

Qing Zhong

List of Publications by Year in descending order

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Version: 2024-02-01

39
papers

1,423
citations

430442

18
h-index

414034

32
g-index

46
all docs

46
docs citations

46
times ranked

2864
citing authors

#	ARTICLE	IF	CITATIONS
1	Machine learning for multi-omics data integration in cancer. <i>IScience</i> , 2022, 25, 103798.	1.9	78
2	Pan-cancer proteomic map of 949 human cell lines. <i>Cancer Cell</i> , 2022, 40, 835-849.e8.	7.7	52
3	PIONEER: Pipeline for Generating High-Quality Spectral Libraries for DIA-MS Data. <i>Current Protocols</i> , 2021, 1, e69.	1.3	4
4	Improved identification and quantification of peptides in mass spectrometry data via chemical and random additive noise elimination (CRANE). <i>Bioinformatics</i> , 2021, 37, 4719-4726.	1.8	4
5	Strategies to enable large-scale proteomics for reproducible research. <i>Nature Communications</i> , 2020, 11, 3793.	5.8	75
6	Convergent network effects along the axis of gene expression during prostate cancer progression. <i>Genome Biology</i> , 2020, 21, 302.	3.8	17
7	Addressing the Challenges of High-Throughput Cancer Tissue Proteomics for Clinical Application: ProCan. <i>Proteomics</i> , 2019, 19, e1900109.	1.3	25
8	High-Throughput proteomic analysis of FFPE tissue samples facilitates tumor stratification. <i>Molecular Oncology</i> , 2019, 13, 2305-2328.	2.1	100
9	Comparative analysis of mRNA and protein degradation in prostate tissues indicates high stability of proteins. <i>Nature Communications</i> , 2019, 10, 2524.	5.8	35
10	Quantitative Proteome Landscape of the NCI-60 Cancer Cell Lines. <i>IScience</i> , 2019, 21, 664-680.	1.9	52
11	Targeted next-generation-sequencing for reliable detection of targetable rearrangements in lung adenocarcinoma—a single center retrospective study. <i>Pathology Research and Practice</i> , 2018, 214, 572-578.	1.0	13
12	Comparison of the Proliferation and Differentiation Potential of Human Urine-, Placenta Decidua Basalis-, and Bone Marrow-Derived Stem Cells. <i>Stem Cells International</i> , 2018, 2018, 1-11.	1.2	41
13	Multi-region proteome analysis quantifies spatial heterogeneity of prostate tissue biomarkers. <i>Life Science Alliance</i> , 2018, 1, e201800042.	1.3	51
14	Prevalence of hypertension and diabetes after exposure to extracorporeal shock-wave lithotripsy in patients with renal calculi: a retrospective non-randomized data analysis. <i>International Urology and Nephrology</i> , 2018, 50, 1227-1233.	0.6	4
15	Multi-laboratory proficiency testing of clinical cancer genomic profiling by next-generation sequencing. <i>Pathology Research and Practice</i> , 2018, 214, 957-963.	1.0	11
16	Application of Nanosecond Laser Photolysis Protein Footprinting to Study EGFR Activation by EGF in Cells. <i>Journal of Proteome Research</i> , 2017, 16, 2282-2293.	1.8	21
17	MP62-11 EXTRACORPOREAL SHOCK-WAVE LITHOTRIPSY (ESWL) FOR RENAL STONES IS ASSOCIATED WITH DECREASED KIDNEY FUNCTION AFTER LONG TERM FOLLOW-UP. <i>Journal of Urology</i> , 2017, 197, .	0.2	0
18	A curated collection of tissue microarray images and clinical outcome data of prostate cancer patients. <i>Scientific Data</i> , 2017, 4, 170014.	2.4	21

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19	Value of postmortem studies in deceased neonatal and pediatric intensive care unit patients. <i>Virchows Archiv Fur Pathologische Anatomie Und Physiologie Und Fur Klinische Medizin</i> , 2017, 470, 217-223.	1.4	18
20	Prostate cancer-associated SPOP mutations confer resistance to BET inhibitors through stabilization of BRD4. <i>Nature Medicine</i> , 2017, 23, 1063-1071.	15.2	240
21	Disease grading of heterogeneous tissue using convolutional autoencoder. , 2017, , .		1
22	Cytology smears as excellent starting material for next-generation sequencing-based molecular testing of patients with adenocarcinoma of the lung. <i>Cancer Cytopathology</i> , 2017, 125, 30-40.	1.4	47
23	Heterogeneity characterization of immunohistochemistry stained tissue using convolutional autoencoder. , 2017, , .		3
24	Detection of <i>CCNE1/UR1</i> (19q12) amplification by <i>in situ</i> hybridisation is common in high grade and type II endometrial cancer. <i>Oncotarget</i> , 2017, 8, 14794-14805.	0.8	16
25	Computational Pathology. , 2017, , 263-279.		0
26	Abstract 5565: Multi-omic profiling of prostate cancer evolution in 39 patients. , 2017, , .		1
27	A computational framework for disease grading using protein signatures. , 2016, , .		7
28	Image-based computational quantification and visualization of genetic alterations and tumour heterogeneity. <i>Scientific Reports</i> , 2016, 6, 24146.	1.6	28
29	TRIM24 Is an Oncogenic Transcriptional Activator in Prostate Cancer. <i>Cancer Cell</i> , 2016, 29, 846-858.	7.7	228
30	Deciphering protein signatures using color, morphological, and topological analysis of immunohistochemically stained human tissues. <i>Proceedings of SPIE</i> , 2016, , .	0.8	2
31	MiR-99b-5p expression and response to tyrosine kinase inhibitor treatment in clear cell renal cell carcinoma patients. <i>Oncotarget</i> , 2016, 7, 78433-78447.	0.8	45
32	Oxygen supply maps for hypoxic microenvironment visualization in prostate cancer. <i>Journal of Pathology Informatics</i> , 2016, 7, 3.	0.8	10
33	Positive fibroblast growth factor receptor 3 immunoreactivity is associated with low-grade non-invasive urothelial bladder cancer. <i>Oncology Letters</i> , 2015, 10, 2753-2760.	0.8	13
34	CD10 expression in 325 testicular germ cell tumours. <i>Journal of Clinical Pathology</i> , 2015, 68, 400-403.	1.0	0
35	Connexin 43 expression predicts poor progression-free survival in patients with non-muscle invasive urothelial bladder cancer. <i>Journal of Clinical Pathology</i> , 2015, 68, 819-824.	1.0	34
36	A novel germline mutation of PDGFR- β might be associated with clinical response of colorectal cancer to regorafenib. <i>Annals of Oncology</i> , 2015, 26, 246-248.	0.6	8

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37	<scp>KPNA2</scp> is overexpressed in human and mouse endometrial cancers and promotes cellular proliferation. <i>Journal of Pathology</i> , 2014, 234, 239-252.	2.1	23
38	Modelling of a genetically diverse evolution of Systemic Mastocytosis with Chronic Myelomonocytic Leukemia (SM-CMML) by Next Generation Sequencing. <i>Experimental Hematology and Oncology</i> , 2014, 3, 18.	2.0	5
39	Unsupervised modeling of cell morphology dynamics for time-lapse microscopy. <i>Nature Methods</i> , 2012, 9, 711-713.	9.0	81