Qi Zhao

List of Publications by Year in descending order

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77 papers	5,687 citations	147801 31 h-index	88630 70 g-index
77 all docs	77 docs citations	77 times ranked	9123 citing authors

#	Article	IF	Citations
1	Genomic temporal heterogeneity of circulating tumour DNA in unresectable metastatic colorectal cancer under first-line treatment. Gut, 2022, 71, 1340-1349.	12.1	17
2	MeRIPseqPipe: an integrated analysis pipeline for MeRIP-seq data based on Nextflow. Bioinformatics, 2022, 38, 2054-2056.	4.1	4
3	Driver mutations in ADGRL3 are involved in the evolution of ependymoma. Laboratory Investigation, 2022, , .	3.7	2
4	Raman Spectroscopy: A Novel Technology for Gastric Cancer Diagnosis. Frontiers in Bioengineering and Biotechnology, 2022, 10, 856591.	4.1	20
5	DrugCVar: a platform for evidence-based drug annotation for genetic variants in cancer. Bioinformatics, 2022, 38, 3094-3098.	4.1	1
6	IBS 2.0: an upgraded illustrator for the visualization of biological sequences. Nucleic Acids Research, 2022, 50, W420-W426.	14.5	22
7	Deciphering clonal dynamics and metastatic routines in a rare patient of synchronous triple-primary tumors and multiple metastases with MPTevol. Briefings in Bioinformatics, 2022, 23, .	6.5	2
8	Integrated analysis of single-cell and bulk RNA sequencing data reveals a pan-cancer stemness signature predicting immunotherapy response. Genome Medicine, 2022, 14, 45.	8.2	73
9	Comprehensive profiling of 1015 patientsâ€™ exomes reveals genomic-clinical associations in colorectal cancer. Nature Communications, 2022, 13, 2342.	12.8	21
10	RMVar: an updated database of functional variants involved in RNA modifications. Nucleic Acids Research, 2021, 49, D1405-D1412.	14.5	112
11	Novel Genetic and Epigenetic Biomarkers of Prognostic and Predictive Significance in Stage II/III Colorectal Cancer. Molecular Therapy, 2021, 29, 587-596.	8.2	52
12	Neoantigen landscape in metastatic nasopharyngeal carcinoma. Theranostics, 2021, 11, 6427-6444.	10.0	14
13	MYC-Activated LncRNA MNX1-AS1 Promotes the Progression of Colorectal Cancer by Stabilizing YB1. Cancer Research, 2021, 81, 2636-2650.	0.9	48
14	MesKit: a tool kit for dissecting cancer evolution of multi-region tumor biopsies through somatic alterations. GigaScience, 2021, 10, .	6.4	13
15	Postoperative circulating tumor DNA as markers of recurrence risk in stages II to III colorectal cancer. Journal of Hematology and Oncology, 2021, 14, 80.	17.0	90
16	FTO downregulation mediated by hypoxia facilitates colorectal cancer metastasis. Oncogene, 2021, 40, 5168-5181.	5.9	77
17	Role of ssDNA as a Noninvasive Indicator for the Diagnosis and Prognosis of Hepatocellular Carcinoma: An Exploratory Study. Disease Markers, 2021, 2021, 1-11.	1.3	0
18	POLE/POLD1 mutation in nonâ€exonuclease domain matters for predicting efficacy of immuneâ€checkpointâ€inhibitor therapy. Clinical and Translational Medicine, 2021, 11, e524.	4.0	6

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19	Image-driven classification of functioning and nonfunctioning pituitary adenoma by deep convolutional neural networks. Computational and Structural Biotechnology Journal, 2021, 19, 3077-3086.	4.1	7
20	PD-1 antibody camrelizumab for Epstein-Barr virus-positive metastatic gastric cancer: a single-arm, open-label, phase 2 trial. American Journal of Cancer Research, 2021, 11, 5006-5015.	1.4	0
21	BBCancer: an expression atlas of blood-based biomarkers in the early diagnosis of cancers. Nucleic Acids Research, 2020, 48, D789-D796.	14.5	29
22	AMPKÎ±1 confers survival advantage of colorectal cancer cells under metabolic stress by promoting redox balance through the regulation of glutathione reductase phosphorylation. Oncogene, 2020, 39, 637-650.	5.9	16
23	CrossICC: iterative consensus clustering of cross-platform gene expression data without adjusting batch effect. Briefings in Bioinformatics, 2020, 21, 1818-1824.	6.5	8
24	Deep learning based prediction of reversible HAT/HDAC-specific lysine acetylation. Briefings in Bioinformatics, 2020, 21, 1798-1805.	6.5	24
25	Inhibition of fatty acid catabolism augments the efficacy of oxaliplatin-based chemotherapy in gastrointestinal cancers. Cancer Letters, 2020, 473, 74-89.	7.2	63
26	Targeting the STING pathway in tumor-associated macrophages regulates innate immune sensing of gastric cancer cells. Theranostics, 2020, 10, 498-515.	10.0	68
27	Circulating tumor DNA methylation profiles enable early diagnosis, prognosis prediction, and screening for colorectal cancer. Science Translational Medicine, 2020, 12, .	12.4	260
28	Systematic analysis of the transcriptome in smallâ€cell carcinoma of the oesophagus reveals its immune microenvironment. Clinical and Translational Immunology, 2020, 9, e1173.	3.8	2
29	p.P476S mutation of RBPJL inhibits the efficacy of antiâ€PDâ€1 therapy in oesophageal squamous cell carcinoma by blunting Tâ€cell responses. Clinical and Translational Immunology, 2020, 9, e1172.	3.8	1
30	PGC1Î± protects against hepatic steatosis and insulin resistance via enhancing IL10â€mediated antiâ€inflammatory response. FASEB Journal, 2020, 34, 10751-10761.	0.5	20
31	Germline mutational profile of Chinese patients under 70 years old with colorectal cancer. Cancer Communications, 2020, 40, 620-632.	9.2	7
32	MUC4, MUC16, and TTN genes mutation correlated with prognosis, and predicted tumor mutation burden and immunotherapy efficacy in gastric cancer and panâ€cancer. Clinical and Translational Medicine, 2020, 10, e155.	4.0	80
33	VDRâ€“SOX2 signaling promotes colorectal cancer stemness and malignancy in an acidic microenvironment. Signal Transduction and Targeted Therapy, 2020, 5, 183.	17.1	30
34	autoRPA: A web server for constructing cancer staging models by recursive partitioning analysis. Computational and Structural Biotechnology Journal, 2020, 18, 3361-3367.	4.1	8
35	Classification of gastric cancer by EBV status combined with molecular profiling predicts patient prognosis. Clinical and Translational Medicine, 2020, 10, 353-362.	4.0	13
36	Investigation of the role and mechanism of ARHGAP5-mediated colorectal cancer metastasis. Theranostics, 2020, 10, 5998-6010.	10.0	16

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37	Clinical and genomic characterization of neutral tumor evolution in Head and Neck Squamous Cell Carcinoma. Genomics, 2020, 112, 3448-3454.	2.9	2
38	Evaluation of POLE/POLD1 Variants as Potential Biomarkers for Immune Checkpoint Inhibitor Treatment Outcomesâ€"Reply. JAMA Oncology, 2020, 6, 590.	7.1	3
39	Systematic Analysis of the Aberrances and Functional Implications of Ferroptosis in Cancer. IScience, 2020, 23, 101302.	4.1	128
40	Single AAV-Mediated CRISPR-SaCas9 Inhibits HSV-1 Replication by Editing ICP4 in Trigeminal Ganglion Neurons. Molecular Therapy - Methods and Clinical Development, 2020, 18, 33-43.	4.1	14
41	IDDF2020-ABS-0110â€...lncRNA MNX1-AS1 promotes the progression of colorectal cancer through stabilizing YB1. , 2020, , .		0
42	IDDF2020-ABS-0177â€...ERBB4 high expression and mutations in gastric cancer present opportunities for clinical landscape and therapeutic development. , 2020, , .		1
43	Whole exome and target sequencing identifies MAP2K5 as novel susceptibility gene for familial nonâ€medullary thyroid carcinoma. International Journal of Cancer, 2019, 144, 1321-1330.	5.1	37
44	Designing gene panels for tumor mutational burden estimation: the need to shift from â€˜correlationâ€™ to â€˜accuracyâ€™. , 2019, 7, 206.		37
45	Evaluation of POLE and POLD1 Mutations as Biomarkers for Immunotherapy Outcomes Across Multiple Cancer Types. JAMA Oncology, 2019, 5, 1504.	7.1	287
46	Alteration in TET1 as potential biomarker for immune checkpoint blockade in multiple cancers. , 2019, 7, 264.		66
47	A circRNA signature predicts postoperative recurrence in stage II/III colon cancer. EMBO Molecular Medicine, 2019, 11, e10168.	6.9	90
48	Excessive miR-25-3p maturation via N6-methyladenosine stimulated by cigarette smoke promotes pancreatic cancer progression. Nature Communications, 2019, 10, 1858.	12.8	242
49	Dysregulation, functional implications, and prognostic ability of the circadian clock across cancers. Cancer Medicine, 2019, 8, 1710-1720.	2.8	23
50	IDDF2019-ABS-0289â€...A circRNA signature predicts postoperative recurrence in stage II/III colon cancer. , 2019, , .		1
51	LncRNA LINRIS stabilizes IGF2BP2 and promotes the aerobic glycolysis in colorectal cancer. Molecular Cancer, 2019, 18, 174.	19.2	315
52	PIWI-interacting RNA-36712 restrains breast cancer progression and chemoresistance by interaction with SEPW1 pseudogene SEPW1P RNA. Molecular Cancer, 2019, 18, 9.	19.2	139
53	qPhos: a database of protein phosphorylation dynamics in humans. Nucleic Acids Research, 2019, 47, D451-D458.	14.5	44
54	Liquid biopsies to track trastuzumab resistance in metastatic HER2-positive gastric cancer. Gut, 2019, 68, 1152-1161.	12.1	118

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55	Tumor mutational and indel burden: a systematic pan-cancer evaluation as prognostic biomarkers. Annals of Translational Medicine, 2019, 7, 640-640.	1.7	103
56	ME1 Regulates NADPH Homeostasis to Promote Gastric Cancer Growth and Metastasis. Cancer Research, 2018, 78, 1972-1985.	0.9	86
57	The genomic landscape of small cell carcinoma of the esophagus. Cell Research, 2018, 28, 771-774.	12.0	23
58	A two-microRNA-based signature predicts first-line chemotherapy outcomes in advanced colorectal cancer patients. Cell Death Discovery, 2018, 4, 116.	4.7	16
59	PIWI-interacting RNA-54265 is oncogenic and a potential therapeutic target in colorectal adenocarcinoma. Theranostics, 2018, 8, 5213-5230.	10.0	115
60	LncPipe: A Nextflow-based pipeline for identification and analysis of long non-coding RNAs from RNA-Seq data. Journal of Genetics and Genomics, 2018, 45, 399-401.	3.9	15
61	CPT1A-mediated fatty acid oxidation promotes colorectal cancer cell metastasis by inhibiting anoikis. Oncogene, 2018, 37, 6025-6040.	5.9	211
62	Firmiana: towards a one-stop proteomic cloud platform for data processing and analysis. Nature Biotechnology, 2017, 35, 409-412.	17.5	80
63	VirusMap: A visualization database for the influenza A virus. Journal of Genetics and Genomics, 2017, 44, 281-284.	3.9	4
64	Expression and regulation of long noncoding RNAs during the osteogenic differentiation of periodontal ligament stem cells in the inflammatory microenvironment. Scientific Reports, 2017, 7, 13991.	3.3	16
65	Circulating tumour DNA methylation markers for diagnosis and prognosis of hepatocellular carcinoma. Nature Materials, 2017, 16, 1155-1161.	27.5	641
66	Functional dissection of the role of UHRF1 in the regulation of retinoblastoma methylome. Oncotarget, 2017, 8, 39497-39511.	1.8	8
67	More precise prediction in Chinese patients with penile squamous cell carcinoma: protein kinase CK2Î± catalytic subunit (CK2Î±) as a poor prognosticator. Oncotarget, 2017, 8, 51542-51550.	1.8	4
68	hTERT promotes cell adhesion and migration independent of telomerase activity. Scientific Reports, 2016, 6, 22886.	3.3	45
69	Conformation Selective Antibody Enables Genome Profiling and Leads to Discovery of Parallel G-Quadruplex in Human Telomeres. Cell Chemical Biology, 2016, 23, 1261-1270.	5.2	102
70	GPS-Lipid: a robust tool for the prediction of multiple lipid modification sites. Scientific Reports, 2016, 6, 28249.	3.3	120
71	Mutation profiling in chinese patients with metastatic colorectal cancer and its correlation with clinicopathological features and anti-EGFR treatment response. Oncotarget, 2016, 7, 28356-28368.	1.8	16
72	Birth-related retinal hemorrhages in healthy full-term newborns and their relationship to maternal, obstetric, and neonatal risk factors. Graefe's Archive for Clinical and Experimental Ophthalmology, 2015, 253, 1021-1025.	1.9	35

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73	IBS: an illustrator for the presentation and visualization of biological sequences. Bioinformatics, 2015, 31, 3359-3361.	4.1	817
74	A systematic simulation of the effect of salicylic acid on sphingolipid metabolism. Frontiers in Plant Science, 2015, 6, 186.	3.6	17
75	GPS-SUMO: a tool for the prediction of sumoylation sites and SUMO-interaction motifs. Nucleic Acids Research, 2014, 42, W325-W330.	14.5	417
76	Determination of anterior segment changes with Pentacam after phacoemulsification in eyes with primary angleâ€closure glaucoma. Clinical and Experimental Ophthalmology, 2012, 40, 786-791.	2.6	9
77	Association study of the endothelial nitric oxide synthase gene polymorphisms with essential hypertension in northern Han Chinese. Chinese Medical Journal, 2006, 119, 1065-71.	2.3	14