

# Caleb A Lareau

## List of Publications by Year in descending order

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Version: 2024-02-01

73  
papers

9,737  
citations

101496

36  
h-index

88593

70  
g-index

99  
all docs

99  
docs citations

99  
times ranked

15596  
citing authors

#	ARTICLE	IF	CITATIONS
1	Heritability enrichment of specifically expressed genes identifies disease-relevant tissues and cell types. <i>Nature Genetics</i> , 2018, 50, 621-629.	9.4	807
2	Activity-by-contact model of enhancer-promoter regulation from thousands of CRISPR perturbations. <i>Nature Genetics</i> , 2019, 51, 1664-1669.	9.4	631
3	Chromatin Potential Identified by Shared Single-Cell Profiling of RNA and Chromatin. <i>Cell</i> , 2020, 183, 1103-1116.e20.	13.5	600
4	Single-cell chromatin state analysis with Signac. <i>Nature Methods</i> , 2021, 18, 1333-1341.	9.0	595
5	Integrated Single-Cell Analysis Maps the Continuous Regulatory Landscape of Human Hematopoietic Differentiation. <i>Cell</i> , 2018, 173, 1535-1548.e16.	13.5	545
6	Transcriptome-wide off-target RNA editing induced by CRISPR-guided DNA base editors. <i>Nature</i> , 2019, 569, 433-437.	13.7	434
7	The Polygenic and Monogenic Basis of Blood Traits and Diseases. <i>Cell</i> , 2020, 182, 1214-1231.e11.	13.5	388
8	Trans-ethnic and Ancestry-Specific Blood-Cell Genetics in 746,667 Individuals from 5 Global Populations. <i>Cell</i> , 2020, 182, 1198-1213.e14.	13.5	353
9	Lineage Tracing in Humans Enabled by Mitochondrial Mutations and Single-Cell Genomics. <i>Cell</i> , 2019, 176, 1325-1339.e22.	13.5	345
10	The cis-Regulatory Atlas of the Mouse Immune System. <i>Cell</i> , 2019, 176, 897-912.e20.	13.5	315
11	Droplet-based combinatorial indexing for massive-scale single-cell chromatin accessibility. <i>Nature Biotechnology</i> , 2019, 37, 916-924.	9.4	315
12	A non-canonical SWI/SNF complex is a synthetic lethal target in cancers driven by BAF complex perturbation. <i>Nature Cell Biology</i> , 2018, 20, 1410-1420.	4.6	265
13	The SARS-CoV-2 RNA-protein interactome in infected human cells. <i>Nature Microbiology</i> , 2021, 6, 339-353.	5.9	245
14	Scalable, multimodal profiling of chromatin accessibility, gene expression and protein levels in single cells. <i>Nature Biotechnology</i> , 2021, 39, 1246-1258.	9.4	244
15	CRISPR DNA base editors with reduced RNA off-target and self-editing activities. <i>Nature Biotechnology</i> , 2019, 37, 1041-1048.	9.4	236
16	Assessment of computational methods for the analysis of single-cell ATAC-seq data. <i>Genome Biology</i> , 2019, 20, 241.	3.8	225
17	Single-cell trajectories reconstruction, exploration and mapping of omics data with STREAM. <i>Nature Communications</i> , 2019, 10, 1903.	5.8	198
18	Dissecting hematopoietic and renal cell heterogeneity in adult zebrafish at single-cell resolution using RNA sequencing. <i>Journal of Experimental Medicine</i> , 2017, 214, 2875-2887.	4.2	168

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19	A dual-deaminase CRISPR base editor enables concurrent adenine and cytosine editing. <i>Nature Biotechnology</i> , 2020, 38, 861-864.	9.4	168
20	Massively parallel single-cell mitochondrial DNA genotyping and chromatin profiling. <i>Nature Biotechnology</i> , 2021, 39, 451-461.	9.4	150
21	Interrogation of human hematopoiesis at single-cell and single-variant resolution. <i>Nature Genetics</i> , 2019, 51, 683-693.	9.4	147
22	Epigenomic State Transitions Characterize Tumor Progression in Mouse Lung Adenocarcinoma. <i>Cancer Cell</i> , 2020, 38, 212-228.e13.	7.7	140
23	hichipper: a preprocessing pipeline for calling DNA loops from HiChIP data. <i>Nature Methods</i> , 2018, 15, 155-156.	9.0	139
24	Large-Scale Topological Changes Restrain Malignant Progression in Colorectal Cancer. <i>Cell</i> , 2020, 182, 1474-1489.e23.	13.5	126
25	Transcript-indexed ATAC-seq for precision immune profiling. <i>Nature Medicine</i> , 2018, 24, 580-590.	15.2	124
26	Transcriptional States and Chromatin Accessibility Underlying Human Erythropoiesis. <i>Cell Reports</i> , 2019, 27, 3228-3240.e7.	2.9	122
27	Spatial genomics enables multi-modal study of clonal heterogeneity in tissues. <i>Nature</i> , 2022, 601, 85-91.	13.7	117
28	Gut CD4+ T cell phenotypes are a continuum molded by microbes, not by TH archetypes. <i>Nature Immunology</i> , 2021, 22, 216-228.	7.0	116
29	Inherited myeloproliferative neoplasm risk affects haematopoietic stem cells. <i>Nature</i> , 2020, 586, 769-775.	13.7	101
30	The ATPase module of mammalian SWI/SNF family complexes mediates subcomplex identity and catalytic activity-independent genomic targeting. <i>Nature Genetics</i> , 2019, 51, 618-626.	9.4	81
31	Control of human hemoglobin switching by LIN28B-mediated regulation of BCL11A translation. <i>Nature Genetics</i> , 2020, 52, 138-145.	9.4	73
32	A B Cell Regulome Links Notch to Downstream Oncogenic Pathways in Small B Cell Lymphomas. <i>Cell Reports</i> , 2017, 21, 784-797.	2.9	65
33	Purifying Selection against Pathogenic Mitochondrial DNA in Human T Cells. <i>New England Journal of Medicine</i> , 2020, 383, 1556-1563.	13.9	62
34	diffloop: a computational framework for identifying and analyzing differential DNA loops from sequencing data. <i>Bioinformatics</i> , 2018, 34, 672-674.	1.8	57
35	Enhancer histone-QTLs are enriched on autoimmune risk haplotypes and influence gene expression within chromatin networks. <i>Nature Communications</i> , 2018, 9, 2905.	5.8	56
36	ImmGen at 15. <i>Nature Immunology</i> , 2020, 21, 700-703.	7.0	55

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37	STAG2 loss rewires oncogenic and developmental programs to promote metastasis in Ewing sarcoma. <i>Cancer Cell</i> , 2021, 39, 827-844.e10.	7.7	49
38	Mitochondrial variant enrichment from high-throughput single-cell RNA sequencing resolves clonal populations. <i>Nature Biotechnology</i> , 2022, 40, 1030-1034.	9.4	45
39	Distinct Foxp3 enhancer elements coordinate development, maintenance, and function of regulatory T cells. <i>Immunity</i> , 2021, 54, 947-961.e8.	6.6	39
40	Single-cell multiomics defines tolerogenic extrathymic Aire-expressing populations with unique homology to thymic epithelium. <i>Science Immunology</i> , 2021, 6, eabl5053.	5.6	39
41	Prioritizing disease and trait causal variants at the TNFAIP3 locus using functional and genomic features. <i>Nature Communications</i> , 2020, 11, 1237.	5.8	38
42	Inference and effects of barcode multiplets in droplet-based single-cell assays. <i>Nature Communications</i> , 2020, 11, 866.	5.8	38
43	Longitudinal Single-Cell Dynamics of Chromatin Accessibility and Mitochondrial Mutations in Chronic Lymphocytic Leukemia Mirror Disease History. <i>Cancer Discovery</i> , 2021, 11, 3048-3063.	7.7	31
44	Single-cell profiling of proteins and chromatin accessibility using PHAGE-ATAC. <i>Nature Biotechnology</i> , 2022, 40, 374-381.	9.4	31
45	Differential co-expression network centrality and machine learning feature selection for identifying susceptibility hubs in networks with scale-free structure. <i>BioData Mining</i> , 2015, 8, 5.	2.2	30
46	Common genes associated with antidepressant response in mouse and man identify key role of glucocorticoid receptor sensitivity. <i>PLoS Biology</i> , 2017, 15, e2002690.	2.6	28
47	Impaired human hematopoiesis due to a cryptic intronic GATA1 splicing mutation. <i>Journal of Experimental Medicine</i> , 2019, 216, 1050-1060.	4.2	27
48	Encore: Genetic Association Interaction Network Centrality Pipeline and Application to SLE Exome Data. <i>Genetic Epidemiology</i> , 2013, 37, 614-621.	0.6	25
49	Response to "Unexpected mutations after CRISPR-Cas9 editing in vivo". <i>Nature Methods</i> , 2018, 15, 238-239.	9.0	25
50	Polygenic risk assessment reveals pleiotropy between sarcoidosis and inflammatory disorders in the context of genetic ancestry. <i>Genes and Immunity</i> , 2017, 18, 88-94.	2.2	21
51	Single Cell Transcriptomics Implicate Novel Monocyte and T Cell Immune Dysregulation in Sarcoidosis. <i>Frontiers in Immunology</i> , 2020, 11, 567342.	2.2	21
52	A microRNA expression and regulatory element activity atlas of the mouse immune system. <i>Nature Immunology</i> , 2021, 22, 914-927.	7.0	19
53	Integrated single-cell transcriptomics and epigenomics reveals strong germinal center-associated etiology of autoimmune risk loci. <i>Science Immunology</i> , 2021, 6, eabh3768.	5.6	19
54	Fine mapping of chromosome 15q25 implicates ZNF592 in neurosarcoidosis patients. <i>Annals of Clinical and Translational Neurology</i> , 2015, 2, 972-977.	1.7	17

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55	Gene-centric functional dissection of human genetic variation uncovers regulators of hematopoiesis. <i>ELife</i> , 2019, 8, .	2.8	14
56	Congenital anemia reveals distinct targeting mechanisms for master transcription factor GATA1. <i>Blood</i> , 2022, 139, 2534-2546.	0.6	14
57	An interaction quantitative trait loci tool implicates epistatic functional variants in an apoptosis pathway in smallpox vaccine eQTL data. <i>Genes and Immunity</i> , 2016, 17, 244-250.	2.2	11
58	Confounding in ex vivo models of Diamond-Blackfan anemia. <i>Blood</i> , 2017, 130, 1165-1168.	0.6	11
59	JAK inhibition in a patient with a STAT1 gain-of-function variant reveals STAT1 dysregulation as a common feature of aplastic anemia. <i>Med</i> , 2022, 3, 42-57.e5.	2.2	11
60	Longitudinal assessment of clonal mosaicism in human hematopoiesis via mitochondrial mutation tracking. <i>Blood Advances</i> , 2019, 3, 4161-4165.	2.5	10
61	Functional dissection of inherited non-coding variation influencing multiple myeloma risk. <i>Nature Communications</i> , 2022, 13, 151.	5.8	10
62	Charting the tumor antigen maps drawn by single-cell genomics. <i>Cancer Cell</i> , 2021, 39, 1553-1557.	7.7	9
63	The Integration of Epistasis Network and Functional Interactions in a GWAS Implicates RXR Pathway Genes in the Immune Response to Smallpox Vaccine. <i>PLoS ONE</i> , 2016, 11, e0158016.	1.1	8
64	Network Theory for Data-Driven Epistasis Networks. <i>Methods in Molecular Biology</i> , 2015, 1253, 285-300.	0.4	7
65	Heritability of fetal hemoglobin, white cell count, and other clinical traits from a sickle cell disease family cohort. <i>American Journal of Hematology</i> , 2019, 94, 522-527.	2.0	6
66	dcVar: a method for identifying common variants that modulate differential correlation structures in gene expression data. <i>Frontiers in Genetics</i> , 2015, 6, 312.	1.1	5
67	Preprocessing and Computational Analysis of Single-Cell Epigenomic Datasets. <i>Methods in Molecular Biology</i> , 2019, 1935, 187-202.	0.4	2
68	Notch-Regulated Enhancers in B-Cell Lymphoma Activate MYC and Potentiate B-Cell Receptor Signaling. <i>Blood</i> , 2016, 128, 457-457.	0.6	2
69	Mitochondrial DNA Mutations Distinguish Individual Donor- and Recipient-Derived Immune Cells Following Matched Unrelated Allogeneic Stem Cell Transplantation. <i>Blood</i> , 2021, 138, 1689-1689.	0.6	2
70	An old BATF's new T-ricks. <i>Nature Immunology</i> , 2020, 21, 1309-1310.	7.0	0
71	Dissecting the Regulation of Human Hematopoiesis at Single-Cell and Single-Variant Resolution. <i>Blood</i> , 2018, 132, 531-531.	0.6	0
72	Abstract 907: Bioinformatic method to define epigenetically regulated enhancer elements associated with cancer. , 2019, , .		0

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73	1508 Single-cell epigenetic profiling highlights genetic impact on chromatin accessibility in SLE. , 2021, ,		0