assistant professor, University of California, Berkeley, Department of Molecular and Cell Biology, 2006-2014.
Visiting faculty member, The Evergreen State College, 2002-2003.

Education

Postdoctoral fellow, lab of Robert Gentleman, Fred Hutchinson Cancer Research Institute, 2005-2006.
Postdoctoral fellow, lab of Leonid Kruglyak, Fred Hutchinson Cancer Research Institute, 2000-2004.
Ph.D. in biophysics, lab of Ken A. Dill, UC San Francisco, September 2000.
B.S. with honors, in biochemistry, Brown University, 1994.
B.A. in French, Brown University, 1994.

Other service to the scientific community

Deputy Editor, *PLoS Computational Biology*, 2013-present.
Associate Editor, *PLoS Computational Biology*, 2011-2013.
Associate Editor, *G3: Genes/Genomes/Genetics*, 2011-2016.
Member, Program Committee, Yeast Genetics Meeting, 2016, 2018.
Chair, Population Genomics and Microevolution session, Asilomar Fungal Genetics Conference, 2015.
Member, Organizing Committee, International Conference on Quantitative Genetics, 2012, 2016.

Honors

Glenn Foundation Glenn Award for Research in Biological Mechanisms of Aging, 2016.
Ellison Medical Foundation New Scholar in Aging, 2008-2012.
UC Berkeley Hellman Family Faculty Fund recipient, 2008-09.
Burroughs-Wellcome Career Award at the Scientific Interface, 2005-2010.
National Institutes of Health Postdoctoral Fellowship, 2001-2003.
University of California Regents' Fellowship, 1999-2000.
National Science Foundation Predoctoral Fellowship, 1995-1998.

Peer-reviewed publications

- Hill RZ, Hoffman B, Morita T, Campos SM, Lumpkin EA, **Brem RB**, Bautista DM. The signaling lipid sphingosine-1-phosphate regulates mechanical pain. *eLife* 7:e33285, 2018.
- Coradetti ST, Pinel D, Geiselman G, Ito M, Mondo S, Reilly MC, Cheng YF, Bauer S, Grigoriev I, Gladden JM, Simmons BA, **Brem RB**, Arkin AP, Skerker JM. Functional genomics of lipid metabolism in the oleaginous yeast *Rhodospiridium toruloides*. *eLife* 7:e32110, 2018. **Featured article, eLife Digest.**
- Bay RA, Rose N, Barrett R, Bernatchez L, Ghalambour CK, Lasky JR, **Brem RB**, Palumbi SR, Ralph P. Predicting evolutionary responses to contemporary environmental change using population genomic data. *American Naturalist* 189(5):463-473, 2017.
- Nelson CS, Beck JN, Wilson KA, Pilcher ER, Kapahi P, **Brem RB**. Cross-phenotype association tests uncover genes mediating nutrient response in *Drosophila*. *BMC Genomics* 17(1):867, 2016.
- Mark KA, Dumas KJ, Bhaumik D, Schilling B, Davis S, Oron TR, Sorensen DJ, **Brem RB**, Melov S, Ramanathan A, Gibson BW, Lithgow GJ. Vitamin D promotes protein homeostasis and longevity via the IRE-1/XBP-1/SKN-1 pathways. *Cell Reports* 17(5):1227-1237, 2016.
- Mostovoy Y, Thiemicke A, Hsu TY, **Brem RB**. The role of transcription factors at antisense-expressing gene pairs in yeast. *Genome Biology and Evolution* 8(6):1748-61, 2016.
- Roop JI, Chang KC, **Brem RB**. Polygenic evolution of a sugar specialization tradeoff in yeast. *Nature* 530(7590):336-9, 2016. **Featured article in Cell Systems, March 2016 issue.**
- Katewa SD, Akagi K, Bose N, Rakshit K, Camarella T, Zheng X, Hall D, Davies S, Nelson C, **Brem RB**, Ramanathan A, Sehgal A, Biebultowicz JM, Kapahi P. Peripheral circadian clocks mediate dietary restriction-dependent changes in lifespan and fat metabolism in *Drosophila*. *Cell Metabolism* 23(1):143-54, 2016.
- McCormick M, ..., **Brem RB**, ..., Kennedy BK. A comprehensive analysis of replicative lifespan in 4,698 single-gene deletion strains uncovers novel mechanisms of aging. *Cell Metabolism* 22(5):895-906, 2015.
- Morita T[^], McClain SP[^], Batia LM, Pellegrino M, Wilson SR, Kienzler MA, Lyman K, Olsen ASB, Wong JF, Zappia KJ, Stucky CL, **Brem RB**^{*}, Bautista DM^{*}. HTR7 mediates serotonergic acute and chronic itch. *Neuron* (87)1:124-38, 2015. [^]Co-author; ^{*}Co-corresponding author
- Kellner R, Bhattacharyya A, Poppe S, Hsu TY, **Brem RB**, Stukenbrock E. Expression profiling of the wheat pathogen *Zymoseptoria tritici* reveals genomic patterns of transcriptions and host-specific regulatory programs. *Genome Biology and Evolution* 6(6):1353-65, 2014.
- Wong VL, Ellison CE, Eisen MB, Pachter L, **Brem RB**. Structural variation among wild and industrial strains of *Penicillium chrysogenum*. *PLoS ONE* 9(5):e96784, 2014.
- Ellison CE, Kowbel D, Glass NL, Taylor JW, **Brem RB**. Discovering functions of unannotated genes from a transcriptome survey of wild fungal isolates. *mBio* 5(2):e01046-13, 2014.
- Lee HN[^], Mostovoy Y[^], Hsu TY, Chang A, **Brem RB**. Divergence of iron metabolism in wild Malaysian yeast. *G3: Genes/Genomes/Genetics* 3(12):2187-94, 2013. [^]Co-author
- Schraiber JG, Mostovoy Y, Hsu TY, **Brem RB**. Inferring pathway evolutionary histories from transcriptional profiling data. *PLoS Computational Biology* 9(10):e1003255, 2013.

- Roop JI, **Brem RB**. Rare variants in hypermutable genes underlie common morphology and growth traits in wild *S. paradoxus* yeasts. *Genetics* 195(2):513-525, 2013.
Cover article, July 2014 issue; featured paper, October 2013 issue highlights.
- Palma-Guerrero J, Hall CR, Kowbel D, Welch J, Taylor JW, **Brem RB***, Glass NL*. Genome-wide association identifies novel loci involved in fungal communication. *PLoS Genetics* 9(8):e1003669, 2013. *Co-corresponding author
- Gerhold KA, Pellegrino M, Tsunozaki M, Morita T, Leitch DB, Tsuruda PR, **Brem RB**, Catania KC, Bautista DM. The star-nosed mole reveals clues to the molecular basis of mammalian touch. *PLoS ONE* 8(1):e55001, 2013.
- Jenkins PA, Song YS, **Brem RB**. Genealogy-based methods for inference of historical recombination and gene flow and their application in *Saccharomyces cerevisiae*. *PLoS ONE* 7(11):e46947, 2012.
- Yoon OK, Hsu TY, Im JH, **Brem RB**. Genetics and regulatory impact of alternative polyadenylation in human B-lymphoblastoid cells. *PLoS Genetics* 8(8):e1002882, 2012.
- Martin HC[^], Roop JI[^], Schraiber JG[^], Hsu TY, **Brem RB**. Evolution of a membrane protein regulon in *Saccharomyces*. *Molecular Biology and Evolution*, 29(7):1747-1756, 2012. [^]Co-author
- Zhu J, Sova P, Xu Q, Dombek KM, Xu EY, Vu H, Tu Z, **Brem RB**, Bumgarner RE, Schadt EE. Stitching together multiple data dimensions reveals interacting metabolic and transcriptomic networks that modulate cell regulation. *PLoS Biology* 10(4):e1001301, 2012.
- Denby CM, Im JH, Yu RC, Pesce CG, **Brem RB**. Negative feedback confers mutational robustness in yeast transcription factor regulation. *PNAS* 109(10):3874-8, 2012.
- Lee HN, Magwene PM, **Brem RB**. Natural variation in *CDC28* underlies morphological phenotypes in an environmental yeast isolate. *Genetics* 188(3):723-30, 2011.
- Ellison CE, Hall C, Kowbel D, Welch J, **Brem RB**, Glass NG, Taylor JW. Population genomics and local adaptation in wild isolates of a model microbial eukaryote. *PNAS* 108(7):2831-6, 2011. **Faculty of 1000 Must Read/Recommended Paper.**
- Levin TC, Glazer AM, Pachter L, **Brem RB**, Eisen MB. Exploring the genetic basis of variation in gene predictions with a synthetic association study. *PLoS ONE* 5(7):e11645, 2010.
- Yoon OK, **Brem RB**. Non-canonical transcript forms in yeast and their regulation during environmental stress. *RNA* 16(6):1256-67, 2010. **Faculty of 1000 Recommended Paper.**
- Bullard JH, Mostovoy J, Dudoit S, **Brem RB**. Polygenic and directional regulatory evolution across pathways in *Saccharomyces*. *PNAS* 107(11):5058-5063, 2010.
- Dmitrov LN, **Brem RB**, Kruglyak L, Gottschling DS. Polymorphisms in multiple genes contribute to the spontaneous mitochondrial genome instability of *Saccharomyces cerevisiae* S288C strains. *Genetics* 183(1):365-83, 2009.
- Zhu J, Zhang B, Smith EN, Drees B, **Brem RB**, Kruglyak L, Bumgarner RE, Schadt EE. Integrating large-scale functional genomic data to dissect the complexity of yeast regulatory networks. *Nature Genetics*, 40(7):854-61, 2008.
- Ronald J, Tang H, **Brem RB**. Genome-wide evolutionary rates in laboratory and wild yeast. *Genetics* 174(1):541-544, 2006.
- Ronald J, **Brem RB**, Whittle J, Kruglyak L. Local regulatory variation in *Saccharomyces cerevisiae*. *PLoS Genetics* 1(2):e25, 2005.
- Brem RB[^]**, Storey JD[^], Whittle J, Kruglyak L. Genetic interactions between polymorphisms that affect gene expression in yeast. *Nature* 436(7051):701-703, 2005. [^]Co-author

- Brem RB**, Kruglyak L. The landscape of genetic complexity across 5700 expression traits in yeast. *PNAS* 102(5):1572-7, 2005.
- Yvert G, **Brem RB**, Whittle J, Akey JM, Foss E, Smith EN, Mackelprang R, Kruglyak L. Trans-acting regulatory variation in *Saccharomyces cerevisiae* and the role of transcription factors. *Nature Genetics* 35(1): 57-64, 2003.
- Brem RB**[^], Yvert G[^], Clinton R, Kruglyak L. Genetic dissection of transcriptional regulation in budding yeast. *Science* 296(5568):752-255, 2002. [^]Co-author.
- Brem R**, Chan HS, Dill KA. Extracting microscopic energies from oil-phase solvation experiments. *Journal of Physical Chemistry B* 104(31):7471-7482, 2000.
- Brem R**, Dill KA. The effect of multiple binding modes on empirical modeling of ligand docking to proteins. *Protein Science* 8:1134-1143, 1999.
- Finer-Moore JS, Liu L, Birdsall DL, **Brem R**, Apfeld J, Santi DV, Stroud RM. Contributions of orientation and hydrogen bonding to catalysis in Asn229 mutants of thymidylate synthase. *Journal of Molecular Biology* 276(1):113-29, 1998.
- Sun S, **Brem R**, Chan HS, Dill KA. Designing amino acid sequences to fold with good hydrophobic cores. *Protein Engineering* 8(12):1205-13, 1995.
- Brem RB**, Robbins SG, Wilson DJ, O'Rourke LM, Mixon RN, Robertson JE, Planck SR, Rosenbaum JT. Immunolocalization of integrins in the human retina. *Investigative Ophthalmology and Visual Science* 35(9):3466-74, 1994.
- Robbins SG, **Brem RB**, Wilson DJ, O'Rourke LM, Robertson JE, Westra I, Planck SR, Rosenbaum JT. Immunolocalization of integrins in proliferative retinal membranes. *Investigative Ophthalmology and Visual Science* 35(9):3475-85, 1994.

Other publications

- Brem RB**. Genomic data analyses unveil cases of polygenic evolution. *Microbe*, January 2014, pp. 18-22.

Patent applications

- Neuronal S1PR3: a biomarker and therapeutic target for acute and chronic itch. U.S. Provisional patent filed, October 2016.

Current grant support

- NIH National Institute of Neurological Disorders and Stroke R56 NS098097-01, Genetic mapping of novel molecular players in itch. Bautista (PI), 9/17-8/18. Role: co-PI.
- NIH National Institute of Aging R21 AG054121-01, The role of natural genetic variants in nutrient-dependent changes in healthspan using *D. melanogaster*. Kapahi (PI), 8/17-7/19. Role: co-PI.
- NIH National Institute of Aging R03 AG056938-01, Screening potassium and phosphate binder drugs for lifespan and healthspan effects in invertebrates. **Brem (PI)**, 7/17-7/19. Role: PI.
- NIH National Institute of General Medical Sciences R01 GM120430-A1, High-resolution, genome-scale mapping of natural variation between reproductively isolated individuals. **Brem (PI)**, 5/17-5/21. Role: PI.
- University of California Office of the President Multicampus Research Programs and Initiatives. UC Valley Fever Research Initiative. Sil (PI). 1/17-12/20. Role: co-PI.
- Glenn Award for Research in Biological Mechanisms of Aging. **Brem (PI)**. 11/16-11/18. Role: PI.

Joint Genome Institute Community Sequencing Project 1460, Pioneering fungal mutagenesis using Tn-seq. **Brem (PI)**. 10/13-10/18. Role: PI.

Completed grant support

US Department of Energy Office of Science, Office of Biological and Environmental Research Project 000213609, Development of the oleaginous yeast *Rhodospiridium toruloides* as a new model organism for a systems-level analysis of lipid productivity. **Brem (PI)**. 9/14-9/17. Role: PI.

NIH National Institute of Aging R01 AG043080, System approaches to determine mechanisms underlying yeast replicative aging. Kennedy (PI). 9/12-8/17. Role: co-PI.

Corporate sponsored research, Calico, Inc. **Brem (PI)**. 11/15-11/16. Role: PI.

NIH National Institute of Neurological Disorders and Stroke R21 NS077224, Analyzing genetic variation in mouse strains to identify molecular players in itch. **Brem (PI)**. 9/12-8/14. Role: PI.

NIH National Institute of General Medicine R01 GM087432, The genetics of dark matter transcription in yeast. **Brem (PI)**. 5/09-4/14. Role: PI.

Ellison Medical Foundation New Scholar in Aging AG-NS-0440-08, Signaling behaviors of the unfolded protein response in aging. **Brem (PI)**. 12/08-7/12. Role: PI.

NIH National Institute of General Medicine R24 GM081597, The development of genetics and genomics for analysis of quantitative traits in *Neurospora crassa*. Taylor (PI). 8/08-7/12. Role: co-PI.

Burroughs-Wellcome Career Award at the Scientific Interface 1005024, The genetics of transcription in budding yeast. **Brem (PI)**. 2/06-1/12. Role: PI.

Invited talks

Departmental seminar, Department of Ecology and Evolutionary Biology, UCLA, Los Angeles, CA, October 11, 2017

California Experimental Evolution Symposium, UC San Diego, January 3-4, 2017.

Cellular and Molecular Fungal Biology Gordon Conference, Holderness School, Plymouth, NH, June 21, 2016

University of Washington Genome Sciences Symposium, Seattle, WA, April 6, 2016

American Society of Naturalists national meeting, Asilomar Conference Center, Pacific Grove, CA, January 13, 2016

XXVIII Fungal Genetics Conference, Asilomar Conference Center, Pacific Grove, CA, March 18, 2015

Research seminar, Center for Computational Molecular Biology, Brown University, Providence, RI, February 11, 2015

Cellular and Molecular Fungal Biology Gordon Conference, Holderness School, Plymouth, NH, June 18, 2014

General meeting of the American Society for Microbiology, Boston, MA, May 20, 2014

Genetics Colloquium, Department of Genetics, University of Wisconsin, Madison, February 12, 2014

Theory Lunch, Department of Systems Biology, Harvard Medical School, November 22, 2013

Research seminar, Hopkins Marine Station, Stanford University, Pacific Grove, CA, September 27, 2013

ASBMB Special Symposium on Evolution and Core Processes in Gene Regulation, University of Chicago, Chicago, IL, July 26, 2013

Symposium on Genomics and Gene Expression, IGERT Program in Genomics, University of Arizona, Tucson, AZ, April 26, 2013

Conference on Predicting Cell Metabolism and Phenotypes, SRI International, Menlo Park, CA, March 5, 2013

Society for Integrative and Comparative Biology Annual Meeting, San Francisco, CA, January 5, 2013

EMBO Conference Series on Experimental Approaches to Evolution and Ecology Using Yeast, Heidelberg, Germany, October 19, 2012 (presented by Jeremy Roop)

Formal research seminar, Buck Institute for Research on Aging, Novato, CA, October 5, 2012

The Biology of Post-transcriptional Gene Regulation Gordon Conference, Salve Regina University, Newport, RI, July 17, 2012

General meeting of the American Society for Microbiology, San Francisco, June 18, 2012

Department seminar, Department of Ecology and Evolution, University of Chicago, March 26, 2012

European Conference on Fungal Genetics, Philipps University, Marburg, Germany, March 29, 2012 (presented by Jeremy Roop)

Department seminar, Cellular and Molecular Medicine, UC San Diego, September 29, 2011

9th Pathways, Networks, and Systems Medicine Conference, Chania, Greece, May 14, 2011

Seminar series for the University Program in Genetics and Genomics, Duke University, April 12, 2011

Genentech, Inc., April 5, 2011

Department seminar, Molecular, Cell, and Developmental Biology, UC Santa Cruz, April 4, 2011

Departmental seminar, Biology, Reed College, April 1, 2011

Amyris, Inc., March 30, 2011

XXVI Fungal Genetics Conference, Asilomar Conference Center, Pacific Grove, CA, March 19, 2011

RNA-Seq: Insights into the Active Genome, Cambridge Healthtech Institute, San Diego, March 2011 (presented by Oh Kyu Yoon)

Frontiers in Bioinformatics & Systems Biology Colloquium, UC San Diego, December 12, 2010

EMBO Conference Series on Experimental Approaches to Evolution and Ecology Using Yeast, Heidelberg, Germany, October 1, 2010

Yeast Genetics Meeting, Vancouver, BC, July 28, 2010

Fungal Cell Biology Gordon Conference, Holderness School, New Hampshire, June 15, 2010

Genetics Graduate Group seminar, UC Davis, May 2010

Keystone Symposium on Biomolecular Interaction Networks: Function and Disease, Quebec City, QC, March 11, 2010

Genome Center seminar series, University of Wisconsin, Madison, October 1, 2009.

BioC 2009: Where Biology and Software Connect, Fred Hutchinson Cancer Research Center, Seattle, WA, July 28, 2009.

Meeting of the Program in Genetic Networks, Canadian Institute for Advanced Research, Whistler, BC, April 3, 2009

XXV Fungal Genetics Conference, Asilomar Conference Center, Pacific Grove, CA, March 19, 2009

CCB/Biophysics Seminar Series, UC San Francisco, San Francisco, CA, May 15, 2008

Annual Meeting of the American Society for Biochemistry and Molecular Biology, San Diego, CA, April 8, 2008
3rd Annual Duke Systems Biology Symposium, Duke University, Durham, NC, October 10, 2008
Gordon Research Conference on Bioinformatics, Proctor Academy, Andover, NH, July 16, 2007
Gordon Research Conference on Evolutionary and Ecological Functional Genomics, Salve Regina University, Newport, RI, July 12, 2007
Department seminar, Molecular Biology and Genetics, Cornell University, May 18, 2007
Seminar, Integrative Graduate Education and Research Traineeship in Evolution, Development, and Genomics, Indiana University, Bloomington, IN, November 6, 2006
Department seminar, Plant and Microbial Biology, UC Berkeley, October 30, 2006
Storer Symposium on Networks in Biology and Computation, UC Davis, September 25, 2006
Banff Computational and Statistical Genomics Workshop, Banff, Canada, July 9, 2006
Evolution Discussion Group, UC Davis, May 25, 2006