

Yong Hou

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2595720/publications.pdf>

Version: 2024-02-01

81
papers

6,732
citations

101543

36
h-index

71685

76
g-index

98
all docs

98
docs citations

98
times ranked

11557
citing authors

#	ARTICLE	IF	CITATIONS
1	Life History Recorded in the Vagino-cervical Microbiome Along with Multi-omes. <i>Genomics, Proteomics and Bioinformatics</i> , 2022, 20, 304-321.	6.9	18
2	Over 50,000 Metagenomically Assembled Draft Genomes for the Human Oral Microbiome Reveal New Taxa. <i>Genomics, Proteomics and Bioinformatics</i> , 2022, 20, 246-259.	6.9	38
3	Mendelian randomization analyses support causal relationships between blood metabolites and the gut microbiome. <i>Nature Genetics</i> , 2022, 54, 52-61.	21.4	134
4	Transcriptomic Profile of the Mouse Postnatal Liver Development by Single-Nucleus RNA Sequencing. <i>Frontiers in Cell and Developmental Biology</i> , 2022, 10, 833392.	3.7	1
5	Single-cell transcriptional diversity of neonatal umbilical cord blood immune cells reveals neonatal immune tolerance. <i>Biochemical and Biophysical Research Communications</i> , 2022, 608, 14-22.	2.1	5
6	Distinct Functional Metagenomic Markers Predict the Responsiveness to Anti-PD-1 Therapy in Chinese Non-Small Cell Lung Cancer Patients. <i>Frontiers in Oncology</i> , 2022, 12, 837525.	2.8	6
7	Cell transcriptomic atlas of the non-human primate <i>Macaca fascicularis</i> . <i>Nature</i> , 2022, 604, 723-731.	27.8	81
8	HBV genome-enriched single cell sequencing revealed heterogeneity in HBV-driven hepatocellular carcinoma (HCC). <i>BMC Medical Genomics</i> , 2022, 15, .	1.5	6
9	Single-cell landscape of the ecosystem in early-relapse hepatocellular carcinoma. <i>Cell</i> , 2021, 184, 404-421.e16.	28.9	399
10	Multiregion single-cell sequencing reveals the transcriptional landscape of the immune microenvironment of colorectal cancer. <i>Clinical and Translational Medicine</i> , 2021, 11, e253.	4.0	48
11	Genome diversity in Ukraine. <i>GigaScience</i> , 2021, 10, .	6.4	9
12	Sex- and age-related trajectories of the adult human gut microbiota shared across populations of different ethnicities. <i>Nature Aging</i> , 2021, 1, 87-100.	11.6	86
13	A genome-wide association study for gut metagenome in Chinese adults illuminates complex diseases. <i>Cell Discovery</i> , 2021, 7, 9.	6.7	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. <i>Aging Cell</i> , 2021, 20, e13323.	6.7	27
15	Single-Nucleus Chromatin Accessibility Landscape Reveals Diversity in Regulatory Regions Across Distinct Adult Rat Cortex. <i>Frontiers in Molecular Neuroscience</i> , 2021, 14, 651355.	2.9	8
16	A transomic cohort as a reference point for promoting a healthy human gut microbiome. <i>Medicine in Microecology</i> , 2021, 8, 100039.	1.6	24
17	scDPN for High-throughput Single-cell CNV Detection to Uncover Clonal Evolution During HCC Recurrence. <i>Genomics, Proteomics and Bioinformatics</i> , 2021, 19, 346-357.	6.9	3
18	Tumor heterogeneity assessed by sequencing and fluorescence <i>in situ</i> hybridization (FISH) data. <i>Bioinformatics</i> , 2021, 37, 4704-4711.	4.1	5

#	ARTICLE	IF	CITATIONS
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.	12.8	90
20	Dairy consumption and physical fitness tests associated with fecal microbiome in a Chinese cohort. <i>Medicine in Microecology</i> , 2021, 9, 100038.	1.6	6
21	Disease trends in a young Chinese cohort according to fecal metagenome and plasma metabolites. <i>Medicine in Microecology</i> , 2021, , 100037.	1.6	2
22	Genome-wide mutational signatures revealed distinct developmental paths for human B cell lymphomas. <i>Journal of Experimental Medicine</i> , 2021, 218, .	8.5	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.	3.9	5
24	Metagenome-genome-wide association studies reveal human genetic impact on the oral microbiome. <i>Cell Discovery</i> , 2021, 7, 117.	6.7	31
25	Embryonic liver developmental trajectory revealed by single-cell RNA sequencing in the Foxa2eGFP mouse. <i>Communications Biology</i> , 2020, 3, 642.	4.4	24
26	Tumor Copy Number Deconvolution Integrating Bulk and Single-Cell Sequencing Data. <i>Journal of Computational Biology</i> , 2020, 27, 565-598.	1.6	10
27	Chromatin accessibility and transcriptome landscapes of <i>Monomorium pharaonis</i> brain. <i>Scientific Data</i> , 2020, 7, 217.	5.3	10
28	Single-cell RNA-seq unveils critical regulators of human FOXP3+ regulatory T cell stability. <i>Science Bulletin</i> , 2020, 65, 1114-1124.	9.0	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.	10.0	33
30	Tumor Copy Number Deconvolution Integrating Bulk and Single-Cell Sequencing Data. <i>Lecture Notes in Computer Science</i> , 2019, , 174-189.	1.3	3
31	Distinct gut metagenomics and metaproteomics signatures in prediabetics and treatment-naïve type 2 diabetics. <i>EBioMedicine</i> , 2019, 47, 373-383.	6.1	101
32	Deconvolution of single-cell multi-omics layers reveals regulatory heterogeneity. <i>Nature Communications</i> , 2019, 10, 470.	12.8	156
33	Viral integration drives multifocal HCC during the occult HBV infection. <i>Journal of Experimental and Clinical Cancer Research</i> , 2019, 38, 261.	8.6	27
34	Genomic Evidence of Recombination in the Basidiomycete <i>Wallemia mellicola</i> . <i>Genes</i> , 2019, 10, 427.	2.4	14
35	Therapeutic potential of CRISPR/Cas9 gene editing in engineered T cell therapy. <i>Cancer Medicine</i> , 2019, 8, 4254-4264.	2.8	57
36	Single-cell transcriptomic landscape of nucleated cells in umbilical cord blood. <i>GigaScience</i> , 2019, 8, .	6.4	24

#	ARTICLE	IF	CITATIONS
37	Comparative analysis of sequencing technologies for single-cell transcriptomics. <i>Genome Biology</i> , 2019, 20, 70.	8.8	82
38	Population Genomics of an Obligately Halophilic Basidiomycete <i>Wallemia ichthyophaga</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 2019.	3.5	9
39	Characterization of circulating tumor cells in breast cancer patients by spiral microfluidics. <i>Cell Biology and Toxicology</i> , 2019, 35, 59-66.	5.3	25
40	1,520 reference genomes from cultivated human gut bacteria enable functional microbiome analyses. <i>Nature Biotechnology</i> , 2019, 37, 179-185.	17.5	402
41	Genetic landscape of hepatitis B virus-associated diffuse large B-cell lymphoma. <i>Blood</i> , 2018, 131, 2670-2681.	1.4	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.	1.9	130
43	Progress and challenges of sequencing and analyzing circulating tumor cells. <i>Cell Biology and Toxicology</i> , 2018, 34, 405-415.	5.3	65
44	Sex Differences in Genetic Associations With Longevity. <i>JAMA Network Open</i> , 2018, 1, e181670.	5.9	60
45	High Throughput Single Cell RNA Sequencing, Bioinformatics Analysis and Applications. <i>Advances in Experimental Medicine and Biology</i> , 2018, 1068, 33-43.	1.6	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, .	6.4	53
47	PSSMHCpan: a novel PSSM-based software for predicting class I peptide-HLA binding affinity. <i>GigaScience</i> , 2017, 6, 1-11.	6.4	67
48	Circumventing intratumoral heterogeneity to identify potential therapeutic targets in hepatocellular carcinoma. <i>Journal of Hepatology</i> , 2017, 67, 293-301.	3.7	79
49	The gut microbiome in atherosclerotic cardiovascular disease. <i>Nature Communications</i> , 2017, 8, 845.	12.8	1,029
50	1D-Reactor Decentralized MDA for Uniform and Accurate Whole Genome Amplification. <i>Analytical Chemistry</i> , 2017, 89, 10147-10152.	6.5	16
51	RED-ML: a novel, effective RNA editing detection method based on machine learning. <i>GigaScience</i> , 2017, 6, 1-8.	6.4	29
52	Population-wide sampling of retrotransposon insertion polymorphisms using deep sequencing and efficient detection. <i>GigaScience</i> , 2017, 6, 1-11.	6.4	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.	1.8	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

#	ARTICLE	IF	CITATIONS
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.	1.8	53
56	Evolution of multiple cell clones over a 29-year period of a CLL patient. <i>Nature Communications</i> , 2016, 7, 13765.	12.8	29
57	Genetic basis of PD-L1 overexpression in diffuse large B-cell lymphomas. <i>Blood</i> , 2016, 127, 3026-3034.	1.4	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.	2.8	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.	1.6	2
60	The stepwise evolution of the exome during acquisition of docetaxel resistance in breast cancer cells. <i>BMC Genomics</i> , 2016, 17, 442.	2.8	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.	0.8	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.	1.6	4
63	Single-cell analyses of transcriptional heterogeneity in squamous cell carcinoma of urinary bladder. <i>Oncotarget</i> , 2016, 7, 66069-66076.	1.8	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.	1.8	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.	1.8	94
66	Frequent alterations in cytoskeleton remodelling genes in primary and metastatic lung adenocarcinomas. <i>Nature Communications</i> , 2015, 6, 10131.	12.8	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.	6.4	51
68	Comparison of variations detection between whole-genome amplification methods used in single-cell resequencing. <i>GigaScience</i> , 2015, 4, 37.	6.4	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.	2.4	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.	13.7	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.	8.8	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.	12.0	123

#	ARTICLE	IF	CITATIONS
73	Current Challenges in the Bioinformatics of Single Cell Genomics. <i>Frontiers in Oncology</i> , 2014, 4, 7.	2.8	40
74	MethylPurify: tumor purity deconvolution and differential methylation detection from single tumor DNA methylomes. <i>Genome Biology</i> , 2014, 15, 419.	8.8	87
75	Sequencing and automated whole-genome optical mapping of the genome of a domestic goat (<i>Capra</i>) Tj ETQq1 1 0.784314 rgBT /Ov	17.5	479
76	Single-Cell Exome Sequencing Reveals Single-Nucleotide Mutation Characteristics of a Kidney Tumor. <i>Cell</i> , 2012, 148, 886-895.	28.9	622
77	Single-Cell Exome Sequencing and Monoclonal Evolution of a JAK2-Negative Myeloproliferative Neoplasm. <i>Cell</i> , 2012, 148, 873-885.	28.9	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.	6.4	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.	0.9	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.	9.1	26
81	M-GWAS for the Gut Microbiome in Chinese Adults Illuminates on Complex Diseases. <i>SSRN Electronic Journal</i> , 0, , .	0.4	4