Xiao Liu

List of Publications by Year in descending order

99 papers	35,277 citations	57631 44 h-index	34900 98 g-index
120 all docs	120 docs citations	120 times ranked	63945 citing authors

#	Article	IF	Citations
1	A global reference for human genetic variation. Nature, 2015, 526, 68-74.	13.7	13,998
2	An integrated map of genetic variation from 1,092 human genomes. Nature, 2012, 491, 56-65.	13.7	7,199
3	The oyster genome reveals stress adaptation and complexity of shell formation. Nature, 2012, 490, 49-54.	13.7	1,966
4	Molecular analysis of gastric cancer identifies subtypes associated with distinct clinical outcomes. Nature Medicine, 2015, 21, 449-456.	15.2	1,592
5	Sequencing of 50 Human Exomes Reveals Adaptation to High Altitude. Science, 2010, 329, 75-78.	6.0	1,339
6	The sequence and de novo assembly of the giant panda genome. Nature, 2010, 463, 311-317.	13.7	1,058
7	Genome-wide survey of recurrent HBV integration in hepatocellular carcinoma. Nature Genetics, 2012, 44, 765-769.	9.4	785
8	An Abundance of Rare Functional Variants in 202 Drug Target Genes Sequenced in 14,002 People. Science, 2012, 337, 100-104.	6.0	626
9	Single-Cell Exome Sequencing Reveals Single-Nucleotide Mutation Characteristics of a Kidney Tumor. Cell, 2012, 148, 886-895.	13.5	622
10	Whole-genome sequencing identifies recurrent mutations in hepatocellular carcinoma. Genome Research, 2013, 23, 1422-1433.	2.4	457
11	Genome-wide profiling of HPV integration in cervical cancer identifies clustered genomic hot spots and a potential microhomology-mediated integration mechanism. Nature Genetics, 2015, 47, 158-163.	9.4	393
12	Resequencing of 200 human exomes identifies an excess of low-frequency non-synonymous coding variants. Nature Genetics, 2010, 42, 969-972.	9.4	297
13	Frequent mutations of genes encoding ubiquitin-mediated proteolysis pathway components in clear cell renal cell carcinoma. Nature Genetics, 2012, 44, 17-19.	9.4	295
14	Genomic and oncogenic preference of HBV integration in hepatocellular carcinoma. Nature Communications, 2016, 7, 12992.	5.8	228
15	Genome-wide characteristics of de novo mutations in autism. Npj Genomic Medicine, 2016, 1, 160271-1602710.	1.7	200
16	Deep sequencing of the MHC region in the Chinese population contributes to studies of complex disease. Nature Genetics, 2016, 48, 740-746.	9.4	188
17	Efficient and unique cobarcoding of second-generation sequencing reads from long DNA molecules enabling cost-effective and accurate sequencing, haplotyping, and de novo assembly. Genome Research, 2019, 29, 798-808.	2.4	176
18	Genomic landscape and genetic heterogeneity in gastric adenocarcinoma revealed by whole-genome sequencing. Nature Communications, 2014, 5, 5477.	5.8	166

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19	BIPES, a cost-effective high-throughput method for assessing microbial diversity. ISME Journal, 2011, 5, 741-749.	4.4	160
20	Rapid detection of structural variation in a human genome using nanochannel-based genome mapping technology. GigaScience, 2014, 3, 34.	3.3	153
21	Association Between Variants of PRDM1 and NDP52 and Crohn's Disease, Based on Exome Sequencing and Functional Studies. Gastroenterology, 2013, 145, 339-347.	0.6	149
22	Comprehensive comparison of three commercial human whole-exome capture platforms. Genome Biology, 2011, 12, R95.	13.9	145
23	Novel loci and pathways significantly associated with longevity. Scientific Reports, 2016, 6, 21243.	1.6	145
24	An Unexpectedly Complex Architecture for Skin Pigmentation in Africans. Cell, 2017, 171, 1340-1353.e14.	13.5	134
25	IMonitor: A Robust Pipeline for TCR and BCR Repertoire Analysis. Genetics, 2015, 201, 459-472.	1.2	119
26	Lung cancer in never-smoker Asian females is driven by oncogenic mutations, most often involving EGFR. Oncotarget, 2015, 6, 5465-5474.	0.8	116
27	Inhibitory Effect of Essential Oils on Aspergillus ochraceus Growth and Ochratoxin A Production. PLoS ONE, 2014, 9, e108285.	1.1	110
28	The Wilms Tumor Gene, Wt1, Is Critical for Mouse Spermatogenesis via Regulation of Sertoli Cell Polarity and Is Associated with Non-Obstructive Azoospermia in Humans. PLoS Genetics, 2013, 9, e1003645.	1.5	109
29	Single-cell sequencing analysis characterizes common and cell-lineage-specific mutations in a muscle-invasive bladder cancer. GigaScience, 2012, 1, 12.	3.3	99
30	T cell receptor Î² repertoires as novel diagnostic markers for systemic lupus erythematosus and rheumatoid arthritis. Annals of the Rheumatic Diseases, 2019, 78, 1070-1078.	0.5	99
31	HIVID: An efficient method to detect HBV integration using low coverage sequencing. Genomics, 2013, 102, 338-344.	1.3	94
32	The Different T-cell Receptor Repertoires in Breast Cancer Tumors, Draining Lymph Nodes, and Adjacent Tissues. Cancer Immunology Research, 2017, 5, 148-156.	1.6	87
33	Clinical implications of systematic phenotyping and exome sequencing in patients with primary antibody deficiency. Genetics in Medicine, 2019, 21, 243-251.	1.1	86
34	History, applications, and challenges of immune repertoire research. Cell Biology and Toxicology, 2018, 34, 441-457.	2.4	81
35	Inhibitory Effect of Cinnamaldehyde, Citral, and Eugenol on Aflatoxin Biosynthetic Gene Expression and Aflatoxin B₁ Biosynthesis in Aspergillus flavus. Journal of Food Science, 2015, 80, M2917-24.	1.5	79
36	PIRD: Pan Immune Repertoire Database. Bioinformatics, 2020, 36, 897-903.	1.8	79

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37	De novo assembly of a haplotype-resolved human genome. Nature Biotechnology, 2015, 33, 617-622.	9.4	73
38	Comprehensive Characterization of Oncogenic Drivers in Asian Lung Adenocarcinoma. Journal of Thoracic Oncology, 2016, 11, 2129-2140.	0.5	70
39	A Cytocompatible Robust Hybrid Conducting Polymer Hydrogel for Use in a Magnesium Battery. Advanced Materials, 2016, 28, 9349-9355.	11.1	67
40	An Integrated Tool to Study MHC Region: Accurate SNV Detection and HLA Genes Typing in Human MHC Region Using Targeted High-Throughput Sequencing. PLoS ONE, 2013, 8, e69388.	1.1	63
41	Sex Differences in Genetic Associations With Longevity. JAMA Network Open, 2018, 1, e181670.	2.8	60
42	Systematic Comparative Evaluation of Methods for Investigating the TCRÎ² Repertoire. PLoS ONE, 2016, 11, e0152464.	1.1	58
43	Aflatoxin B 1 inhibition in Aspergillus flavus by Aspergillus niger through down-regulating expression of major biosynthetic genes and AFB 1 degradation by atoxigenic A . flavus. International Journal of Food Microbiology, 2017, 256, 1-10.	2.1	54
44	Decoding complex patterns of genomic rearrangement in hepatocellular carcinoma. Genomics, 2014, 103, 189-203.	1.3	49
45	Comparative Analysis of Immune Repertoires between Bactrian Camel's Conventional and Heavy-Chain Antibodies. PLoS ONE, 2016, 11, e0161801.	1.1	49
46	A genome-wide association study for gut metagenome in Chinese adults illuminates complex diseases. Cell Discovery, 2021, 7, 9.	3.1	49
47	IMPre: An Accurate and Efficient Software for Prediction of T- and B-Cell Receptor Germline Genes and Alleles from Rearranged Repertoire Data. Frontiers in Immunology, 2016, 7, 457.	2.2	47
48	Characterization of the human skin resistome and identification of two microbiota cutotypes. Microbiome, 2021, 9, 47.	4.9	42
49	Diversity in immunogenomics: the value and the challenge. Nature Methods, 2021, 18, 588-591.	9.0	40
50	Excess of Rare Variants in Genes that are Key Epigenetic Regulators of Spermatogenesis in the Patients with Non-Obstructive Azoospermia. Scientific Reports, 2015, 5, 8785.	1.6	39
51	Characterization of the B Cell Receptor Repertoire in the Intestinal Mucosa and of Tumor-Infiltrating Lymphocytes in Colorectal Adenoma and Carcinoma. Journal of Immunology, 2017, 198, 3719-3728.	0.4	39
52	Effect of Cinnamaldehyde on Morphological Alterations of Aspergillus ochraceus and Expression of Key Genes Involved in Ochratoxin A Biosynthesis. Toxins, 2018, 10, 340.	1.5	38
53	Distinct human Langerhans cell subsets orchestrate reciprocal functions and require different developmental regulation. Immunity, 2021, 54, 2305-2320.e11.	6.6	38
54	Variation in fungal microbiome (mycobiome) and aflatoxin in stored in-shell peanuts at four different areas of China. Frontiers in Microbiology, 2015, 6, 1055.	1.5	37

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55	Minimal Residual Disease Detection and Evolved IGH Clones Analysis in Acute B Lymphoblastic Leukemia Using IGH Deep Sequencing. Frontiers in Immunology, 2016, 7, 403.	2.2	37
56	Exome capture from saliva produces high quality genomic and metagenomic data. BMC Genomics, 2014, 15, 262.	1.2	34
57	Variation in fungal microbiome (mycobiome) and aflatoxins during simulated storage of in-shell peanuts and peanut kernels. Scientific Reports, 2016, 6, 25930.	1.6	33
58	Sevoflurane inhibits ferroptosis: A new mechanism to explain its protective role against lipopolysaccharide-induced acute lung injury. Life Sciences, 2021, 275, 119391.	2.0	31
59	Alterations in the human gut microbiome associated with HelicobacterÂpylori infection. FEBS Open Bio, 2019, 9, 1552-1560.	1.0	30
60	Comprehensive TCR repertoire analysis of CD4+ T-cell subsets in rheumatoid arthritis. Journal of Autoimmunity, 2020, 109, 102432.	3.0	29
61	Integrated genetic analyses revealed novel human longevity loci and reduced risks of multiple diseases in a cohort study of 15,651 Chinese individuals. Aging Cell, 2021, 20, e13323.	3.0	27
62	Genetic Aberrations in Imatinib-Resistant Dermatofibrosarcoma Protuberans Revealed by Whole Genome Sequencing. PLoS ONE, 2013, 8, e69752.	1.1	25
63	The landscape and diagnostic potential of T and B cell repertoire in Immunoglobulin A Nephropathy. Journal of Autoimmunity, 2019, 97, 100-107.	3.0	25
64	The correlation of copy number variations with longevity in a genome-wide association study of Han Chinese. Aging, 2018, 10, 1206-1222.	1.4	25
65	Single-cell transcriptomic landscape of nucleated cells in umbilical cord blood. GigaScience, 2019, 8, .	3.3	24
66	A transomic cohort as a reference point for promoting a healthy human gut microbiome. Medicine in Microecology, 2021, 8, 100039.	0.7	24
67	A Comprehensive Analysis of the T and B Lymphocytes Repertoire Shaped by HIV Vaccines. Frontiers in Immunology, 2018, 9, 2194.	2.2	23
68	A Novel Excitation Assistance Switched Reluctance Wind Power Generator. IEEE Transactions on Magnetics, 2014, 50, 1-4.	1.2	21
69	Novel genetic loci associated HLA-B*08:01 positive myasthenia gravis. Journal of Autoimmunity, 2018, 88, 43-49.	3.0	20
70	The bZIP transcription factor Afap1 mediates the oxidative stress response and aflatoxin biosynthesis in Aspergillus flavus. Revista Argentina De Microbiologia, 2019, 51, 292-301.	0.4	20
71	Life History Recorded in the Vagino-cervical Microbiome Along with Multi-omes. Genomics, Proteomics and Bioinformatics, 2022, 20, 304-321.	3.0	18
72	A comprehensive profiling of T- and B-lymphocyte receptor repertoires from a Chinese-origin rhesus macaque by high-throughput sequencing. PLoS ONE, 2017, 12, e0182733.	1.1	18

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73	Detection and Analysis of Human Papillomavirus (HPV) DNA in Breast Cancer Patients by an Effective Method of HPV Capture. PLoS ONE, 2014, 9, e90343.	1.1	15
74	Germline-Encoded TCR-MHC Contacts Promote TCR V Gene Bias in Umbilical Cord Blood T Cell Repertoire. Frontiers in Immunology, 2019, 10, 2064.	2.2	15
75	A regulatory mutant on <scp>TRIM</scp>26 conferring the risk of nasopharyngeal carcinoma by inducing low immune response. Cancer Medicine, 2018, 7, 3848-3861.	1.3	14
76	A population model for genotyping indels from next-generation sequence data. Nucleic Acids Research, 2013, 41, e46-e46.	6.5	12
77	Dissecting the Landscape of Activated CMV-Stimulated CD4+ T Cells in Humans by Linking Single-Cell RNA-Seq With T-Cell Receptor Sequencing. Frontiers in Immunology, 2021, 12, 779961.	2.2	12
78	Novel Y-chromosomal microdeletions associated with non-obstructive azoospermia uncovered by high throughput sequencing of sequence-tagged sites (STSs). Scientific Reports, 2016, 6, 21831.	1.6	11
79	Single-cell RNA-seq unveils critical regulators of human FOXP3+Âregulatory T cell stability. Science Bulletin, 2020, 65, 1114-1124.	4.3	10
80	Characteristics of serum metabolites in sporadic amyotrophic lateral sclerosis patients based on gas chromatography-mass spectrometry. Scientific Reports, 2021, 11, 20786.	1.6	10
81	Heterogeneous origin of IgE in atopic dermatitis and psoriasis revealed by B cell receptor repertoire analysis. Allergy: European Journal of Allergy and Clinical Immunology, 2022, 77, 559-568.	2.7	10
82	T Cell Repertoire Abnormality in Immunodeficiency Patients with DNA Repair and Methylation Defects. Journal of Clinical Immunology, 2022, 42, 375-393.	2.0	10
83	Identification of Variable and Joining Germline Genes and Alleles for Rhesus Macaque from B Cell Receptor Repertoires. Journal of Immunology, 2019, 202, 1612-1622.	0.4	9
84	Compound Heterozygous Mutations of IL2-Inducible T cell Kinase in a Swedish Patient: the Importance of Early Genetic Diagnosis. Journal of Clinical Immunology, 2019, 39, 131-134.	2.0	9
85	Tâ€cell receptor repertoire data provides new evidence for hygiene hypothesis of allergic diseases. Allergy: European Journal of Allergy and Clinical Immunology, 2020, 75, 681-683.	2.7	9
86	Case report of a Liâ€“Fraumeni syndrome-like phenotype with a de novo mutation in CHEK2. Medicine (United States), 2016, 95, e4251.	0.4	8
87	Deep sequencing identifies regulated small RNAs in Dugesia japonica. Molecular Biology Reports, 2013, 40, 4075-4081.	1.0	7
88	Myopia disease mouse models: a missense point mutation (S673G) and a protein-truncating mutation of the Zfp644 mimic human disease phenotype. Cell and Bioscience, 2019, 9, 21.	2.1	5
89	New genetic variants associated with major adverse cardiovascular events in patients with acute coronary syndromes and treated with clopidogrel and aspirin. Pharmacogenomics Journal, 2021, 21, 664-672.	0.9	5
90	Developing an Unbiased Multiplex PCR System to Enrich the TRB Repertoire Toward Accurate Detection in Leukemia. Frontiers in Immunology, 2020, 11, 1631.	2.2	4

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91	M-GWAS for the Gut Microbiome in Chinese Adults Illuminates on Complex Diseases. SSRN Electronic Journal, 0, , .	0.4	4
92	Archaeology Augments Tibet's Genetic Historyâ€"Response. Science, 2010, 329, 1467-1468.	6.0	3
93	Species specific exome probes reveal new insights in positively selected genes in nonhuman primates. Scientific Reports, 2016, 6, 33876.	1.6	3
94	The effects of CYP1A1 gene polymorphism and p16 gene methylation on the risk of lung cancer in a Chinese population. Chinese-German Journal of Clinical Oncology, 2007, 6, 350-356.	0.1	2
95	Selection of potential cytokeratin-18 monoclonal antibodies following IGH repertoire evaluation in mice. Journal of Immunological Methods, 2019, 474, 112647.	0.6	2
96	The complete mitochondrial genome of the white-tailed tropicbird, Phaethon lepturus. Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2016, 27, 4259-4260.	0.7	1
97	A Positively Selected MAGEE2 LoF Allele Is Associated with Sexual Dimorphism in Human Brain Size and Shows Similar Phenotypes in Magee2 Null Mice. Molecular Biology and Evolution, 2021, 38, 5655-5663.	3.5	1
98	Abstract LB-229: Whole genome sequencing reveals genetic landscape of hepatocellular carcinoma.. , 2013, , .		0
99	Abstract LB-231: Decoding complex patterns of structural variations in hepatocellular carcinoma.. , 2013, , .		0