Christine S. Cheng

Assistant Professor
Department of Biology
Bioinformatics Program
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EDUCATION

University of California, San Diego La Jolla, CA
Ph.D. Bioinformatics and Systems Biology
2011
Advisor: Professor Alexander Hoffmann

Stanford University Stanford, CA
M.S. Computer Science
2001

National Taiwan University Taipei, Taiwan
B.S. Plant Biology
1996

PROFESSIONAL EXPERIENCE

Assistant Professor, Department of Biology, Boston University Boston, MA
Single cell epigenetic/transcriptomic, immunology, bioinformatics 2016 – present

Postdoctoral Fellow, Broad Institute of MIT and Harvard Cambridge, MA
Epigenetic, immunology, bioinformatics 2011 – 2016
Advisor: Professor Aviv Regev

AWARDS

NIH Ruth L. Kirschstein National Research Service Award Individual Postdoctoral Fellowship 2012-2015

DOD Army Breast Cancer Predoctoral Traineeship 2005-2008

PUBLICATIONS

In review:

1. **Cheng CS***[§], Gate R*, Siba A, Tabaka M, Lituiev D, Subramaniam M, Hougen KL, Shamim M, Wortman I, Aiden AP, Machol I, Feng T, de Jager P, Chang H, Aiden EL, Benoist C, Beer M, Ye C[§], Regev A[§]. Genetic determinants of chromatin accessibility and gene regulation in T cell activation across human individuals. ***Submitted to Nature Genetics, in revision.*** (Contributions: conceived study, designed/performed experiments and computational analysis, wrote manuscript)

Published:

1. Soto-Feliciano YM, Bartlebaugh JME, Liu Y, Sánchez-Rivera FJ, Bhutkar A, Weintraub AS, Buenrostro JD, **Cheng CS**, Regev A, Jacks TE, Young RA, Hemann MT. PHF6 regulates phenotypic plasticity through chromatin organization within lineage-specific genes. **Genes & development. 2017; 31(10):973-989.**

2. Fiziev P, Akdemir KC, Miller JP, Keung EZ, Samant NS, Sharma S, Natale CA Terranova CJ, Maitituoheti M, Amin SB, Martinez-Ledesma E, Dhamdhere M, Axelrad JB, Shah A, **Cheng CS**, Mahadeshwar H, Seth S, Barton MC, Protopopov A Tsai KY, Davies MA, Garcia BA, Amit I, Chin L,

Ernst J, Rai K. Systematic Epigenomic Analysis Reveals Chromatin States Associated with Melanoma Progression. **Cell Report. 2017 Apr 25;19(4):875-889. doi: 10.1016/j.celrep.2017.03.078.**

3. **Cheng CS***, Behar M*, Suryawanshi GW, Feldman KE, Spreafico R, Hoffmann A. Iterative modeling reveals evidence of sequential transcriptional control mechanisms. ***Cell Systems.*** **2017 Feb 10. pii: S2405-4712(17)30012-1.** (Contributions: conceived study, designed/performed experiments and computational analysis, wrote manuscript)

4. Sanjana NE, Wright J, Zheng K, Shalem O, Fontanillas P, Joung J, Cheng CS, Regev A, Zhang F. High-resolution interrogation of functional elements in the noncoding genome. ***Science.*** **2016; 353(6307):1545-1549** (Contributions: designed/performed experiments)

5. **Cheng CS**, Rai K, Garber M, Hollinger A, Robbins D, Anderson S, Macbeth A, Tzou A, Carneiro MO, Raychowdhury R, Russ C, Hacohen N, Gershenwald JE, Lennon N, Nusbaum C, Chin L, Regev A, Amit I. Semiconductor-based DNA sequencing of histone modification states. **Nature Communications. 2013;4:2672.** (Contributions: conceived study, designed/performed experiments and computational analysis, wrote manuscript)

6. Garber M, Yosef N, Goren A, Raychowdhury R, Thielke A, Guttman M, Robinson J, Minie B, Chevrier N, Itzhaki Z, Blecher-Gonen R, Bornstein C, Amann-Zalcenstein D, Weiner A, Friedrich D, Meldrim J, Ram O, **Cheng C**, Gnirke A, Fisher S, Friedman N, Wong B, Bernstein BE, Nusbaum C, Hacohen N, Regev A, Amit I. A high-throughput chromatin immunoprecipitation approach reveals principles of dynamic gene regulation in mammals. **Mol Cell. 2012 Sep 14;47(5):810-22.** PMCID: PMC3873101 (Contribution: designed and performed experiments)

7. **Cheng CS**, Feldman KE, Lee J, Verma S, Huang DB, Huynh K, Chang M, Ponomarenko JC, Sun SC, Benedict CA, Ghosh G, Hoffmann A. The specificity of innate immune responses is enforced by repression of interferon response elements by NF□B p50. **Science Signaling. 2011 Feb 22;4(161):ra11.** PMCID: PMC3096068 (Contributions: conceived study, designed/performed experiments and computational analysis, wrote manuscript)

8. Escoubet-Lozach L, Benner C, Kaikkonen MU, Lozach J, Heinz S, Spann NJ, Crotti A, Stender J, Ghisletti S, Reichart D, **Cheng CS**, Luna R, Ludka C, Sasik R, Garcia-Bassets I, Hoffmann A, Subramaniam S, Hardiman G, Rosenfeld MG, Glass CK. Mechanisms establishing TLR4-responsive activation states of inflammatory response genes. **PLoS Genet. 2011 Dec;7(12):e1002401.** PMCID: PMC3234212 (Contribution: designed and performed experiments)

9. Ramirez-Carrozzi VR, Braas D, Bhatt DM, **Cheng CS**, Hong C, Doty KR, Black JC, Hoffmann A, Carey M, Smale ST. A unifying model for the selective regulation of inducible transcription by CpG islands and nucleosome remodeling. **Cell. 2009 Jul 10;138(1):114-28.** PMCID: PMC2712736 (Contribution: designed and performed computational analysis)

10. **Cheng CS**, Johnson TL, Hoffmann A. Epigenetic control: slow and global, nimble and local. **Genes and Development. 2008 May 1;22(9):1110-4.** PMCID: PMC2732403

11. Garcia-Bassets I, Kwon YS, Telese F, Prefontaine GG, Hutt KR, **Cheng CS**, Ju BG, Ohgi KA, Wang J, Escoubet-Lozach L, Rose DW, Glass CK, Fu XD, Rosenfeld MG. Histone methylation-dependent mechanisms impose ligand dependency for gene activation by nuclear receptors. **Cell. 2007 Feb 9;128(3):505-18**. PMCID: PMC1994663 (Contribution: designed and performed computational analysis)

12. Kwon YS, Garcia-Bassets I, Hutt KR, **Cheng CS**, Jin M, Liu D, Benner C, Wang D, Ye Z, Bibikova M, Fan JB, Duan L, Glass CK, Rosenfeld MG, Fu XD. Sensitive ChIP-DSL technology reveals an extensive estrogen receptor alpha-binding program on human gene promoters. **Proc Natl Acad Sci U S A. 2007 Mar 20;104(12):4852-7**. PMCID: PMC1821125 (Contribution: designed and performed computational analysis)

INVITED TALKS

15. Boston University, BU Data Science Day, 2018
14. NIH NIDA Genetics Consortium Meeting, 2018
13. Boston University, Medical School, Microbial Pathogenesis, Inflammation and Immunology Seminar, 2017
12. National Taiwan University, Medical School, Taiwan, 2016
11. Academic Sinica, Taiwan, 2016
10. Cold Spring Harbor Epigenetic and Chromatin Meeting, 2016
9. Cell Circuits and Epigenomics Program Meeting, Broad Institute of MIT and Harvard, 2016
8. Medical and Population Genomics Meeting, Broad Institute of MIT and Harvard, 2016
7. New Initiative in Precision Medicine, Epigenetics and Genomics, School of Medicine, University of California, San Diego, 2016
6. Department of Immunology, UT Southwestern, 2016
5. Department of Pharmaceutical Chemistry, University of California, San Francisco, 2016
4. Department of Biology, Boston University, 2016
3. Department of Biomedical Engineering, Johns Hopkins University, 2015
2. Klarman Cell Observatory Annual Retreat, Broad Institute of MIT and Harvard, 2015
1. Keytone NFkB in Inflammation and Disease Meeting, 2010