

EDUCATION

- 2008 **University of California, Berkeley**
PhD in Molecular and Cell Biology with designated emphasis in Computational and Genomic Biology
- 2000 **Massachusetts Institute of Technology**
SB, Mathematics; SB, Biology

RESEARCH POSITIONS

- Assistant Professor **University of California, Berkeley** 2019-
Department of Bioengineering
- Fellow **University of California, Berkeley** 2013-2018
California Institute for Quantitative Biosciences (QB3)
- Postdoctoral fellow **University of California, Santa Cruz** 2012-2013
Department of Biomolecular Engineering
with Richard (Ed) Green
- Postdoctoral fellow **Stanford University** 2009-2012
Department of Biochemistry
with Pat Brown
- Graduate student **University of California, Berkeley** 2002-2008
Department of Molecular and Cell Biology
with Steven Brenner

AWARDS AND HONORS

- 2019-2021 Shurl & Kay Curci Foundation Faculty Scholar (*\$200,000 research funding*)
- 2009-2012 Damon Runyon Postdoctoral Research Fellowship
- 2009 NSF Postdoctoral Research Fellowship in Biological Informatics (*declined*)

FUNDING

- 2019-2024 **NIH/NIGMS R01** Determinants and consequences of translation elongation rate. PI: **Lareau**. Annual direct costs \$210,000.
- 2019-2022 **NSF + UK BBSRC** RiboViz for reliable, reproducible and rigorous quantification of protein synthesis from ribosome profiling data. PI: **Lareau**, Shah, Wallace. Total direct costs to Berkeley \$113,484.
- 2015-2018 **NIH/NCI R21** A computational framework for statistical analysis of ribosome profiling data. PI: **Lareau**. Annual direct costs \$130,500.

PREPRINTS

1. Buen Abad Najar CF, Yosef N, **Lareau LF**. 2019. Coverage-dependent bias creates the appearance of binary splicing in single cells. *bioRxiv* 2019.12.19.883256.

RESEARCH PUBLICATIONS

1. Tunney RJ*, McGlincy NJ*, Graham ME, Naddaf N, Pachter L, **Lareau LF**. 2018. Accurate design of translational output by a neural network model of ribosome distribution. *Nature Structural & Molecular Biology* 25 (7): 577-582.
2. Rice ES, Kohno S, St John J, Pham S, Howard J, **Lareau LF**, O'Connell BL, Hickey G, Armstrong J, Deran A, Fiddes I, Platt RN, Gresham C, McCarthy F, Kern C, Haan D, Phan T, Schmidt C, Sanford JR, Ray DA, Paten B, Guillette LJ, Green RE. 2017. Improved genome assembly of American alligator genome reveals conserved architecture of estrogen signaling. *Genome Research* 27 (5): 686-696.
3. **Lareau LF**, Brenner SE. 2015. Regulation of splicing factors by alternative splicing and NMD is conserved between kingdoms yet evolutionarily flexible. *Molecular Biology and Evolution* 32 (4): 1072-1079.
4. **Lareau LF***, Hite DH*, Hogan GJ, Brown PO. 2014. Distinct stages of the translation elongation cycle revealed by sequencing ribosome-protected mRNA fragments. *eLife* 2014 (3): e01257.
5. Ingolia NT, **Lareau LF**, Weissman JS. 2011. Ribosome profiling of mouse embryonic stem cells reveals the complexity and dynamics of mammalian proteomes. *Cell* 147 (4): 789-802.
6. Hansen KD*, **Lareau LF***, Blanchette M, Green RE, Meng Q, Rehwinkel J, Galluser FL, Izaurralde E, Rio DC, Dudoit S, Brenner SE. 2009. Genome-wide identification of alternative splice forms down-regulated by nonsense-mediated mRNA decay in *Drosophila*. *PLoS Genetics* 5 (6): e1000525.
7. **Lareau LF***, Inada M*, Green RE, Wengrod JC, Brenner SE. 2007. Unproductive splicing of SR genes associated with highly and ultraconserved DNA elements. *Nature* 447 (2138): 926-929.
8. Carnici P, ...76 authors..., **Lareau LF**, ...115 authors..., Hayashizaki Y; FANTOM Consortium. 2005. The transcriptional landscape of the mammalian genome. *Science* 309 (5740): 1559-1563.
9. Green RE, Lewis BP, Hillman RT, Blanchette M, **Lareau LF**, Garnett A, Rio DC, Brenner SE. 2003. Widespread predicted nonsense-mediated mRNA decay of alternatively-spliced transcripts of human normal and disease genes. *Bioinformatics* 19 (S1): i118-121.

*contributed equally

REVIEW PUBLICATIONS

1. **Lareau LF**, Brooks AN, Soergel DAW, Meng Q, Brenner SE. 2007. The coupling of alternative splicing and nonsense-mediated mRNA decay. In Blencowe B and Graveley B, ed., *Alternative Splicing in the Postgenomic Era*, Landes Bioscience.
2. Soergel DAW, **Lareau LF**, Brenner SE. 2006. Regulation of gene expression by the coupling of alternative splicing and nonsense-mediated mRNA decay. In Maquat L, ed., *Nonsense-Mediated mRNA Decay*, Landes Bioscience.
3. **Lareau LF**, Green RE, Bhatnagar RS, Brenner SE. 2004. The evolving roles of alternative splicing. *Current Opinion in Structural Biology* 14 (3): 273-282.

CONFERENCE TALKS

CSHL meeting on Eukaryotic mRNA Processing, Cold Spring Harbor NY	August 2019
Society for Developmental Biology annual meeting, Boston MA (<i>invited speaker</i>)	July 2019
RNA Society annual meeting, Berkeley CA	June 2018

CSHL meeting on Eukaryotic mRNA Processing, Cold Spring Harbor NY	August 2017
CSHL meeting on Systems Biology, Cold Spring Harbor NY	March 2017
CSHL meeting on Translational Control, Cold Spring Harbor NY	September 2016
Society for Molecular Biology and Evolution, Vienna Austria	July 2015
Intelligent Systems for Molecular Biology, Dublin Ireland	July 2015
EMBL Symposium on The Complex Life of mRNA, Heidelberg Germany	October 2014
Gordon Research Conference on Nucleic Acids, Maine	June 2013
RNA Society annual meeting, Seattle WA	June 2006

SEMINARS

University of Colorado School of Medicine, RNA Biosciences Initiative	November 2019
Rockefeller University, Center for Studies in Physics and Biology	May 2019
Columbia University, Department of Biological Sciences	February 2019
University of California Santa Cruz, Department of Biomolecular Engineering	March 2018
University of California Los Angeles, Molecular Biology Institute	October 2017
Johns Hopkins University, Genomics seminar series	November 2011
MRC Human Genetics Unit, Edinburgh	August 2007

PATENTS

Lareau LF, Tunney R. Optimization of gene sequences for protein expression. Filed 2019.

Green RE, **Lareau LF**. Methods for genome assembly and haplotype phasing. US Patent 9411930, issued 2016.

MENTORING

Graduate students

2019-	Karina Vivanco, Bioengineering Graduate Program.
2019-	Amanda Mok, Computational Biology PhD Program.
2016-	Carlos Buen Abad Najar, Computational Biology PhD Program (<i>co-advisor: Nir Yosef</i>). UC MEXUS Doctoral Fellowship.
2014-2018	Robert Tunney, Computational Biology PhD Program (<i>co-advisor: Lior Pachter</i>). National Defense Science & Engineering Graduate Fellowship. PhD awarded May 2018.

Undergraduate students

2016	Jordan Wilson, Diablo Valley Community College. Transfer-to-Excellence Research Experiences for Undergraduates (REU). Now PhD student, Johns Hopkins University.
2014, 2015	Emily Powers, Ithaca College. Amgen Summer Scholar program. Now PhD student, University of California, Berkeley.

TEACHING

2015-2018	Guest lectures in Classics in Computational Biology (CMPBIO 201) and Genomics and Bioinformatics (MCB 280C)
2005	Graduate student instructor, Computational Biology and Genomics (MCB 246)
2003	Graduate student instructor, Biochemistry and Molecular Biology (MCB 102)

SERVICE & PROFESSIONAL ACTIVITIES

Bioengineering PhD Program admissions committee, 2019.

Computational Biology PhD Program admissions committee, 2018, 2019.

Reviewer for *Nature*, *Science*, *Cell*, *Nature Methods*, *Nature Structural & Molecular Biology*, *Molecular Biology and Evolution*, *Genome Research*, *Trends in Genetics*, *Nucleic Acids Research*, *PLoS Biology*, *PLoS Genetics*, *RNA*, *Genetics*, *Bioinformatics*, *PLoS Computational Biology* (guest editor), *BMC Evolutionary Biology*, *PLoS One*.

Co-maintainer of WebLogo, a tool for visualizing motifs in sequence data.

Chairman, MIT Student Information Processing Board (computer society), 2001.