Caleb A Lareau

List of Publications by Year
in descending order

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	Single-cell profiling of proteins and chromatin accessibility using PHAGE-ATAC. Nature Biotechnology, 2022, 40, 374-381.	9.4	31
2	JAK inhibition in a patient with a STAT1 gain-of-function variant reveals STAT1 dysregulation as a common feature of aplastic anemia. Med, 2022, 3, 42-57.e5.	2.2	11
3	Congenital anemia reveals distinct targeting mechanisms for master transcription factor GATA1. Blood, 2022, 139, 2534-2546.	0.6	14
4	Functional dissection of inherited non-coding variation influencing multiple myeloma risk. Nature Communications, 2022, 13, 151.	5.8	10
5	Spatial genomics enables multi-modal study of clonal heterogeneity in tissues. Nature, 2022, 601, 85-91.	13.7	117
6	Mitochondrial variant enrichment from high-throughput single-cell RNA sequencing resolves clonal populations. Nature Biotechnology, 2022, 40, 1030-1034.	9.4	45
7	Massively parallel single-cell mitochondrial DNA genotyping and chromatin profiling. Nature Biotechnology, 2021, 39, 451-461.	9.4	150
8	The SARS-CoV-2 RNA–protein interactome in infected human cells. Nature Microbiology, 2021, 6, 339-353.	5.9	245
9	Gut CD4+ T cell phenotypes are a continuum molded by microbes, not by TH archetypes. Nature Immunology, 2021, 22, 216-228.	7.0	116
10	Distinct Foxp3 enhancer elements coordinate development, maintenance, and function of regulatory T cells. Immunity, 2021, 54, 947-961.e8.	6.6	39
11	STAG2 loss rewires oncogenic and developmental programs to promote metastasis in Ewing sarcoma. Cancer Cell, 2021, 39, 827-844.e10.	7.7	49
12	A microRNA expression and regulatory element activity atlas of the mouse immune system. Nature Immunology, 2021, 22, 914-927.	7.0	19
13	Scalable, multimodal profiling of chromatin accessibility, gene expression and protein levels in single cells. Nature Biotechnology, 2021, 39, 1246-1258.	9.4	244
14	Longitudinal Single-Cell Dynamics of Chromatin Accessibility and Mitochondrial Mutations in Chronic Lymphocytic Leukemia Mirror Disease History. Cancer Discovery, 2021, 11, 3048-3063.	7.7	31
15	Integrated single-cell transcriptomics and epigenomics reveals strong germinal center–associated etiology of autoimmune risk loci. Science Immunology, 2021, 6, eabh3768.	5.6	19
16	Single-cell chromatin state analysis with Signac. Nature Methods, 2021, 18, 1333-1341.	9.0	595
17	1508…Single-cell epigenetic profiling highlights genetic impact on chromatin accessibility in SLE. , 2021, , .		0
18	Single-cell multiomics defines tolerogenic extrathymic Aire-expressing populations with unique homology to thymic epithelium. Science Immunology, 2021, 6, eabl5053.	5.6	39

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19	Mitochondrial DNA Mutations Distinguish Individual Donor- and Recipient-Derived Immune Cells Following Matched Unrelated Allogeneic Stem Cell Transplantation. Blood, 2021, 138, 1689-1689.	0.6	2
20	Charting the tumor antigen maps drawn by single-cell genomics. Cancer Cell, 2021, 39, 1553-1557.	7.7	9
21	The Polygenic and Monogenic Basis of Blood Traits and Diseases. Cell, 2020, 182, 1214-1231.e11.	13.5	388
22	Inherited myeloproliferative neoplasm risk affects haematopoietic stem cells. Nature, 2020, 586, 769-775.	13.7	101
23	An old BATF's new T-ricks. Nature Immunology, 2020, 21, 1309-1310.	7.0	0
24	Purifying Selection against Pathogenic Mitochondrial DNA in Human T Cells. New England Journal of Medicine, 2020, 383, 1556-1563.	13.9	62
25	Epigenomic State Transitions Characterize Tumor Progression in Mouse Lung Adenocarcinoma. Cancer Cell, 2020, 38, 212-228.e13.	7.7	140
26	Chromatin Potential Identified by Shared Single-Cell Profiling of RNA and Chromatin. Cell, 2020, 183, 1103-1116.e20.	13.5	600
27	Large-Scale Topological Changes Restrain Malignant Progression in Colorectal Cancer. Cell, 2020, 182, 1474-1489.e23.	13.5	126
28	Trans-ethnic and Ancestry-Specific Blood-Cell Genetics in 746,667 Individuals from 5 Global Populations. Cell, 2020, 182, 1198-1213.e14.	13.5	353
29	Single Cell Transcriptomics Implicate Novel Monocyte and T Cell Immune Dysregulation in Sarcoidosis. Frontiers in Immunology, 2020, 11, 567342.	2.2	21
30	A dual-deaminase CRISPR base editor enables concurrent adenine and cytosine editing. Nature Biotechnology, 2020, 38, 861-864.	9.4	168
31	Prioritizing disease and trait causal variants at the TNFAIP3 locus using functional and genomic features. Nature Communications, 2020, 11, 1237.	5.8	38
32	ImmGen at 15. Nature Immunology, 2020, 21, 700-703.	7.0	55
33	Inference and effects of barcode multiplets in droplet-based single-cell assays. Nature Communications, 2020, 11, 866.	5.8	38
34	Control of human hemoglobin switching by LIN28B-mediated regulation of BCL11A translation. Nature Genetics, 2020, 52, 138-145.	9.4	73
35	CRISPR DNA base editors with reduced RNA off-target and self-editing activities. Nature Biotechnology, 2019, 37, 1041-1048.	9.4	236
36	The cis-Regulatory Atlas of the Mouse Immune System. Cell, 2019, 176, 897-912.e20.	13.5	315

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37	Heritability of fetal hemoglobin, white cell count, and other clinical traits from a sickle cell disease family cohort. American Journal of Hematology, 2019, 94, 522-527.	2.0	6
38	Droplet-based combinatorial indexing for massive-scale single-cell chromatin accessibility. Nature Biotechnology, 2019, 37, 916-924.	9.4	315
39	Transcriptional States and Chromatin Accessibility Underlying Human Erythropoiesis. Cell Reports, 2019, 27, 3228-3240.e7.	2.9	122
40	Transcriptome-wide off-target RNA editing induced by CRISPR-guided DNA base editors. Nature, 2019, 569, 433-437.	13.7	434
41	Single-cell trajectories reconstruction, exploration and mapping of omics data with STREAM. Nature Communications, 2019, 10, 1903.	5.8	198
42	Impaired human hematopoiesis due to a cryptic intronic GATA1 splicing mutation. Journal of Experimental Medicine, 2019, 216, 1050-1060.	4.2	27
43	Interrogation of human hematopoiesis at single-cell and single-variant resolution. Nature Genetics, 2019, 51, 683-693.	9.4	147
44	The ATPase module of mammalian SWI/SNF family complexes mediates subcomplex identity and catalytic activityâ€"independent genomic targeting. Nature Genetics, 2019, 51, 618-626.	9.4	81
45	Lineage Tracing in Humans Enabled by Mitochondrial Mutations and Single-Cell Genomics. Cell, 2019, 176, 1325-1339.e22.	13.5	345
46	Preprocessing and Computational Analysis of Single-Cell Epigenomic Datasets. Methods in Molecular Biology, 2019, 1935, 187-202.	0.4	2
47	Longitudinal assessment of clonal mosaicism in human hematopoiesis via mitochondrial mutation tracking. Blood Advances, 2019, 3, 4161-4165.	2.5	10
48	Assessment of computational methods for the analysis of single-cell ATAC-seq data. Genome Biology, 2019, 20, 241.	3.8	225
49	Activity-by-contact model of enhancerâ€"promoter regulation from thousands of CRISPR perturbations. Nature Genetics, 2019, 51, 1664-1669.	9.4	631
50	Gene-centric functional dissection of human genetic variation uncovers regulators of hematopoiesis. ELife, 2019, 8, .	2.8	14
51	Abstract 907: Bioinformatic method to define epigenetically regulated enhancer elements associated with cancer. , 2019, , .		0
52	hichipper: a preprocessing pipeline for calling DNA loops from HiChIP data. Nature Methods, 2018, 15, 155-156.	9.0	139
53	Transcript-indexed ATAC-seq for precision immune profiling. Nature Medicine, 2018, 24, 580-590.	15.2	124
54	Heritability enrichment of specifically expressed genes identifies disease-relevant tissues and cell types. Nature Genetics, 2018, 50, 621-629.	9.4	807

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55	diffloop: a computational framework for identifying and analyzing differential DNA loops from sequencing data. Bioinformatics, 2018, 34, 672-674.	1.8	57
56	Integrated Single-Cell Analysis Maps the Continuous Regulatory Landscape of Human Hematopoietic Differentiation. Cell, 2018, 173, 1535-1548.e16.	13.5	545
57	Response to â€œUnexpected mutations after CRISPRâ€"Cas9 editing in vivoâ€. Nature Methods, 2018, 15, 238-239.	9.0	25
58	A non-canonical SWI/SNF complex is a synthetic lethal target in cancers driven by BAF complex perturbation. Nature Cell Biology, 2018, 20, 1410-1420.	4.6	265
59	Enhancer histone-QTLs are enriched on autoimmune risk haplotypes and influence gene expression within chromatin networks. Nature Communications, 2018, 9, 2905.	5.8	56
60	Dissecting the Regulation of Human Hematopoiesis at Single-Cell and Single-Variant Resolution. Blood, 2018, 132, 531-531.	0.6	0
61	Polygenic risk assessment reveals pleiotropy between sarcoidosis and inflammatory disorders in the context of genetic ancestry. Genes and Immunity, 2017, 18, 88-94.	2.2	21
62	Confounding in ex vivo models of Diamond-Blackfan anemia. Blood, 2017, 130, 1165-1168.	0.6	11
63	A B Cell Regulome Links Notch to Downstream Oncogenic Pathways in Small B Cell Lymphomas. Cell Reports, 2017, 21, 784-797.	2.9	65
64	Dissecting hematopoietic and renal cell heterogeneity in adult zebrafish at single-cell resolution using RNA sequencing. Journal of Experimental Medicine, 2017, 214, 2875-2887.	4.2	168
65	Common genes associated with antidepressant response in mouse and man identify key role of glucocorticoid receptor sensitivity. PLoS Biology, 2017, 15, e2002690.	2.6	28
66	The Integration of Epistasis Network and Functional Interactions in a GWAS Implicates RXR Pathway Genes in the Immune Response to Smallpox Vaccine. PLoS ONE, 2016, 11, e0158016.	1.1	8
67	An interaction quantitative trait loci tool implicates epistatic functional variants in an apoptosis pathway in smallpox vaccine eQTL data. Genes and Immunity, 2016, 17, 244-250.	2.2	11
68	Notch-Regulated Enhancers in B-Cell Lymphoma Activate MYC and Potentiate B-Cell Receptor Signaling. Blood, 2016, 128, 457-457.	0.6	2
69	Fine mapping of chromosome 15q25 implicates <scp>ZNF</scp>592 in neurosarcoidosis patients. Annals of Clinical and Translational Neurology, 2015, 2, 972-977.	1.7	17
70	dcVar: a method for identifying common variants that modulate differential correlation structures in gene expression data. Frontiers in Genetics, 2015, 6, 312.	1.1	5
71	Differential co-expression network centrality and machine learning feature selection for identifying susceptibility hubs in networks with scale-free structure. BioData Mining, 2015, 8, 5.	2.2	30
72	Network Theory for Data-Driven Epistasis Networks. Methods in Molecular Biology, 2015, 1253, 285-300.	0.4	7

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73	Encore: Genetic Association Interaction Network Centrality Pipeline and Application to SLE Exome Data. Genetic Epidemiology, 2013, 37, 614-621.	0.6	25