

# Yi Zhu

## List of Publications by Year in descending order

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Version: 2024-02-01

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	Potential Use of Serum Proteomics for Monitoring COVID-19 Progression to Complement RT-PCR Detection. <i>Journal of Proteome Research</i> , 2022, 21, 90-100.	1.8	19
2	Proteomics profiling of colorectal cancer progression identifies PLOD2 as a potential therapeutic target. <i>Cancer Communications</i> , 2022, 42, 164-169.	3.7	7
3	Proteomic and metabolomic profiling of urine uncovers immune responses in patients with COVID-19. <i>Cell Reports</i> , 2022, 38, 110271.	2.9	66
4	DIA-Based Proteomics Identifies IDH2 as a Targetable Regulator of Acquired Drug Resistance in Chronic Myeloid Leukemia. <i>Molecular and Cellular Proteomics</i> , 2022, 21, 100187.	2.5	4
5	Stratification of follicular thyroid tumours using data-independent acquisition proteomics and a comprehensive thyroid tissue spectral library. <i>Molecular Oncology</i> , 2022, 16, 1611-1624.	2.1	14
6	PulseDIA: Data-Independent Acquisition Mass Spectrometry Using Multi-Injection Pulsed Gas-Phase Fractionation. <i>Journal of Proteome Research</i> , 2021, 20, 279-288.	1.8	37
7	Eleven routine clinical features predict COVID-19 severity uncovered by machine learning of longitudinal measurements. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 3640-3649.	1.9	28
8	Multi-organ proteomic landscape of COVID-19 autopsies. <i>Cell</i> , 2021, 184, 775-791.e14.	13.5	272
9	Gut microbiota, inflammation, and molecular signatures of host response to infection. <i>Journal of Genetics and Genomics</i> , 2021, 48, 792-802.	1.7	49
10	Proteomic and metabolomic investigation of serum lactate dehydrogenase elevation in COVID-19 patients. <i>Proteomics</i> , 2021, 21, e2100002.	1.3	18
11	METTL9 mediated N1-histidine methylation of zinc transporters is required for tumor growth. <i>Protein and Cell</i> , 2021, 12, 965-970.	4.8	20
12	The Hippo-TAZ axis mediates vascular endothelial growth factor C in glioblastoma-derived exosomes to promote angiogenesis. <i>Cancer Letters</i> , 2021, 513, 1-13.	3.2	18
13	SnapShot: Clinical proteomics. <i>Cell</i> , 2021, 184, 4840-4840.e1.	13.5	29
14	High-throughput proteomics and AI for cancer biomarker discovery. <i>Advanced Drug Delivery Reviews</i> , 2021, 176, 113844.	6.6	54
15	DPHL: A DIA Pan-human Protein Mass Spectrometry Library for Robust Biomarker Discovery. <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 104-119.	3.0	51
16	Generating Proteomic Big Data for Precision Medicine. <i>Proteomics</i> , 2020, 20, 1900358.	1.3	7
17	Convergent network effects along the axis of gene expression during prostate cancer progression. <i>Genome Biology</i> , 2020, 21, 302.	3.8	17
18	Proteomic and Metabolomic Characterization of COVID-19 Patient Sera. <i>Cell</i> , 2020, 182, 59-72.e15.	13.5	1,137

#	ARTICLE	IF	CITATIONS
19	Accelerated Lysis and Proteolytic Digestion of Biopsy-Level Fresh-Frozen and FFPE Tissue Samples Using Pressure Cycling Technology. <i>Journal of Proteome Research</i> , 2020, 19, 1982-1990.	1.8	47
20	Accelerated Protein Biomarker Discovery from FFPE Tissue Samples Using Single-Shot, Short Gradient Microflow SWATH MS. <i>Journal of Proteome Research</i> , 2020, 19, 2732-2741.	1.8	27
21	A circulating extracellular vesicles-based novel screening tool for colorectal cancer revealed by shotgun and data-independent acquisition mass spectrometry. <i>Journal of Extracellular Vesicles</i> , 2020, 9, 1750202.	5.5	70
22	High-throughput proteomic analysis of FFPE tissue samples facilitates tumor stratification. <i>Molecular Oncology</i> , 2019, 13, 2305-2328.	2.1	100
23	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
24	In-depth serum proteomics reveals biomarkers of psoriasis severity and response to traditional Chinese medicine. <i>Theranostics</i> , 2019, 9, 2475-2488.	4.6	76
25	Quantitative Proteome Landscape of the NCI-60 Cancer Cell Lines. <i>IScience</i> , 2019, 21, 664-680.	1.9	52
26	Identification of Protein Abundance Changes in Hepatocellular Carcinoma Tissues Using PCT-SWATH. <i>Proteomics - Clinical Applications</i> , 2019, 13, e1700179.	0.8	32
27	Towards a one-stop solution for large-scale proteomics data analysis. <i>Science China Life Sciences</i> , 2018, 61, 351-354.	2.3	2
28	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
29	High-Throughput Proteomic Analysis of Fresh-Frozen Biopsy Tissue Samples Using Pressure Cycling Technology Coupled with SWATH Mass Spectrometry. <i>Methods in Molecular Biology</i> , 2017, 1788, 279-287.	0.4	19
30	Homozygous Deletions and Recurrent Amplifications Implicate New Genes Involved in Prostate Cancer. <i>Neoplasia</i> , 2008, 10, 897-IN37.	2.3	99
31	Optimization of Microflow LC Coupled with Scanning SWATH and Its Application in Hepatocellular Carcinoma Tissues. <i>Journal of Proteome Research</i> , 0, , .	1.8	5