

# Yang Luo

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

36  
papers

2,713  
citations

15  
h-index

46  
g-index

46  
ext. papers

3,930  
ext. citations

26  
avg, IF

3.73  
L-index

#	Paper	IF	Citations
36	Single-cell eQTL models reveal dynamic T cell state dependence of disease loci.. <i>Nature</i> , <b>2022</b> ,	50.4	4
35	A high-resolution HLA reference panel capturing global population diversity enables multi-ancestry fine-mapping in HIV host response. <i>Nature Genetics</i> , <b>2021</b> , 53, 1504-1516	36.3	7
34	Multimodally profiling memory T cells from a tuberculosis cohort identifies cell state associations with demographics, environment and disease. <i>Nature Immunology</i> , <b>2021</b> , 22, 781-793	19.1	13
33	HATK: HLA analysis toolkit. <i>Bioinformatics</i> , <b>2021</b> , 37, 416-418	7.2	4
32	Estimating heritability and its enrichment in tissue-specific gene sets in admixed populations. <i>Human Molecular Genetics</i> , <b>2021</b> , 30, 1521-1534	5.6	6
31	Population-specific causal disease effect sizes in functionally important regions impacted by selection. <i>Nature Communications</i> , <b>2021</b> , 12, 1098	17.4	16
30	Accurate imputation of human leukocyte antigens with CookHLA. <i>Nature Communications</i> , <b>2021</b> , 12, 1264	17.4	5
29	A positively selected FBN1 missense variant reduces height in Peruvian individuals. <i>Nature</i> , <b>2020</b> , 582, 234-239	50.4	15
28	Allele-specific expression changes dynamically during T cell activation in HLA and other autoimmune loci. <i>Nature Genetics</i> , <b>2020</b> , 52, 247-253	36.3	33
27	Genome-wide Study Identifies Association between HLA-B55:01 and Self-Reported Penicillin Allergy. <i>American Journal of Human Genetics</i> , <b>2020</b> , 107, 612-621	11	17
26	Advances in genetics toward identifying pathogenic cell states of rheumatoid arthritis. <i>Immunological Reviews</i> , <b>2020</b> , 294, 188-204	11.3	9
25	Early progression to active tuberculosis is a highly heritable trait driven by 3q23 in Peruvians. <i>Nature Communications</i> , <b>2019</b> , 10, 3765	17.4	18
24	IMPACT: Genomic Annotation of Cell-State-Specific Regulatory Elements Inferred from the Epigenome of Bound Transcription Factors. <i>American Journal of Human Genetics</i> , <b>2019</b> , 104, 879-895	11	21
23	Discovering in vivo cytokine-eQTL interactions from a lupus clinical trial. <i>Genome Biology</i> , <b>2018</b> , 19, 168	18.3	19
22	Fine-mapping and functional studies highlight potential causal variants for rheumatoid arthritis and type 1 diabetes. <i>Nature Genetics</i> , <b>2018</b> , 50, 1366-1374	36.3	82
21	Genome-wide association study implicates immune activation of multiple integrin genes in inflammatory bowel disease. <i>Nature Genetics</i> , <b>2017</b> , 49, 256-261	36.3	462
20	Exploring the genetic architecture of inflammatory bowel disease by whole-genome sequencing identifies association at ADCY7. <i>Nature Genetics</i> , <b>2017</b> , 49, 186-192	36.3	104

19	A reference panel of 64,976 haplotypes for genotype imputation. <i>Nature Genetics</i> , <b>2016</b> , 48, 1279-83	36.3	1447
18	Intra-host dynamics of Ebola virus during 2014. <i>Nature Microbiology</i> , <b>2016</b> , 1, 16151	26.6	54
17	HLA class II sequence variants influence tuberculosis risk in populations of European ancestry. <i>Nature Genetics</i> , <b>2016</b> , 48, 318-22	36.3	92
16	Genetic diversity and evolutionary dynamics of Ebola virus in Sierra Leone. <i>Nature</i> , <b>2015</b> , 524, 93-6	50.4	121
15	Susceptibility to tuberculosis is associated with variants in the ASAP1 gene encoding a regulator of dendritic cell migration. <i>Nature Genetics</i> , <b>2015</b> , 47, 523-527	36.3	112
14	Trans-ancestry genome-wide association study identifies novel genetic mechanisms in rheumatoid arthritis		2
13	Genome-wide study identifies association between HLA-B*55:01 and penicillin allergy		2
12	IMPACT: Genomic annotation of cell-state-specific regulatory elements inferred from the epigenome of bound transcription factors		1
11	Genome-wide association study implicates immune activation of multiple integrin genes in inflammatory bowel disease		4
10	Discovering in vivo cytokine eQTL interactions from a lupus clinical trial		3
9	Fine-mapping identifies causal variants for RA and T1D in DNASE1L3, SIRPG, MEG3, TNFAIP3 and CD28/CTLA4 loci		4
8	Multimodal memory T cell profiling identifies a reduction in a polyfunctional Th17 state associated with tuberculosis progression		7
7	A high-resolution HLA reference panel capturing global population diversity enables multi-ethnic fine-mapping in HIV host response		6
6	HLA autoimmune risk alleles restrict the hypervariable region of T cell receptors		4
5	Progression of recent Mycobacterium tuberculosis exposure to active tuberculosis is a highly heritable complex trait driven by 3q23 in Peruvians		2
4	Estimating heritability and its enrichment in tissue-specific gene sets in admixed populations		4
3	Allele-specific expression changes dynamically during T cell activation in HLA and other autoimmune loci		4
2	Population-specific causal disease effect sizes in functionally important regions impacted by selection		4

1 Modeling memory T cell states at single-cell resolution identifies in vivo state-dependence of eQTLs influencing disease

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