

Yang Liao

List of Publications by Citations

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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.

40
papers

12,314
citations

20
h-index

43
g-index

43
ext. papers

19,658
ext. citations

13.6
avg, IF

7.14
L-index

#	Paper	IF	Citations
40	featureCounts: an efficient general purpose program for assigning sequence reads to genomic features. <i>Bioinformatics</i> , 2014 , 30, 923-30	7.2	7883
39	The Subread aligner: fast, accurate and scalable read mapping by seed-and-vote. <i>Nucleic Acids Research</i> , 2013 , 41, e108	20.1	1489
38	The R package Rsubread is easier, faster, cheaper and better for alignment and quantification of RNA sequencing reads. <i>Nucleic Acids Research</i> , 2019 , 47, e47	20.1	635
37	Hobit and Blimp1 instruct a universal transcriptional program of tissue residency in lymphocytes. <i>Science</i> , 2016 , 352, 459-63	33.3	495
36	The transcriptional regulators IRF4, BATF and IL-33 orchestrate development and maintenance of adipose tissue-resident regulatory T cells. <i>Nature Immunology</i> , 2015 , 16, 276-85	19.1	356
35	Transcriptional profiling of mouse B cell terminal differentiation defines a signature for antibody-secreting plasma cells. <i>Nature Immunology</i> , 2015 , 16, 663-73	19.1	239
34	Blimp-1 controls plasma cell function through the regulation of immunoglobulin secretion and the unfolded protein response. <i>Nature Immunology</i> , 2016 , 17, 323-30	19.1	194
33	Transcription Factor IRF4 Promotes CD8 T Cell Exhaustion and Limits the Development of Memory-like T Cells during Chronic Infection. <i>Immunity</i> , 2017 , 47, 1129-1141.e5	32.3	178
32	A molecular threshold for effector CD8(+) T cell differentiation controlled by transcription factors Blimp-1 and T-bet. <i>Nature Immunology</i> , 2016 , 17, 422-32	19.1	98
31	Assessing technical performance in differential gene expression experiments with external spike-in RNA control ratio mixtures. <i>Nature Communications</i> , 2014 , 5, 5125	17.4	89
30	The TNF Receptor Superfamily-NF- κ B Axis Is Critical to Maintain Effector Regulatory T Cells in Lymphoid and Non-lymphoid Tissues. <i>Cell Reports</i> , 2017 , 20, 2906-2920	10.6	77
29	Sex-specific adipose tissue imprinting of regulatory T cells. <i>Nature</i> , 2020 , 579, 581-585	50.4	72
28	c-Maf-dependent T cell control of intestinal T17 cells and IgA establishes host-microbiota homeostasis. <i>Nature Immunology</i> , 2019 , 20, 471-481	19.1	72
27	Pax5 loss imposes a reversible differentiation block in B-progenitor acute lymphoblastic leukemia. <i>Genes and Development</i> , 2014 , 28, 1337-50	12.6	62
26	Effector Regulatory T Cell Differentiation and Immune Homeostasis Depend on the Transcription Factor Myb. <i>Immunity</i> , 2017 , 46, 78-91	32.3	48
25	IMiDs prime myeloma cells for daratumumab-mediated cytotoxicity through loss of Ikaros and Aiolos. <i>Blood</i> , 2018 , 132, 2166-2178	2.2	42
24	Environmental sensing by mature B cells is controlled by the transcription factors PU.1 and SpiB. <i>Nature Communications</i> , 2017 , 8, 1426	17.4	39

23	Dynamic changes in Id3 and E-protein activity orchestrate germinal center and plasma cell development. <i>Journal of Experimental Medicine</i> , 2016 , 213, 1095-111	16.6	38
22	Attenuation of TCR-induced transcription by Bach2 controls regulatory T cell differentiation and homeostasis. <i>Nature Communications</i> , 2020 , 11, 252	17.4	28
21	TCF-1 limits the formation of Tc17 cells via repression of the MAF-ROR β axis. <i>Journal of Experimental Medicine</i> , 2019 , 216, 1682-1699	16.6	27
20	IRF4 Activity Is Required in Established Plasma Cells to Regulate Gene Transcription and Mitochondrial Homeostasis. <i>Cell Reports</i> , 2019 , 29, 2634-2645.e5	10.6	20
19	An update on using CRISPR/Cas9 in the one-cell stage mouse embryo for generating complex mutant alleles. <i>Cell Death and Differentiation</i> , 2017 , 24, 1821-1822	12.7	18
18	Transcription Factor T-bet in B Cells Modulates Germinal Center Polarization and Antibody Affinity Maturation in Response to Malaria. <i>Cell Reports</i> , 2019 , 29, 2257-2269.e6	10.6	16
17	Quantitative proteomic profiling reveals novel region-specific markers in the adult mouse brain. <i>Proteomics</i> , 2014 , 14, 241-61	4.8	10
16	The R package Rsubread is easier, faster, cheaper and better for alignment and quantification of RNA sequencing reads		10
15	Tailored NEOadjuvant epirubicin, cyclophosphamide and Nanoparticle Albumin-Bound paclitaxel for breast cancer: The phase II NEONAB trial-Clinical outcomes and molecular determinants of response. <i>PLoS ONE</i> , 2019 , 14, e0210891	3.7	9
14	Mining Micro-blogs: Opportunities and Challenges 2012 , 129-159		9
13	Plasmacytoid dendritic cell heterogeneity is defined by CXCL10 expression following TLR7 stimulation. <i>Immunology and Cell Biology</i> , 2018 , 96, 1083-1094	5	8
12	Read trimming is not required for mapping and quantification of RNA-seq reads at the gene level. <i>NAR Genomics and Bioinformatics</i> , 2020 , 2, lqaa068	3.7	8
11	The transcription factor IRF4 represses proapoptotic BMF and BIM to licence multiple myeloma survival. <i>Leukemia</i> , 2021 , 35, 2114-2118	10.7	8
10	Impact of RNA-seq data analysis algorithms on gene expression estimation and downstream prediction. <i>Scientific Reports</i> , 2020 , 10, 17925	4.9	7
9	A point mutation in the signal peptide impairs the development of innate lymphoid cell subsets. <i>Oncolmmunology</i> , 2018 , 7, e1475875	7.2	7
8	Mining the Plasma Cell Transcriptome for Novel Cell Surface Proteins. <i>International Journal of Molecular Sciences</i> , 2018 , 19,	6.3	4
7	Read trimming is not required for mapping and quantification of RNA-seq reads		3
6	ScoreFinder: A method for collaborative quality inference on user-generated content 2010 ,		2

5	Dynamic changes in Id3 and E-protein activity orchestrate germinal center and plasma cell development. <i>Journal of Cell Biology</i> , 2016 , 213, 2135OIA110	7.3	1
4	Decentralisation of ScoreFinder: A Framework for Credibility Management on User-Generated Contents. <i>Lecture Notes in Computer Science</i> , 2010 , 272-282	0.9	1
3	Impact of gene annotation choice on the quantification of RNA-seq data.. <i>BMC Bioinformatics</i> , 2022 , 23, 107	3.6	0
2	Molecular profiling reveals features of clinical immunity and immunosuppression in asymptomatic <i>P. falciparum</i> malaria.. <i>Molecular Systems Biology</i> , 2022 , 18, e10824	12.2	0
1	ScoreTree: A Decentralised Framework for Credibility Management of User-Generated Content. <i>Lecture Notes in Computer Science</i> , 2011 , 249-256	0.9	