Ruibin Xi

List of Publications by Year
in descending order

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49	23,836	126858	161767
papers	citations	33 h-index	54 g-index

57	57	57	38327
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Comprehensive molecular characterization of human colon and rectal cancer. Nature, 2012, 487, 330-337.	13.7	7,168
2	Comprehensive molecular characterization of gastric adenocarcinoma. Nature, 2014, 513, 202-209.	13.7	5,055
3	Integrated genomic characterization of endometrial carcinoma. Nature, 2013, 497, 67-73.	13.7	4,075
4	Genomic Classification of Cutaneous Melanoma. Cell, 2015, 161, 1681-1696.	13.5	2,562
5	Comprehensive analysis of the chromatin landscape in Drosophila melanogaster. Nature, 2011, 471, 480-485.	13.7	781
6	A Pan-Cancer Proteogenomic Atlas of PI3K/AKT/mTOR Pathway Alterations. Cancer Cell, 2017, 31, 820-832.e3.	7.7	433
7	Comprehensive analysis of chromothripsis in 2,658 human cancers using whole-genome sequencing. Nature Genetics, 2020, 52, 331-341.	9.4	431
8	Hallmarks of pluripotency. Nature, 2015, 525, 469-478.	13.7	338
9	Diverse Mechanisms of Somatic Structural Variations in Human Cancer Genomes. Cell, 2013, 153, 919-929.	13.5	308
10	Spatiotemporal Immune Landscape of Colorectal Cancer Liver Metastasis at Single-Cell Level. Cancer Discovery, 2022, 12, 134-153.	7.7	286
11	Copy number variation detection in whole-genome sequencing data using the Bayesian information criterion. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, E1128-36.	3.3	200
12	Genomic analysis of oesophageal squamous-cell carcinoma identifies alcohol drinking-related mutation signature and genomic alterations. Nature Communications, 2017, 8, 15290.	5.8	195
13	Functional genomic analysis of chromosomal aberrations in a compendium of 8000 cancer genomes. Genome Research, 2013, 23, 217-227.	2.4	139
14	Whole-genome sequencing of 508 patients identifies key molecular features associated with poor prognosis in esophageal squamous cell carcinoma. Cell Research, 2020, 30, 902-913.	5.7	132
15	Copy number analysis of whole-genome data using BIC-seq2 and its application to detection of cancer susceptibility variants. Nucleic Acids Research, 2016, 44, 6274-6286.	6.5	117
16	Activated and Exhausted MAIT Cells Foster Disease Progression and Indicate Poor Outcome in Hepatocellular Carcinoma. Clinical Cancer Research, 2019, 25, 3304-3316.	3.2	109
17	Systematic identification of synergistic drug pairs targeting HIV. Nature Biotechnology, 2012, 30, 1125-1130.	9.4	108
18	Cell Culture System for Analysis of Genetic Heterogeneity WithinÂHepatocellular Carcinomas and Response to Pharmacologic Agents. Gastroenterology, 2017, 152, 232-242.e4.	0.6	107

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19	Diverse modes of clonal evolution in HBV-related hepatocellular carcinoma revealed by single-cell genome sequencing. Cell Research, 2018, 28, 359-373.	5.7	106
20	CCL15 Recruits Suppressive Monocytes to Facilitate Immune Escape and Disease Progression in Hepatocellular Carcinoma. Hepatology, 2019, 69, 143-159.	3.6	105
21	Aggregated estimating equation estimation. Statistics and Its Interface, 2011, 4, 73-83.	0.2	92
22	Genomic footprints of activated telomere maintenance mechanisms in cancer. Nature Communications, 2020, 11, 733.	5.8	87
23	Global immune characterization of HBV/HCV-related hepatocellular carcinoma identifies macrophage and T-cell subsets associated with disease progression. Cell Discovery, 2020, 6, 90.	3.1	84
24	Evidence for dosage compensation between the X chromosome and autosomes in mammals. Nature Genetics, 2011, 43, 1167-1169.	9.4	81
25	A Pan-Cancer Compendium of Genes Deregulated by Somatic Genomic Rearrangement across More Than 1,400 Cases. Cell Reports, 2018, 24, 515-527.	2.9	70
26	Spatial and temporal clonal evolution of intrahepatic cholangiocarcinoma. Journal of Hepatology, 2018, 69, 89-98.	1.8	63
27	Detecting structural variations in the human genome using next generation sequencing. Briefings in Functional Genomics, 2010, 9, 405-415.	1.3	54
28	Differential network analysis via lasso penalized D-trace loss. Biometrika, 2017, 104, 755-770.	1.3	49
29	rSW-seq: Algorithm for detection of copy number alterations in deep sequencing data. BMC Bioinformatics, 2010, 11, 432.	1.2	47
30	Evaluation of somatic copy number estimation tools for whole-exome sequencing data. Briefings in Bioinformatics, 2016, 17, 185-192.	3.2	44
31	scRMD: imputation for single cell RNA-seq data via robust matrix decomposition. Bioinformatics, 2020, 36, 3156-3161.	1.8	42
32	Global impact of somatic structural variation on the DNA methylome of human cancers. Genome Biology, 2019, 20, 209.	3.8	40
33	Single-cell transcriptomic analysis suggests two molecularly distinct subtypes of intrahepatic cholangiocarcinoma. Nature Communications, 2022, 13, 1642.	5.8	40
34	Patient-derived tumor-like cell clusters for drug testing in cancer therapy. Science Translational Medicine, 2020, 12, .	5.8	39
35	Inferring the progression of multifocal liver cancer from spatial and temporal genomic heterogeneity. Oncotarget, 2016, 7, 2867-2877.	0.8	38
36	A microscopic landscape of the invasive breast cancer genome. Scientific Reports, 2016, 6, 27545.	1.6	33

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37	Compression and Aggregation for Logistic Regression Analysis in Data Cubes. IEEE Transactions on Knowledge and Data Engineering, 2009, 21, 479-492.	4.0	28
38	Detecting virus integration sites based on multiple related sequencing data by VirTect. BMC Medical Genomics, 2019, 12, 19.	0.7	27
39	Pysim-sv: a package for simulating structural variation data with GC-biases. BMC Bioinformatics, 2017, 18, 53.	1.2	22
40	A Survey of Copyâ€Number Variation Detection Tools Based on Highâ€Throughput Sequencing Data. Current Protocols in Human Genetics, 2012, 75, Unit7.19.	3.5	18
41	Fast surrogates of U-statistics. Computational Statistics and Data Analysis, 2010, 54, 16-24.	0.7	8
42	Genomics landscape of 185 Streptococcus thermophilus and identification of fermentation biomarkers. Food Research International, 2021, 150, 110711.	2.9	8
43	Single-cell gene fusion detection by scFusion. Nature Communications, 2022, 13, 1084.	5.8	8
44	SVmine improves structural variation detection by integrative mining of predictions from multiple algorithms. Bioinformatics, 2017, 33, 3348-3354.	1.8	6
45	Somatic mutations in renal cell carcinomas from Chinese patients revealed by targeted gene panel sequencing and their associations with prognosis and PDâ€L1 expression. Cancer Communications, 2019, 39, 1-6.	3.7	4
46	CNV-BAC: Copy number Variation Detection in Bacterial Circular Genome. Bioinformatics, 2020, 36, 3890-3891.	1.8	4
47	Compression and aggregation of Bayesian estimates for data intensive computing. Knowledge and Information Systems, 2012, 33, 191-212.	2.1	3
48	Community detection by L_{0}-penalized graph Laplacian. Electronic Journal of Statistics, 2018, 12, .	0.4	2
49	Direct regression modelling of high-order moments in big data. Statistics and Its Interface, 2016, 9, 445-452.	0.2	2