

Xianwen Ren

List of Publications by Year in descending order

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56
papers

7,443
citations

201575

27
h-index

161767

54
g-index

64
all docs

64
docs citations

64
times ranked

10342
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	Landscape and Dynamics of Single Immune Cells in Hepatocellular Carcinoma. <i>Cell</i> , 2019, 179, 829-845.e20.	13.5	897
3	Lineage tracking reveals dynamic relationships of T cells in colorectal cancer. <i>Nature</i> , 2018, 564, 268-272.	13.7	742
4	Single-Cell Analyses Inform Mechanisms of Myeloid-Targeted Therapies in Colon Cancer. <i>Cell</i> , 2020, 181, 442-459.e29.	13.5	741
5	A pan-cancer single-cell transcriptional atlas of tumor infiltrating myeloid cells. <i>Cell</i> , 2021, 184, 792-809.e23.	13.5	563
6	COVID-19 immune features revealed by a large-scale single-cell transcriptome atlas. <i>Cell</i> , 2021, 184, 1895-1913.e19.	13.5	512
7	Pan-cancer single-cell landscape of tumor-infiltrating T cells. <i>Science</i> , 2021, 374, abe6474.	6.0	460
8	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
9	Virome Analysis for Identification of Novel Mammalian Viruses in Bat Species from Chinese Provinces. <i>Journal of Virology</i> , 2012, 86, 10999-11012.	1.5	244
10	Direct Comparative Analyses of 10X Genomics Chromium and Smart-seq2. <i>Genomics, Proteomics and Bioinformatics</i> , 2021, 19, 253-266.	3.0	167
11	Understanding tumor ecosystems by single-cell sequencing: promises and limitations. <i>Genome Biology</i> , 2018, 19, 211.	3.8	161
12	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
13	Novel Henipa-like Virus, Mojiang Paramyxovirus, in Rats, China, 2012. <i>Emerging Infectious Diseases</i> , 2014, 20, 1064-6.	2.0	134
14	Immune phenotypic linkage between colorectal cancer and liver metastasis. <i>Cancer Cell</i> , 2022, 40, 424-437.e5.	7.7	129
15	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
16	Novel SARS-like Betacoronaviruses in Bats, China, 2011. <i>Emerging Infectious Diseases</i> , 2013, 19, 989-91.	2.0	93
17	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
18	MERSâ€“Related Betacoronavirus in<i>Vespertilio superans</i>Bats, China. <i>Emerging Infectious Diseases</i> , 2014, 20, 1260-2.	2.0	90

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19	SciBet as a portable and fast single cell type identifier. <i>Nature Communications</i> , 2020, 11, 1818.	5.8	90
20	An entropy-based metric for assessing the purity of single cell populations. <i>Nature Communications</i> , 2020, 11, 3155.	5.8	83
21	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
22	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
23	Comparative Study of the Cytokine/Chemokine Response in Children with Differing Disease Severity in Enterovirus 71-Induced Hand, Foot, and Mouth Disease. <i>PLoS ONE</i> , 2013, 8, e67430.	1.1	50
24	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
25	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
26	ellipsoidFN: a tool for identifying a heterogeneous set of cancer biomarkers based on gene expressions. <i>Nucleic Acids Research</i> , 2013, 41, e53-e53.	6.5	34
27	Analysis of the Secretome and Identification of Novel Constituents from Culture Filtrate of <i>Bacillus Calmette-Guérin</i> Using High-resolution Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 2081-2095.	2.5	31
28	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
29	Full Genome of Influenza A (H7N9) Virus Derived by Direct Sequencing without Culture. <i>Emerging Infectious Diseases</i> , 2013, 19, 1881-4.	2.0	30
30	iPcc: a novel feature extraction method for accurate disease class discovery and prediction. <i>Nucleic Acids Research</i> , 2013, 41, e143-e143.	6.5	26
31	Evaluating de Bruijn Graph Assemblers on 454 Transcriptomic Data. <i>PLoS ONE</i> , 2012, 7, e51188.	1.1	24
32	Understanding tumor-infiltrating lymphocytes by single cell RNA sequencing. <i>Advances in Immunology</i> , 2019, 144, 217-245.	1.1	21
33	Distinct lung microbial community states in patients with pulmonary tuberculosis. <i>Science China Life Sciences</i> , 2020, 63, 1522-1533.	2.3	18
34	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
35	Discovering cooperative biomarkers for heterogeneous complex disease diagnoses. <i>Briefings in Bioinformatics</i> , 2019, 20, 89-101.	3.2	12
36	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

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37	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
38	A unified computational model for revealing and predicting subtle subtypes of cancers. <i>BMC Bioinformatics</i> , 2012, 13, 70.	1.2	11
39	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
40	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
41	PEG10 amplification at 7q21.3 potentiates large-cell transformation in cutaneous T-cell lymphoma. <i>Blood</i> , 2022, 139, 554-571.	0.6	9
42	Mutations of Novel Influenza A(H10N8) Virus in Chicken Eggs and MDCK Cells. <i>Emerging Infectious Diseases</i> , 2014, 20, 1541-1543.	2.0	8
43	Proteogenomic Analysis of <i>Trichophyton rubrum</i> Aided by RNA Sequencing. <i>Journal of Proteome Research</i> , 2015, 14, 2207-2218.	1.8	7
44	scRNAAss: a single-cell RNA-seq assembler via imputing dropouts and combing junctions. <i>Bioinformatics</i> , 2019, 35, 4264-4271.	1.8	7
45	Applying modularity analysis of PPI networks to sequenced organisms. <i>Virulence</i> , 2012, 3, 459-463.	1.8	6
46	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
47	Integrating heterogeneous genomic data to accurately identify disease subtypes. <i>BMC Medical Genomics</i> , 2015, 8, 78.	0.7	3
48	Rapid genome sequencing and characterization of novel avian-origin influenza A H7N9 virus directly from clinical sample by semiconductor sequencing. <i>Journal of Clinical Virology</i> , 2015, 73, 84-88.	1.6	3
49	Safe sequencing depth to estimate the intra-host heterogeneity of viruses. <i>Briefings in Functional Genomics</i> , 2016, 15, 275-277.	1.3	3
50	Identification of transcriptional isoforms associated with survival in cancer patient. <i>Journal of Genetics and Genomics</i> , 2019, 46, 413-421.	1.7	3
51	Distinctive Network Topology of Phase-Separated Proteins in Human Interactome. <i>Journal of Molecular Biology</i> , 2022, 434, 167292.	2.0	3
52	Toward a more systematic understanding of bacterial virulence factors and establishing Koch postulates in silico. <i>Virulence</i> , 2013, 4, 437-438.	1.8	2
53	Interrogating noise in protein sequences from the perspective of protein-protein interactions prediction. <i>Journal of Theoretical Biology</i> , 2012, 315, 64-70.	0.8	1
54	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

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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	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