

# Leif S Ludwig

## List of Publications by Year in descending order

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Version: 2024-02-01

33  
papers

2,988  
citations

304743

22  
h-index

395702

33  
g-index

43  
all docs

43  
docs citations

43  
times ranked

5535  
citing authors

#	ARTICLE	IF	CITATIONS
1	Lineage Tracing in Humans Enabled by Mitochondrial Mutations and Single-Cell Genomics. <i>Cell</i> , 2019, 176, 1325-1339.e22.	28.9	345
2	Ribosome Levels Selectively Regulate Translation and Lineage Commitment in Human Hematopoiesis. <i>Cell</i> , 2018, 173, 90-103.e19.	28.9	296
3	Single-cell meta-analysis of SARS-CoV-2 entry genes across tissues and demographics. <i>Nature Medicine</i> , 2021, 27, 546-559.	30.7	261
4	Scalable, multimodal profiling of chromatin accessibility, gene expression and protein levels in single cells. <i>Nature Biotechnology</i> , 2021, 39, 1246-1258.	17.5	244
5	Altered translation of GATA1 in Diamond-Blackfan anemia. <i>Nature Medicine</i> , 2014, 20, 748-753.	30.7	243
6	Methylation matters: binding of Ets-1 to the demethylated Foxp3 gene contributes to the stabilization of Foxp3 expression in regulatory T cells. <i>Journal of Molecular Medicine</i> , 2010, 88, 1029-1040.	3.9	188
7	The Genetic Landscape of Diamond-Blackfan Anemia. <i>American Journal of Human Genetics</i> , 2018, 103, 930-947.	6.2	184
8	Massively parallel single-cell mitochondrial DNA genotyping and chromatin profiling. <i>Nature Biotechnology</i> , 2021, 39, 451-461.	17.5	150
9	Interrogation of human hematopoiesis at single-cell and single-variant resolution. <i>Nature Genetics</i> , 2019, 51, 683-693.	21.4	147
10	Transcriptional States and Chromatin Accessibility Underlying Human Erythropoiesis. <i>Cell Reports</i> , 2019, 27, 3228-3240.e7.	6.4	122
11	Skin-resident innate lymphoid cells converge on a pathogenic effector state. <i>Nature</i> , 2021, 592, 128-132.	27.8	119
12	Cyclin D3 coordinates the cell cycle during differentiation to regulate erythrocyte size and number. <i>Genes and Development</i> , 2012, 26, 2075-2087.	5.9	100
13	Targeted Application of Human Genetic Variation Can Improve Red Blood Cell Production from Stem Cells. <i>Cell Stem Cell</i> , 2016, 18, 73-78.	11.1	78
14	Purifying Selection against Pathogenic Mitochondrial DNA in Human T Cells. <i>New England Journal of Medicine</i> , 2020, 383, 1556-1563.	27.0	62
15	Insight into GATA1 transcriptional activity through interrogation of cis elements disrupted in human erythroid disorders. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 4434-4439.	7.1	56
16	Mitochondrial variant enrichment from high-throughput single-cell RNA sequencing resolves clonal populations. <i>Nature Biotechnology</i> , 2022, 40, 1030-1034.	17.5	45
17	X-linked macrocytic dyserythropoietic anemia in females with an ALAS2 mutation. <i>Journal of Clinical Investigation</i> , 2015, 125, 1665-1669.	8.2	43
18	Prioritizing disease and trait causal variants at the TNFAIP3 locus using functional and genomic features. <i>Nature Communications</i> , 2020, 11, 1237.	12.8	38

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19	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.	9.4	31
20	Single-cell profiling of proteins and chromatin accessibility using PHAGE-ATAC. <i>Nature Biotechnology</i> , 2022, 40, 374-381.	17.5	31
21	Impaired human hematopoiesis due to a cryptic intronic GATA1 splicing mutation. <i>Journal of Experimental Medicine</i> , 2019, 216, 1050-1060.	8.5	27
22	Induction of antigen-specific tolerance by nanobodyâ€“antigen adducts that target class-II major histocompatibility complexes. <i>Nature Biomedical Engineering</i> , 2021, 5, 1389-1401.	22.5	26
23	Familial thrombocytopenia due to a complex structural variant resulting in a <i>WAC-ANKRD26</i> fusion transcript. <i>Journal of Experimental Medicine</i> , 2021, 218, .	8.5	20
24	Genome-wide association study follow-up identifies cyclin A2 as a regulator of the transition through cytokinesis during terminal erythropoiesis. <i>American Journal of Hematology</i> , 2015, 90, 386-391.	4.1	15
25	Gene-centric functional dissection of human genetic variation uncovers regulators of hematopoiesis. <i>ELife</i> , 2019, 8, .	6.0	14
26	Congenital anemia reveals distinct targeting mechanisms for master transcription factor GATA1. <i>Blood</i> , 2022, 139, 2534-2546.	1.4	14
27	Confounding in ex vivo models of Diamond-Blackfan anemia. <i>Blood</i> , 2017, 130, 1165-1168.	1.4	11
28	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.	4.4	11
29	Longitudinal assessment of clonal mosaicism in human hematopoiesis via mitochondrial mutation tracking. <i>Blood Advances</i> , 2019, 3, 4161-4165.	5.2	10
30	Emerging cellular and gene therapies for congenital anemias. <i>American Journal of Medical Genetics, Part C: Seminars in Medical Genetics</i> , 2016, 172, 332-348.	1.6	6
31	cDNA-detector: detection and removal of cDNA contamination in DNA sequencing libraries. <i>BMC Bioinformatics</i> , 2021, 22, 611.	2.6	3
32	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.	1.4	2
33	Dissecting the Regulation of Human Hematopoiesis at Single-Cell and Single-Variant Resolution. <i>Blood</i> , 2018, 132, 531-531.	1.4	0