

# Yang Liao

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7059313/publications.pdf>

Version: 2024-02-01

39  
papers

24,562  
citations

279778

23  
h-index

330122

37  
g-index

43  
all docs

43  
docs citations

43  
times ranked

49897  
citing authors

#	ARTICLE	IF	CITATIONS
1	featureCounts: an efficient general purpose program for assigning sequence reads to genomic features. <i>Bioinformatics</i> , 2014, 30, 923-930.	4.1	16,839
2	The Subread aligner: fast, accurate and scalable read mapping by seed-and-vote. <i>Nucleic Acids Research</i> , 2013, 41, e108-e108.	14.5	2,389
3	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-e47.	14.5	1,744
4	Hobit and Blimp1 instruct a universal transcriptional program of tissue residency in lymphocytes. <i>Science</i> , 2016, 352, 459-463.	12.6	721
5	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, 276-285.	14.5	442
6	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.	14.3	335
7	Transcriptional profiling of mouse B cell terminal differentiation defines a signature for antibody-secreting plasma cells. <i>Nature Immunology</i> , 2015, 16, 663-673.	14.5	332
8	Blimp-1 controls plasma cell function through the regulation of immunoglobulin secretion and the unfolded protein response. <i>Nature Immunology</i> , 2016, 17, 323-330.	14.5	310
9	A molecular threshold for effector CD8+ T cell differentiation controlled by transcription factors Blimp-1 and T-bet. <i>Nature Immunology</i> , 2016, 17, 422-432.	14.5	145
10	Sex-specific adipose tissue imprinting of regulatory T cells. <i>Nature</i> , 2020, 579, 581-585.	27.8	141
11	c-Maf-dependent Treg cell control of intestinal TH17 cells and IgA establishes host-microbiota homeostasis. <i>Nature Immunology</i> , 2019, 20, 471-481.	14.5	138
12	Assessing technical performance in differential gene expression experiments with external spike-in RNA control ratio mixtures. <i>Nature Communications</i> , 2014, 5, 5125.	12.8	122
13	The TNF Receptor Superfamily-NF- $\kappa$ B Axis Is Critical to Maintain Effector Regulatory T Cells in Lymphoid and Non-lymphoid Tissues. <i>Cell Reports</i> , 2017, 20, 2906-2920.	6.4	115
14	Effector Regulatory T Cell Differentiation and Immune Homeostasis Depend on the Transcription Factor Myb. <i>Immunity</i> , 2017, 46, 78-91.	14.3	83
15	Pax5 loss imposes a reversible differentiation block in B-progenitor acute lymphoblastic leukemia. <i>Genes and Development</i> , 2014, 28, 1337-1350.	5.9	73
16	Environmental sensing by mature B cells is controlled by the transcription factors PU.1 and SpiB. <i>Nature Communications</i> , 2017, 8, 1426.	12.8	71
17	IMiDs prime myeloma cells for daratumumab-mediated cytotoxicity through loss of Ikaros and Aiolos. <i>Blood</i> , 2018, 132, 2166-2178.	1.4	65
18	Attenuation of TCR-induced transcription by Bach2 controls regulatory T cell differentiation and homeostasis. <i>Nature Communications</i> , 2020, 11, 252.	12.8	59

#	ARTICLE	IF	CITATIONS
19	Dynamic changes in Id3 and E-protein activity orchestrate germinal center and plasma cell development. <i>Journal of Experimental Medicine</i> , 2016, 213, 1095-1111.	8.5	53
20	TCF-1 limits the formation of Tc17 cells via repression of the MAF-ROR $\beta$ t axis. <i>Journal of Experimental Medicine</i> , 2019, 216, 1682-1699.	8.5	48
21	IRF4 Activity Is Required in Established Plasma Cells to Regulate Gene Transcription and Mitochondrial Homeostasis. <i>Cell Reports</i> , 2019, 29, 2634-2645.e5.	6.4	47
22	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.	11.2	38
23	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.	6.4	36
24	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.	3.2	22
25	Impact of RNA-seq data analysis algorithms on gene expression estimation and downstream prediction. <i>Scientific Reports</i> , 2020, 10, 17925.	3.3	18
26	The transcription factor IRF4 represses proapoptotic BMF and BIM to licence multiple myeloma survival. <i>Leukemia</i> , 2021, 35, 2114-2118.	7.2	18
27	Mining the Plasma Cell Transcriptome for Novel Cell Surface Proteins. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2161.	4.1	17
28	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.	2.5	13
29	Mining Micro-blogs: Opportunities and Challenges. , 2012, , 129-159.		13
30	Quantitative proteomic profiling reveals novel region-specific markers in the adult mouse brain. <i>Proteomics</i> , 2014, 14, 241-261.	2.2	12
31	Plasmacytoid dendritic cell heterogeneity is defined by CXCL10 expression following TLR7 stimulation. <i>Immunology and Cell Biology</i> , 2018, 96, 1083-1094.	2.3	12
32	A point mutation in the <i>Ncr1</i> signal peptide impairs the development of innate lymphoid cell subsets. <i>Oncolmmunology</i> , 2018, 7, e1475875.	4.6	9
33	Molecular profiling reveals features of clinical immunity and immunosuppression in asymptomatic <i>P. falciparum</i> malaria. <i>Molecular Systems Biology</i> , 2022, 18, e10824.	7.2	9
34	Impact of gene annotation choice on the quantification of RNA-seq data. <i>BMC Bioinformatics</i> , 2022, 23, 107.	2.6	8
35	Epithelial de-differentiation triggered by co-ordinate epigenetic inactivation of the EHF and CDX1 transcription factors drives colorectal cancer progression. <i>Cell Death and Differentiation</i> , 2022, 29, 2288-2302.	11.2	6
36	ScoreFinder: A method for collaborative quality inference on user-generated content. , 2010, , .		2

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37	Dynamic changes in Id3 and E-protein activity orchestrate germinal center and plasma cell development. <i>Journal of Cell Biology</i> , 2016, 213, 2135OIA110.	5.2	1
38	Decentralisation of ScoreFinder: A Framework for Credibility Management on User-Generated Contents. <i>Lecture Notes in Computer Science</i> , 2010, , 272-282.	1.3	1
39	ScoreTree: A Decentralised Framework for Credibility Management of User-Generated Content. <i>Lecture Notes in Computer Science</i> , 2011, , 249-256.	1.3	0