## GLORIA A. BRAR, PH.D

**Assistant 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,**

 **Assistant Professor of Molecular and Cell Biology** 2014- present

* + 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), Postdoctoral Fellow**

2008-2013

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**

Summer 2000

Integrated Protein Technologies group under Dr. Ronald Bassuner

**University of Wisconsin-Madison, Research Assistant**

Summer 1999

Laboratory of Dr. Richard A. Proctor

**University of Wisconsin-Madison, Research Assistant**

 Summer 1998

Laboratory of Dr. David Brow

### HONORS AND AWARDS

 **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

Tw-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

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

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**.**](https://www.ncbi.nlm.nih.gov/pubmed/30503772) *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.](https://www.ncbi.nlm.nih.gov/pubmed/30590036) *Cell Reports*. 2018.

Van Dalfsen 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 eIF2α-p Team Up to Tackle ATF4 Translation during Stress.](https://www.ncbi.nlm.nih.gov/pubmed/29452634) *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](http://www.weizmann.ac.il/molgen/new_pages/members/Stern_Ginossar.html), Harris N,  Talhouarne GJS, Jackson SE, Wills MR, and [Weissman JS](http://weissmanlab.ucsf.edu/). Ribosome Profiling Reveals Pervasive Translation Outside of Annotated Protein-Coding Genes. *Cell Reports.* 2014 Sep8(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.](http://www.ncbi.nlm.nih.gov/pubmed/22194413) *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, Futcher 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.](http://www.ncbi.nlm.nih.gov/pubmed/22836135) *Nature Protocols*. 2012 Jul 26;7(8):1534-50.

Carvunis AR, Rolland T, Wapinski I, Calderwood MA, Yildirim MA, Simonis N, Charloteaux 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.](http://www.ncbi.nlm.nih.gov/pubmed/22722833) *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.](http://www.ncbi.nlm.nih.gov/pubmed/19064917)*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

***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*, t*eam 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’