Ruibin Xi

List of Publications by Citations

51 papers	16,971 citations	28 h-index	57 g-index
57 ext. papers	21,091 ext. citations	18.1 avg, IF	7.96 L-index

#	Paper	IF	Citations
51	Comprehensive molecular characterization of human colon and rectal cancer. *Nature*, **2012**, 487, 330-7	50.4	5640
50	Comprehensive molecular characterization of gastric adenocarcinoma. *Nature*, **2014**, 513, 202-9	50.4	3659
49	Integrated genomic characterization of endometrial carcinoma. *Nature*, **2013**, 497, 67-73	50.4	2800
48	Genomic Classification of Cutaneous Melanoma. *Cell*, **2015**, 161, 1681-96	56.2	1807
47	Comprehensive analysis of the chromatin landscape in Drosophila melanogaster. *Nature*, **2011**, 471, 480-5	50.4	641
46	A Pan-Cancer Proteogenomic Atlas of PI3K/AKT/mTOR Pathway Alterations. *Cancer Cell*, **2017**, 31, 820-832.e3	24.3	286
45	Hallmarks of pluripotency. *Nature*, **2015**, 525, 469-78	50.4	253
44	Diverse mechanisms of somatic structural variations in human cancer genomes. *Cell*, **2013**, 153, 919-29	56.2	238
43	Comprehensive analysis of chromothripsis in 2,658 human cancers using whole-genome sequencing. *Nature Genetics*, **2020**, 52, 331-341	36.3	168
42	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	11.5	163
41	Functional genomic analysis of chromosomal aberrations in a compendium of 8000 cancer genomes. *Genome Research*, **2013**, 23, 217-27	9.7	111
40	Genomic analysis of oesophageal squamous-cell carcinoma identifies alcohol drinking-related mutation signature and genomic alterations. *Nature Communications*, **2017**, 8, 15290	17.4	109
39	Systematic identification of synergistic drug pairs targeting HIV. *Nature Biotechnology*, **2012**, 30, 1125-30	44.5	84
38	Copy number analysis of whole-genome data using BIC-seq2 and its application to detection of cancer susceptibility variants. *Nucleic Acids Research*, **2016**, 44, 6274-86	20.1	82
37	Cell Culture System for Analysis of Genetic Heterogeneity Within Hepatocellular Carcinomas and Response to Pharmacologic Agents. *Gastroenterology*, **2017**, 152, 232-242.e4	13.3	81
36	Evidence for dosage compensation between the X chromosome and autosomes in mammals. *Nature Genetics*, **2011**, 43, 1167-9; author reply 1171-2	36.3	65
35	Aggregated estimating equation estimation. *Statistics and Its Interface*, **2011**, 4, 73-83	0.4	65

34	CCL15 Recruits Suppressive Monocytes to Facilitate Immune Escape and Disease Progression in Hepatocellular Carcinoma. *Hepatology*, **2019**, 69, 143-159	11.2	61
33	Diverse modes of clonal evolution in HBV-related hepatocellular carcinoma revealed by single-cell genome sequencing. *Cell Research*, **2018**, 28, 359-373	24.7	60
32	Activated and Exhausted MAIT Cells Foster Disease Progression and Indicate Poor Outcome in Hepatocellular Carcinoma. *Clinical Cancer Research*, **2019**, 25, 3304-3316	12.9	57
31	A Pan-Cancer Compendium of Genes Deregulated by Somatic Genomic Rearrangement across More Than 1,400 Cases. *Cell Reports*, **2018**, 24, 515-527	10.6	49
30	Detecting structural variations in the human genome using next generation sequencing. *Briefings in Functional Genomics*, **2010**, 9, 405-15	4.9	48
29	rSW-seq: algorithm for detection of copy number alterations in deep sequencing data. *BMC Bioinformatics*, **2010**, 11, 432	3.6	43
28	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	24.7	42
27	Genomic footprints of activated telomere maintenance mechanisms in cancer. *Nature Communications*, **2020**, 11, 733	17.4	40
26	Evaluation of somatic copy number estimation tools for whole-exome sequencing data. *Briefings in Bioinformatics*, **2016**, 17, 185-92	13.4	35
25	Inferring the progression of multifocal liver cancer from spatial and temporal genomic heterogeneity. *Oncotarget*, **2016**, 7, 2867-77	3.3	35
24	Spatial and temporal clonal evolution of intrahepatic cholangiocarcinoma. *Journal of Hepatology*, **2018**, 69, 89-98	13.4	33
23	Differential network analysis via lasso penalized D-trace loss. *Biometrika*, **2017**, 104, 755-770	2	27
22	A microscopic landscape of the invasive breast cancer genome. *Scientific Reports*, **2016**, 6, 27545	4.9	19
21	Compression and Aggregation for Logistic Regression Analysis in Data Cubes. *IEEE Transactions on Knowledge and Data Engineering*, **2009**, 21, 479-492	4.2	19
20	A survey of copy-number variation detection tools based on high-throughput sequencing data. *Current Protocols in Human Genetics*, **2012**, Chapter 7, Unit7.19	3.2	18
19	Global immune characterization of HBV/HCV-related hepatocellular carcinoma identifies macrophage and T-cell subsets associated with disease progression. *Cell Discovery*, **2020**, 6, 90	22.3	17
18	Spatiotemporal Immune Landscape of Colorectal Cancer Liver Metastasis at Single-Cell Level. *Cancer Discovery*, **2021**,	24.4	17
17	scRMD: imputation for single cell RNA-seq data via robust matrix decomposition. *Bioinformatics*, **2020**, 36, 3156-3161	7.2	15

16	Patient-derived tumor-like cell clusters for drug testing in cancer therapy. *Science Translational Medicine*, **2020**, 12,	17.5	14
15	Comprehensive analysis of chromothripsis in 2,658 human cancers using whole-genome sequencing		12
14	Pysim-sv: a package for simulating structural variation data with GC-biases. *BMC Bioinformatics*, **2017**, 18, 53	3.6	10
13	Detecting virus integration sites based on multiple related sequencing data by VirTect. *BMC Medical Genomics*, **2019**, 12, 19	3.7	9
12	Global impact of somatic structural variation on the DNA methylome of human cancers. *Genome Biology*, **2019**, 20, 209	18.3	9
11	SVmine improves structural variation detection by integrative mining of predictions from multiple algorithms. *Bioinformatics*, **2017**, 33, 3348-3354	7.2	5
10	Somatic mutations in renal cell carcinomas from Chinese patients revealed by targeted gene panel sequencing and their associations with prognosis and PD-L1 expression. *Cancer Communications*, **2019**, 39, 37	9.4	4
9	Fast surrogates of U-statistics. *Computational Statistics and Data Analysis*, **2010**, 54, 16-24	1.6	3
8	Compression and aggregation of Bayesian estimates for data intensive computing. *Knowledge and Information Systems*, **2012**, 33, 191-212	2.4	2
7	Single-cell transcriptomic analysis suggests two molecularly subtypes of intrahepatic cholangiocarcinoma.. *Nature Communications*, **2022**, 13, 1642	17.4	2
6	CNV-BAC: Copy number Variation Detection in Bacterial Circular Genome. *Bioinformatics*, **2020**, 36, 3890-3891	7.2	1
5	CNV-BAC: Copy Number Variation Detection in Bacterial Circular Genome		1
4	Direct regression modelling of high-order moments in big data. *Statistics and Its Interface*, **2016**, 9, 445-452	0.4	1
3	Community detection by L_{0}-penalized graph Laplacian. *Electronic Journal of Statistics*, **2018**, 12,	1.2	1
2	Single-cell gene fusion detection by scFusion.. *Nature Communications*, **2022**, 13, 1084	17.4	1
1	Genomics landscape of 185 Streptococcus thermophilus and identification of fermentation biomarkers. *Food Research International*, **2021**, 150, 110711	7	0