## Jin Yan Huang

List of Publications by Year in descending order

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257450 128289 7,016 63 24 60 h-index citations g-index papers 70 70 70 16774 docs citations times ranked citing authors all docs

#	Article	IF	CITATIONS
1	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	27.8	3,823
2	The genetic architecture of type 2 diabetes. Nature, 2016, 536, 41-47.	27.8	952
3	Directional dominance on stature and cognition inÂdiverse human populations. Nature, 2015, 523, 459-462.	27.8	173
4	Genome-wide association study identifies multiple susceptibility loci for diffuse large B cell lymphoma. Nature Genetics, 2014, 46, 1233-1238.	21.4	147
5	Genomic and Transcriptomic Characterization of Natural Killer T Cell Lymphoma. Cancer Cell, 2020, 37, 403-419.e6.	16.8	136
6	Association of homocysteine with type 2 diabetes: a meta-analysis implementing Mendelian randomization approach. BMC Genomics, 2013, 14, 867.	2.8	115
7	Meta-analysis of genome-wide association studies of adult height in East Asians identifies 17 novel loci. Human Molecular Genetics, 2015, 24, 1791-1800.	2.9	105
8	Inhibition of mTORC1 by IncRNA H19 via disrupting 4E-BP1/Raptor interaction in pituitary tumours. Nature Communications, 2018, 9, 4624.	12.8	104
9	Genome-wide Association Study Identifies Five Susceptibility Loci for Follicular Lymphoma outside the HLA Region. American Journal of Human Genetics, 2014, 95, 462-471.	6.2	96
10	Meta-analysis of genome-wide association studies discovers multiple loci for chronic lymphocytic leukemia. Nature Communications, 2016, 7, 10933.	12.8	94
11	CREBBP/EP300 mutations promoted tumor progression in diffuse large B-cell lymphoma through altering tumor-associated macrophage polarization via FBXW7-NOTCH-CCL2/CSF1 axis. Signal Transduction and Targeted Therapy, 2021, 6, 10.	17.1	93
12	Associations of autozygosity with a broad range of human phenotypes. Nature Communications, 2019, 10, 4957.	12.8	84
13	Genome-Wide Analysis of DNA Methylation and Acute Coronary Syndrome. Circulation Research, 2017, 120, 1754-1767.	4.5	70
14	Whole genome and transcriptome sequencing of matched primary and peritoneal metastatic gastric carcinoma. Scientific Reports, 2015, 5, 13750.	3.3	69
15	Characterization of gene expression profiles in HBV-related liver fibrosis patients and identification of ITGBL1 as a key regulator of fibrogenesis. Scientific Reports, 2017, 7, 43446.	3.3	68
16	Multiple Nonglycemic Genomic Loci Are Newly Associated With Blood Level of Glycated Hemoglobin in East Asians. Diabetes, 2014, 63, 2551-2562.	0.6	61
17	A genome-wide association study of marginal zone lymphoma shows association to the HLA region. Nature Communications, 2015, 6, 5751.	12.8	58
18	Homoharringtonine deregulates <i>MYC</i> transcriptional expression by directly binding NF-κB repressing factor. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 2220-2225.	7.1	55

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19	Fast and robust adjustment of cell mixtures in epigenome-wide association studies with SmartSVA. BMC Genomics, 2017, 18, 413.	2.8	54
20	A comprehensive survey of genetic variation in 20,691 subjects from four large cohorts. PLoS ONE, 2017, 12, e0173997.	2.5	52
21	A Low-Frequency Inactivating <i>AKT2</i> Variant Enriched in the Finnish Population Is Associated With Fasting Insulin Levels and Type 2 Diabetes Risk. Diabetes, 2017, 66, 2019-2032.	0.6	47
22	USP7 deubiquitinates and stabilizes NOTCH1 in T-cell acute lymphoblastic leukemia. Signal Transduction and Targeted Therapy, 2018, 3, 29.	17.1	38
23	<i>PCSK7</i> Genotype Modifies Effect of a Weight-Loss Diet on 2-Year Changes of Insulin Resistance: The POUNDS LOST Trial. Diabetes Care, 2015, 38, 439-444.	8.6	35
24	Rare coding variants and X-linked loci associated with age at menarche. Nature Communications, 2015, 6, 7756.	12.8	32
25	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. Scientific Data, 2017, 4, 170179.	5.3	31
26	Multidimensional study of the heterogeneity of leukemia cells in t(8;21) acute myelogenous leukemia identifies the subtype with poor outcome. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 20117-20126.	7.1	31
27	Gene mutational pattern and expression level in 560 acute myeloid leukemia patients and their clinical relevance. Journal of Translational Medicine, 2017, 15, 178.	4.4	24
28	SLC1A1 mediated glutamine addiction and contributed to natural killer T-cell lymphoma progression with immunotherapeutic potential. EBioMedicine, 2021, 72, 103614.	6.1	24
29	eQTL mapping identifies insertion- and deletion-specific eQTLs in multiple tissues. Nature Communications, 2015, 6, 6821.	12.8	18
30	Different roles of E proteins in t(8;21) leukemia: E2-2 compromises the function of AETFC and negatively regulates leukemogenesis. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 890-899.	7.1	18
31	CytoTree: an R/Bioconductor package for analysis and visualization of flow and mass cytometry data. BMC Bioinformatics, 2021, 22, 138.	2.6	18
32	Transcriptome-wide subtyping of pediatric and adult T cell acute lymphoblastic leukemia in an international study of 707 cases. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2120787119.	7.1	18
33	A tool for RNA sequencing sample identity check. Bioinformatics, 2013, 29, 1463-1464.	4.1	17
34	Genetic variants in desaturase gene, erythrocyte fatty acids, and risk for type 2 diabetes in Chinese Hans. Nutrition, 2014, 30, 897-902.	2.4	17
35	DEPTOR inhibits cell proliferation and confers sensitivity to dopamine agonist in pituitary adenoma. Cancer Letters, 2019, 459, 135-144.	7.2	17
36	PHF8 and REST/NRSF co-occupy gene promoters to regulate proximal gene expression. Scientific Reports, 2014, 4, 5008.	3.3	16

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37	Training in Swallowing Prevents Aspiration Pneumonia in Stroke Patients with Dysphagia. Journal of International Medical Research, 2006, 34, 303-306.	1.0	15
38	N-Arachidonoyl Dopamine Inhibits NRAS Neoplastic Transformation by Suppressing Its Plasma Membrane Translocation. Molecular Cancer Therapeutics, 2017, 16, 57-67.	4.1	13
39	Clinical significance of CD34+CD117dim/CD34+CD117bri myeloblast-associated gene expression in t(8;21) acute myeloid leukemia. Frontiers of Medicine, 2021, 15, 608-620.	3.4	13
40	Generalizability Theory as Evidence of Concerns About Fairness in Largeâ€Scale ESL Writing Assessments. TESOL Journal, 2011, 2, 423-443.	0.9	10
41	Leveraging biological and statistical covariates improves the detection power in epigenome-wide association testing. Genome Biology, 2020, 21, 88.	8.8	9
42	Case Report: Temozolomide Treatment of Refractory Prolactinoma Resistant to Dopamine Agonists. Frontiers in Endocrinology, 2021, 12, 616339.	3.5	9
43	Fucosylation of anti-dsDNA IgG1 correlates with disease activity of treatment-naÃve systemic lupus erythematosus patients. EBioMedicine, 2022, 77, 103883.	6.1	9
44	RTeQTL: Real-Time Online Engine for Expression Quantitative Trait Loci Analyses. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau066-bau066.	3.0	7
45	Human NUP98-IQCG fusion protein induces acute myelomonocytic leukemia in mice by dysregulating the Hox/Pbx3 pathway. Leukemia, 2016, 30, 1590-1593.	7.2	6
46	Estimating the Number of 2019 Novel Coronavirus Cases in Chinese Mainland. SSRN Electronic Journal, 0, , .	0.4	6
47	TRIM65 determines the fate of a novel subtype of pituitary neuroendocrine tumors via ubiquitination and degradation of TPIT. Neuro-Oncology, 2022, 24, 1286-1297.	1.2	6
48	Inhibition of the nuclear export of p65 and IQCG in leukemogenesis by NUP98-IQCG. Frontiers of Medicine, 2016, 10, 410-419.	3.4	5
49	An integrated software for virus community sequencing data analysis. BMC Genomics, 2020, 21, 363.	2.8	5
50	InterCellDB: A Userâ€Defined Database for Inferring Intercellular Networks. Advanced Science, 2022, 9, .	11.2	5
51	Kinase-associated gene mutation pattern and clinical relevance in 205 patients with core binding factor leukemias. Blood Cancer Journal, 2016, 6, e494-e494.	6.2	4
52	Single-Cell Transcriptome Analysis Identifies Ligand–Receptor Pairs Associated With BCP-ALL Prognosis. Frontiers in Oncology, 2021, 11, 639013.	2.8	4
53	Identification of a t(X;17)(q28;q21) generating a <scp><i>KANSL1â€MTCP1</i></scp> gene fusion leading to dysregulated expression of <scp><i>MTCP1</i></scp> in acute myeloid leukemia. Genes Chromosomes and Cancer, 2020, 59, 417-421.	2.8	3
54	Differential Expression of CD49f Discriminates the Independently Emerged Hematopoietic Stem Cells and Erythroid-Biased Progenitors. Blood, 2019, 134, 3700-3700.	1.4	3

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55	Development of a Model for Predicting the Effectiveness of Pulsed Radiofrequency on Zoster-Associated Pain. Pain and Therapy, 2022, 11, 253-267.	3.2	3
56	2dFDR: a new approach to confounder adjustment substantially increases detection power in omics association studies. Genome Biology, 2021, 22, 208.	8.8	2
57	BioInstaller: a comprehensive R package to construct interactive and reproducible biological data analysis applications based on the R platform. PeerJ, 2018, 6, e5853.	2.0	2
58	Teacher Perceptions of Strategies for Improving ESOL Students' Academic English Skills: A K-12 Perspective. Comparative and International Education, 2011, 40, .	0.3	1
59	Functional Study of Novel Gene Fusions and Patterns of Epigenetic Regulator Mutations in Adult and Childhood B-Cell Acute Lymphoblastic Leukemia. Blood, 2016, 128, 4076-4076.	1.4	O
60	Knock-in of Dnmt3a R878H Recapitulates Human Acute Myeloid Leukemia Harboring DNMT3A Mutation and Is Highly Responsive to mTOR Inhibitor Rapamycin. Blood, 2016, 128, 2836-2836.	1.4	0
61	The Three E Proteins Define a Heterogeneity of the AML1-ETO-Containing Transcription Factor Complex (AETFC) and Differentially Regulate t(8;21) Leukemogenesis. Blood, 2018, 132, 5247-5247.	1.4	0
62	Phase- and Epidemic Regions- Adjusted Estimation of the Number of Coronavirus Disease 2019 Cases in China. SSRN Electronic Journal, $\dot{0}$ , , .	0.4	0
63	Increase the Power of Epigenome-Wide Association Testing Using ICC-Based Hypothesis Weighting. Methods in Molecular Biology, 2022, 2432, 113-122.	0.9	0