Jacob C Ulirsch

List of Publications by Year
in descending order

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Version: 2024-02-01

36 papers	3,769 citations	236833 25 h-index	360920 35 g-index
46 all docs	46 docs citations	46 times ranked	7384 citing authors

#	Article	IF	Citations
1	Genome-wide enhancer maps link risk variants to disease genes. Nature, 2021, 593, 238-243.	13.7	332
2	Leveraging supervised learning for functionallyÂinformed fine-mapping of cis-eQTLs identifies an additional 20,913 putative causal eQTLs. Nature Communications, 2021, 12, 3394.	5.8	44
3	Direct characterization of cis-regulatory elements and functional dissection of complex genetic associations using HCRâ€“FlowFISH. Nature Genetics, 2021, 53, 1166-1176.	9.4	36
4	Genome-wide functional screen of 3â€²UTR variants uncovers causal variants for human disease and evolution. Cell, 2021, 184, 5247-5260.e19.	13.5	62
5	Functional characterization of T2D-associated SNP effects on baseline and ER stress-responsive Î² cell transcriptional activation. Nature Communications, 2021, 12, 5242.	5.8	13
6	Tractor uses local ancestry to enable the inclusion of admixed individuals in GWAS and to boost power. Nature Genetics, 2021, 53, 195-204.	9.4	125
7	Functionally informed fine-mapping and polygenic localization of complex trait heritability. Nature Genetics, 2020, 52, 1355-1363.	9.4	185
8	Prioritizing disease and trait causal variants at the TNFAIP3 locus using functional and genomic features. Nature Communications, 2020, 11, 1237.	5.8	38
9	Control of human hemoglobin switching by LIN28B-mediated regulation of BCL11A translation. Nature Genetics, 2020, 52, 138-145.	9.4	73
10	Transcriptional States and Chromatin Accessibility Underlying Human Erythropoiesis. Cell Reports, 2019, 27, 3228-3240.e7.	2.9	122
11	Impaired human hematopoiesis due to a cryptic intronic GATA1 splicing mutation. Journal of Experimental Medicine, 2019, 216, 1050-1060.	4.2	27
12	Interrogation of human hematopoiesis at single-cell and single-variant resolution. Nature Genetics, 2019, 51, 683-693.	9.4	147
13	Lineage Tracing in Humans Enabled by Mitochondrial Mutations and Single-Cell Genomics. Cell, 2019, 176, 1325-1339.e22.	13.5	345
14	Genetic predisposition to mosaic Y chromosome loss in blood. Nature, 2019, 575, 652-657.	13.7	198
15	Gene-centric functional dissection of human genetic variation uncovers regulators of hematopoiesis. ELife, 2019, 8, .	2.8	14
16	HRI coordinates translation necessary for protein homeostasis and mitochondrial function in erythropoiesis. ELife, 2019, 8, .	2.8	47
17	Ribosome Levels Selectively Regulate Translation and Lineage Commitment in Human Hematopoiesis. Cell, 2018, 173, 90-103.e19.	13.5	296
18	The Genetic Landscape of Diamond-Blackfan Anemia. American Journal of Human Genetics, 2018, 103, 930-947.	2.6	184

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19	Detecting genome-wide directional effects of transcription factor binding on polygenic disease risk. Nature Genetics, 2018, 50, 1483-1493.	9.4	55
20	The NORAD lncRNA assembles a topoisomerase complex critical for genome stability. Nature, 2018, 561, 132-136.	13.7	303
21	Common Î±-globin variants modify hematologic and other clinical phenotypes in sickle cell trait and disease. PLoS Genetics, 2018, 14, e1007293.	1.5	45
22	Functional Selectivity in Cytokine Signaling Revealed Through a Pathogenic EPO Mutation. Cell, 2017, 168, 1053-1064.e15.	13.5	98
23	Confounding in ex vivo models of Diamond-Blackfan anemia. Blood, 2017, 130, 1165-1168.	0.6	11
24	Comprehensive population-based genome sequencing provides insight into hematopoietic regulatory mechanisms. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E327-E336.	3.3	39
25	Developmentallyâ€faithful and effective human erythropoiesis in immunodeficient and Kit mutant mice. American Journal of Hematology, 2017, 92, E513-E519.	2.0	20
26	Whole-exome sequencing identifies an Î±-globin cluster triplication resulting in increased clinical severity of Î²-thalassemia. Journal of Physical Education and Sports Management, 2017, 3, a001941.	0.5	13
27	Advances in understanding erythropoiesis: evolving perspectives. British Journal of Haematology, 2016, 173, 206-218.	1.2	109
28	Exome sequencing results in successful diagnosis and treatment of a severe congenital anemia. Journal of Physical Education and Sports Management, 2016, 2, a000885.	0.5	10
29	Insight into GATA1 transcriptional activity through interrogation of cis elements disrupted in human erythroid disorders. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 4434-4439.	3.3	56
30	A novel pathogenic mutation in RPL11 identified in a patient diagnosed with diamond Blackfan anemia as a young adult. Blood Cells, Molecules, and Diseases, 2016, 61, 46-47.	0.6	9
31	Systematic Functional Dissection of Common Genetic Variation Affecting Red Blood Cell Traits. Cell, 2016, 165, 1530-1545.	13.5	294
32	Targeted Application of Human Genetic Variation Can Improve Red Blood Cell Production from Stem Cells. Cell Stem Cell, 2016, 18, 73-78.	5.2	78
33	BCL11A deletions result in fetal hemoglobin persistence and neurodevelopmental alterations. Journal of Clinical Investigation, 2015, 125, 2363-2368.	3.9	122
34	Biallelic Mutations in PARP4 Are Linked to a Variant Form of Congenital Dyserythropoietic Anemia. Blood, 2015, 126, 272-272.	0.6	2
35	Temporally Distinct Developmental Waves of Erythropoiesis from Human Pluripotent Stem Cells. Blood, 2015, 126, 1170-1170.	0.6	0
36	Altered Chromatin Occupancy of Master Regulators Underlies Evolutionary Divergence in the Transcriptional Landscape of Erythroid Differentiation. PLoS Genetics, 2014, 10, e1004890.	1.5	42