Yi Zhu

List of Publications by Year
in descending order

31 papers	2,556 citations	394286 19 h-index	454834 30 g-index
47 all docs	47 docs citations	47 times ranked	5084 citing authors

#	Article	IF	Citations
1	Proteomic and Metabolomic Characterization of COVID-19 Patient Sera. Cell, 2020, 182, 59-72.e15.	13.5	1,137
2	Multi-organ proteomic landscape of COVID-19 autopsies. Cell, 2021, 184, 775-791.e14.	13.5	272
3	High‑throughput proteomic analysis of <scp>FFPE</scp> tissue samples facilitates tumor stratification. Molecular Oncology, 2019, 13, 2305-2328.	2.1	100
4	Homozygous Deletions and Recurrent Amplifications Implicate New Genes Involved in Prostate Cancer. Neoplasia, 2008, 10, 897-IN37.	2.3	99
5	In-depth serum proteomics reveals biomarkers of psoriasis severity and response to traditional Chinese medicine. Theranostics, 2019, 9, 2475-2488.	4.6	76
6	A circulating extracellular vesicles‑based novel screening tool for colorectal cancer revealed by shotgun and data‑independent acquisition mass spectrometry. Journal of Extracellular Vesicles, 2020, 9, 1750202.	5.5	70
7	Proteomic and metabolomic profiling of urine uncovers immune responses in patients with COVID-19. Cell Reports, 2022, 38, 110271.	2.9	66
8	High-throughput proteomics and AI for cancer biomarker discovery. Advanced Drug Delivery Reviews, 2021, 176, 113844.	6.6	54
9	Quantitative Proteome Landscape of the NCI-60 Cancer Cell Lines. IScience, 2019, 21, 664-680.	1.9	52
10	DPHL: A DIA Pan-human Protein Mass Spectrometry Library for Robust Biomarker Discovery. Genomics, Proteomics and Bioinformatics, 2020, 18, 104-119.	3.0	51
11	Gut microbiota, inflammation, and molecular signatures of host response to infection. Journal of Genetics and Genomics, 2021, 48, 792-802.	1.7	49
12	Accelerated Lysis and Proteolytic Digestion of Biopsy-Level Fresh-Frozen and FFPE Tissue Samples Using Pressure Cycling Technology. Journal of Proteome Research, 2020, 19, 1982-1990.	1.8	47
13	PulseDIA: Data-Independent Acquisition Mass Spectrometry Using Multi-Injection Pulsed Gas-Phase Fractionation. Journal of Proteome Research, 2021, 20, 279-288.	1.8	37
14	Comparative analysis of mRNA and protein degradation in prostate tissues indicates high stability of proteins. Nature Communications, 2019, 10, 2524.	5.8	35
15	Identification of Protein Abundance Changes in Hepatocellular Carcinoma Tissues Using PCT–SWATH. Proteomics - Clinical Applications, 2019, 13, e1700179.	0.8	32
16	SnapShot: Clinical proteomics. Cell, 2021, 184, 4840-4840.e1.	13.5	29
17	Eleven routine clinical features predict COVID-19 severity uncovered by machine learning of longitudinal measurements. Computational and Structural Biotechnology Journal, 2021, 19, 3640-3649.	1.9	28
18	Accelerated Protein Biomarker Discovery from FFPE Tissue Samples Using Single-Shot, Short Gradient Microflow SWATH MS. Journal of Proteome Research, 2020, 19, 2732-2741.	1.8	27

#	Article	IF	Citations
19	A curated collection of tissue microarray images and clinical outcome data of prostate cancer patients. Scientific Data, 2017, 4, 170014.	2.4	21
20	METTL9 mediated N1-histidine methylation of zinc transporters is required for tumor growth. Protein and Cell, 2021, 12, 965-970.	4.8	20
21	High-Throughput Proteomic Analysis of Fresh-Frozen Biopsy Tissue Samples Using Pressure Cycling Technology Coupled with SWATH Mass Spectrometry. Methods in Molecular Biology, 2017, 1788, 279-287.	0.4	19
22	Potential Use of Serum Proteomics for Monitoring COVID-19 Progression to Complement RT-PCR Detection. Journal of Proteome Research, 2022, 21, 90-100.	1.8	19
23	Proteomic and metabolomic investigation of serum lactate dehydrogenase elevation in COVIDâ€19 patients. Proteomics, 2021, 21, e2100002.	1.3	18
24	The Hippo-TAZ axis mediates vascular endothelial growth factor C in glioblastoma-derived exosomes to promote angiogenesis. Cancer Letters, 2021, 513, 1-13.	3.2	18
25	Convergent network effects along the axis of gene expression during prostate cancer progression. Genome Biology, 2020, 21, 302.	3.8	17
26	Stratification of follicular thyroid tumours using dataâ€independent acquisition proteomics and a comprehensive thyroid tissue spectral library. Molecular Oncology, 2022, 16, 1611-1624.	2.1	14
27	Generating Proteomic Big Data for Precision Medicine. Proteomics, 2020, 20, 1900358.	1.3	7
28	Proteomics profiling of colorectal cancer progression identifies PLOD2 as a potential therapeutic target. Cancer Communications, 2022, 42, 164-169.	3.7	7
29	Optimization of Microflow LC Coupled with Scanning SWATH and Its Application in Hepatocellular Carcinoma Tissues. Journal of Proteome Research, 0, , .	1.8	5
30	DIA-Based Proteomics Identifies IDH2 as a Targetable Regulator of Acquired Drug Resistance in Chronic Myeloid Leukemia. Molecular and Cellular Proteomics, 2022, 21, 100187.	2.5	4
31	Towards a one-stop solution for large-scale proteomics data analysis. Science China Life Sciences, 2018, 61, 351-354.	2.3	2