

CALEB LAREAU

clareau@stanford.edu

ORCID: 0000-0003-4179-4807



CURRENT APPOINTMENT

I am currently a **Stanford Science Fellow** in the School of Medicine at Stanford University and a **Parker Scholar** at the Parker Institute of Cancer Immunotherapy. My research concerns the development and application of single-cell technologies to inform properties of human physiology, including the somatic changes in tissues and the dynamics of immune cells within the tumor microenvironment. I am particularly interested in studying and increasing the efficacy of immunotherapies.

EDUCATION

Doctor of Philosophy , [‡] Biological and Biomedical Sciences Harvard University (Cambridge, MA)	May 2020
Master of Arts , Biostatistics Harvard University (Cambridge, MA)	May 2017
Bachelor of Science , <i>summa cum laude</i> , Biochemistry and Mathematics University of Tulsa (Tulsa, OK)	May 2015

[‡]Advisory committee: Martin J. Aryee, Bradley E. Bernstein, Jason D. Buenrostro, Vijay G. Sankaran (advisor)

RESEARCH EXPERIENCE

Parker Institute for Cancer Immunotherapy , Stanford Campus	2021- Present
Stanford University , Departments of Genetics and Pathology	2020- Present
Harvard University , Stem Cell and Regenerative Biology Department	2018- 2020
Boston Children's Hospital , Division of Hematology/Oncology	2017- 2020
Massachusetts General Hospital , Department of Pathology	2016- 2020
Broad Institute of Harvard and MIT , Cell Circuits and Epigenomics Program	2016- 2020
Max Planck Institute of Psychiatry , Translational Research in Psychiatry Division	2013- 2014
Oklahoma Medical Research Foundation , Arthritis and Clinical Immunology Program	2011- 2015
University of Tulsa , Department of Computer Science	2011- 2015

AWARDS AND HONORS

Parker Institute for Cancer Immunotherapy - Parker Scholar	2021
Stanford Science Fellowship	2020
Deutsche Forschungsgemeinschaft Mercator Fellowship	2020
Ruth L. Kirschstein National Research Service Award Individual Predoctoral Fellowship (F31)	2018
Harvard University Certificate of Distinction in Teaching	2017
National Science Foundation Graduate Research Fellowship (NSF-GRFP)	2015
Phi Kappa Phi Walter and Adelheid Hohenstein Fellow	2015
Pi Kappa Alpha Robertson Most Outstanding Undergraduate Student	2014
Jess Choteau Outstanding Senior	2014
Deutscher Akademischer Austauschdienst RISE Scholar	2013, 2014
Barry M. Goldwater Scholar	2013
University of Tulsa Presidential Scholar	2011
Oklahoma Medical Research Foundation Sir Alexander Fleming Scholar	2011

PATENTS

PCT/US2019/036583; Lineage tracing using mitochondrial genome mutations and single-cell genomics (**co-inventor**)
PPA/62;881,148; Lineage inference from single-cell transcriptomics (**co-inventor**)
PPA/63;034,740; Methods of detecting mitochondrial disease (**co-inventor**)

TEACHING EXPERIENCE

Stanford University

Teaching Associate, Developmental Biology and Genetics PhD Bootcamp

Summer 2020

Harvard University

Teaching Associate, Introduction to Computational Biology and Bioinformatics

Spring 2017, 2020

Teaching Associate, Introduction to Statistical Genetics

Fall 2016, 2017

Cold Spring Harbor Laboratory

Lecturer, Advanced Sequencing Technologies

Fall 2019

University of Tulsa

Teaching Associate, Molecular Modeling

Spring 2014, 2015

Teaching Associate, Energy Technology for the Future

Spring 2013

PUBLICATIONS

* Denotes equal contributions; ‡ Denotes corresponding author(s)

FIRST AUTHOR

1. **C.A. Lareau**,*[‡], L.S. Ludwig,*[‡], C. Muus, *et al.* (2020) Massively parallel single-cell mitochondrial DNA genotyping and chromatin profiling. *Nature Biotechnology*. DOI: 10.1038/s41587-020-0645-6.
2. N. Schmidt*, **C.A. Lareau***, H. Keshishian* *et al.* (2020) A direct RNA-protein interaction atlas of the SARS-CoV-2 RNA in infected human cells. *Nature Microbiology*. DOI: 10.1101/2020.07.15.204404.
3. M. A. Walker,* **C.A. Lareau***, L.S. Ludwig,* *et al.* (2020) Purifying Selection against Pathogenic Mitochondrial DNA in Human T cells. *New England Journal of Medicine*. DOI: 10.1056/NEJMoa2001265.
4. **C.A. Lareau** and A.T. Satpathy. (2020) An old BATF's new T-ricks. *Nature Immunology*. DOI: 10.1038/s41590-020-0796-0.
5. **C.A. Lareau**[‡], S. Ma, F.M. Duarte, J.D. Buenrostro[‡]. (2020) Inference and effects of barcode multiplets in droplet-based single-cell assays. *Nature Communications*. DOI: 10.1038/s41467-020-14667-5.
6. D. Vuckovic*, E. Bao*, P. Akbari*, **C.A. Lareau***, *et al.* (2020) The Polygenic and Monogenic Basis of Blood Traits and Diseases. *Cell*. DOI: 10.1101/2020.02.02.20020065.
7. **C.A. Lareau***, F.M. Duarte,* J.G. Chew,* *et al.* (2019) Droplet-based combinatorial indexing for massive-scale single-cell chromatin accessibility. *Nature Biotechnology*. DOI: 10.1038/s41587-019-0147-6.
8. L.S. Ludwig,* **C.A. Lareau***, J.C. Ulirsch*, *et al.* (2019) Lineage tracing in humans enabled by mitochondrial mutations and single cell genomics. *Cell*. DOI: 10.1016/j.cell.2019.01.022.
9. **C.A. Lareau**, L.S. Ludwig, V.G. Sankaran. (2019) Longitudinal assessment of clonal mosaicism in human hematopoiesis via mitochondrial mutation tracking. *Blood Advances*. DOI: 10.1182/bloodadvances.2019001196.

10. J.C. Ulirsch,* **C.A. Lareau,*** E.L. Bao,* *et al.* (2019) Interrogation of human hematopoiesis at single-cell and single-variant resolution. *Nature Genetics*. DOI: 10.1038/s41588-019-0362-6.
11. **C.A. Lareau,** D. Kangeyan, M.J. Aryee. (2019) Preprocessing and computational analysis of single-cell epigenomic datasets. *Methods in Molecular Biology - Computational Methods for Single-Cell Data Analysis*. DOI: 10.1007/978-1-4939-9057-3.
12. E.L. Bao,* **C.A. Lareau,*** C. Brugnara, I.R. Fulcher, *et al.* (2019) Heritability of fetal hemoglobin, white cell count, and other clinical traits from a sickle cell disease family cohort. *American Journal of Hematology*. DOI: 10.1002/ajh.25421.
13. L.S. Ludwig,* , **C.A. Lareau,*** *et al.* (2019) Transcriptional States and Chromatin Accessibility Underlying Human Erythropoiesis. *Cell Reports*. DOI: 10.1016/j.celrep.2019.05.046.
14. **C.A. Lareau,*** K. Clement,* J.Y. Hsu,* *et al.* (2018) Response to "Unexpected mutations after CRISPR-Cas9 editing *in vivo*." *Nature Methods*. DOI: 10.1038/nmeth.4541.
15. **C.A. Lareau** and M.J. Aryee. (2018) hichipper: A preprocessing pipeline for assessing library quality and DNA loops from HiChIP data. *Nature Methods*. DOI: 10.1038/nmeth.4583.
16. **C.A. Lareau,** C.F. DeWeese *et al.* (2017) Polygenic risk assessment reveals pleiotropy between sarcoidosis and inflammatory disorders in the context of genetic ancestry. *Genes and Immunity*. DOI: 10.1038/gene.2017.3
17. **C.A. Lareau** and M.J. Aryee. (2017) diffloop: a novel computational framework for identifying and functionalizing differential topological features in DNA. *Bioinformatics*. DOI: 10.1093/bioinformatics/btx623.
18. **C.A. Lareau,** B.C. White, *et al.* (2016) An interaction quantitative trait loci tool implicates epistatic functional variants in an apoptosis pathway in smallpox vaccine eQTL data. *Genes and Immunity*. DOI: 10.1038/gene.2016.15.
19. **C.A. Lareau,** B.C. White, C.G. Montgomery, and B.A. McKinney. (2015) Common Variants Modulate Differential Correlation Structures in Gene Expression Data. *Frontiers in Genetics*. DOI: 10.3389/fgene.2015.00312.
20. **C.A. Lareau,** I.A. Adrianto, *et al.* (2015) Fine mapping of Chromosome 15q25 in Sarcoidosis Implicates Zinc Finger Protein 592 in Patients with Neurological Involvement. *Annals of Translational and Clinical Neurology*. DOI: 10.1002/acn3.229.
21. **C.A. Lareau,** B.C. White, A.L. Oberg, and B.A. McKinney. (2015) Differential co-expression network centrality and machine learning feature selection for identifying susceptibility hubs in networks with scale-free structure. *BioData Mining*, DOI: 10.1186/s13040-015-0040-x.
22. **C.A. Lareau** and B.A. McKinney. (2015) Network Theory for Data-Driven Epistasis Networks. *Epistasis: Methods and Protocols, Methods in Molecular Biology*, DOI: 10.1007/978-1-4939-2155-3.
23. N.A. Davis,* **C.A. Lareau,*** *et al.* (2013) Encore: Genetic association interaction network centrality pipeline and application to SLE exome data. *Genetic Epidemiology*. DOI: 10.1002/gepi.21739.

CO-AUTHOR

24. S. Ma, B. Zhang, L.M. LaFave, Z. Chiang, Y. Hu, J. Ding, A. Brack, V.K. Kartha, T. Law, **C.A. Lareau,** *et al.* Chromatin potential identified by shared single cell profiling of RNA and chromatin. *Cell*. DOI: 10.1016/j.cell.2020.09.056.
25. E. Bao, S. Nandakumar, X. Liao, A. Bick, J. Karjalainen, M. Tabaka, O.I. Gan, A. Havulinna, T. Kiiskinen, **C.A. Lareau,** *et al.* (2020) Genetic predisposition to myeloproliferative neoplasms implicates hematopoietic stem cell biology. *Nature*. DOI: 10.1038/s41586-020-2786-7.
26. M. Chen, L. Raffield, A. Mousas, S. Sakaue, J. Huffman, T. Jiang, P. Akbari, D. Vuckovic, E. Bao, A. Moscati, X. Zhong, R. Manansala, V. Laplante, M. Chen, K. Lo, H Qian, **C.A. Lareau,** *et al.* (2020) Trans-ethnic and ancestry-specific blood-cell genetics in 746,667 individuals from 5 global populations. *Cell*. DOI: 10.1016/j.cell.2020.06.045.

27. S. Johnstone, A. Reyes, Y. Qi, E. Hegazi, K. Pelka, J. Chen, L. Zou, Y. Drier, V. Hecht, N. Shores, **C.A. Lareau**, *et al.* (2020) A topological atlas reveals layers of genome reorganization in colorectal cancer. *Cell*. DOI: 10.1016/j.cell.2020.07.030.
28. L. Garman, R. Pelikan, A. Rasmussen, **C.A. Lareau**, *et al.* (2020) Single cell transcriptomics implicate novel T cell and monocyte immune dysregulation in sarcoidosis. *Frontiers in Immunology*. DOI: 10.3389/fimmu.2020.01901.
29. J. Grünewald, R. Zhao, **C.A. Lareau**, *et al.* (2020) A dual-deaminase CRISPR base editor enables concurrent adenine and cytosine editing. *Nature Biotechnology*. DOI: 10.1038/s41587-020-0535-y.
30. L.M. LaFave, V.K. Kartha, S. Ma, K. Meli, I. Del Priore, **C.A. Lareau**, *et al.* (2020) Epigenetic state transitions characterize tumor progression in lung adenocarcinoma. *Cancer Cell*. DOI: 10.1016/j.ccell.2020.06.006.
31. A.L. Basak, M. Munschauer, **C.A. Lareau**, *et al.* (2020) Control of human hemoglobin switching by LIN28B-mediated regulation of BCL11A translation. *Nature Genetics*. DOI: 10.1038/s41588-019-0568-7.
32. J. Ray, C. de Boer, C. Fulco, **C.A. Lareau**, *et al.* (2020) Prioritizing disease and trait causal variants at the TNFAIP3 locus using functional and genomic features. *Nature Communications*. DOI: 10.1038/s41467-020-15022-4.
33. H. Yoshida, **C.A. Lareau**, R.N. Ramirez, S.A. Rose, *et al.* (2019) The cis-regulatory atlas of the mouse immune system. *Cell*. DOI: 10.1016/j.cell.2018.12.036.
34. J. Grünewald, R. Zhao, S. Garcia,* S. Iyer,* **C.A. Lareau**,* *et al.* (2019) Transcriptome-wide off-target RNA editing induced by CRISPR-guided DNA base editors. *Nature*. DOI: 10.1038/s41586-019-1161-z.
35. H. Chen, **C.A. Lareau**, T. Andreani, *et al.* (2019) Assessment of computational methods for the analysis of single-cell ATAC-seq data. *Genome Biology*. DOI: 10.1186/s13059-019-1854-5.
36. H. Chen, L. Albergante, J.Y. Hsu, **C.A. Lareau**, *et al.* (2019) STREAM: Single-cell Trajectories Reconstruction, Exploration And Mapping of omics data. *Nature Communications*. DOI: 10.1038/s41467-019-09670-4.
37. J. Grünewald, R. Zhao, S. Iyer,* **C.A. Lareau**,* S. Garcia,* *et al.* (2019) CRISPR adenine and cytosine base editors with reduced RNA off-target activities. *Nature Biotechnology*. DOI: 10.1038/s41587-019-0236-6.
38. C. Fulco, J. Nasser, T. Jones, G. Munson, D. Bergman, V. Subramanian, S. Grossman, R. Anyoha, B. Doughty, T. Patwardhan, T. Nguyen, M. Kane, E. Perez, N. Durand, **C.A. Lareau**, *et al.* (2019) Activity-by-Contact model of enhancer-promoter regulation from thousands of CRISPR perturbations. *Nature Genetics*. DOI: 10.1038/s41588-019-0538-0.
39. S.K. Nandakumar, S.K. McFarland, L.M. Mateyka,* **C.A. Lareau**,* *et al.* (2019) Gene-centric functional dissection of human genetic variation uncovers regulators of hematopoiesis. *eLife*: DOI: 10.7554/eLife.44080.
40. J. Pan, Z. McKenzie, A. D'Avino, N. Mashtalir, **C.A. Lareau**, *et al.* (2019) The ATPase module of mammalian SWI/SNF family complexes mediates subcomplex identity and catalytic activity-independent genomic targeting. *Nature Genetics*. DOI: 10.1038/s41588-019-0363-5.
41. N. Abdulhay, C. Fiorini, J. Verboon, L. Ludwig, J. Ulirsch, B. Zieger, **C.A. Lareau**, *et al.* (2019) Impaired Human Hematopoiesis Due to a Cryptic Intronic GATA1 Splicing Mutation. *Journal of Experimental Medicine*. DOI: 10.1084/jem.20181625.
42. J.D. Buenrostro, M.R. Corces, **C.A. Lareau**, *et al.* (2018) Integrated Single-Cell Analysis Maps the Continuous Regulatory Landscape of Human Hematopoietic Differentiation. *Cell*. DOI: 10.1016/j.cell.2018.03.074.
43. R.C. Pelikan, J.A. Kelly, Y. Fu, **C.A. Lareau**, *et al.* (2018) Enhancer histone-QTLs are enriched on autoimmune risk haplotypes and influence gene expression within chromatin networks. *Nature Communications*, DOI: 10.1038/s41467-018-05328-9.

44. H. Finucane, Y. Reshef, V. Anttila, K. Slowikowski, A. Gusev, A. Byrnes, S. Gazal, P.-R. Loh, **C.A. Lareau**, *et al.* (2018) Heritability enrichment of specifically expressed genes identifies disease-relevant tissues and cell types. *Nature Genetics*. DOI: 10.1038/s41588-018-0081-4.
45. B. Michel, A. D'Avino, S. Cassel, N. Mashtalir, Z. McKenzie, M. McBride, A. Valencia, Q. Zhou, M. Bocker, L. Soares, J. Pan, D. Remillard, **C.A. Lareau**, *et al.* (2018) A non-canonical SWI/SNF complex is a synthetic lethal target in cancers driven by BAF complex perturbation. *Nature Cell Biology*. DOI: 10.1038/s41556-018-0221-1.
46. A.T. Satpathy, N. Saligrama, J.D. Buenrostro, Y. Wei, B. Wu, A.J. Rubin, J.M. Granja, **C.A. Lareau**, *et al.* (2018) Transcript-indexed ATAC-seq reveals paired single-cell T cell receptor identity and chromatin accessibility for precision immune profiling. *Nature Medicine*. DOI: 10.1038/nm.4520.
47. J.C. Ulirsch, **C.A. Lareau**, *et al.* (2017) Confounding in *ex vivo* models of Diamond-Blackfan anemia. *Blood*. DOI: 10.1182/blood-2017-05-783191.
48. T. Carrillo-Roa, C. Labermier, P. Weber, D.P. Herzog, **C.A. Lareau**, *et al.* (2017) Common Genes Associated With Antidepressant Response In Mouse And Man Identify Key Role Of Glucocorticoid Receptor Sensitivity. *PLoS Biology*. DOI: 10.1371/journal.pbio.2002690.
49. R.J.H. Ryan, J. Petrovic, D.M. Rausch, Y. Zhou, **C.A. Lareau** *et al.* (2017) AB Cell Regulome Links Notch to Downstream Oncogenic Pathways in Small B Cell Lymphomas. *Cell Reports*. DOI: 10.1016/j.celrep.2017.09.066.
50. Q. Tang, S. Iyer, R. Lobbardi, J. C. Moore, H. Chen, **C.A. Lareau**, *et al.* (2017) Dissecting hematopoietic and renal cell heterogeneity in adult zebrafish at single-cell resolution using RNA sequencing. *Journal of Experimental Medicine*. DOI: 10.1084/jem.20170976.
51. B.A. McKinney, **C.A. Lareau**, *et al.* (2016) The Integration of Epistasis Network and Functional Interactions in a GWAS Implicates RXR Pathway Genes in the Immune Response to Smallpox Vaccine. *PLoS One*. DOI: 10.1371/journal.pone.0158016.

PRE-PRINT

52. E. Mimitou*, **C.A. Lareau***, K.Y. Chen* *et al.* (2020) Scalable, multimodal profiling of chromatin accessibility and protein levels in single cells. *bioRxiv*. DOI: 10.1101/2020.09.08.286914.
53. E. Fiskin, **C.A. Lareau**, *et al.* (2020) Single-cell multimodal profiling of proteins and chromatin accessibility using PHAGE-ATAC. *bioRxiv*. DOI: 10.1101/2020.10.01.322420.
54. T. Stuart, A. Srivastava, **C.A. Lareau**, R. Satija. (2020) Multimodal single-cell chromatin analysis with Signac. *bioRxiv*. DOI: 10.1101/2020.11.09.373613

ACADEMIC SERVICE

AD HOC PEER REVIEW

Nature Biotechnology, Nature Communications, BioData Mining, Bioinformatics, BMC Medical Genomics, The R Journal

MENTORSHIP EXPERIENCE

Stanford undergraduate and graduate computer science research (2020-present)

Research Science Institute (2016, 2018, 2019)

MIT undergraduate research (2016-2020)

PROFESSIONAL MEMBERSHIP

Associate Member, American Association for Cancer Research

Developer, Bioconductor Project

Supporting Member, R and Python Software Foundations

INVITED TALKS AND PRESENTATIONS

UCSF Diabetes Center*, San Francisco, CA; February 2021.

Recent advances in single-cell multiomics

Wellcome Trust Mitochondrial Medicine*, Hinxton, UK; December 2020.

Applications and development of massively parallel single-cell mitochondrial DNA sequencing.

American Society of Human Genetics Annual Meeting*, San Diego, CA; October 2020.

Massively parallel single-cell mitochondrial DNA genotyping and chromatin profiling.

Single Cell Technology Symposium,*, Mount Sinai, NY; October 2020.

Massively parallel single-cell mitochondrial DNA genotyping and chromatin profiling.

American Society of Human Genetics Annual Meeting, Houston, TX; October 2019.

Droplet-based combinatorial indexing for massive-scale single-cell chromatin accessibility.

Computational Genomics Workshop, Cambridge, MA; September 2019.

Computational analyses of single-cell chromatin accessibility data.

HHMI / High-Throughput Dense Reconstruction of Cell Lineages, Janelia, VA; April 2019.

Lineage tracing in humans enabled by mitochondrial mutations and single cell genomics.

Broad Institute Cell Circuits and Epigenomics Program meeting, Boston, MA; July 2018.

Lineage tracing in humans enabled by mitochondrial mutations and single cell genomics.

American Association for Cancer Research Annual Meeting. Washington, D.C. April 2017.

Genome-wide examination of topological variability reveals mechanisms of oncogene activation.

*Virtual presentation due to COVID-19