Yang Luo

List of Publications by Year in descending order

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361045 580395 4,907 25 25 20 h-index citations g-index papers 46 46 46 14525 all docs docs citations times ranked citing authors

#	Article	IF	CITATIONS
1	A reference panel of 64,976 haplotypes for genotype imputation. Nature Genetics, 2016, 48, 1279-1283.	9.4	2,421
2	Genome-wide association study implicates immune activation of multiple integrin genes in inflammatory bowel disease. Nature Genetics, 2017, 49, 256-261.	9.4	943
3	Susceptibility to tuberculosis is associated with variants in the ASAP1 gene encoding a regulator of dendritic cell migration. Nature Genetics, 2015, 47, 523-527.	9.4	156
4	Exploring the genetic architecture of inflammatory bowel disease by whole-genome sequencing identifies association at ADCY7. Nature Genetics, 2017, 49, 186-192.	9.4	153
5	Genetic diversity and evolutionary dynamics of Ebola virus in Sierra Leone. Nature, 2015, 524, 93-96.	13.7	150
6	HLA class II sequence variants influence tuberculosis risk in populations of European ancestry. Nature Genetics, 2016, 48, 318-322.	9.4	123
7	Fine-mapping and functional studies highlight potential causal variants for rheumatoid arthritis and type 1 diabetes. Nature Genetics, 2018, 50, 1366-1374.	9.4	122
8	Allele-specific expression changes dynamically during T cell activation in HLA and other autoimmune loci. Nature Genetics, 2020, 52, 247-253.	9.4	85
9	Single-cell eQTL models reveal dynamic T cell state dependence of disease loci. Nature, 2022, 606, 120-128.	13.7	75
10	Intra-host dynamics of Ebola virus during 2014. Nature Microbiology, 2016, 1, 16151.	5.9	70
11	A high-resolution HLA reference panel capturing global population diversity enables multi-ancestry fine-mapping in HIV host response. Nature Genetics, 2021, 53, 1504-1516.	9.4	69
12	Population-specific causal disease effect sizes in functionally important regions impacted by selection. Nature Communications, 2021, 12, 1098.	5.8	68
13	Multimodally profiling memory T cells from a tuberculosis cohort identifies cell state associations with demographics, environment and disease. Nature Immunology, 2021, 22, 781-793.	7.0	52
14	IMPACT: Genomic Annotation of Cell-State-Specific Regulatory Elements Inferred from the Epigenome of Bound Transcription Factors. American Journal of Human Genetics, 2019, 104, 879-895.	2.6	49
15	Early progression to active tuberculosis is a highly heritable trait driven by 3q23 in Peruvians. Nature Communications, 2019, 10, 3765.	5.8	43
16	HLA autoimmune risk alleles restrict the hypervariable region of T cell receptors. Nature Genetics, 2022, 54, 393-402.	9.4	40
17	A positively selected FBN1 missense variant reduces height in Peruvian individuals. Nature, 2020, 582, 234-239.	13.7	39
18	Discovering in vivo cytokine-eQTL interactions from a lupus clinical trial. Genome Biology, 2018, 19, 168.	3.8	36

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#	Article	IF	CITATION
19	Genome-wide Study Identifies Association between HLA-Bâ^—55:01 and Self-Reported Penicillin Allergy. American Journal of Human Genetics, 2020, 107, 612-621.	2.6	34
20	OUP accepted manuscript. Human Molecular Genetics, 2021, 30, 1521-1534.	1.4	32
21	Advances in genetics toward identifying pathogenic cell states of rheumatoid arthritis. Immunological Reviews, 2020, 294, 188-204.	2.8	23
22	Accurate imputation of human leukocyte antigens with CookHLA. Nature Communications, 2021, 12, 1264.	5.8	21
23	HATK: HLA analysis toolkit. Bioinformatics, 2021, 37, 416-418.	1.8	13
24	A sex-specific evolutionary interaction between ADCY9 and CETP. ELife, 2021, 10, .	2.8	8
25	Higher native Peruvian genetic ancestry proportion is associated with tuberculosis progression risk. Cell Genomics, 2022, 2, 100151.	3.0	5