

FAN LI

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PROFESSIONAL/WORK EXPERIENCE

Sr. Bioinformatics Scientist Single Cell, Sequencing, and CyTOF (SC ²) Core Facility Division of Infectious Diseases, Children's Hospital Los Angeles	2014 – current
Postdoctoral Researcher Department of Biology, University of Pennsylvania	2014
Graduate Researcher University of Pennsylvania Perelman School of Medicine	2009 – 2013
Programmer/Analyst II Department of Biology, University of California, San Diego	2008 – 2009

EDUCATION

Ph.D., Genomics and Computational Biology Dissertation: Genome-wide analysis of RNA secondary structure in eukaryotes Advisors: Brian D. Gregory and Li-San Wang University of Pennsylvania Perelman School of Medicine	2013
B.S., Electrical Engineering and Computer Sciences University of California, Berkeley	2008

AWARDS

Travel Award, 1 st International Workshop on Microbiome in HIV Pathogenesis, Prevention, and Treatment	2015
Saul Winegrad Award for Outstanding Dissertation in Genomics and Computational Biology	2014
NIH T32 Computational Genomics	2011 – 2013
Excellence in Genome Science Graduate Student Award Penn Genome Frontiers Institute	2009 – 2013

PUBLICATIONS

Microbiome/Metagenomics

Tobin NH, Woodward C, Zabih S, Lee DJ, **Li F**, and Aldrovandi GM. A method for targeted 16S sequencing of human milk samples. *J Vis Exp*, *in press*.

Lee HR, **Li F**, Choi UY, Yu HR, Aldrovandi GM, Feng P, Gao SJ, Hong YK, and Jung J. Deregulation of HDAC5 by vIRF3 plays an essential role in the Kaposi Sarcoma-associated herpesvirus-induced lymphangiogenesis. *mBio*, *in press*.

Pannaraj PS, **Li F**, Cerini C, Bender JM, Yang S, Rollie A, Adisetiyo H, Zabih S, Lincez P, Bittinger K, Bailey A, Bushman FD, Sleasman JW, and Aldrovandi GM. Association between breast milk bacterial communities and establishment and development of the infant gut microbiome. *JAMA Pediatrics*, doi:10.1001/jamapediatrics.2017.0378 (2017).

Bender JM, **Li F**, Martelly S, Byrt E, Rouzier V, Leo M, Tobin NH, Pannaraj PS, Adisetiyo H, Santiskulvong C, Wang S, Autran C, Bode L, Fitzgerald D, Kuhn L, and Aldrovandi GM. Maternal HIV infection influences the microbiome of HIV-uninfected infants. *Sci Transl Med*, doi: 10.1126/scitranslmed.aaf510 (2016).

Francis N, **Li F**, Zabih S, Oberai A, Chavez T, Purswani H, Capretz T, Chin S, and Bender JM. The effect of gastroschisis on the developing infant gut microbiome. *In review*.

Bender JM, **Li F**, Adisetiyo H, Yang S, Zabih S, Pannaraj PS, Hung L, Wilkinson T, Dien-Bard J, She R, and Aldrovandi GM. Input biomass contributes to variation in microbiome profiling. *Submitted*.

Infectious diseases

Yang S, Hemarajata P, Hindler J, **Li F**, Adisetiyo H, Aldrovandi GM, Sebra R, Kasarskis A, MacCannell D, Didelot X, Russell D, Rubin Z, and Humphries RM. Evolution and transmission of carbapenem-resistant *Klebsiella pneumoniae* expressing the blaOXA-232 gene during an institutional outbreak associated with endoscopic retrograde cholangiopancreatography. *Clin Infect Dis*, doi: 10.1093/cid/ciw876 (2017).

Yang S, Hemarajata P, Hindler J, Ward K, Adisetiyo H, **Li F**, Aldrovandi GM, Green NM, Russell D, Rubin Z, and Humphries RM. Investigation of a suspected nosocomial transmission of blaKPC3-mediated carbapenem-resistant *Klebsiella pneumoniae* by whole genome sequencing. *Diagn Microbiol Infect Dis*, doi: 10.1016/j.diagmicrobio.2015.12.019 (2016).

Ruan A, Tobin NH, Mulligan K, Rollie A, **Li F**, Sleasman JW, and Aldrovandi GM. Macrophage activation in HIV-infected adolescent males contributes to differential bone loss by sex: adolescent trials network study 021. *J Acquir Immune Defic Syndr*, doi: 10.1097/QAI.0000000000000953 (2016).

RNA structure and function

Kuksa PP*, **Li F***, Kannan S, Gregory BD, and Wang LS. HiPR: High-throughput probabilistic RNA structure inference. *In revision*.

Li N, Yousefi M, Nakauka-Ddamba A, **Li F**, Vandivier LE, Parada K, Woo DH, Wang S, Naqvi AS, Rao S, Tobias J, Cedeno RJ, Minuesa G, Katz Y, Barlowe TS, Valvezan A, Shankar S, Deering RP, Klein PS, Jensen ST, Kharas MG, Gregory BD, Yu Z, and Lengner CJ. The Msi family of RNA-binding proteins function redundantly as intestinal oncoproteins. *Cell Rep*, doi: 10.1016/j.celrep.2015.11.022 (2015).

Wang S, Li N, Yousefi M, Nakauka-Ddamba A, **Li F**, Parada K, Rao S, Minuesa G, Katz Y, Gregory BD, Kharas MG, Yu Z, and Lengner CJ. Transformation of the intestinal epithelium by the MSI2 RNA-binding protein. *Nat Commun*, 2015 Mar 16;6:6517 doi: 10.1038/ncomms7517 (2015).

Vandivier LE, **Li F**, and Gregory BD. High-throughput nuclease-mediated probing of RNA secondary structure in plant transcriptomes. *Methods Mol Biol*, doi: 10.1007/978-1-4939-2444-8_3 (2015).

Stein P, Rozhkov NV, **Li F**, Cardenas FL, Davydenk O, Vandivier LE, Gregory BD, Hannon GJ, and Schultz RM. Essential role for endogenous siRNAs during meiosis in mouse oocytes. *PLoS Genet*. 2015 Feb 19;11(2):e1005013. doi: 10.1371/journal.pgen.1005013 (2015).

Silverman IM*, **Li F***, Alexander A, Goff L, Trapnell C, Rinn JL, and Gregory BD. RNase-mediated protein footprint sequencing reveals protein-binding sites throughout the human transcriptome. *Genome Biol*, 15:R3 doi:10.1186/gb-2014-15-1-r3 (2014).

Ihara M, Meyer-Ficca ML, Leu NA, Rao S, Gregory BD, **Li F**, Zalenskaya IA, Schultz RM, and Meyer RG. Paternal poly(ADP-ribose) metabolism regulates retention of inheritable sperm histones and early embryonic gene expression. *PLoS Genet*, 10(5):e1004317 doi: 10.1371/journal.pgen.1004317 (2014).

Elliott R, **Li F**, Dragomir I, Chua MW, Gregory BD, and Weiss SR. Analysis of the host transcriptome from demyelinating spinal cord of murine coronavirus-infected mice. *PLoS One*, 8(9):e75346 doi: 10.1371/journal.pone.0075346 (2013).

Vandivier LE, **Li F**, Zheng Q, Willmann MR, Chen Y, and Gregory BD. *Arabidopsis* mRNA secondary structure correlates with protein function and domains. *Plant Signal Behav*, 8(6). pii: e24301 (2013).

Silverman IM*, **Li F***, and Gregory BD. Review: Genomic era analyses of RNA secondary structure and RNA-binding proteins reveal their significance to post-transcriptional regulation in plants. *Plant Science*, 205-206 (p55-62) <http://dx.doi.org/10.1016/j.plantsci.2013.01.009> (2013).

Li F, Zheng Q, Vandivier LE, M.R. Willmann, Y. Chen, and Gregory BD. Regulatory impact of RNA secondary structure across the *Arabidopsis thaliana* transcriptome. *Plant Cell*, 24(11):4346-59 (2012).

Li F, Ryvkin P, Childress M, Valladares O, Gregory BD, and Wang LS. SAVoR: a server for sequencing annotation and visualization of RNA structures. *Nucleic Acids Res*, 40(W1):W59-W64 (2012).

Li F*, Zheng Q*, Ryvkin P, Dragomir I, Desai Y, Aiyer S, Valladares O, Yang J, Sabin LR, Murray JI, Lamitina T, Raj A, Cherry S, Wang LS, and Gregory BD. Global analysis of RNA secondary structure in two metazoans. *Cell Rep*, 1:69-82 (2012).

Zheng Q, Ryvkin P, **Li F**, Dragomir I, Valladares O, Yang J, Cao K, Wang LS, and Gregory BD. Genome-wide double-stranded RNA sequencing reveals the functional significance of base-paired RNAs in *Arabidopsis*. *PLoS Genet*, 6(9), pii: e1001141 (2010).

Other

Ha VL, Luong A, **Li F**, Casero D, Malvar J, Kim YM, Bhatia R, Crooks GM, and Parekh C. The T-ALL related gene BCL11B regulates the initial stages of human T-cell differentiation. *Leukemia*, doi:10.1038/leu.2017.70 (2017).

Yang Y, He S, Wang Q, **Li F**, Kwak M, Chen S, O'Connell D, Zhang T, Priooz SD, Jeon Y, Chimge N, Frenkel B, Choi Y, Aldrovandi GM, Oh B, Zan Y, and Liang C. Autophagic UVRAG promotes UV-induced photolesion repair by activation of the CRL4^{DDb2} E3 ligase. *Mol Cell*, doi: 10.1016/j.molcel.2016.04.014 (2016).

Li F, Thiele I, Jamshidi N, and Palsson BO. Identification of potential pathway mediation targets in Toll-like receptor signaling. *PLoS Comput Biol*, 5:2, e1000292 (2009).

* Authors contributed equally to this work

TALKS

New methods in microbiome data analysis. Gut Microbiome Interest Group, Children's Hospital Los Angeles, 2017.

Microbiome data analysis: hidden assumptions and common pitfalls. Advancing the Field of Microbiome Research for HIV Positive and At-risk Populations, Center for AIDS Research, University of California, Los Angeles, 2017.

The SC² core facility: case studies in multi-omics data analysis. Research Seminar Series, Children's Hospital Los Angeles, 2016.

Feeding practices and HIV exposure modulate infant gut microbiota maturity. 1st International Workshop on Microbiome in HIV Pathogenesis, Prevention and Treatment, 2015.

The Mi Next Generation Science (MiNGS) core. Developmental Biology and Regenerative Medicine Annual Retreat, Children's Hospital Los Angeles, 2015.

Sequencing-based approaches to study RNA structure and function. The Saban Research Institute Seminar Series, Children's Hospital Los Angeles, 2014.

Regulatory impact of secondary structure in the *Arabidopsis* transcriptome. Plant Biology Seminar Series, University of Pennsylvania, 2013.

Global analysis of RNA-protein interactions across the human transcriptome. PCBI/GCB Annual Retreat, 2012.

ABH1 regulates mRNA secondary structure in *Arabidopsis*. Plant Biology Seminar Series, University of Pennsylvania, 2012.