

Xianwen Ren

List of Publications by Year in descending order

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Version: 2024-02-01

56
papers

7,443
citations

201385

27
h-index

161609

54
g-index

64
all docs

64
docs citations

64
times ranked

10342
citing authors

#	ARTICLE	IF	CITATIONS
1	Single-cell RNA sequencing reveals intrahepatic and peripheral immune characteristics related to disease phases in HBV-infected patients. <i>Gut</i> , 2023, 72, 153-167.	6.1	42
2	PEG10 amplification at 7q21.3 potentiates large-cell transformation in cutaneous T-cell lymphoma. <i>Blood</i> , 2022, 139, 554-571.	0.6	9
3	Distinctive Network Topology of Phase-Separated Proteins in Human Interactome. <i>Journal of Molecular Biology</i> , 2022, 434, 167292.	2.0	3
4	Identification of Distinct Immune Cell Subsets Associated With Asymptomatic Infection, Disease Severity, and Viral Persistence in COVID-19 Patients. <i>Frontiers in Immunology</i> , 2022, 13, 812514.	2.2	12
5	Immune phenotypic linkage between colorectal cancer and liver metastasis. <i>Cancer Cell</i> , 2022, 40, 424-437.e5.	7.7	129
6	Editorial: The Genetic Causes Underlying Immune Mediated Disease: A Focus on Autoimmunity and Cancer. <i>Frontiers in Genetics</i> , 2022, 13, 889160.	1.1	0
7	A pan-cancer single-cell transcriptional atlas of tumor infiltrating myeloid cells. <i>Cell</i> , 2021, 184, 792-809.e23.	13.5	563
8	Direct Comparative Analyses of 10X Genomics Chromium and Smart-seq2. <i>Genomics, Proteomics and Bioinformatics</i> , 2021, 19, 253-266.	3.0	167
9	Insights Gained from Single-Cell Analysis of Immune Cells in the Tumor Microenvironment. <i>Annual Review of Immunology</i> , 2021, 39, 583-609.	9.5	153
10	COVID-19 immune features revealed by a large-scale single-cell transcriptome atlas. <i>Cell</i> , 2021, 184, 1895-1913.e19.	13.5	512
11	SARS-CoV-2 exacerbates proinflammatory responses in myeloid cells through C-type lectin receptors and Tweety family member 2. <i>Immunity</i> , 2021, 54, 1304-1319.e9.	6.6	115
12	Pan-cancer single-cell landscape of tumor-infiltrating T cells. <i>Science</i> , 2021, 374, abe6474.	6.0	460
13	Distinct epigenetic features of tumor-reactive CD8+ T cells in colorectal cancer patients revealed by genome-wide DNA methylation analysis. <i>Genome Biology</i> , 2020, 21, 2.	3.8	77
14	scTIM: seeking cell-type-indicative marker from single cell RNA-seq data by consensus optimization. <i>Bioinformatics</i> , 2020, 36, 2474-2485.	1.8	12
15	Landscape of transcript isoforms in single T cells infiltrating in non-small-cell lung cancer. <i>Journal of Genetics and Genomics</i> , 2020, 47, 373-388.	1.7	10
16	Reconstruction of cell spatial organization from single-cell RNA sequencing data based on ligand-receptor mediated self-assembly. <i>Cell Research</i> , 2020, 30, 763-778.	5.7	92
17	An entropy-based metric for assessing the purity of single cell populations. <i>Nature Communications</i> , 2020, 11, 3155.	5.8	83
18	Distinct lung microbial community states in patients with pulmonary tuberculosis. <i>Science China Life Sciences</i> , 2020, 63, 1522-1533.	2.3	18

#	ARTICLE	IF	CITATIONS
19	Single-Cell Analyses Inform Mechanisms of Myeloid-Targeted Therapies in Colon Cancer. <i>Cell</i> , 2020, 181, 442-459.e29.	13.5	741
20	SciBet as a portable and fast single cell type identifier. <i>Nature Communications</i> , 2020, 11, 1818.	5.8	90
21	Deep single-cell RNA sequencing data of individual T cells from treatment-naïve colorectal cancer patients. <i>Scientific Data</i> , 2019, 6, 131.	2.4	49
22	Identification of transcriptional isoforms associated with survival in cancer patient. <i>Journal of Genetics and Genomics</i> , 2019, 46, 413-421.	1.7	3
23	Landscape and Dynamics of Single Immune Cells in Hepatocellular Carcinoma. <i>Cell</i> , 2019, 179, 829-845.e20.	13.5	897
24	Understanding tumor-infiltrating lymphocytes by single cell RNA sequencing. <i>Advances in Immunology</i> , 2019, 144, 217-245.	1.1	21
25	SSCC: A Novel Computational Framework for Rapid and Accurate Clustering Large-scale Single Cell RNA-seq Data. <i>Genomics, Proteomics and Bioinformatics</i> , 2019, 17, 201-210.	3.0	31
26	scRNAAss: a single-cell RNA-seq assembler via imputing dropouts and combing junctions. <i>Bioinformatics</i> , 2019, 35, 4264-4271.	1.8	7
27	Discovering cooperative biomarkers for heterogeneous complex disease diagnoses. <i>Briefings in Bioinformatics</i> , 2019, 20, 89-101.	3.2	12
28	Evaluating the Value of Defensins for Diagnosing Secondary Bacterial Infections in Influenza-Infected Patients. <i>Frontiers in Microbiology</i> , 2018, 9, 2762.	1.5	5
29	Global characterization of T cells in non-small-cell lung cancer by single-cell sequencing. <i>Nature Medicine</i> , 2018, 24, 978-985.	15.2	1,044
30	Lineage tracking reveals dynamic relationships of T cells in colorectal cancer. <i>Nature</i> , 2018, 564, 268-272.	13.7	742
31	Understanding tumor ecosystems by single-cell sequencing: promises and limitations. <i>Genome Biology</i> , 2018, 19, 211.	3.8	161
32	An elaborate landscape of the human antibody repertoire against enterovirus 71 infection is revealed by phage display screening and deep sequencing. <i>MAbs</i> , 2017, 9, 342-349.	2.6	13
33	A case report demonstrating the utility of next generation sequencing in analyzing serial samples from the lung following an infection with influenza A (H7N9) virus. <i>Journal of Clinical Virology</i> , 2016, 76, 45-50.	1.6	9
34	Safe sequencing depth to estimate the intra-host heterogeneity of viruses. <i>Briefings in Functional Genomics</i> , 2016, 15, 275-277.	1.3	3
35	Deciphering the bat virome catalog to better understand the ecological diversity of bat viruses and the bat origin of emerging infectious diseases. <i>ISME Journal</i> , 2016, 10, 609-620.	4.4	249
36	ORF8-Related Genetic Evidence for Chinese Horseshoe Bats as the Source of Human Severe Acute Respiratory Syndrome Coronavirus. <i>Journal of Infectious Diseases</i> , 2016, 213, 579-583.	1.9	77

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37	Integrating heterogeneous genomic data to accurately identify disease subtypes. BMC Medical Genomics, 2015, 8, 78.	0.7	3
38	Proteogenomic Analysis of <i>Trichophyton rubrum</i> Aided by RNA Sequencing. Journal of Proteome Research, 2015, 14, 2207-2218.	1.8	7
39	Rapid genome sequencing and characterization of novel avian-origin influenza A H7N9 virus directly from clinical sample by semiconductor sequencing. Journal of Clinical Virology, 2015, 73, 84-88.	1.6	3
40	Mutations of Novel Influenza A(H10N8) Virus in Chicken Eggs and MDCK Cells. Emerging Infectious Diseases, 2014, 20, 1541-1543.	2.0	8
41	Novel Henipa-like Virus, Mojiang Paramyxovirus, in Rats, China, 2012. Emerging Infectious Diseases, 2014, 20, 1064-6.	2.0	134
42	MERS-Related Betacoronavirus in <i>Vespertilio superans</i> Bats, China. Emerging Infectious Diseases, 2014, 20, 1260-2.	2.0	90
43	Analysis of the Secretome and Identification of Novel Constituents from Culture Filtrate of <i>Bacillus Calmette-Guérin</i> Using High-resolution Mass Spectrometry. Molecular and Cellular Proteomics, 2013, 12, 2081-2095.	2.5	31
44	Full Genome of Influenza A (H7N9) Virus Derived by Direct Sequencing without Culture. Emerging Infectious Diseases, 2013, 19, 1881-4.	2.0	30
45	iPcc: a novel feature extraction method for accurate disease class discovery and prediction. Nucleic Acids Research, 2013, 41, e143-e143.	6.5	26
46	ellipsoidFN: a tool for identifying a heterogeneous set of cancer biomarkers based on gene expressions. Nucleic Acids Research, 2013, 41, e53-e53.	6.5	34
47	Toward a more systematic understanding of bacterial virulence factors and establishing Koch postulates in silico. Virulence, 2013, 4, 437-438.	1.8	2
48	Novel SARS-like Betacoronaviruses in Bats, China, 2011. Emerging Infectious Diseases, 2013, 19, 989-91.	2.0	93
49	Comparative Study of the Cytokine/Chemokine Response in Children with Differing Disease Severity in Enterovirus 71-Induced Hand, Foot, and Mouth Disease. PLoS ONE, 2013, 8, e67430.	1.1	50
50	Virome Analysis for Identification of Novel Mammalian Viruses in Bat Species from Chinese Provinces. Journal of Virology, 2012, 86, 10999-11012.	1.5	244
51	Applying modularity analysis of PPI networks to sequenced organisms. Virulence, 2012, 3, 459-463.	1.8	6
52	Interrogating noise in protein sequences from the perspective of protein-protein interactions prediction. Journal of Theoretical Biology, 2012, 315, 64-70.	0.8	1
53	A unified computational model for revealing and predicting subtle subtypes of cancers. BMC Bioinformatics, 2012, 13, 70.	1.2	11
54	Evaluating de Bruijn Graph Assemblers on 454 Transcriptomic Data. PLoS ONE, 2012, 7, e51188.	1.1	24

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55	The network properties of myelodysplastic syndromes pathogenesis revealed by an integrative systems biological method. <i>Molecular BioSystems</i> , 2011, 7, 2048.	2.9	0
56	A linear programming model based on network flow for pathway inference. <i>Journal of Systems Science and Complexity</i> , 2010, 23, 971-977.	1.6	0