

Yong Hou

List of Publications by Year in descending order

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Version: 2024-02-01

81
papers

6,732
citations

116194

36
h-index

81351

76
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98
all docs

98
docs citations

98
times ranked

12716
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	Over 50,000 Metagenomically Assembled Draft Genomes for the Human Oral Microbiome Reveal New Taxa. Genomics, Proteomics and Bioinformatics, 2022, 20, 246-259.	3.0	38
3	Mendelian randomization analyses support causal relationships between blood metabolites and the gut microbiome. Nature Genetics, 2022, 54, 52-61.	9.4	134
4	Transcriptomic Profile of the Mouse Postnatal Liver Development by Single-Nucleus RNA Sequencing. Frontiers in Cell and Developmental Biology, 2022, 10, 833392.	1.8	1
5	Single-cell transcriptional diversity of neonatal umbilical cord blood immune cells reveals neonatal immune tolerance. Biochemical and Biophysical Research Communications, 2022, 608, 14-22.	1.0	5
6	Distinct Functional Metagenomic Markers Predict the Responsiveness to Anti-PD-1 Therapy in Chinese Non-Small Cell Lung Cancer Patients. Frontiers in Oncology, 2022, 12, 837525.	1.3	6
7	Cell transcriptomic atlas of the non-human primate <i>Macaca fascicularis</i> . Nature, 2022, 604, 723-731.	13.7	81
8	HBV genome-enriched single cell sequencing revealed heterogeneity in HBV-driven hepatocellular carcinoma (HCC). BMC Medical Genomics, 2022, 15, .	0.7	6
9	Single-cell landscape of the ecosystem in early-relapse hepatocellular carcinoma. Cell, 2021, 184, 404-421.e16.	13.5	399
10	Multiregion single-cell sequencing reveals the transcriptional landscape of the immune microenvironment of colorectal cancer. Clinical and Translational Medicine, 2021, 11, e253.	1.7	48
11	Genome diversity in Ukraine. GigaScience, 2021, 10, .	3.3	9
12	Sex- and age-related trajectories of the adult human gut microbiota shared across populations of different ethnicities. Nature Aging, 2021, 1, 87-100.	5.3	86
13	A genome-wide association study for gut metagenome in Chinese adults illuminates complex diseases. Cell Discovery, 2021, 7, 9.	3.1	49
14	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
15	Single-Nucleus Chromatin Accessibility Landscape Reveals Diversity in Regulatory Regions Across Distinct Adult Rat Cortex. Frontiers in Molecular Neuroscience, 2021, 14, 651355.	1.4	8
16	A transomic cohort as a reference point for promoting a healthy human gut microbiome. Medicine in Microecology, 2021, 8, 100039.	0.7	24
17	scDPN for High-throughput Single-cell CNV Detection to Uncover Clonal Evolution During HCC Recurrence. Genomics, Proteomics and Bioinformatics, 2021, 19, 346-357.	3.0	3
18	Tumor heterogeneity assessed by sequencing and fluorescence <i>in situ</i> hybridization (FISH) data. Bioinformatics, 2021, 37, 4704-4711.	1.8	5

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19	Dissecting spatial heterogeneity and the immune-evasion mechanism of CTCs by single-cell RNA-seq in hepatocellular carcinoma. <i>Nature Communications</i> , 2021, 12, 4091.	5.8	90
20	Dairy consumption and physical fitness tests associated with fecal microbiome in a Chinese cohort. <i>Medicine in Microecology</i> , 2021, 9, 100038.	0.7	6
21	Disease trends in a young Chinese cohort according to fecal metagenome and plasma metabolites. <i>Medicine in Microecology</i> , 2021, , 100037.	0.7	2
22	Genome-wide mutational signatures revealed distinct developmental paths for human B cell lymphomas. <i>Journal of Experimental Medicine</i> , 2021, 218, .	4.2	29
23	Network of Interactions Between Gut Microbiome, Host Biomarkers, and Urine Metabolome in Carotid Atherosclerosis. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 708088.	1.8	5
24	Metagenome-genome-wide association studies reveal human genetic impact on the oral microbiome. <i>Cell Discovery</i> , 2021, 7, 117.	3.1	31
25	Embryonic liver developmental trajectory revealed by single-cell RNA sequencing in the Foxa2eGFP mouse. <i>Communications Biology</i> , 2020, 3, 642.	2.0	24
26	Tumor Copy Number Deconvolution Integrating Bulk and Single-Cell Sequencing Data. <i>Journal of Computational Biology</i> , 2020, 27, 565-598.	0.8	10
27	Chromatin accessibility and transcriptome landscapes of <i>Monomorium pharaonis</i> brain. <i>Scientific Data</i> , 2020, 7, 217.	2.4	10
28	Single-cell RNA-seq unveils critical regulators of human FOXP3+ regulatory T cell stability. <i>Science Bulletin</i> , 2020, 65, 1114-1124.	4.3	10
29	Selective targeting of the oncogenic <i>KRAS</i> G12S mutant allele by CRISPR/Cas9 induces efficient tumor regression. <i>Theranostics</i> , 2020, 10, 5137-5153.	4.6	33
30	Tumor Copy Number Deconvolution Integrating Bulk and Single-Cell Sequencing Data. <i>Lecture Notes in Computer Science</i> , 2019, , 174-189.	1.0	3
31	Distinct gut metagenomics and metaproteomics signatures in prediabetics and treatment-naïve type 2 diabetics. <i>EBioMedicine</i> , 2019, 47, 373-383.	2.7	101
32	Deconvolution of single-cell multi-omics layers reveals regulatory heterogeneity. <i>Nature Communications</i> , 2019, 10, 470.	5.8	156
33	Viral integration drives multifocal HCC during the occult HBV infection. <i>Journal of Experimental and Clinical Cancer Research</i> , 2019, 38, 261.	3.5	27
34	Genomic Evidence of Recombination in the Basidiomycete <i>Wallemia mellicola</i> . <i>Genes</i> , 2019, 10, 427.	1.0	14
35	Therapeutic potential of CRISPR/Cas9 gene editing in engineered T cell therapy. <i>Cancer Medicine</i> , 2019, 8, 4254-4264.	1.3	57
36	Single-cell transcriptomic landscape of nucleated cells in umbilical cord blood. <i>GigaScience</i> , 2019, 8, .	3.3	24

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37	Comparative analysis of sequencing technologies for single-cell transcriptomics. <i>Genome Biology</i> , 2019, 20, 70.	3.8	82
38	Population Genomics of an Obligately Halophilic Basidiomycete <i>Wallemia ichthyophaga</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 2019.	1.5	9
39	Characterization of circulating tumor cells in breast cancer patients by spiral microfluidics. <i>Cell Biology and Toxicology</i> , 2019, 35, 59-66.	2.4	25
40	1,520 reference genomes from cultivated human gut bacteria enable functional microbiome analyses. <i>Nature Biotechnology</i> , 2019, 37, 179-185.	9.4	402
41	Genetic landscape of hepatitis B virus-associated diffuse large B-cell lymphoma. <i>Blood</i> , 2018, 131, 2670-2681.	0.6	77
42	Whole-genome and Transcriptome Sequencing of Prostate Cancer Identify New Genetic Alterations Driving Disease Progression. <i>European Urology</i> , 2018, 73, 322-339.	0.9	130
43	Progress and challenges of sequencing and analyzing circulating tumor cells. <i>Cell Biology and Toxicology</i> , 2018, 34, 405-415.	2.4	65
44	Sex Differences in Genetic Associations With Longevity. <i>JAMA Network Open</i> , 2018, 1, e181670.	2.8	60
45	High Throughput Single Cell RNA Sequencing, Bioinformatics Analysis and Applications. <i>Advances in Experimental Medicine and Biology</i> , 2018, 1068, 33-43.	0.8	50
46	Establishment of a <i>Macaca fascicularis</i> gut microbiome gene catalog and comparison with the human, pig, and mouse gut microbiomes. <i>GigaScience</i> , 2018, 7, .	3.3	53
47	PSSMHCpan: a novel PSSM-based software for predicting class I peptide-HLA binding affinity. <i>GigaScience</i> , 2017, 6, 1-11.	3.3	67
48	Circumventing intratumoral heterogeneity to identify potential therapeutic targets in hepatocellular carcinoma. <i>Journal of Hepatology</i> , 2017, 67, 293-301.	1.8	79
49	The gut microbiome in atherosclerotic cardiovascular disease. <i>Nature Communications</i> , 2017, 8, 845.	5.8	1,029
50	1D-Reactor Decentralized MDA for Uniform and Accurate Whole Genome Amplification. <i>Analytical Chemistry</i> , 2017, 89, 10147-10152.	3.2	16
51	RED-ML: a novel, effective RNA editing detection method based on machine learning. <i>GigaScience</i> , 2017, 6, 1-8.	3.3	29
52	Population-wide sampling of retrotransposon insertion polymorphisms using deep sequencing and efficient detection. <i>GigaScience</i> , 2017, 6, 1-11.	3.3	11
53	Conditionally reprogrammed normal and primary tumor prostate epithelial cells: a novel patient-derived cell model for studies of human prostate cancer. <i>Oncotarget</i> , 2017, 8, 22741-22758.	0.8	51
54	Abstract LB-202: A novel neoepitope screening platform for generating effective and safe neoantigen-based vaccines and immunotherapeutics in a hepatocellular carcinoma model. , 2017, , .		0

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55	An epigenetic biomarker combination of PCDH17 and POU4F2 detects bladder cancer accurately by methylation analyses of urine sediment DNA in Han Chinese. <i>Oncotarget</i> , 2016, 7, 2754-2764.	0.8	53
56	Evolution of multiple cell clones over a 29-year period of a CLL patient. <i>Nature Communications</i> , 2016, 7, 13765.	5.8	29
57	Genetic basis of PD-L1 overexpression in diffuse large B-cell lymphomas. <i>Blood</i> , 2016, 127, 3026-3034.	0.6	168
58	Single-cell RNA sequencing reveals dynamic changes in A-to-I RNA editome during early human embryogenesis. <i>BMC Genomics</i> , 2016, 17, 766.	1.2	49
59	First report of human salivirus/klassevirus in respiratory specimens of a child with fatal adenovirus infection. <i>Virus Genes</i> , 2016, 52, 620-624.	0.7	2
60	The stepwise evolution of the exome during acquisition of docetaxel resistance in breast cancer cells. <i>BMC Genomics</i> , 2016, 17, 442.	1.2	25
61	Multiple IgH Isotypes Including IgD, Subclasses of IgM, and IgY Are Expressed in the Common Ancestors of Modern Birds. <i>Journal of Immunology</i> , 2016, 196, 5138-5147.	0.4	25
62	Diverse evolutionary dynamics in glioblastoma inference by multi-region and single-cell sequencing. <i>Journal of Clinical Oncology</i> , 2016, 34, 11580-11580.	0.8	4
63	Single-cell analyses of transcriptional heterogeneity in squamous cell carcinoma of urinary bladder. <i>Oncotarget</i> , 2016, 7, 66069-66076.	0.8	31
64	Novel variants in <i>MLL</i> confer to bladder cancer recurrence identified by whole-exome sequencing. <i>Oncotarget</i> , 2016, 7, 2629-2645.	0.8	25
65	A comparison of isolated circulating tumor cells and tissue biopsies using whole-genome sequencing in prostate cancer. <i>Oncotarget</i> , 2015, 6, 44781-44793.	0.8	94
66	Frequent alterations in cytoskeleton remodelling genes in primary and metastatic lung adenocarcinomas. <i>Nature Communications</i> , 2015, 6, 10131.	5.8	93
67	Full-length single-cell RNA-seq applied to a viral human cancer: applications to HPV expression and splicing analysis in HeLa S3 cells. <i>GigaScience</i> , 2015, 4, 51.	3.3	51
68	Comparison of variations detection between whole-genome amplification methods used in single-cell resequencing. <i>GigaScience</i> , 2015, 4, 37.	3.3	141
69	Mutational bias of Turnip Yellow Mosaic Virus in the context of host anti-viral gene silencing. <i>Virology</i> , 2015, 486, 2-6.	1.1	2
70	Viral integration signature in multifocal hepatocellular carcinoma during occult hepatitis B virus infection: a single-cell sequencing analysis. <i>Lancet</i> , The, 2015, 386, S30.	6.3	1
71	Genomic signatures of near-extinction and rebirth of the crested ibis and other endangered bird species. <i>Genome Biology</i> , 2014, 15, 557.	3.8	83
72	Discovery of biclonal origin and a novel oncogene SLC12A5 in colon cancer by single-cell sequencing. <i>Cell Research</i> , 2014, 24, 701-712.	5.7	123

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73	Current Challenges in the Bioinformatics of Single Cell Genomics. <i>Frontiers in Oncology</i> , 2014, 4, 7.	1.3	40
74	MethylPurify: tumor purity deconvolution and differential methylation detection from single tumor DNA methylomes. <i>Genome Biology</i> , 2014, 15, 419.	3.8	87
75	Sequencing and automated whole-genome optical mapping of the genome of a domestic goat (<i>Capra</i>) Tj ETQq1 1 0.784314 9.4 479 BT /Ov	0.784314	479
76	Single-Cell Exome Sequencing Reveals Single-Nucleotide Mutation Characteristics of a Kidney Tumor. <i>Cell</i> , 2012, 148, 886-895.	13.5	622
77	Single-Cell Exome Sequencing and Monoclonal Evolution of a JAK2-Negative Myeloproliferative Neoplasm. <i>Cell</i> , 2012, 148, 873-885.	13.5	503
78	Single-cell sequencing analysis characterizes common and cell-lineage-specific mutations in a muscle-invasive bladder cancer. <i>GigaScience</i> , 2012, 1, 12.	3.3	99
79	Near-Infrared Fluorescence Labeling of Iron Nanoparticles and Applications for Cell Labeling and In Vivo Imaging. <i>Methods in Molecular Biology</i> , 2012, 906, 221-237.	0.4	3
80	Manufacture of IRDye800CW-coupled Fe ₃ O ₄ nanoparticles and their applications in cell labeling and in vivo imaging. <i>Journal of Nanobiotechnology</i> , 2010, 8, 25.	4.2	26
81	M-GWAS for the Gut Microbiome in Chinese Adults Illuminates on Complex Diseases. <i>SSRN Electronic Journal</i> , 0, , .	0.4	4