# Xiao Liu

## List of Publications by Year in descending order



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|---|---|---|---|
| 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 | Life History Recorded in the Vagino-cervical Microbiome Along with Multi-omes. Genomics, Proteomics and Bioinformatics, 2022, 20, 304-321. | 3.0 | 18 |
| 2 | 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 |
| 3 | T Cell Repertoire Abnormality in Immunodeficiency Patients with DNA Repair and Methylation Defects. Journal of Clinical Immunology, 2022, 42, 375-393. | 2.0 | 10 |
| 4 | A genome-wide association study for gut metagenome in Chinese adults illuminates complex diseases. Cell Discovery, 2021, 7, 9. | 3.1 | 49 |
| 5 | Characterization of the human skin resistome and identification of two microbiota cutotypes. Microbiome, 2021, 9, 47. | 4.9 | 42 |
| 6 | 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 |
| 7 | Diversity in immunogenomics: the value and the challenge. Nature Methods, 2021, 18, 588-591. | 9.0 | 40 |
| 8 | 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 |
| 9 | A transomic cohort as a reference point for promoting a healthy human gut microbiome. Medicine in Microecology, 2021, 8, 100039. | 0.7 | 24 |
| 10 | 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 |
| 11 | 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 |
| 12 | Distinct human Langerhans cell subsets orchestrate reciprocal functions and require different developmental regulation. Immunity, 2021, 54, 2305-2320.e11. | 6.6 | 38 |
| 13 | Characteristics of serum metabolites in sporadic amyotrophic lateral sclerosis patients based on gas chromatography-mass spectrometry. Scientific Reports, 2021, 11, 20786. | 1.6 | 10 |
| 14 | 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 |
| 15 | PIRD: Pan Immune Repertoire Database. Bioinformatics, 2020, 36, 897-903. | 1.8 | 79 |
| 16 | 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 |
| 17 | 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 |
| 18 | Comprehensive TCR repertoire analysis of CD4+ T-cell subsets in rheumatoid arthritis. Journal of Autoimmunity, 2020, 109, 102432. | 3.0 | 29 |

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|---|---|---|---|
| 19 | Single-cell RNA-seq unveils critical regulators of human FOXP3+Âregulatory T cell stability. Science Bulletin, 2020, 65, 1114-1124. | 4.3 | 10 |
| 20 | Clinical implications of systematic phenotyping and exome sequencing in patients with primary antibody deficiency. Genetics in Medicine, 2019, 21, 243-251. | 1.1 | 86 |
| 21 | Alterations in the human gut microbiome associated with HelicobacterÂpylori infection. FEBS Open Bio, 2019, 9, 1552-1560. | 1.0 | 30 |
| 22 | Selection of potential cytokeratin-18 monoclonal antibodies following IGH repertoire evaluation in mice. Journal of Immunological Methods, 2019, 474, 112647. | 0.6 | 2 |
| 23 | 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 |
| 24 | 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 |
| 25 | 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 |
| 26 | Single-cell transcriptomic landscape of nucleated cells in umbilical cord blood. GigaScience, 2019, 8, . | 3.3 | 24 |
| 27 | 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 |
| 28 | 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 |
| 29 | 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 |
| 30 | 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 |
| 31 | 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 |
| 32 | History, applications, and challenges of immune repertoire research. Cell Biology and Toxicology, 2018, 34, 441-457. | 2.4 | 81 |
| 33 | Novel genetic loci associated HLA-B*08:01 positive myasthenia gravis. Journal of Autoimmunity, 2018, 88, 43-49. | 3.0 | 20 |
| 34 | A Comprehensive Analysis of the T and B Lymphocytes Repertoire Shaped by HIV Vaccines. Frontiers in Immunology, 2018, 9, 2194. | 2.2 | 23 |
| 35 | Sex Differences in Genetic Associations With Longevity. JAMA Network Open, 2018, 1, e181670. | 2.8 | 60 |
| 36 | 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 |

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|---|---|---|---|
| 37 | 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 |
| 38 | 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 |
| 39 | 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 |
| 40 | 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 |
| 41 | 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 |
| 42 | An Unexpectedly Complex Architecture for Skin Pigmentation in Africans. Cell, 2017, 171, 1340-1353.e14. | 13.5 | 134 |
| 43 | 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 |
| 44 | 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 |
| 45 | 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 |
| 46 | Systematic Comparative Evaluation of Methods for Investigating the TCRÎ² Repertoire. PLoS ONE, 2016, 11, e0152464. | 1.1 | 58 |
| 47 | Comparative Analysis of Immune Repertoires between Bactrian Camel's Conventional and Heavy-Chain Antibodies. PLoS ONE, 2016, 11, e0161801. | 1.1 | 49 |
| 48 | Species specific exome probes reveal new insights in positively selected genes in nonhuman primates. Scientific Reports, 2016, 6, 33876. | 1.6 | 3 |
| 49 | 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 |
| 50 | Novel loci and pathways significantly associated with longevity. Scientific Reports, 2016, 6, 21243. | 1.6 | 145 |
| 51 | 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 |
| 52 | 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 |
| 53 | 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 |
| 54 | Comprehensive Characterization of Oncogenic Drivers in Asian Lung Adenocarcinoma. Journal of Thoracic Oncology, 2016, 11, 2129-2140. | 0.5 | 70 |

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|---|---|---|---|
| 55 | A Cytocompatible Robust Hybrid Conducting Polymer Hydrogel for Use in a Magnesium Battery. Advanced Materials, 2016, 28, 9349-9355. | 11.1 | 67 |
| 56 | Genome-wide characteristics of de novo mutations in autism. Npj Genomic Medicine, 2016, 1, 160271-1602710. | 1.7 | 200 |
| 57 | Genomic and oncogenic preference of HBV integration in hepatocellular carcinoma. Nature Communications, 2016, 7, 12992. | 5.8 | 228 |
| 58 | 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 |
| 59 | Inhibitory Effect of Cinnamaldehyde, Citral, and Eugenol on Aflatoxin Biosynthetic Gene Expression and Aflatoxin B<sub>1</sub> Biosynthesis in Aspergillus flavus. Journal of Food Science, 2015, 80, M2917-24. | 1.5 | 79 |
| 60 | 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 |
| 61 | Lung cancer in never-smoker Asian females is driven by oncogenic mutations, most often involving EGFR. Oncotarget, 2015, 6, 5465-5474. | 0.8 | 116 |
| 62 | De novo assembly of a haplotype-resolved human genome. Nature Biotechnology, 2015, 33, 617-622. | 9.4 | 73 |
| 63 | 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 |
| 64 | 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 |
| 65 | Molecular analysis of gastric cancer identifies subtypes associated with distinct clinical outcomes. Nature Medicine, 2015, 21, 449-456. | 15.2 | 1,592 |
| 66 | A global reference for human genetic variation. Nature, 2015, 526, 68-74. | 13.7 | 13,998 |
| 67 | IMonitor: A Robust Pipeline for TCR and BCR Repertoire Analysis. Genetics, 2015, 201, 459-472. | 1.2 | 119 |
| 68 | 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 |
| 69 | Inhibitory Effect of Essential Oils on Aspergillus ochraceus Growth and Ochratoxin A Production. PLoS ONE, 2014, 9, e108285. | 1.1 | 110 |
| 70 | A Novel Excitation Assistance Switched Reluctance Wind Power Generator. IEEE Transactions on Magnetics, 2014, 50, 1-4. | 1.2 | 21 |
| 71 | Genomic landscape and genetic heterogeneity in gastric adenocarcinoma revealed by whole-genome sequencing. Nature Communications, 2014, 5, 5477. | 5.8 | 166 |
| 72 | Exome capture from saliva produces high quality genomic and metagenomic data. BMC Genomics, 2014, 15, 262. | 1.2 | 34 |

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|---|---|---|---|
| 73 | Decoding complex patterns of genomic rearrangement in hepatocellular carcinoma. Genomics, 2014, 103, 189-203. | 1.3 | 49 |
| 74 | Rapid detection of structural variation in a human genome using nanochannel-based genome mapping technology. GigaScience, 2014, 3, 34. | 3.3 | 153 |
| 75 | 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 |
| 76 | Deep sequencing identifies regulated small RNAs in Dugesia japonica. Molecular Biology Reports, 2013, 40, 4075-4081. | 1.0 | 7 |
| 77 | HIVID: An efficient method to detect HBV integration using low coverage sequencing. Genomics, 2013, 102, 338-344. | 1.3 | 94 |
| 78 | 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 |
| 79 | A population model for genotyping indels from next-generation sequence data. Nucleic Acids Research, 2013, 41, e46-e46. | 6.5 | 12 |
| 80 | Whole-genome sequencing identifies recurrent mutations in hepatocellular carcinoma. Genome Research, 2013, 23, 1422-1433. | 2.4 | 457 |
| 81 | 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 |
| 82 | Genetic Aberrations in Imatinib-Resistant Dermatofibrosarcoma Protuberans Revealed by Whole Genome Sequencing. PLoS ONE, 2013, 8, e69752. | 1.1 | 25 |
| 83 | Abstract LB-229: Whole genome sequencing reveals genetic landscape of hepatocellular carcinoma.. , 2013, , . | | 0 |
| 84 | Abstract LB-231: Decoding complex patterns of structural variations in hepatocellular carcinoma.. , 2013, , . | | 0 |
| 85 | Genome-wide survey of recurrent HBV integration in hepatocellular carcinoma. Nature Genetics, 2012, 44, 765-769. | 9.4 | 785 |
| 86 | Single-Cell Exome Sequencing Reveals Single-Nucleotide Mutation Characteristics of a Kidney Tumor. Cell, 2012, 148, 886-895. | 13.5 | 622 |
| 87 | Single-cell sequencing analysis characterizes common and cell-lineage-specific mutations in a muscle-invasive bladder cancer. GigaScience, 2012, 1, 12. | 3.3 | 99 |
| 88 | An integrated map of genetic variation from 1,092 human genomes. Nature, 2012, 491, 56-65. | 13.7 | 7,199 |
| 89 | The oyster genome reveals stress adaptation and complexity of shell formation. Nature, 2012, 490, 49-54. | 13.7 | 1,966 |
| 90 | 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 |

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|---|---|---|---|
| 91 | An Abundance of Rare Functional Variants in 202 Drug Target Genes Sequenced in 14,002 People. Science, 2012, 337, 100-104. | 6.0 | 626 |
| 92 | Comprehensive comparison of three commercial human whole-exome capture platforms. Genome Biology, 2011, 12, R95. | 13.9 | 145 |
| 93 | BIPES, a cost-effective high-throughput method for assessing microbial diversity. ISME Journal, 2011, 5, 741-749. | 4.4 | 160 |
| 94 | Sequencing of 50 Human Exomes Reveals Adaptation to High Altitude. Science, 2010, 329, 75-78. | 6.0 | 1,339 |
| 95 | The sequence and de novo assembly of the giant panda genome. Nature, 2010, 463, 311-317. | 13.7 | 1,058 |
| 96 | Resequencing of 200 human exomes identifies an excess of low-frequency non-synonymous coding variants. Nature Genetics, 2010, 42, 969-972. | 9.4 | 297 |
| 97 | Archaeology Augments Tibet's Genetic Historyâ€"Response. Science, 2010, 329, 1467-1468. | 6.0 | 3 |
| 98 | 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 |
| 99 | M-GWAS for the Gut Microbiome in Chinese Adults Illuminates on Complex Diseases. SSRN Electronic Journal, 0, , . | 0.4 | 4 |