Xin Jin

List of Publications by Year in descending order

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85 papers	28,764 citations	136950 32 h-index	64796 79 g-index
94 all docs	94 docs citations	94 times ranked	53529 citing authors

#	Article	IF	Citations
1	VThunter: a database for single-cell screening of virus target cells in the animal kingdom. Nucleic Acids Research, 2022, 50, D934-D942.	14.5	13
2	Phytochemical wedelolactone reverses obesity by prompting adipose browning through SIRT1/AMPK/ PPARÎ± pathway via targeting nicotinamide N-methyltransferase. Phytomedicine, 2022, 94, 153843.	5.3	6
3	hsa_circWDR37_016 Regulates Hypoxia-Induced Proliferation of Pulmonary Arterial Smooth Muscle Cells. Cardiovascular Therapeutics, 2022, 2022, 1-12.	2.5	6
4	Novel mutations in the BEST1 gene cause distinct retinopathies in two Chinese families. International Journal of Ophthalmology, 2022, 15, 205-212.	1.1	0
5	Effective Identification of Maternal Malignancies in Pregnancies Undergoing Noninvasive Prenatal Testing. Frontiers in Genetics, 2022, 13, 802865.	2.3	5
6	A Prospective Trial Comparing Haploidentical Donor Transplantation With Cord Blood Versus HLA-Matched Sibling Donor Transplantation for Hematologic Malignancy Patients. Cell Transplantation, 2022, 31, 096368972210760.	2.5	2
7	Drugâ€grafted DNA as a novel chemogene for targeted combinatorial cancer therapy. Exploration, 2022, 2, .	11.0	12
8	Progesterone Changes the Pregnancy-Induced Adaptation of Cardiomyocyte Kv2.1 Channels via MicroRNA-29b. Cardiovascular Therapeutics, 2022, 2022, 1-19.	2.5	2
9	AÎ²-responsive metformin-based supramolecular synergistic nanodrugs for Alzheimer's disease via enhancing microglial AÎ² clearance. Biomaterials, 2022, 283, 121452.	11.4	19
10	Singleâ€cell atlas of peripheral blood mononuclear cells from pregnant women. Clinical and Translational Medicine, 2022, 12, e821.	4.0	12
11	Rare Variants in Inborn Errors of Immunity Genes Associated With Covid-19 Severity. Frontiers in Cellular and Infection Microbiology, 2022, 12, .	3.9	5
12	Lineage-specific positive selection on ACE2 contributes to the genetic susceptibility of COVID-19. National Science Review, 2022, 9, .	9.5	2
13	hsa_circNFXL1_009 modulates apoptosis, proliferation, migration, and potassium channel activation in pulmonary hypertension. Molecular Therapy - Nucleic Acids, 2021, 23, 1007-1019.	5.1	23
14	Noninvasive tools based on immune biomarkers for the diagnosis of central nervous system graft-vs-host disease: Two case reports and a review of the literature. World Journal of Clinical Cases, 2021, 9, 1359-1366.	0.8	3
15	Longitudinal multi-omics transition associated with fatality in critically ill COVID-19 patients. Intensive Care Medicine Experimental, 2021, 9, 13.	1.9	9
16	CD19 CAR-T cell treatment conferred sustained remission in B-ALL patients with minimal residual disease. Cancer Immunology, Immunotherapy, 2021, 70, 3501-3511.	4.2	12
17	Deep sequencing of 1320 genes reveals the landscape of protein-truncating variants and their contribution to psoriasis in 19,973 Chinese individuals. Genome Research, 2021, 31, 1150-1158.	5.5	5
18	Circular RNA profiling reveals a potential role of hsa_circ_IPCEF1 in papillary thyroid carcinoma. Molecular Medicine Reports, 2021, 24, .	2.4	8

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19	The trans-omics landscape of COVID-19. Nature Communications, 2021, 12, 4543.	12.8	75
20	Cell-free DNA as a diagnostic tool for human echinococcosis. Trends in Parasitology, 2021, 37, 943-946.	3.3	5
21	Genome-wide association study of COVID-19 severity among the Chinese population. Cell Discovery, 2021, 7, 76.	6.7	41
22	Trans-ethnic genome-wide association study of severe COVID-19. Communications Biology, 2021, 4, 1034.	4.4	29
23	A Chinese host genetic study discovered IFNs and causality of laboratory traits on COVID-19 severity. IScience, 2021, 24, 103186.	4.1	10
24	Estimation of cell-free fetal DNA fraction from maternal plasma based on linkage disequilibrium information. Npj Genomic Medicine, 2021, 6, 85.	3.8	3
25	BDdb: a comprehensive platform for exploration and utilization of birth defect multi-omics data. BMC Medical Genomics, 2021, 14, 260.	1.5	1
26	Single cell atlas for 11 non-model mammals, reptiles and birds. Nature Communications, 2021, 12, 7083.	12.8	32
27	HLA-matched and HLA-haploidentical allogeneic CD19-directed chimeric antigen receptor T-cell infusions are feasible in relapsed or refractory B-cell acute lymphoblastic leukemia before hematopoietic stem cell transplantation. Leukemia, 2020, 34, 909-913.	7.2	15
28	Umbilical cord blood-derived mesenchymal stromal cells promote myeloid-derived suppressor cell proliferation by secreting HLA-G to reduce acute graft-versus-host disease after hematopoietic stem cell transplantation. Cytotherapy, 2020, 22, 718-733.	0.7	20
29	The genetic architecture of sporadic and multiple consecutive miscarriage. Nature Communications, 2020, 11, 5980.	12.8	52
30	Initial whole-genome sequencing and analysis of the host genetic contribution to COVID-19 severity and susceptibility. Cell Discovery, 2020, 6, 83.	6.7	159
31	Suppression of PTTG1 inhibits cell angiogenesis, migration and invasion in glioma cells. Medical Oncology, 2020, 37, 73.	2.5	13
32	Identification and Verification on Prognostic Index of Lower-Grade Glioma Immune-Related LncRNAs. Frontiers in Oncology, 2020, 10, 578809.	2.8	7
33	Identifying Occult Maternal Malignancies From 1.93 Million Pregnant Women Undergoing Noninvasive Prenatal Screening Tests. Obstetrical and Gynecological Survey, 2020, 75, 155-157.	0.4	0
34	Methylglyoxal-induced miR-223 suppresses rat vascular KATP channel activity by downregulating Kir6.1 mRNA in carbonyl stress. Vascular Pharmacology, 2020, 128-129, 106666.	2.1	3
35	Oleoylethanolamide Increases Glycogen Synthesis and Inhibits Hepatic Gluconeogenesis via the LKB1/AMPK Pathway in Type 2 Diabetic Model. Journal of Pharmacology and Experimental Therapeutics, 2020, 373, 81-91.	2.5	14
36	Circulating miRâ€‘451a levels as a potential biomarker to predict the prognosis of patients with multiple myeloma. Oncology Letters, 2020, 20, 1-1.	1.8	5

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37	miRâ€‘451a suppression of ILâ€‘6R can inhibit proliferation and increase apoptosis through the JAK2/STAT3 pathway in multiple myeloma. Oncology Letters, 2020, 20, 1-1.	1.8	11
38	STAT3â€‘PTTG11 abrogation inhibits proliferation and induces apoptosis in malignant glioma cells. Oncology Letters, 2020, 20, 6.	1.8	6
39	CD19 CAR-T Cells Treatment Conferred a Sustained Remission in Patients with Chemotherapy-Refractory MRD in B-ALL. Blood, 2020, 136, 48-48.	1.4	0
40	Low-Dose Decitabine Plus Venetoclax Maintenance Therapy Can Decrease the Relapse after Allogeneic Stem Cell Transplantation for MRD Positive High-Risk Acute Myeloid Leukemia and Myelodysplastic Syndrome. Blood, 2020, 136, 33-33.	1.4	2
41	Chronic oleoylethanolamide treatment attenuates diabetes-induced mice encephalopathy by triggering peroxisome proliferator-activated receptor alpha in the hippocampus. Neurochemistry International, 2019, 129, 104501.	3.8	12
42	Oleoylethanolamide inhibits glial activation via moudulating PPARÎ± and promotes motor function recovery after brain ischemia. Pharmacological Research, 2019, 141, 530-540.	7.1	37
43	Effect of Moringa oleifera stem extract on hydrogen peroxide-induced opacity of cultured mouse lens. BMC Complementary and Alternative Medicine, 2019, 19, 144.	3.7	7
44	Moringa oleifera seed extract protects against brain damage in both the acute and delayed stages of ischemic stroke. Experimental Gerontology, 2019, 122, 99-108.	2.8	23
45	Identifying occult maternal malignancies from 1.93 million pregnant women undergoing noninvasive prenatal screening tests. Genetics in Medicine, 2019, 21, 2293-2302.	2.4	36
46	Copy number variation profile in noninvasive prenatal testing (NIPT) can identify co-existing maternal malignancies: Case reports and a literature review. Taiwanese Journal of Obstetrics and Gynecology, 2018, 57, 871-877.	1.3	10
47	Genomic Analyses from Non-invasive Prenatal Testing Reveal Genetic Associations, Patterns of Viral Infections, and Chinese Population History. Cell, 2018, 175, 347-359.e14.	28.9	213
48	Genomic landscapes of Chinese sporadic autism spectrum disorders revealed by whole-genome sequencing. Journal of Genetics and Genomics, 2018, 45, 527-538.	3.9	33
49	CD19-CAR T Cells Treatment for Minimal Residual Disease in B-Cell Lymphoma with a Higher Response Rate and Fewer Adverse Reactions. Blood, 2018, 132, 3714-3714.	1.4	1
50	A copy-number variation detection pipeline for single cell sequencing data on BGI online. , 2017, , .		0
51	Deep sequencing of the MHC region in the Chinese population contributes to studies of complex disease. Nature Genetics, 2016, 48, 740-746.	21.4	188
52	Genome-wide characteristics of de novo mutations in autism. Npj Genomic Medicine, 2016, 1, 160271-1602710.	3.8	200
53	New loci and coding variants confer risk for age-related macular degeneration in East Asians. Nature Communications, 2015, 6, 6063.	12.8	147
54	Lanosterol reverses protein aggregation in cataracts. Nature, 2015, 523, 607-611.	27.8	351

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55	Inference of Purifying and Positive Selection in Three Subspecies of Chimpanzees (Pan troglodytes) from Exome Sequencing. Genome Biology and Evolution, 2015, 7, 1122-1132.	2.5	33
56	A global reference for human genetic variation. Nature, 2015, 526, 68-74.	27.8	13,998
57	A Novel DFNA36 Mutation in TMC1 Orthologous to the Beethoven (Bth) Mouse Associated with Autosomal Dominant Hearing Loss in a Chinese Family. PLoS ONE, 2014, 9, e97064.	2.5	61
58	Whole genome sequencing of Ethiopian highlanders reveals conserved hypoxia tolerance genes. Genome Biology, 2014, 15, R36.	9.6	71
59	A large-scale screen for coding variants predisposing to psoriasis. Nature Genetics, 2014, 46, 45-50.	21.4	183
60	Nitrogen-doped carbon dots as multifunctional fluorescent probes. Journal of Nanoparticle Research, 2014, 16, 1.	1.9	20
61	Sequencing-based approach identified three new susceptibility loci for psoriasis. Nature Communications, 2014, 5, 4331.	12.8	67
62	Altitude adaptation in Tibetans caused by introgression of Denisovan-like DNA. Nature, 2014, 512, 194-197.	27.8	904
63	A common Greenlandic TBC1D4 variant confers muscle insulin resistance and type 2 diabetes. Nature, 2014, 512, 190-193.	27.8	338
64	Whole-Genome Sequencing Uncovers the Genetic Basis of Chronic Mountain Sickness in Andean Highlanders. American Journal of Human Genetics, 2013, 93, 452-462.	6.2	115
65	Detection of Clinically Relevant Genetic Variants in Autism Spectrum Disorder by Whole-Genome Sequencing. American Journal of Human Genetics, 2013, 93, 249-263.	6.2	429
66	Effects of Fluid Shear Stress on Expression of Smac/DIABLO in Human Umbilical Vein Endothelial Cells. Current Therapeutic Research, 2013, 74, 36-40.	1.2	6
67	Exome Sequencing and Linkage Analysis Identified Tenascin-C (TNC) as a Novel Causative Gene in Nonsyndromic Hearing Loss. PLoS ONE, 2013, 8, e69549.	2.5	46
68	Genes Contributing to Pain Sensitivity in the Normal Population: An Exome Sequencing Study. PLoS Genetics, 2012, 8, e1003095.	3.5	49
69	An exome sequencing pipeline for identifying and genotyping common CNVs associated with disease with application to psoriasis. Bioinformatics, 2012, 28, i370-i374.	4.1	24
70	Extensive X-linked adaptive evolution in central chimpanzees. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 2054-2059.	7.1	79
71	Whole-Genome Sequencing in Autism Identifies Hot Spots for De Novo Germline Mutation. Cell, 2012, 151, 1431-1442.	28.9	501
72	An integrated map of genetic variation from 1,092 human genomes. Nature, 2012, 491, 56-65.	27.8	7,199

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73	An Effort to Use Human-Based Exome Capture Methods to Analyze Chimpanzee and Macaque Exomes. PLoS ONE, 2012, 7, e40637.	2.5	28
74	Exome Sequencing Identifies ZNF644 Mutations in High Myopia. PLoS Genetics, 2011, 7, e1002084.	3.5	164
75	Sequencing of 50 Human Exomes Reveals Adaptation to High Altitude. Science, 2010, 329, 75-78.	12.6	1,339
76	Building the sequence map of the human pan-genome. Nature Biotechnology, 2010, 28, 57-63.	17.5	237
77	Resequencing of 200 human exomes identifies an excess of low-frequency non-synonymous coding variants. Nature Genetics, 2010, 42, 969-972.	21.4	297
78	Archaeology Augments Tibet's Genetic Historyâ€"Response. Science, 2010, 329, 1467-1468.	12.6	3
79	The DNA Methylome of Human Peripheral Blood Mononuclear Cells. PLoS Biology, 2010, 8, e1000533.	5.6	290
80	TGM6 identified as a novel causative gene of spinocerebellar ataxias using exome sequencing. Brain, 2010, 133, 3510-3518.	7.6	243
81	Shear stress-induced collagen XII expression is associated with atherogenesis. Biochemical and Biophysical Research Communications, 2003, 308, 152-158.	2.1	33
82	Induction of human inhibitor of apoptosis protein-2 by shear stress in endothelial cells. FEBS Letters, 2002, 529, 286-292.	2.8	24
83	Laminar Shear Stressâ€"Induced GRO mRNA and Protein Expression in Endothelial Cells. Circulation, 1998, 98, 2584-2590.	1.6	36
84	Low Pass Genomes of 141,431 Chinese Reveal Patterns of Viral Infection, Novel Phenotypic Associations, and the Genetic History of China. SSRN Electronic Journal, 0, , .	0.4	2
85	How robust are cross-population signatures of polygenic adaptation in humans?. , 0, 1, .		3