

GLORIA A. BRAR, PH.D

Associate Professor of Molecular and Cell Biology
University of California – Berkeley

CONTACT INFORMATION

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EDUCATION

- Ph.D., Biology 2002-2008
Massachusetts Institute of Technology (MIT), Cambridge, MA
Thesis: 'The mechanisms controlling meiotic chromosome segregation'
- B.A., Molecular and Cell Biology 1998-2002
University of California-Berkeley (UC-Berkeley), Berkeley, CA
Honors Thesis: 'Broccoli and Breast Cancer: Examination of the mechanisms of I3C and N-benzyl in arresting the growth of MCF-7 human breast cancer cells'

RESEARCH AND PROFESSIONAL EXPERIENCE

- University of California-Berkeley,**
Associate Professor of Molecular and Cell Biology 2020- present
- University of California-Berkeley,**
Assistant Professor of Molecular and Cell Biology 2014- 2020
- My lab uses integrated classical and high-throughput approaches to probe the link between gene expression regulation and cellular remodeling during meiosis, the process by which gametes are produced.
- University of California-San Francisco (UCSF),** 2008-2013
Postdoctoral Fellow
Advisor: Jonathan Weissman
- Using a combination of high-throughput genomic and classical methods to study stress pathway co-option for cell remodeling, translational regulation in meiosis, and the significance of non-canonical meiotic coding regions.
- MIT, Graduate Researcher** 2003-2008
Advisor: Angelika Amon
- Determined phosphorylation of the cohesin Rec8 to contribute to stepwise cohesion loss in meiosis in a mechanism dependent on recombination.

UC-Berkeley, Undergraduate Researcher Laboratory of Dr. Gary Firestone	2000-2002
Agracetus, Biotechnology Internship Integrated Protein Technologies group under Dr. Ronald Bassuner	Summer 2000
University of Wisconsin-Madison, Research Assistant Laboratory of Dr. Richard A. Proctor	Summer 1999
University of Wisconsin-Madison, Research Assistant Laboratory of Dr. David Brow	Summer 1998

OTHER PROFESSIONAL ACTIVITIES

- Standing member of MRAA study section, NIGMS (2020-2026)
- Co-Chair Graduate Admissions, MCB, Berkeley (2021-2024)
- Co-Organizer Yeast Genetics Meeting (TAGC, 2024)
- Reviewer for the 2023 Next Generation Faculty Symposium
- Campus reviewer Pew Scholars program (2017-2023)
- Ad hoc reviewer for manuscripts at *Cell*, *PLoS Genetics*, *MBoC*, *PNAS*, *Genome Research*, *Cell Reports*, *Genome Biology*, *Nature Communications*, *Molecular Cell*, *Nature*, *Nature Protocols*, *Developmental Cell*, *Cell Reports Methods*, *eLife*, *Science*, *Life Science Alliance*
- Ad hoc reviewer for grants for EMBO Young Investigator program, Wellcome Trust, Netherlands Organization for Scientific research, Israeli Science Foundation, Biotechnology and Biological Sciences Research Council (UK), NSF, Wellcome Trust/DBT India Alliance, and the Ireland Frontiers for the Future Programme

HONORS AND AWARDS

Pew Innovation Fund Award, 2021

With Elçin Ünal, one of six teams chosen to pursue a high-risk/high-reward project by the Pew Charitable trusts

R.R. Bensley Award in Cell Biology, 2017

Early career award given to one cell biologist per year by the American Association of Anatomists for discovery, ingenuity, and publications in the field of cell biology

Pew Scholar in the Biomedical Sciences, 2016

Early career award, awarded based on scientific proposal and achievements

Sloan Research Fellowship, 2016

Early career award, awarded based on achievements and scientific potential

NIH New Innovator Award, 2015

5-year, \$1.5M grant awarded based on study section review of a “high-risk, high-reward” proposal

Winkler Family Biological Sciences Award, 2014

Chosen by Matthew Winkler and family as the annual awardee among UC-Berkeley junior faculty.

March of Dimes Basil O’Conner Starter Award, 2015

Two-year grant awarded based on achievements and scientific proposal

One of Cell’s ’40 under 40’, 2014

Nominated and selected based on age, research background and accomplishments as part of the *Cell* 40th anniversary features

American Cancer Society Postdoctoral Fellow, 2009-2012

Awarded based on review of research proposal, references, and academic achievements

National Science Foundation Predoctoral Research Fellow, 2002-2005

Awarded based on review of research proposal, references, and academic achievements

UC-Berkeley Molecular and Cell Biology Departmental Citation, 2002

Awarded to one student per UC-Berkeley graduating class for outstanding academic and research achievement

UC-Berkeley Edward M. Blount Award for Genetics, 2002

Awarded to one student per year for an outstanding honors thesis presentation

Phi Beta Kappa, UC-Berkeley, 2002

Awarded based on undergraduate academic record

Golden Key Honor Society, UC-Berkeley, 2002

Awarded based on undergraduate academic record

Haas Scholar- Undergraduate Research Fellow, 2001-2002

Awarded based on research application, references, and academic achievements

UC-Berkeley Chancellor's Scholar, 1998-2002

Merit-based undergraduate scholarship

National Merit Scholar, 1998-2002

Merit-based undergraduate scholarship

All-State Scholar (Wisconsin), 1998-2002

Merit-based undergraduate scholarship

Dean's Honor List, UC-Berkeley, 1998-2002

Kraft Scholar, 1998-1999

Merit-based freshman undergraduate scholarship

PEER-REVIEWED PUBLICATIONS

Higdon AL, Won NH, **Brar GA**. Truncated protein isoforms generate diversity of protein localization and function in yeast. *bioRxiv*. 2023. [in press, *Cell Systems*]

Powers EN, Reynaud K, Sousa C, Kuwayama N, Diamond P, Ingolia NT, Jovanovic M, **Brar GA**. Dbp1 is a low performance paralog of RNA helicase Ded1 that drives impaired translation and heat stress response. *bioRxiv*. 2024.

Spiri S, **Brar GA**. Fix it, don't trash it: Ribosome maintenance by chaperone-mediated repair of damaged subunits. *Mol Cell* 2023.

Vander Wende HM, Gopi M, Onyundo M, Medrano C, Adanlawo T, **Brar GA**. Meiotic resetting of the cellular Sod1 pool is driven by protein aggregation, degradation, and transient LUTI-mediated repression. *J Cell Biol*. 2023.

Powers EN, Chan C, Doron-Mandel E, Llacsahuanga Allcca L, Kim Kim J, Jovanovic M, **Brar GA**. Bidirectional promoter activity from expression cassettes can drive off-target repression of neighboring gene translation. *Elife*. 2022.

Sing TL, **Brar GA**, Ünal E. Gametogenesis: Exploring an Endogenous Rejuvenation Program to Understand Cellular Aging and Quality Control. *Annu Rev Genet*. 2022.

Barna M, Karbstein K, Tollervey D, Ruggero D, **Brar G**, Greer EL, Dinman JD. The promises and pitfalls of specialized ribosomes. *Mol Cell*. 2022.

Sing TL, Conlon K, Lu SH, Madrazo N, Morse K, Barker JC, Hollerer I, **Brar GA**, Sudmant PH, Ünal E. Meiotic cDNA libraries reveal gene truncations and mitochondrial proteins important for competitive fitness in *Saccharomyces cerevisiae*. *Genetics*. 2022.

Otto GM, **Brar GA**. Developmentally regulated selective autophagy determines ER inheritance by gametes. *Autophagy*. 2022.

Otto GM, Cheunkarndee T, Leslie J, **Brar GA**. Programmed cortical ER collapse drives selective ER degradation and inheritance in yeast meiosis. *JCB*. 2021.

Hollerer I, Powers EN, **Brar GA**. Global mapping of translation initiation sites by TIS profiling in budding yeast. *STAR Protocols*. 2020.

Powers EN & **Brar GA**. Performing Ribosome Profiling to Assess Translation in Vegetative and Meiotic Yeast Cells. *Methods in Molecular Biology*. 2021.

Higdon AL, **Brar GA**. Rules are made to be broken: a "simple" model organism reveals the complexity of gene regulation. *Current Genetics*. 2021

Eisenberg AR, Higdon AL, Hollerer I, Fields AP, Jungreis I, Diamond PD, Kellis M, Jovanovic M, **Brar GA**. Translation Initiation Site Profiling Reveals Widespread Synthesis of Non-AUG-Initiated Protein Isoforms in Yeast. *Cell Systems*. 2020.

Jorgensen V, Chen J, Vander Wende H, Harris DE, McCarthy A, Breznak S, Wong-Deyrup SW, Chen Y, Rangan P, **Brar GA**, Sawyer EM, Chan LY, Ünal E. Tunable transcriptional interference at the endogenous alcohol dehydrogenase gene locus in *Drosophila melanogaster*. *G3*. 2020.

Cheng Z and **Brar GA**. Global translation inhibition yields condition-dependent de-repression of ribosome biogenesis mRNAs. *Nucleic Acids Research*. 2019.

Cheng Z, Mugler CF, Keskin A, Hodapp S, Chan LY, Weis K, Mertins P, Regev A, Jovanovic M, **Brar GA**. Small and Large Ribosomal Subunit Deficiencies Lead to Distinct Gene Expression Signatures that Reflect Cellular Growth Rate. *Molecular Cell*. 2019.

Eisenberg AR, Higdon A, Keskin A, Hodapp S, Jovanovic M, **Brar GA**. Precise Post-translational Tuning Occurs for Most Protein Complex Components during Meiosis. *Cell Reports*. 2018.

Van Daltsen KM, Hodapp S, Keskin A, Otto GM, Berdan CA, Higdon A, Cheunkarndee T, Nomura DK, Jovanovic M, **Brar GA**. Global Proteome Remodeling during ER Stress Involves Hac1-Driven Expression of Long Undecoded Transcript Isoforms. *Developmental Cell*. 2018.

Otto GM and **Brar GA**. Seq-ing answers: uncovering the unexpected in global gene regulation. *Curr Genetics*. 2018

Hollerer I, Barker JC, Jorgenson V, Tresenrider A, Dugast-Darzacq C, Chan LY, Darzacq X, Tjian R, Ünal, E*, **Brar GA***. Evidence for an Integrated Gene Repression Mechanism based on mRNA Isoform Toggling in Human Cells *G3*. 2019 (*equal contributions)

Guenther U-P, Weinberg DE, Zubradt MM, Tedeschi FA, Stawicki BN, Zagore LL, **Brar GA**, Licatalosi DD, Bartel DP, Weissman JS & Jankowsky E. The helicase Ded1p controls use of near-cognate translation initiation codons in 5' UTRs. *Nature*. 2018.

Cheng Z*, Otto GM*, Powers EN, Keskin A, Mertins P, Carr SA, Jovanovic M, **Brar GA**. Pervasive, coordinated protein level changes driven by transcript isoform switching during meiosis. *Cell*. 2018 (*equal contributions)

Powers EN, **Brar GA**. m6A and eIF2 α -p Team Up to Tackle ATF4 Translation during Stress. *Mol Cell*. 2018

Hollerer I, Higdon A, **Brar GA**. Strategies and Challenges in Identifying Function for Thousands of sORF-Encoded Peptides in Meiosis. *Proteomics*. 2017.

Brar GA. Beyond the Triplet Code: Context Cues Transform Translation. *Cell Review*. 2016 Dec 15;167(7):1681-1692

Ingolia NT, **Brar GA**, Stern-Ginossar N, Harris N, Talhouarne GJS, Jackson SE, Wills MR, and Weissman JS. Ribosome Profiling Reveals Pervasive Translation Outside of Annotated Protein-Coding Genes. *Cell Reports*. 2014 Sep 8(5), 1365-79.

Brar GA and Weissman JS. Ribosome profiling reveals the what, when, where, and how of protein synthesis. *Nature Reviews Molecular and Cell Biology*. 2015 Nov;16(11):651-64.

Brar GA, Yassour M, Friedman N, Regev A, Ingolia NT, Weissman JS. High-Resolution View of the Yeast Meiotic Program Revealed by Ribosome Profiling. *Science*. Article. 2012 Feb 3;335(6068):552-7.

Berchowitz LE, Gajadhar AS, van Werven FJ, De Rosa AA, Samoylova ML, **Brar GA**, Xu Y, Xiao C, Fitcher B, Weissman JS, White FM, Amon A. A developmentally regulated translational control pathway establishes the meiotic chromosome segregation pattern. *Genes Dev*. 2013 Oct 1.

Gilbert LA, Larson MH, Morsut L, Liu Z, **Brar GA**, Torres SE, Stern-Ginossar N, Brandman O, Whitehead EH, Doudna JA, Lim WA, Weissman JS, Qi LS. CRISPR-mediated modular RNA-guided regulation of transcription in eukaryotes. *Cell*. 2013 Jul 18;154(2):442-51.

Thorburn RR, Gonzalez C, **Brar GA**, Christen S, Carlile TM, Ingolia NT, Sauer U, Weissman JS, Amon A. Aneuploid yeast strains exhibit defects in cell growth and passage through START. *Mol Biol Cell*. 2013 May;24(9):1274-89. PMID: 23468524.

Miller, M.P.*, Ünal, E.*, **Brar, GA**, Amon, A. (*equal contributions) Meiosis I chromosome segregation is established by inhibiting microtubule-kinetochore interactions in Prophase I. *eLife*. 2012.

Ingolia NT, **Brar GA**, Rouskin S, McGeachy AM, Weissman JS. The ribosome profiling strategy for monitoring translation in vivo by deep sequencing of ribosome-protected mRNA fragments. *Nature Protocols*. 2012 Jul 26;7(8):1534-50.

Carvunis AR, Rolland T, Wapinski I, Calderwood MA, Yildirim MA, Simonis N, Charlotteaux B, Hidalgo CA, Barbette J, Santhanam B, **Brar GA**, Weissman JS, Regev A, Thierry-Mieg N, Cusick ME, Vidal M. Proto-genes and de novo gene birth. *Nature*. 2012 Jul 19;487(7407):370-4.

Brar GA and Amon A. Emerging roles for centromeres in meiosis I chromosome segregation. *Nature Reviews Genetics*. Review. 2008 Dec;9(12):899-910.

Nguyen HH, Aronchik I, **Brar GA**, Nguyen DH, Bjeldanes LF, Firestone GL. The dietary phytochemical indole-3-carbinol is a natural elastase enzymatic inhibitor that disrupts cyclin E protein processing. *PNAS*. 2008 Dec 16;105(50):19750-5.

Brar GA, Hochwagen A, Ee L, Amon A. The multiple roles of cohesin in meiotic chromosome morphogenesis and pairing. *Mol Biol Cell*. 2009 Feb;20(3):1030-47.

Brar GA, Kiburz BM, Zhang Y, Kim JE, White F, Amon A. Rec8 phosphorylation and recombination promote the step-wise loss of cohesins in meiosis. *Nature*. 2006 May 25;441(7092):532-6.

Hochwagen A, Tham WH, **Brar GA**, Amon A. The FK506 binding protein Fpr3 counteracts protein phosphatase 1 to maintain meiotic recombination checkpoint activity. *Cell*. 2005 Sep 23;122(6):861-73.

Garcia HH, **Brar GA**, Nguyen DH, Bjeldanes LF, Firestone GL. Indole-3-carbinol (I3C) inhibits cyclin-dependent kinase-2 function in human breast cancer cells by regulating the size distribution, associated cyclin E forms, and subcellular localization of the CDK2 protein complex. *J Biol Chem*. 2005 Mar 11;280(10):8756-64.

INVITED RESEARCH TALKS

UC Riverside RNA Symposium: November 3rd, 2023. Riverside, CA. 'Temporary repression driven by alternative transcripts is common, impactful'

Cold Spring Harbor Asia Yeast and Life Sciences: October 6th, 2023. Matsue, Japan. 'Budding yeast genome organization is complex, interesting.'

RNA Society Collaborative Seminar: April 26th, 2023. Zoom. 'Genomic expression cassettes drive unexpected RNAs and off-target effects'

Hexagon Bio: April 18th, 2023. Menlo Park, CA. 'Global expression measurements reveal complex gene regulatory strategies, even in yeast'

UC Davis: March 21st, 2023. Davis, CA. 'Temporary repression driven by alternative transcripts underlies meiotic success'

GRC Stress Proteins: July 5th, 2023. Barga, Italy. 'Resetting of Sod1 in gametes by programmed aggregation and degradation'

Georgetown University: November 3rd, 2022. Washington DC. 'Temporary repression driven by alternative transcripts underlies meiotic success'

MIT Colloquium: November 1st, 2022. Cambridge, MA. 'Temporary repression driven by alternative transcripts underlies meiotic success'

GRC for Posttranscriptional Gene Regulation: July 13th, 2022. Newry, MA. 'LUTI mRNAs are repressive, common, and an overlooked side-effect of genome editing'

CU Boulder SCR Symposium Plenary Address: May 9th, 2022. Boulder, CO. 'Unconventional gene regulatory circuitry underlies meiosis (and beyond)'

Ohio State MLS Seminar Series: April 12th, 2022. 'Unconventional gene regulatory circuitry underlies meiosis (and beyond)'

Scripps Institute Integrative Structural and Computational Biology: April 6th, 2022. 'Unconventional gene regulatory circuitry underlies meiosis (and beyond)'

CSHL Postdoc Retreat Keynote: September 17th, 2021. 'Teaming up to investigate meiotic differentiation' (with Elçin Ünal).

Amgen Summer Program Series: August 6th, 2021. 'How does gene expression control meiosis?'

Cleveland State University: April 16th, 2021. 'Uncovering the unconventional gene regulation that underlies meiotic differentiation'

Meiosis in Quarantine Series: July 2nd, 2020. 'Programmed disassembly and destruction of the ER during meiosis in budding yeast'

University of Toronto Donnelly Center Seminar Series: March 5th, 2020. Toronto, Canada. 'Uncovering the complex, unconventional gene regulation underlying meiotic differentiation'

UCSF Basic Science Seminar Series: January 21st, 2020. San Francisco, CA. 'Uncovering the non-canonical gene regulation underlying meiosis''

Vienna BioCenter Seminar Series: June 27, 2019. Vienna, Austria
'Regulated transcript toggling and protein degradation set meiotic protein levels'

Stowers Institute Seminar Series: May 1, 2019. Kansas City, MO
'Regulated transcript toggling and protein degradation set meiotic protein levels'

Carnegie Mellon University Department of Biological Sciences Seminar Series: April 24, 2019. Pittsburgh, PA
'Regulated transcript toggling and protein degradation set meiotic protein levels'

UMass Amherst MCB Seminar Series: March 26, 2019. Amherst, MA
'Regulated transcript toggling and protein degradation set meiotic protein levels'

Columbia University Biological Sciences Seminar Series: March 11, 2019. New York, NY
'Regulated transcript toggling and protein degradation set meiotic protein levels'

CSU Stanislas Biology Colloquium for Undergraduates: February 22, 2019. Turlock, CA
'How to globally measure gene expression and what this can tell us about meiosis'

- Brandeis Joint Biology Colloquium:** January 15, 2019; Waltham, MA
'Regulated transcript toggling and protein degradation set meiotic protein levels'
- UC Davis Molecular Genetics Seminar Series:** November 5, 2018; Davis, CA
'Pervasive, coordinated protein-level changes are driven by transcript toggling'
- UW Madison Biochemistry Colloquium;** October 22, 2018; Madison, WI
'Pervasive, coordinated protein-level changes are driven by transcript toggling'
- Post-transcriptional Gene Regulation Gordon Conference;** July 17, 2018; Newry, ME
Invited speaker, talk presented by my postdoc (Ina Hollerer) because I was unable to attend the conference due to late term pregnancy, 'Pervasive, coordinated protein-level changes are driven by transcript toggling'
- Meiosis Gordon Conference;** June 12, 2018; Colby-Sawyer, NH
Speaker, 'Perfection is over-rated: Meiotic yeast synthesize complex components sloppily, clean up later'
- RNA Society Annual Meeting,** June 2018; Berkeley, CA
Session chair, Interconnected RNA processes
Speaker, 'Pervasive, coordinated protein-level changes are driven by transcript toggling'
- Experimental Biology Conference,** April 2018; San Diego, CA
Session chair, AAA Cell Biology Hybrid Award Symposium
Speaker, ASBMB session on Ribosomes and translation, 'Pervasive, coordinated protein-level changes are driven by transcript toggling'
- UCSD Genetics, Bioinformatics, and Systems Biology Colloquium,** April 5th, 2018; La Jolla, CA, 'Pervasive, coordinated protein-level changes are driven by transcript toggling'
- Stanford Frontiers in Biology Seminar Series Speaker,** March 28th, 2018; Palo Alto, CA, 'Pervasive, coordinated protein-level changes are driven by transcript toggling'
- Cold Spring Harbor Yeast Genetics Course;** *Guest lecturer,* August 2017, Cold Spring Harbor, NY, 'Decoding Meiosis'
- ASBMB Evolution and Core Processes in Gene Expression;** July 2017, Kansas City, MO, 'Meiotic protein levels are pervasively set by transcript toggling rather than mRNA abundance'
- R.R. Bensley Award Seminar at the 2017 Experimental Biology Conference;** April 2017, Chicago, IL, 'Unraveling gene regulatory mechanisms underlying meiotic differentiation'
- Stony Brook University Department of Biochemistry and Cell Biology weekly seminar;** April 13, 2017; Stony Brook, NY, 'Unraveling gene regulatory mechanisms underlying meiotic differentiation'
- Canadian Institute for Advanced Research (CIFAR) Genetic Networks workshop;** *Invited guest speaker,* December 2, 2016; Santa Cruz, CA, 'Using ribosome profiling data to annotate surprising complexity in decoding of a simple genome'

University of North Carolina Department of Physiology weekly seminar; November 29, 2016; Chapel Hill, NC, 'Decoding meiotic translation'

Science Leadership and Management seminar series; *Invited guest speaker, team seminar with Elçin Ünal*, November 7, 2016; Berkeley, CA, 'Establishing a positive lab culture'

Max Planck Institute of Molecular Physiology weekly seminar; September 16, 2016; Dortmund, Germany, 'Decoding meiotic translation'

13th Horizons in Molecular Biology Symposium; *Invited guest speaker at annual international event organized by the Max Planck Institute of Göttingen and the University of Göttingen*, September 13, 2016; Göttingen, Germany, 'Decoding meiotic translation'

Meiosis Gordon Conference; June 28, 2016; Colby-Sawyer, NH,
Speaker, 'Probing the Basis for Non-Canonical Translation in Meiosis'
Session Chair, 'Chromosome Segregation: Kinetochores, Cohesion, Chiasmata and Spindles'

University of California, San Francisco Center for Reproductive Sciences Annual Retreat; *Invited guest speaker*, June 3, 2016; San Francisco, CA, 'Decoding meiotic translation'

Texas A&M Department of Biochemistry and Biophysics weekly seminar; March 9, 2016; College Station, TX, 'Unraveling meiotic translation'

MCBcDNA Featured Speaker Night; *Invited guest speaker*, February 25, 2016; Berkeley, CA, 'Decoding meiosis'

Sierra Systems and SynBio Symposium; *Keynote speaker*, August 2015; Reno, NV, 'Bridging systems and molecular biology in meiosis'

Amgen Scholars Symposium; *Invited guest speaker*, July 15, 2015; Berkeley, CA, 'Ribosome profiling reveals surprises in translation: short ORFs and stress in meiosis'

Bay Area Organelle Meeting; *Invited guest speaker*, March 18, 2015; San Francisco, CA, 'Towards a molecular description of organelle remodeling through meiosis'

University of Washington Genome Sciences weekly seminar; February 25, 2015; Seattle, WA, 'Ribosome profiling reveals surprises in translation: short ORFs and stress in meiosis'

Protein Society Annual Symposium; July 27, 2014; San Diego, CA. 'Probing meiotic gene regulation and genome decoding by ribosome profiling'

Salk Institute Seminar; April 2013, La Jolla, CA, 'Using high-resolution translation measurements to define meiotic cellular remodeling and redefine genome coding'

Rockefeller University Institute Seminar; March 2013, New York, NY, 'Using high-resolution translation measurements to define meiotic cellular remodeling and redefine genome coding'

Johns Hopkins University, High Throughput Biology Center Seminar: February 2013, Baltimore, MD, 'Using high-resolution translation measurements to define meiotic cellular remodeling and redefine genome coding'

UCLA, Department of Biochemistry and Chemistry: February 2013, Los Angeles, CA, 'Using high-resolution translation measurements to define meiotic cellular remodeling and redefine genome coding'

Harvard Medical School, BCMP Departmental Seminar: January 2013, Boston, MA, 'Using high-resolution translation measurements to define meiotic cellular remodeling and redefine genome coding'

Northwestern University, Molecular Biosciences Seminar: January 2013, Evanston, IL, 'Using high-resolution translation measurements to define meiotic cellular remodeling and redefine genome coding'

UC-Davis Biology Seminar: January 2013, Davis, CA, 'Using high-resolution translation measurements to define meiotic cellular remodeling and redefine genome coding'

UC-Berkeley, Molecular and Cell Biology Department Seminar: January 2013, Berkeley, CA, 'Using high-resolution translation measurements to define meiotic cellular remodeling and redefine genome coding'

UT-Southwestern Department of Pharmacology: December 2012, Dallas, TX, 'Using high-resolution translation measurements to define meiotic cellular remodeling and redefine genome coding'

Princeton University, Lewis-Sigler Institute Seminar: November 2012, Princeton, NH, 'Using high-resolution translation measurements to define meiotic cellular remodeling and redefine genome coding'

Stanford University, Department of Biochemistry Seminar: November 2012, Stanford, CA, 'Using high-resolution translation measurements to define meiotic cellular remodeling and redefine genome coding'

National Institutes of Health Earl Stadtman Investigator Symposium: November 2012, Bethesda, MD, 'Using high-resolution translation measurements to define meiotic cellular remodeling and redefine genome coding'

MIT Koch Institute Special Seminar; September 24, 2012; Cambridge, MA. 'Ribosome profiling meiosis: high-resolution translation measurements define cell remodeling and redefine elements of genome coding'

Bay Area Meiosis Meeting; October 27, 2012; Berkeley, CA. 'Defining cellular remodeling and protein coding in meiosis by ribosome profiling'

Stanford Biology Department 'Think and Drink' Seminar; October 5, 2012; Stanford, CA. 'Defining cellular remodeling and protein coding in meiosis by ribosome profiling'

Yeast Genetics and Molecular Biology Meeting; July/August 2012; Princeton, NJ. 'Illuminating gene function and regulation through meiosis by ribosome profiling'

Gordon Research Conference: The Biology of Post-Transcriptional Gene Regulation;
July 2012; Salve Regina University, RI. 'Illuminating gene function and regulation
through meiosis by ribosome profiling'

Institute for Molecular Pathology (IMP) Seminar; February 20, 2012; Vienna, Austria. 'High-
Resolution View of the Yeast Meiotic Program Revealed by Ribosome Profiling'


EMBO Conference: Protein Synthesis and Translational Control; September 2011;
Heidelberg, Germany. 'A Genome-Wide view of Protein Synthesis Through Meiosis:
Identifying New Meiotic Factors and Probing Noncanonical Translation'

Stowers Institute Seminar; November 16, 2010; Kansas City, MO. 'Translation profiling in
meiosis: Uncovering specific biology and global surprises'

Gordon Research Conference: Meiosis; June 2010; Colby-Sawyer College, NH.
'Translation in meiosis: Using ribosome profiling to uncover specific biology and global
surprises'

Carnegie Institution: Department of Embryology Seminar; May 2007; Baltimore, MD.
'Investigating mechanisms for proper meiotic chromosome segregation'

PROFESSIONAL ORGANIZATIONS

- American Society of Cell Biology (ASCB; 2014-present) 
- RNA Society (2014-present) 
- Genetics Society of America (GSA; 2014-present)

SERVICE TO PROFESSIONAL PUBLICATIONS AND ORGANIZATIONS

- Member of the first NIH R35 MIRA review study section (MRAA, 2020-2026)
- Ad hoc reviewer for manuscripts at *Cell*, *PLoS Genetics*, *MBoC*, *PNAS*, *Genome Research*, *Cell Reports*, *Genome Biology*, *Nature Communications*, *Molecular Cell*, *Nature*, *Nature Protocols*, *Developmental Cell*, *Cell Reports Methods*
- Ad hoc reviewer for grants for EMBO Young Investigator program, Wellcome Trust, Netherlands Organization for Scientific research, Israeli Science Foundation, Biotechnology and Biological Sciences Research Council (UK), NSF, Wellcome Trust/DBT India Alliance, Ireland Frontiers for the Future Programme
- Member of and contributor to Faculty of 1000 Prime (2018-present)

Ongoing research support

1R35GM134886 (Brar)

01/01/2020-12/31/2024

Illuminating the gene regulation underlying meiotic differentiation
NIH

Pew Innovation Fund

11/01/2021-10/31/2023

Repurposing Endogenous Stress Pathway Activity To Drive Cellular Rejuvenation

Pew Charitable Trusts

GLORIA A. BRAR, Ph.D.

1R01AG071869 (Brar)

9/01/21-5/31/2026

Defining the programmed proteome rejuvenation underlying gametogenesis

NIH