

Xiao Liu

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.

103
papers

24,771
citations

39
h-index

120
g-index

120
ext. papers

31,444
ext. citations

13.2
avg, IF

5.74
L-index

#	Paper	IF	Citations
103	A global reference for human genetic variation. <i>Nature</i> , 2015 , 526, 68-74	50.4	8599
102	An integrated map of genetic variation from 1,092 human genomes. <i>Nature</i> , 2012 , 491, 56-65	50.4	6049
101	The oyster genome reveals stress adaptation and complexity of shell formation. <i>Nature</i> , 2012 , 490, 49-54	50.4	1464
100	Molecular analysis of gastric cancer identifies subtypes associated with distinct clinical outcomes. <i>Nature Medicine</i> , 2015 , 21, 449-56	50.5	1031
99	Sequencing of 50 human exomes reveals adaptation to high altitude. <i>Science</i> , 2010 , 329, 75-8	33.3	1020
98	The sequence and de novo assembly of the giant panda genome. <i>Nature</i> , 2010 , 463, 311-7	50.4	864
97	Genome-wide survey of recurrent HBV integration in hepatocellular carcinoma. <i>Nature Genetics</i> , 2012 , 44, 765-9	36.3	627
96	An abundance of rare functional variants in 202 drug target genes sequenced in 14,002 people. <i>Science</i> , 2012 , 337, 100-4	33.3	523
95	Single-cell exome sequencing reveals single-nucleotide mutation characteristics of a kidney tumor. <i>Cell</i> , 2012 , 148, 886-95	56.2	511
94	Whole-genome sequencing identifies recurrent mutations in hepatocellular carcinoma. <i>Genome Research</i> , 2013 , 23, 1422-33	9.7	371
93	Genome-wide profiling of HPV integration in cervical cancer identifies clustered genomic hot spots and a potential microhomology-mediated integration mechanism. <i>Nature Genetics</i> , 2015 , 47, 158-63	36.3	264
92	Resequencing of 200 human exomes identifies an excess of low-frequency non-synonymous coding variants. <i>Nature Genetics</i> , 2010 , 42, 969-72	36.3	264
91	Frequent mutations of genes encoding ubiquitin-mediated proteolysis pathway components in clear cell renal cell carcinoma. <i>Nature Genetics</i> , 2011 , 44, 17-9	36.3	248
90	Genomic and oncogenic preference of HBV integration in hepatocellular carcinoma. <i>Nature Communications</i> , 2016 , 7, 12992	17.4	151
89	BIPES, a cost-effective high-throughput method for assessing microbial diversity. <i>ISME Journal</i> , 2011 , 5, 741-9	11.9	136
88	Genomic landscape and genetic heterogeneity in gastric adenocarcinoma revealed by whole-genome sequencing. <i>Nature Communications</i> , 2014 , 5, 5477	17.4	130
87	Deep sequencing of the MHC region in the Chinese population contributes to studies of complex disease. <i>Nature Genetics</i> , 2016 , 48, 740-6	36.3	129

86	Genome-wide characteristics of mutations in autism. <i>Npj Genomic Medicine</i> , 2016 , 1, 160271-1602710	6.2	126
85	Comprehensive comparison of three commercial human whole-exome capture platforms. <i>Genome Biology</i> , 2011 , 12, R95	18.3	126
84	Association between variants of PRDM1 and NDP52 and Crohn's disease, based on exome sequencing and functional studies. <i>Gastroenterology</i> , 2013 , 145, 339-47	13.3	125
83	Rapid detection of structural variation in a human genome using nanochannel-based genome mapping technology. <i>GigaScience</i> , 2014 , 3, 34	7.6	113
82	Novel loci and pathways significantly associated with longevity. <i>Scientific Reports</i> , 2016 , 6, 21243	4.9	105
81	An Unexpectedly Complex Architecture for Skin Pigmentation in Africans. <i>Cell</i> , 2017 , 171, 1340-1353.e14	6.2	85
80	Inhibitory effect of essential oils on <i>Aspergillus ochraceus</i> growth and ochratoxin A production. <i>PLoS ONE</i> , 2014 , 9, e108285	3.7	82
79	Single-cell sequencing analysis characterizes common and cell-lineage-specific mutations in a muscle-invasive bladder cancer. <i>GigaScience</i> , 2012 , 1, 12	7.6	82
78	The Wilms tumor gene, <i>Wt1</i> , is critical for mouse spermatogenesis via regulation of sertoli cell polarity and is associated with non-obstructive azoospermia in humans. <i>PLoS Genetics</i> , 2013 , 9, e1003645	6	81
77	Lung cancer in never-smoker Asian females is driven by oncogenic mutations, most often involving EGFR. <i>Oncotarget</i> , 2015 , 6, 5465-74	3.3	78
76	Efficient and unique cobarcoding of second-generation sequencing reads from long DNA molecules enabling cost-effective and accurate sequencing, haplotyping, and de novo assembly. <i>Genome Research</i> , 2019 , 29, 798-808	9.7	74
75	IMonitor: A Robust Pipeline for TCR and BCR Repertoire Analysis. <i>Genetics</i> , 2015 , 201, 459-72	4	73
74	HIVID: an efficient method to detect HBV integration using low coverage sequencing. <i>Genomics</i> , 2013 , 102, 338-44	4.3	65
73	Clinical implications of systematic phenotyping and exome sequencing in patients with primary antibody deficiency. <i>Genetics in Medicine</i> , 2019 , 21, 243-251	8.1	64
72	De novo assembly of a haplotype-resolved human genome. <i>Nature Biotechnology</i> , 2015 , 33, 617-22	44.5	57
71	Inhibitory Effect of Cinnamaldehyde, Citral, and Eugenol on Aflatoxin Biosynthetic Gene Expression and Aflatoxin B1 Biosynthesis in <i>Aspergillus flavus</i> . <i>Journal of Food Science</i> , 2015 , 80, M2917-24	3.4	50
70	Comprehensive Characterization of Oncogenic Drivers in Asian Lung Adenocarcinoma. <i>Journal of Thoracic Oncology</i> , 2016 , 11, 2129-2140	8.9	50
69	The Different T-cell Receptor Repertoires in Breast Cancer Tumors, Draining Lymph Nodes, and Adjacent Tissues. <i>Cancer Immunology Research</i> , 2017 , 5, 148-156	12.5	49

68	A Cytocompatible Robust Hybrid Conducting Polymer Hydrogel for Use in a Magnesium Battery. <i>Advanced Materials</i> , 2016 , 28, 9349-9355	24	46
67	T cell receptor \mathbb{R} epertoires as novel diagnostic markers for systemic lupus erythematosus and rheumatoid arthritis. <i>Annals of the Rheumatic Diseases</i> , 2019 , 78, 1070-1078	2.4	41
66	Sex Differences in Genetic Associations With Longevity. <i>JAMA Network Open</i> , 2018 , 1, e181670	10.4	40
65	Decoding complex patterns of genomic rearrangement in hepatocellular carcinoma. <i>Genomics</i> , 2014 , 103, 189-203	4.3	39
64	History, applications, and challenges of immune repertoire research. <i>Cell Biology and Toxicology</i> , 2018 , 34, 441-457	7.4	36
63	An integrated tool to study MHC region: accurate SNV detection and HLA genes typing in human MHC region using targeted high-throughput sequencing. <i>PLoS ONE</i> , 2013 , 8, e69388	3.7	34
62	Aflatoxin B inhibition in <i>Aspergillus flavus</i> by <i>Aspergillus niger</i> through down-regulating expression of major biosynthetic genes and AFB degradation by atoxigenic <i>A. flavus</i> . <i>International Journal of Food Microbiology</i> , 2017 , 256, 1-10	5.8	29
61	Excess of rare variants in genes that are key epigenetic regulators of spermatogenesis in the patients with non-obstructive azoospermia. <i>Scientific Reports</i> , 2015 , 5, 8785	4.9	29
60	Systematic Comparative Evaluation of Methods for Investigating the TCR \mathbb{R} epertoire. <i>PLoS ONE</i> , 2016 , 11, e0152464	3.7	29
59	IMPre: An Accurate and Efficient Software for Prediction of T- and B-Cell Receptor Germline Genes and Alleles from Rearranged Repertoire Data. <i>Frontiers in Immunology</i> , 2016 , 7, 457	8.4	28
58	Comparative Analysis of Immune Repertoires between Bactrian Camel's Conventional and Heavy-Chain Antibodies. <i>PLoS ONE</i> , 2016 , 11, e0161801	3.7	27
57	Exome capture from saliva produces high quality genomic and metagenomic data. <i>BMC Genomics</i> , 2014 , 15, 262	4.5	26
56	Characterization of the B Cell Receptor Repertoire in the Intestinal Mucosa and of Tumor-Infiltrating Lymphocytes in Colorectal Adenoma and Carcinoma. <i>Journal of Immunology</i> , 2017 , 198, 3719-3728	5.3	25
55	Effect of Cinnamaldehyde on Morphological Alterations of and Expression of Key Genes Involved in Ochratoxin A Biosynthesis. <i>Toxins</i> , 2018 , 10,	4.9	25
54	Minimal Residual Disease Detection and Evolved Clones Analysis in Acute B Lymphoblastic Leukemia Using Deep Sequencing. <i>Frontiers in Immunology</i> , 2016 , 7, 403	8.4	24
53	Variation in fungal microbiome (mycobiome) and aflatoxins during simulated storage of in-shell peanuts and peanut kernels. <i>Scientific Reports</i> , 2016 , 6, 25930	4.9	23
52	Variation in fungal microbiome (mycobiome) and aflatoxin in stored in-shell peanuts at four different areas of China. <i>Frontiers in Microbiology</i> , 2015 , 6, 1055	5.7	22
51	Genetic aberrations in imatinib-resistant dermatofibrosarcoma protuberans revealed by whole genome sequencing. <i>PLoS ONE</i> , 2013 , 8, e69752	3.7	20

50	Alterations in the human gut microbiome associated with <i>Helicobacter pylori</i> infection. <i>FEBS Open Bio</i> , 2019 , 9, 1552-1560	2.7	18
49	Comprehensive TCR repertoire analysis of CD4 T-cell subsets in rheumatoid arthritis. <i>Journal of Autoimmunity</i> , 2020 , 109, 102432	15.5	17
48	A genome-wide association study for gut metagenome in Chinese adults illuminates complex diseases. <i>Cell Discovery</i> , 2021 , 7, 9	22.3	17
47	A Novel Excitation Assistance Switched Reluctance Wind Power Generator. <i>IEEE Transactions on Magnetics</i> , 2014 , 50, 1-4	2	15
46	The landscape and diagnostic potential of T and B cell repertoire in Immunoglobulin A Nephropathy. <i>Journal of Autoimmunity</i> , 2019 , 97, 100-107	15.5	15
45	Novel genetic loci associated HLA-B*08:01 positive myasthenia gravis. <i>Journal of Autoimmunity</i> , 2018 , 88, 43-49	15.5	14
44	The bZIP transcription factor Afap1 mediates the oxidative stress response and aflatoxin biosynthesis in <i>Aspergillus flavus</i> . <i>Revista Argentina De Microbiologia</i> , 2019 , 51, 292-301	1.8	13
43	A transomic cohort as a reference point for promoting a healthy human gut microbiome. <i>Medicine in Microecology</i> , 2021 , 8, 100039	4.3	13
42	Germline-Encoded TCR-MHC Contacts Promote TCR V Gene Bias in Umbilical Cord Blood T Cell Repertoire. <i>Frontiers in Immunology</i> , 2019 , 10, 2064	8.4	12
41	Single-cell transcriptomic landscape of nucleated cells in umbilical cord blood. <i>GigaScience</i> , 2019 , 8,	7.6	12
40	PIRD: Pan Immune Repertoire Database. <i>Bioinformatics</i> , 2020 , 36, 897-903	7.2	12
39	A population model for genotyping indels from next-generation sequence data. <i>Nucleic Acids Research</i> , 2013 , 41, e46	20.1	12
38	The correlation of copy number variations with longevity in a genome-wide association study of Han Chinese. <i>Aging</i> , 2018 , 10, 1206-1222	5.6	12
37	Diversity in immunogenomics: the value and the challenge. <i>Nature Methods</i> , 2021 , 18, 588-591	21.6	11
36	A regulatory mutant on TRIM26 conferring the risk of nasopharyngeal carcinoma by inducing low immune response. <i>Cancer Medicine</i> , 2018 , 7, 3848-3861	4.8	10
35	Detection and analysis of human papillomavirus (HPV) DNA in breast cancer patients by an effective method of HPV capture. <i>PLoS ONE</i> , 2014 , 9, e90343	3.7	10
34	Sevoflurane inhibits ferroptosis: A new mechanism to explain its protective role against lipopolysaccharide-induced acute lung injury. <i>Life Sciences</i> , 2021 , 275, 119391	6.8	9
33	Life History Recorded in the Vagino-cervical Microbiome Along with Multi-omics. <i>Genomics, Proteomics and Bioinformatics</i> , 2021 ,	6.5	8

32	Novel Y-chromosomal microdeletions associated with non-obstructive azoospermia uncovered by high throughput sequencing of sequence-tagged sites (STSs). <i>Scientific Reports</i> , 2016 , 6, 21831	4.9	8
31	Characterization of the human skin resistome and identification of two microbiota cutotypes. <i>Microbiome</i> , 2021 , 9, 47	16.6	8
30	Deep sequencing identifies regulated small RNAs in <i>Dugesia japonica</i> . <i>Molecular Biology Reports</i> , 2013 , 40, 4075-81	2.8	7
29	A comprehensive profiling of T- and B-lymphocyte receptor repertoires from a Chinese-origin rhesus macaque by high-throughput sequencing. <i>PLoS ONE</i> , 2017 , 12, e0182733	3.7	7
28	A multi-omic cohort as a reference point for promoting a healthy human gut microbiome		7
27	Integrated genetic analyses revealed novel human longevity loci and reduced risks of multiple diseases in a cohort study of 15,651 Chinese individuals. <i>Aging Cell</i> , 2021 , 20, e13323	9.9	7
26	T-cell receptor repertoire data provides new evidence for hygiene hypothesis of allergic diseases. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2020 , 75, 681-683	9.3	7
25	A Comprehensive Analysis of the T and B Lymphocytes Repertoire Shaped by HIV Vaccines. <i>Frontiers in Immunology</i> , 2018 , 9, 2194	8.4	7
24	Identification of Variable and Joining Germline Genes and Alleles for Rhesus Macaque from B Cell Receptor Repertoires. <i>Journal of Immunology</i> , 2019 , 202, 1612-1622	5.3	6
23	Distinct human Langerhans cell subsets orchestrate reciprocal functions and require different developmental regulation. <i>Immunity</i> , 2021 , 54, 2305-2320.e11	32.3	6
22	Compound Heterozygous Mutations of IL2-Inducible T cell Kinase in a Swedish Patient: the Importance of Early Genetic Diagnosis. <i>Journal of Clinical Immunology</i> , 2019 , 39, 131-134	5.7	5
21	Single-cell RNA-seq unveils critical regulators of human FOXP3+ regulatory T cell stability. <i>Science Bulletin</i> , 2020 , 65, 1114-1124	10.6	5
20	Case report of a Li-Fraumeni syndrome-like phenotype with a de novo mutation in CHEK2. <i>Medicine (United States)</i> , 2016 , 95, e4251	1.8	4
19	M-GWAS for the Gut Microbiome in Chinese Adults Illuminates on Complex Diseases. <i>SSRN Electronic Journal</i> ,	1	4
18	The vagino-cervical microbiome as a woman's life history		4
17	Archaeology Augments Tibet's Genetic History--Response. <i>Science</i> , 2010 , 329, 1467-1468	33.3	3
16	Species specific exome probes reveal new insights in positively selected genes in nonhuman primates. <i>Scientific Reports</i> , 2016 , 6, 33876	4.9	3
15	Myopia disease mouse models: a missense point mutation (S673G) and a protein-truncating mutation of the mimic human disease phenotype. <i>Cell and Bioscience</i> , 2019 , 9, 21	9.8	2

14	The effects of CYP1A1 gene polymorphism and p16 gene methylation on the risk of lung cancer in a Chinese population. <i>Chinese-German Journal of Clinical Oncology</i> , 2007 , 6, 350-356		2
13	Characteristics of serum metabolites in sporadic amyotrophic lateral sclerosis patients based on gas chromatography-mass spectrometry. <i>Scientific Reports</i> , 2021 , 11, 20786	4.9	2
12	Germline-encoded TCR-MHC contacts promote TCR V gene bias in umbilical cord blood T cell repertoire		2
11	New genetic variants associated with major adverse cardiovascular events in patients with acute coronary syndromes and treated with clopidogrel and aspirin. <i>Pharmacogenomics Journal</i> , 2021 , 21, 664-672	3.5	2
10	Selection of potential cytokeratin-18 monoclonal antibodies following IGH repertoire evaluation in mice. <i>Journal of Immunological Methods</i> , 2019 , 474, 112647	2.5	1
9	T Cell Repertoire Abnormality in Immunodeficiency Patients with DNA Repair and Methylation Defects. <i>Journal of Clinical Immunology</i> , 2021 , 1	5.7	1
8	M-GWAS for the gut microbiome in Chinese adults illuminates on complex diseases		1
7	Identification of Variable and Joining germline genes and alleles for Rhesus macaque from B-cell receptor repertoires		1
6	PIRD: Pan immune repertoire database		1
5	New genetic variants associated with major adverse cardiovascular events in patients with acute coronary syndromes and treated with clopidogrel and aspirin		1
4	Developing an Unbiased Multiplex PCR System to Enrich the Repertoire Toward Accurate Detection in Leukemia. <i>Frontiers in Immunology</i> , 2020 , 11, 1631	8.4	1
3	The complete mitochondrial genome of the white-tailed tropicbird, <i>Phaethon lepturus</i> . <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016 , 27, 4259-4260	1.3	1
2	Dissecting the Landscape of Activated CMV-Stimulated CD4+ T Cells in Humans by Linking Single-Cell RNA-Seq With T-Cell Receptor Sequencing.. <i>Frontiers in Immunology</i> , 2021 , 12, 779961	8.4	1
1	A Positively Selected MAGEE2 LoF Allele Is Associated with Sexual Dimorphism in Human Brain Size and Shows Similar Phenotypes in Magee2 Null Mice. <i>Molecular Biology and Evolution</i> , 2021 , 38, 5655-5663	8.3	0