

CALEB LAREAU

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INTRODUCTION

I am a scientist with expertise in single-cell genomics, immunotherapy, and computational biology. My laboratory focuses on how cells evolve within an individual's lifetime from molecular triggers, including somatic mutations and exposures to viruses, and how these changes impact the ability of the immune system to respond to cancers and infections.

CURRENT APPOINTMENT

Assistant Member, Program in Computational and Systems Biology
Memorial Sloan Kettering Cancer Center (New York, NY)

September 2023 - Present

EDUCATION AND TRAINING

Postdoctoral Fellowship , Departments of Pathology and Genetics Stanford University (Palo Alto, CA)	2023
Doctor of Philosophy , Biological and Biomedical Sciences Harvard University (Cambridge, MA)	2020
Master of Arts , Biostatistics Harvard University (Cambridge, MA)	2017
Bachelor of Science , <i>summa cum laude</i> , Biochemistry and Mathematics University of Tulsa (Tulsa, OK)	2015

AWARDS AND HONORS

Society for Immunotherapy of Cancer - Sparkathon Emerging Leader	2023
Memorial Sloan Kettering Emerging Leader in Computational Oncology	2023
Gladstone Institutes Distinguished Achievement in Science Award (Genomic Immunology)	2023
National Human Genome Research Institute - Pathway to Independence Award (K99/R00)	2022
STAT Wunderkind	2022
Forbes 30 Under 30 - Science	2022
Parker Institute for Cancer Immunotherapy - Parker Scholar	2021
Broad Institute Next Generation in Biomedicine	2021
10x Genomics Featured Scientist in Innovator Series	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

PUBLICATIONS

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

CORRESPONDING AUTHOR

1. **C.A. Lareau**[‡], *et al.* (2023) Single-cell multi-omics reveals dynamics of purifying selection of pathogenic mitochondrial DNA across human immune cells. *Nature Genetics*. DOI: 10.1038/s41588-023-01433-8.
2. **C.A. Lareau**[‡], *et al.* (2023) Mitochondrial single cell ATAC-seq for high-throughput multi-omic detection of mitochondrial genotypes and chromatin accessibility. *Nature Protocols*. DOI: 10.1038/s41596-022-00795-3.
3. **C.A. Lareau**[‡], K.R. Parker[‡], A.T. Satpathy[‡]. (2021) Charting the tumor antigen maps drawn by single-cell genomics. *Cancer Cell*. DOI: 10.1016/j.ccell.2021.11.005.
4. **C.A. Lareau**^{*,‡}, L.S. Ludwig^{*,‡}, C. Muus, *et al.* (2021) Massively parallel single-cell mitochondrial DNA genotyping and chromatin profiling. *Nature Biotechnology*. DOI: 10.1038/s41587-020-0645-6.
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.

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6. L.S. Ludwig^{*}, **C.A. Lareau**^{*}, *et al.* (2022) A Congenital Anemia Dissociates the Pleiotropic Functions of Master Transcription Factor GATA1. *Blood*. DOI: 10.1182/blood.2021013753.
7. J. Wang^{*}, **C.A. Lareau**^{*}, *et al.* (2021) Single-Cell Multiomics Defines Tolerogenic Extrathymic Aire-Expressing Populations with Unique Homology to Thymic Epithelium. *Science Immunology*. DOI: 10.1126/sciimmunol.abl5053.
8. E. Mimitou^{*}, **C.A. Lareau**^{*}, K.Y. Chen^{*} *et al.* (2021) Scalable, multimodal profiling of chromatin accessibility, RNA, and protein levels in single cells. *Nature Biotechnology*. DOI: 10.1038/s41587-021-00927-2
9. N. Schmidt^{*}, **C.A. Lareau**^{*}, H. Keshishian^{*} *et al.* (2021) 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.
10. 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.
11. 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.
12. **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.
13. 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.
14. **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.
15. 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.
16. 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.
17. 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.

18. **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.
19. **C.A. Lareau** and M.J. Aryee. (2018) hitchhiker: A preprocessing pipeline for assessing library quality and DNA loops from HiChIP data. *Nature Methods*. DOI: 10.1038/nmeth.4583.
20. **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
21. **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.
22. **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.
23. **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.
24. **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.
25. **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.
26. 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.

INVITED COMMENTARY

27. **C.A. Lareau**[‡]. (2023). Resolving subtle cell states in sparse single-cell data. *Nature Biotechnology* DOI: 10.1038/s41587-023-01797-6.
28. **C.A. Lareau**[‡], C. Romagnani, L. Ludwig. (2022) Lineage tracing, hematopoietic stem cell and immune cell dynamics. *Frontiers in Immunology* DOI: 10.3389/fimmu.2022.1062415.
29. **C.A. Lareau** and A.T. Satpathy. (2020) An old BATF's new T-ricks. *Nature Immunology*. DOI: 10.1038/s41590-020-0796-0.

BOOK CHAPTERS

30. E.P. Mimitou[‡], P. Smibert[‡], and **C.A. Lareau**[‡] (2022) Massively parallel profiling of accessible chromatin and proteins with ASAP-seq. *Methods in Molecular Biology - Chromatin Accessibility: Methods and Protocols*. DOI: 10.1007/978-1-0716-2899-7_13.
31. L.S. Ludwig and **C.A. Lareau**[‡] (2022) Concomitant sequencing of accessible chromatin and mitochondrial genomes in single cells using mtscATAC-seq. *Methods in Molecular Biology - Chromatin Accessibility: Methods and Protocols*. DOI: 10.1007/978-1-0716-2899-7_14.
32. **C.A. Lareau**, *et al.* (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.
33. **C.A. Lareau** and B.A. McKinney. (2015) Network Theory for Data-Driven Epistasis Networks. *Methods in Molecular Biology—Epistasis: Methods and Protocols*, DOI: 10.1007/978-1-4939-2155-3.

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34. A.M Tousley, M.C. Rotiroti, L Labanieh, L.W. Rysavy, W. Kim, **C.A. Lareau**, *et al.* (2023). Co-opting T cell proximal signaling molecules enables Boolean logic-gated CAR T cell control. *Nature*. DOI: 10.1038/s41586-023-05778-2.
35. R. Fonseca, T. Burn, L. Gandolfo, S. Devi, S. Park, A. Obers, M Evrard, S. N. Christo, F. A. Buquicchio, **C.A. Lareau**, *et al.* (2022). Runx3 drives a tissue residency program that is absent in CD4+ T cells. *Nature Immunology*. DOI: 10.1038/s41590-022-01273-4.
36. T. Ruckert, **C.A. Lareau**, *et al.* (2022) Clonal expansion and epigenetic inheritance of long-lasting NK cell memory. *Nature Immunology*. DOI: 10.1038/s41590-022-01327-7.
37. T. Miller, **C.A. Lareau**, *et al.* (2022) Mitochondrial variant enrichment from high-throughput single-cell RNA-seq resolves clonal populations. *Nature Biotechnology*. DOI: 10.1101/2021.03.08.434450v1.
38. L. Penter, E. ten Hacken, J. Southard, **C.A. Lareau**, *et al.* (2022) Mitochondrial DNA mutations as natural barcodes for lineage tracing of murine tumor models. *Cancer Research*. DOI: 10.1158/0008-5472.CAN-22-0275.
39. J. Rosenberg, J. Peters, T. Hughes, **C.A. Lareau** *et al.* (2022) JAK-inhibition in a patient with a STAT1 gain-of-function variant reveals dysregulation as a common feature of aplastic anemia. *Med*. DOI: 10.1016/j.medj.2021.12.003.
40. S. Bucktrout, N. Banovich, L. Butterfield, C. Cimen-Bozkus, J. Giles, Z. Good, D. Goodman, V. Jonsson, **C.A. Lareau**, *et al.* (2022) Advancing T cell-based cancer therapy with single-cell technologies. *Nature Medicine*. DOI: 10.1038/s41591-022-01986-x.
41. V.K. Kartha, F.M. Duarte, Y. Hu, S. Ma, J.G. Chew, **C.A. Lareau**, *et al.* (2022) Functional Inference of Gene Regulation using Single-Cell Multi-Omics. *Cell Genomics*. DOI: 10.1016/j.xgen.2022.100166.
42. R. Kedmi, T. Najjar, K. Mesa, A. Grayson, L. Kroehling, Y. Hao, S. Hao, M. Pokrovskii, M. Xu, J. Talbot, J. Wang, J. Germino, **C.A. Lareau**, *et al.* (2022). Microbiota-instructed regulatory T cell differentiation is mediated by a distinct RORgt+ antigen presenting cell subset. *Nature*. DOI: 10.1038/s41586-022-05089-y.
43. E. Panditharatna, J. Marques, T. Wang, M. Trissal, I. Liu, L. Jiang, A. Beck, A. Groves, N. Dharia, D. Li, S. Hoffman, G. Kugener, M. Shaw, H. Mire, O. Hack, J. Dempster, **C.A. Lareau**, *et al.* (2022) BAF complex maintains glioma stem cells in pediatric H3K27M-glioma. *Cancer Discovery*. DOI: 10.1158/2159-8290.CD-21-1491.
44. T. Zhao, Z Chiang, J. Morriss, L. LaFave, E.M. Murray, I. Del Priore, K. Meli, **C.A. Lareau** *et al.* (2022). Spatial genomics enables multi-modal study of clonal heterogeneity in tissues. *Nature*. DOI: 10.1038/s41586-021-04217-4.
45. R. Ajore, A. Niroula, M. Pertesi, C. Cafaro, M. Thodberg, M. Went, E. Bao, L. Duran-Lozano, A. de Lapuente Portilla, T. Olafsdottir, N. Ugidos-Damboriena, O. Magnusson, M. Samur, **C.A. Lareau**, *et al.* (2022) Functional dissection of inherited non-coding variation influencing multiple myeloma risk. *Nature Communications*. DOI: 10.1038/s41467-021-27666.
46. T. Stuart, A. Srivastava, S. Madad, **C.A. Lareau**, R. Satija. (2021) Multimodal single-cell chromatin analysis with Signac. *Nature Methods*. DOI: 10.1101/2020.11.09.373613.
47. E. Fiskin, **C.A. Lareau**, *et al.* (2021) Single-cell multimodal profiling of proteins and chromatin accessibility using PHAGE-ATAC. *Nature Biotechnology*. DOI: 10.1038/s41587-021-01065-5.
48. H. King, K. Wells, Z. Shipony, A. Kathiria, L Wager, **C.A. Lareau**, *et al.* (2021) Integrated single-cell transcriptomics and epigenomics reveals strong germinal center-associated etiology of autoimmune risk loci. *Science Immunology*. DOI: 10.1126/sciimmunol.abh3768.
49. L. Penter, S. Gohil, **C.A. Lareau**, *et al.* (2021) Longitudinal single-cell dynamics of chromatin accessibility and mitochondrial mutations in chronic lymphocytic leukemia mirror disease history. *Cancer Discovery*. DOI: 10.1158/2159-8290.CD-21-0276.

50. R. Kawakami, Y. Kitagawa, K. Chen, M. Arai, D. Ohara, Y. Nakamura, K. Yasuda, M. Osaki, N. Mikami, **C.A. Lareau, et al.** (2021) Distinct Foxp3 enhancer elements coordinate development, maintenance, and function of regulatory T cells. *Immunity*. DOI: 10.1016/j.immuni.2021.04.005
51. B. Adane, G. Alexe, B Seong, D. Lu, E. Hwang, D. Hsinz, **C.A. Lareau, et al.** (2021) STAG2 Loss Rewires Oncogenic and Developmental Programs to Promote Metastasis in Ewing Sarcoma. *Cancer Cell*. DOI: 10.1016/j.ccell.2021.05.007
52. S. Ma, B. Zhang, L. LaFave, Z. Chiang, Y. Hu, J. Ding, A. Brack, V. Kartha, T. Law, **C.A. Lareau, et al.** (2020) Chromatin potential identified by shared single cell profiling of RNA and chromatin. *Cell*. DOI: 10.1016/j.cell.2020.09.056.
53. 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.
54. 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.
55. 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.
56. 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.2020.567342.
57. J. Grünwald, 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.
58. 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.
59. 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.
60. 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.
61. ImmGen Consortium, 149 authors including **C.A. Lareau**. (2020) ImmGen at 15. *Nature Immunology*. DOI: 10.1038/s41590-020-0687-4.
62. 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.
63. J. Grünwald, 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.
64. 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.
65. 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.
66. J. Grünwald, 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.
67. 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.

68. 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.
69. 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.
70. 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.
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75. 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/S41591-018-0008-8.
76. 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.
77. 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.
78. 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.
79. 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.
80. 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-PRINTS

81. **C.A. Lareau**[‡], *et al.* (2023) Codon affinity in mitochondrial DNA shapes evolutionary and somatic fitness. *bioRxiv*. DOI: 10.1101/2023.04.23.537997v1.
82. **C.A. Lareau**[‡], *et al.* (2022) Latent human herpesvirus 6 is reactivated in chimeric antigen receptor T cells. *bioRxiv*. DOI: 10.1101/2022.08.12.503683.
83. K. Hiam-Galvez, R. Debarge, **C.A. Lareau**, *et al.* (2022) Transient dendritic cell activation diversifies the T cell response to acute infection. *bioRxiv*. DOI: 10.1101/2021.09.26.461821v1.

84. C. Liu, H. Nagashima, P. Wang, A. Lim, S. Signorella, W. Montgomery, N. Fernando, V. Bass, L. Reich, Z. Tang, O. Harrison, C. Yao, H. Sun, S. Brooks, J. Kan, V. Nagarajan, R. Phillips, Y. Mikami, **C.A. Lareau**, *et al.* (2023) CTCF-mediated topologically associated domains delineates super-enhancer territories and selective cytokine expression at the Mdm1-Il22-Ifng. **Cell Press Sneak Peek**. https://papers.ssrn.com/sol3/papers.cfm?abstract_id=4271102.

PATENTS

GRANTED

1. **PCT/US2019/036583**; Lineage tracing using mitochondrial genome mutations and single-cell genomics
2. **PCT/US2021/035951**; Methods of detecting mitochondrial disease
3. **PCT/US2021/032702**; Lineage inference from single-cell transcriptomics

PENDING

4. **PPA 63/314,980**; Massively integrated analysis of single cell RNA sequencing data
5. **PPA 63/353,715**; Methods of genetically modifying cells for altered codon-anti-codon interactions
6. **PPA 63/397,515**; Methods of assessing *in vitro* therapeutic T cells for latent and reactivated human herpesvirus 6B
7. **PPA 63/397,519**; Methods of assessing therapeutic T cells for latent and reactivated human herpesvirus 6B

RESEARCH SUPPORT

ONGOING

K99/R00 HG012579 , National Human Genome Research Institute <i>Charting somatic evolution via single-cell multiomics</i> Role: PI; Funding: \$1,020,800	08/2022-07/2027
Pilot Project , Stanford Alzheimer's Disease Research Center <i>Somatic mitochondrial DNA mutations in single synaptosomes via multimodal proteo-genomics</i> Role: PI; Funding: \$250,000	04/2022-03/2024
Seed Project , Stanford Institute for Immunity, Transplantation and Infection <i>Methods for studying human viral reactivation at single cell resolution</i> Role: PI; Funding: \$100,000	04/2022-03/2024

COMPLETED

Parker Scholarship , Parker Institute for Cancer Immunotherapy <i>Mapping the immune microenvironment in pre-malignant human tissue</i> Role: PI; Funding: \$168,000	03/2021-02/2023
Stanford Science Fellowship , Stanford University School of Humanities and Sciences <i>Clonal properties of single cells in human health and disease</i> Role: PI; Funding: \$254,000	07/2020-08/2022
F31 CA232670 , National Cancer Institute <i>Inference of variable chromatin loops in glioblastoma tumors and single-cells</i> Role: PI; Funding: \$63,415	09/2018-06/2020
GRFP DGE1144152 , National Science Foundation <i>Methods for stratifying diverse disease populations for genome-wide association studies</i> Role: PI; Funding: \$138,000	08/2015-08/2018

TEACHING EXPERIENCE

Stanford University

Course Head; Cell, Gene, and Immune Therapies

Spring 2023

Lecturer; Single-cell Immunogenomics

Spring 2022, 2023

Lecturer; Introduction to Applied Computational Tools in Immunology

Winter 2022, 2023

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

ACADEMIC SERVICE

SCIENTIFIC MENTORSHIP

Stanford Institutes of Medicine Summer Research Program (2022-2023)

Stanford undergraduate and graduate students in: Genetics, Computer Science, and Immunology research (2020-2023)

MIT undergraduate research (2016-2020)

OUTREACH

Public Journal Club Presenter (2022-2023)

Project SHORT Mentor (2020-2023)

Speaker, Gateway High School and Fremont High School, High School Career Day (2020-2023)

Mentor, Research Science Institute, MIT (2016-2019)

Volunteer computer science instructor, Will Rogers High School, Tulsa, OK (2014-2015)

GUEST EDITOR

Frontiers in Immunology

AD HOC PEER REVIEW - GRANTS

UK Medical Research Council, European Research Council (ERC), Dutch Research Council (NWO), Italian Science Fund

AD HOC PEER REVIEW - JOURNALS

Cell, Science, Nature Biotechnology, Nature Genetics, Nature Methods, Nature Communications, Science Advances, Bioinformatics, BMC Biology, BMC Bioinformatics, Nature Protocols, Cancers, Communications Biology, Frontiers in Cell and Development Biology, Frontiers in Immunology, Frontiers in Medicine, Molecular Cancer, The R Journal, BioData Mining, BMC Medical Genomics, BMJ Open

PROFESSIONAL MEMBERSHIP

Member, Society for Immunotherapy of Cancer

Trainee Member, American Society of Human Genetics; American Association for Cancer Research

Developer, Bioconductor Project

Supporting Member, R and Python Software Foundations

INVITED TALKS AND PRESENTATIONS (2021-)

Human Cell Atlas, General Meeting , Toronto, ON, Canada	July 2023
Memorial Sloan Kettering Institute, Emerging Leader Symposium , New York, NY	May 2023
Dana Farber Cancer Institute, Medical Oncology Seminar Series , Boston, MA	March 2023
Genentech, Distinguished Scientific Speaker Seminar Series , San Francisco, CA	February 2023
UCSF, Microbiology and Immunology Seminar , San Francisco, CA	February 2023
Sloan Kettering Institute, Computational and Systems Biology Seminar , New York, NY	February 2023
Fred Hutchinson Cancer Center, Translational Data Science Center Seminar , Seattle, WA	January 2023
Northwestern University, Biochemistry and Molecular Genetics Seminar , Chicago, IL	January 2023
University of Pennsylvania, Department of Pediatrics Seminar , Philadelphia, PA	January 2023
Massachusetts General Hospital, Department of Pathology Seminar Series , Boston, MA	January 2023
New York University, Department of Pathology Seminar Seminar Series , New York, NY	December 2022
Stanford University EpiBio Seminar Series , Stanford, CA	December 2022
Parker Institute for Cancer Immunotherapy, Winter Meeting , Santa Rosa, CA	November 2022
Stanford Cancer Institute Cell Therapy Seminar Series , Stanford, CA	October 2022
Max Planck Systems Immunology Seminar Series , Wurzburg, Germany	September 2022
Immunotherapy of Cancer Conference, Annual Meeting , Munich, Germany	September 2022
Stanford Center for Human Systems Immunology SAB Meeting , Stanford, CA	September 2022
Stanford Alzheimer's Disease Research Center Seminar Series , Stanford, CA	September 2022
Impact of Genomic Variation on Function Seminar Series , Bethesda, MD	June 2022
Probing Human Disease Using Single-Cell Technologies, Annual Meeting , Cancun, Mexico	May 2022
Parker Institute for Cancer Immunotherapy, Annual Meeting , Sonoma, CA	April 2022
Dana Farber Center for Functional Cancer Epigenetics Seminar Series , Boston, MA	April 2022
Immunai Visiting Scientist Seminar Series , New York, NY	January 2022
Broad Institute Next Generation Faculty Symposium , Cambridge, MA	November 2021
UCSF Single-cell Seminar Series San Francisco, CA	July 2021
10x Genomics Global Cancer Symposium , Pleasanton, CA	April 2021
Max Delbrück Medical Systems Biology Lecture , Berlin, Germany	April 2021
UCSF Diabetes Center Seminar , San Francisco, CA	February 2021