

Tiannan Guo

List of Publications by Year in descending order

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86
papers

5,038
citations

159358

30
h-index

110170

64
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114
all docs

114
docs citations

114
times ranked

8630
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	PROTREC: A probability-based approach for recovering missing proteins based on biological networks. <i>Journal of Proteomics</i> , 2022, 250, 104392.	1.2	8
3	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
4	A prostate cancer tissue specific spectral library for targeted proteomic analysis. <i>Proteomics</i> , 2022, 22, e2100147.	1.3	10
5	Proteomics profiling of colorectal cancer progression identifies PLOD2 as a potential therapeutic target. <i>Cancer Communications</i> , 2022, 42, 164-169.	3.7	7
6	Proteomic and metabolomic profiling of urine uncovers immune responses in patients with COVID-19. <i>Cell Reports</i> , 2022, 38, 110271.	2.9	66
7	sRAGE alleviates SARS-CoV-2-induced pneumonia in hamster. <i>Signal Transduction and Targeted Therapy</i> , 2022, 7, 36.	7.1	1
8	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
9	Proteomic datasets of HeLa and SiHa cell lines acquired by DDA-PASEF and diaPASEF. <i>Data in Brief</i> , 2022, 41, 107919.	0.5	5
10	Circulating Proteome and Progression of Type 2 Diabetes. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2022, 107, 1616-1625.	1.8	4
11	Multi-omics in COVID-19: Seeing the unseen but overlooked in the clinic. <i>Cell Reports Medicine</i> , 2022, 3, 100580.	3.3	9
12	RAB2A promotes cervical cancer progression as revealed by comprehensive analysis of HPV integration and proteome in longitudinal cervical samples. <i>Clinical and Translational Medicine</i> , 2022, 12, e767.	1.7	2
13	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
14	Understudied proteins: opportunities and challenges for functional proteomics. <i>Nature Methods</i> , 2022, 19, 774-779.	9.0	83
15	An open invitation to the Understudied Proteins Initiative. <i>Nature Biotechnology</i> , 2022, 40, 815-817.	9.4	25
16	Proteomic characterization of Omicron SARS-CoV-2 host response. <i>Cell Discovery</i> , 2022, 8, 46.	3.1	8
17	Molecular Subgroups of Intrahepatic Cholangiocarcinoma Discovered by Single-Cell RNA Sequencing-Assisted Multiomics Analysis. <i>Cancer Immunology Research</i> , 2022, 10, 811-828.	1.6	21
18	An in-library ligation strategy and its application in CRISPR/Cas9 screening of high-order gRNA combinations. <i>Nucleic Acids Research</i> , 2022, 50, 6575-6586.	6.5	1

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19	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
20	BatchServer: A Web Server for Batch Effect Evaluation, Visualization, and Correction. <i>Journal of Proteome Research</i> , 2021, 20, 1079-1086.	1.8	10
21	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
22	Multi-organ proteomic landscape of COVID-19 autopsies. <i>Cell</i> , 2021, 184, 775-791.e14.	13.5	272
23	Immunometabolism the CyTOF way. <i>Immunity</i> , 2021, 54, 610-613.	6.6	6
24	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
25	Proteomic and metabolomic investigation of serum lactate dehydrogenase elevation in COVID-19 patients. <i>Proteomics</i> , 2021, 21, e2100002.	1.3	18
26	On the feasibility of deep learning applications using raw mass spectrometry data. <i>Bioinformatics</i> , 2021, 37, i245-i253.	1.8	10
27	Phenotypic characterization of two novel cell line models of castration-resistant prostate cancer. <i>Prostate</i> , 2021, 81, 1159-1171.	1.2	9
28	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
29	SnapShot: Clinical proteomics. <i>Cell</i> , 2021, 184, 4840-4840.e1.	13.5	29
30	High-throughput proteomics and AI for cancer biomarker discovery. <i>Advanced Drug Delivery Reviews</i> , 2021, 176, 113844.	6.6	54
31	ProteomeExpert: a Docker image-based web server for exploring, modeling, visualizing and mining quantitative proteomic datasets. <i>Bioinformatics</i> , 2021, 37, 273-275.	1.8	12
32	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
33	Novel deep learning radiomics model for preoperative evaluation of hepatocellular carcinoma differentiation based on computed tomography data. <i>Clinical and Translational Medicine</i> , 2021, 11, e570.	1.7	11
34	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
35	Generating Proteomic Big Data for Precision Medicine. <i>Proteomics</i> , 2020, 20, 1900358.	1.3	7
36	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

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37	Convergent network effects along the axis of gene expression during prostate cancer progression. <i>Genome Biology</i> , 2020, 21, 302.	3.8	17
38	Proteomic and Metabolomic Characterization of COVID-19 Patient Sera. <i>Cell</i> , 2020, 182, 59-72.e15.	13.5	1,137
39	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
40	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
41	Data-Independent Acquisition Mass Spectrometry-Based Proteomics and Software Tools: A Glimpse in 2020. <i>Proteomics</i> , 2020, 20, e1900276.	1.3	222
42	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
43	IDDF2020-ABS-0073...Proteomics reveals that rectal cancer patients with neoadjuvant radiochemotherapy reach pCR through immune activation. , 2020, , .		0
44	Proteomic investigation of intra-tumor heterogeneity using network-based contextualization " A case study on prostate cancer. <i>Journal of Proteomics</i> , 2019, 206, 103446.	1.2	3
45	High-throughput proteomic analysis of FFPE tissue samples facilitates tumor stratification. <i>Molecular Oncology</i> , 2019, 13, 2305-2328.	2.1	100
46	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
47	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
48	Quantitative Proteome Landscape of the NCI-60 Cancer Cell Lines. <i>IScience</i> , 2019, 21, 664-680.	1.9	52
49	Arabidopsis proteome and the mass spectral assay library. <i>Scientific Data</i> , 2019, 6, 278.	2.4	39
50	Identification of Protein Abundance Changes in Hepatocellular Carcinoma Tissues Using PCT-SWATH. <i>Proteomics - Clinical Applications</i> , 2019, 13, e1700179.	0.8	32
51	Towards a one-stop solution for large-scale proteomics data analysis. <i>Science China Life Sciences</i> , 2018, 61, 351-354.	2.3	2
52	Multi-region proteome analysis quantifies spatial heterogeneity of prostate tissue biomarkers. <i>Life Science Alliance</i> , 2018, 1, e201800042.	1.3	51
53	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
54	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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55	Phosphatase POPX2 Exhibits Dual Regulatory Functions in Cancer Metastasis. <i>Journal of Proteome Research</i> , 2017, 16, 698-711.	1.8	13
56	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
57	Image-based computational quantification and visualization of genetic alterations and tumour heterogeneity. <i>Scientific Reports</i> , 2016, 6, 24146.	1.6	28
58	TRIM24 Is an Oncogenic Transcriptional Activator in Prostate Cancer. <i>Cancer Cell</i> , 2016, 29, 846-858.	7.7	228
59	Reproducible Tissue Homogenization and Protein Extraction for Quantitative Proteomics Using MicroPestle-Assisted Pressure-Cycling Technology. <i>Journal of Proteome Research</i> , 2016, 15, 1821-1829.	1.8	41
60	Minimal sample requirement for highly multiplexed protein quantification in cell lines and tissues by PCT-SWATH mass spectrometry. <i>Proteomics</i> , 2015, 15, 3711-3721.	1.3	44
61	Quantitative proteomics signature profiling based on network contextualization. <i>Biology Direct</i> , 2015, 10, 71.	1.9	34
62	Mass spectrometry-based proteomic quest for diabetes biomarkers. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2015, 1854, 519-527.	1.1	42
63	The methyltransferase Ezh2 controls cell adhesion and migration through direct methylation of the extranuclear regulatory protein talin. <i>Nature Immunology</i> , 2015, 16, 505-516.	7.0	144
64	Rapid mass spectrometric conversion of tissue biopsy samples into permanent quantitative digital proteome maps. <i>Nature Medicine</i> , 2015, 21, 407-413.	15.2	358
65	Global Metabonomic and Proteomic Analysis of Human Conjunctival Epithelial Cells (IOBA-NHC) in Response to Hyperosmotic Stress. <i>Journal of Proteome Research</i> , 2015, 14, 3982-3995.	1.8	25
66	LEO1 Is Regulated by PRL-3 and Mediates Its Oncogenic Properties in Acute Myelogenous Leukemia. <i>Cancer Research</i> , 2014, 74, 3043-3053.	0.4	29
67	Quantitative proteomics reveals differential biological processes in healthy neonatal cord neutrophils and adult neutrophils. <i>Proteomics</i> , 2014, 14, 1688-1697.	1.3	22
68	A repository of assays to quantify 10,000 human proteins by SWATH-MS. <i>Scientific Data</i> , 2014, 1, 140031.	2.4	370
69	Integrative Transcriptome and Proteome Study to Identify the Signaling Network Regulated by POPX2 Phosphatase. <i>Journal of Proteome Research</i> , 2013, 12, 2525-2536.	1.8	18
70	Multidimensional Identification of Tissue Biomarkers of Gastric Cancer. <i>Journal of Proteome Research</i> , 2012, 11, 3405-3413.	1.8	14
71	Abstract 2460: Extracellular matrix protein expression is associated with chemotherapy resistance in breast cancer. , 2012, , .		0
72	Global molecular dysfunctions in gastric cancer revealed by an integrated analysis of the phosphoproteome and transcriptome. <i>Cellular and Molecular Life Sciences</i> , 2011, 68, 1983-2002.	2.4	32

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73	Investigation of POPX2 phosphatase functions by comparative phosphoproteomic analysis. <i>Proteomics</i> , 2011, 11, 2891-2900.	1.3	20
74	Elucidating Structural Dynamics of Integral Membrane Proteins on Native Cell Surface by Hydroxyl Radical Footprinting and Nano LC-MS/MS. <i>Methods in Molecular Biology</i> , 2011, 790, 287-303.	0.4	5
75	Simultaneous Analysis of Proteome, Phospho- and Glycoproteome of Rat Kidney Tissue with Electrostatic Repulsion Hydrophilic Interaction Chromatography. <i>PLoS ONE</i> , 2011, 6, e16884.	1.1	54
76	Quantitative Proteomics Discloses MET Expression in Mitochondria as a Direct Target of MET Kinase Inhibitor in Cancer Cells. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 2629-2641.	2.5	22
77	Simultaneous Characterization of Glyco- and Phosphoproteomes of Mouse Brain Membrane Proteome with Electrostatic Repulsion Hydrophilic Interaction Chromatography. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 635-647.	2.5	90
78	Novel Application of Electrostatic Repulsion-Hydrophilic Interaction Chromatography (ERLIC) in Shotgun Proteomics: Comprehensive Profiling of Rat Kidney Proteome. <i>Journal of Proteome Research</i> , 2010, 9, 3520-3526.	1.8	84
79	Elucidating in Vivo Structural Dynamics in Integral Membrane Protein by Hydroxyl Radical Footprinting. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 1999-2010.	2.5	56
80	Elucidating the Structure of Cyclotides by Partial Acid Hydrolysis and LC-MS/MS Analysis. <i>Analytical Chemistry</i> , 2009, 81, 1079-1088.	3.2	33
81	One-Step Procedure for Peptide Extraction from In-Gel Digestion Sample for Mass Spectrometric Analysis. <i>Analytical Chemistry</i> , 2008, 80, 9797-9805.	3.2	19
82	A Comparative Study of Electrostatic Repulsion-Hydrophilic Interaction Chromatography (ERLIC) versus SCX-IMAC-Based Methods for Phosphopeptide Isolation/Enrichment. <i>Journal of Proteome Research</i> , 2008, 7, 4869-4877.	1.8	88
83	Hybridization of Pulsed-Q Dissociation and Collision-Activated Dissociation in Linear Ion Trap Mass Spectrometer for iTRAQ Quantitation. <i>Journal of Proteome Research</i> , 2008, 7, 4831-4840.	1.8	63
84	Expression and functional role of HERG1, K ⁺ channels in leukemic cells and leukemic stem cells. <i>Journal of Huazhong University of Science and Technology [Medical Sciences]</i> , 2007, 27, 257-260.	1.0	8
85	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
86	Proteotypic Differences of Follicular-Patterned Thyroid Neoplasms. <i>Frontiers in Endocrinology</i> , 0, 13, .	1.5	3