

Yang Luo

List of Publications by Citations

Source: <https://exaly.com/author-pdf/1142068/yang-luo-publications-by-citations.pdf>

Version: 2024-04-24

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

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	A reference panel of 64,976 haplotypes for genotype imputation. <i>Nature Genetics</i> , 2016 , 48, 1279-83	36.3	1447
35	Genome-wide association study implicates immune activation of multiple integrin genes in inflammatory bowel disease. <i>Nature Genetics</i> , 2017 , 49, 256-261	36.3	462
34	Genetic diversity and evolutionary dynamics of Ebola virus in Sierra Leone. <i>Nature</i> , 2015 , 524, 93-6	50.4	121
33	Susceptibility to tuberculosis is associated with variants in the ASAP1 gene encoding a regulator of dendritic cell migration. <i>Nature Genetics</i> , 2015 , 47, 523-527	36.3	112
32	Exploring the genetic architecture of inflammatory bowel disease by whole-genome sequencing identifies association at ADCY7. <i>Nature Genetics</i> , 2017 , 49, 186-192	36.3	104
31	HLA class II sequence variants influence tuberculosis risk in populations of European ancestry. <i>Nature Genetics</i> , 2016 , 48, 318-22	36.3	92
30	Fine-mapping and functional studies highlight potential causal variants for rheumatoid arthritis and type 1 diabetes. <i>Nature Genetics</i> , 2018 , 50, 1366-1374	36.3	82
29	Intra-host dynamics of Ebola virus during 2014. <i>Nature Microbiology</i> , 2016 , 1, 16151	26.6	54
28	Allele-specific expression changes dynamically during T cell activation in HLA and other autoimmune loci. <i>Nature Genetics</i> , 2020 , 52, 247-253	36.3	33
27	IMPACT: Genomic Annotation of Cell-State-Specific Regulatory Elements Inferred from the Epigenome of Bound Transcription Factors. <i>American Journal of Human Genetics</i> , 2019 , 104, 879-895	11	21
26	Discovering in vivo cytokine-eQTL interactions from a lupus clinical trial. <i>Genome Biology</i> , 2018 , 19, 168	18.3	19
25	Early progression to active tuberculosis is a highly heritable trait driven by 3q23 in Peruvians. <i>Nature Communications</i> , 2019 , 10, 3765	17.4	18
24	Genome-wide Study Identifies Association between HLA-B55:01 and Self-Reported Penicillin Allergy. <i>American Journal of Human Genetics</i> , 2020 , 107, 612-621	11	17
23	Population-specific causal disease effect sizes in functionally important regions impacted by selection. <i>Nature Communications</i> , 2021 , 12, 1098	17.4	16
22	A positively selected FBN1 missense variant reduces height in Peruvian individuals. <i>Nature</i> , 2020 , 582, 234-239	50.4	15
21	Multimodally profiling memory T cells from a tuberculosis cohort identifies cell state associations with demographics, environment and disease. <i>Nature Immunology</i> , 2021 , 22, 781-793	19.1	13
20	Advances in genetics toward identifying pathogenic cell states of rheumatoid arthritis. <i>Immunological Reviews</i> , 2020 , 294, 188-204	11.3	9

19	A high-resolution HLA reference panel capturing global population diversity enables multi-ancestry fine-mapping in HIV host response. <i>Nature Genetics</i> , 2021 , 53, 1504-1516	36.3	7
18	Multimodal memory T cell profiling identifies a reduction in a polyfunctional Th17 state associated with tuberculosis progression		7
17	A high-resolution HLA reference panel capturing global population diversity enables multi-ethnic fine-mapping in HIV host response		6
16	Estimating heritability and its enrichment in tissue-specific gene sets in admixed populations. <i>Human Molecular Genetics</i> , 2021 , 30, 1521-1534	5.6	6
15	Accurate imputation of human leukocyte antigens with CookHLA. <i>Nature Communications</i> , 2021 , 12, 1264	17.4	5
14	Genome-wide association study implicates immune activation of multiple integrin genes in inflammatory bowel disease		4
13	Fine-mapping identifies causal variants for RA and T1D in DNASE1L3, SIRPG, MEG3, TNFAIP3 and CD28/CTLA4 loci		4
12	HLA autoimmune risk alleles restrict the hypervariable region of T cell receptors		4
11	Estimating heritability and its enrichment in tissue-specific gene sets in admixed populations		4
10	Allele-specific expression changes dynamically during T cell activation in HLA and other autoimmune loci		4
9	Population-specific causal disease effect sizes in functionally important regions impacted by selection		4
8	HATK: HLA analysis toolkit. <i>Bioinformatics</i> , 2021 , 37, 416-418	7.2	4
7	Single-cell eQTL models reveal dynamic T cell state dependence of disease loci.. <i>Nature</i> , 2022 ,	50.4	4
6	Discovering in vivo cytokine eQTL interactions from a lupus clinical trial		3
5	Trans-ancestry genome-wide association study identifies novel genetic mechanisms in rheumatoid arthritis		2
4	Genome-wide study identifies association between HLA-B*55:01 and penicillin allergy		2
3	Progression of recent Mycobacterium tuberculosis exposure to active tuberculosis is a highly heritable complex trait driven by 3q23 in Peruvians		2
2	IMPACT: Genomic annotation of cell-state-specific regulatory elements inferred from the epigenome of bound transcription factors		1

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

1