

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 Department of Bioengineering	2019-
Fellow (PI)	University of California, Berkeley California Institute for Quantitative Biosciences (QB3)	2013-2018
Postdoctoral fellow	University of California, Santa Cruz Department of Biomolecular Engineering <i>with Richard (Ed) Green</i>	2012-2013
Postdoctoral fellow	Stanford University Department of Biochemistry <i>with Pat Brown</i>	2009-2012
Graduate student	University of California, Berkeley Department of Molecular and Cell Biology <i>with Steven Brenner</i>	2002-2008
Technical associate	Massachusetts Institute of Technology Department of Biology <i>with Chris Burge</i>	2000-2002

AWARDS AND HONORS

2009-2012	Damon Runyon Postdoctoral Research Fellowship
2009	NSF Postdoctoral Research Fellowship in Biological Informatics (<i>declined</i>)

FUNDING

A computational framework for statistical analysis of ribosome profiling data. NIH/NCI R21 CA202960, 12/16/2015 - 11/30/2018.

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. [800+ citations]
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. [300+ citations]
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

Accurate design of translational output by a neural network model of ribosome distribution. RNA Society annual meeting. Berkeley, June 2018.

A neural network to model translation and design sequences optimized for expression. CSHL meeting on Eukaryotic mRNA Processing. Cold Spring Harbor, August 2017.

A neural network to model translation and design sequences optimized for expression. CSHL meeting on Systems Biology. Cold Spring Harbor, March 2017.

Deep learning reveals variation in translation elongation along human mRNAs. CSHL meeting on Translational Control. Cold Spring Harbor, September 2016.

Regulation of splicing factors by alternative splicing and NMD is conserved between kingdoms yet evolutionarily flexible. Society for Molecular Biology and Evolution. Vienna, July 2015.

Ribosome motion revealed by RNA sequencing. Intelligent Systems for Molecular Biology, Integrative RNA Biology SIG. Dublin, July 2015.

Distinct ribosome states revealed by sequencing of ribosome-protected mRNA fragments. EMBL Symposium on The Complex Life of mRNA. Heidelberg, October 2014.

Distinct ribosome states revealed by sequencing of ribosome-protected mRNA fragments. Gordon Research Conference on Nucleic Acids. Maine, June 2013.

Conserved unproductive splicing of SR proteins. RNA Society annual meeting. Seattle, June 2006.

INVITED SEMINARS

Center for Studies in Physics and Biology, Rockefeller University. May 7, 2019. (*upcoming*)

Department of Biological Sciences, Columbia University. February 11, 2019. (*upcoming*)

Translation revealed by deep sequencing and deep learning. Department of Biomolecular Engineering, University of California, Santa Cruz. March 15, 2018.

Ribosome dynamics captured by deep sequencing and deep learning. Molecular Biology Institute, University of California, Los Angeles. October 5, 2017.

Ribosome profiling of mouse embryonic stem cells reveals the complexity and dynamics of mammalian proteomes. Genomics seminar series, Johns Hopkins University. November 21, 2011.

Regulation of SR proteins by unproductive splicing associated with ultraconserved DNA elements. MRC Human Genetics Unit, Edinburgh. August 17, 2007.

PATENTS

Lareau LF, Tunney R. Optimization of gene sequences for protein expression. Provisional application filed October 11, 2018.

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

MENTORING

Graduate students

2016- Carlos Buen Abad Najar, Computational Biology PhD Program (*co-advisor: Nir Yosef*). UC MEXUS Doctoral Fellowship.

2014-2018 Robert Tunney, Computational Biology PhD Program (*co-advisor: Lior Pachter*). 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 postbac researcher, Johns Hopkins University.

2014, 2015 Emily Powers, Ithaca College. Amgen Summer Scholar program. Now PhD student, University of California, Berkeley.

TEACHING EXPERIENCE

2015-2018 Guest lectures in Classics in Computational Biology (CMPBIO 201) and Genomics and Bioinformatics (MCB 280C)

2005 Graduate student instructor, Topics in Computational Biology and Genomics (MCB 246)

2003 Graduate student instructor, Principles of Biochemistry and Molecular Biology (MCB 102)

SERVICE & ACTIVITIES

Computational Biology PhD Program admissions committee, fall 2017.

Reviewer for *Nature*, *Cell*, *Molecular Biology and Evolution*, *NSMB*, *Genome Research*, *Trends in Genetics*, *Nucleic Acids Research*, *PLoS Biology*, *PLoS Genetics*, *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.