

# Xiao Yi

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5405289/publications.pdf>

Version: 2024-02-01

15  
papers

1,977  
citations

759055

12  
h-index

996849

15  
g-index

23  
all docs

23  
docs citations

23  
times ranked

4306  
citing authors

#	ARTICLE	IF	CITATIONS
1	Quantitative proteomic landscapes of primary and recurrent glioblastoma reveal a protumorigenic role for FBXO2-dependent glioma-microenvironment interactions. <i>Neuro-Oncology</i> , 2023, 25, 290-302.	0.6	8
2	Proteomic and metabolomic profiling of urine uncovers immune responses in patients with COVID-19. <i>Cell Reports</i> , 2022, 38, 110271.	2.9	66
3	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
4	BatchServer: A Web Server for Batch Effect Evaluation, Visualization, and Correction. <i>Journal of Proteome Research</i> , 2021, 20, 1079-1086.	1.8	10
5	Multi-organ proteomic landscape of COVID-19 autopsies. <i>Cell</i> , 2021, 184, 775-791.e14.	13.5	272
6	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
7	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
8	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
9	Computational Optimization of Spectral Library Size Improves DIA-MS Proteome Coverage and Applications to 15 Tumors. <i>Journal of Proteome Research</i> , 2021, 20, 5392-5401.	1.8	21
10	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
11	Phenotype Classification using Proteome Data in a Data-Independent Acquisition Tensor Format. <i>Journal of the American Society for Mass Spectrometry</i> , 2020, 31, 2296-2304.	1.2	7
12	Proteomic and Metabolomic Characterization of COVID-19 Patient Sera. <i>Cell</i> , 2020, 182, 59-72.e15.	13.5	1,137
13	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
14	High-throughput proteomic analysis of FFPE tissue samples facilitates tumor stratification. <i>Molecular Oncology</i> , 2019, 13, 2305-2328.	2.1	100
15	Identification of Protein Abundance Changes in Hepatocellular Carcinoma Tissues Using PCT-SWATH. <i>Proteomics - Clinical Applications</i> , 2019, 13, e1700179.	0.8	32