

Siqi Liu

List of Publications by Year in descending order

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57
papers

6,718
citations

218677

26
h-index

149698

56
g-index

65
all docs

65
docs citations

65
times ranked

12299
citing authors

#	ARTICLE	IF	CITATIONS
1	Profiling the Bisecting N-acetylglucosamine Modification in Amniotic Membrane via Mass Spectrometry. <i>Genomics, Proteomics and Bioinformatics</i> , 2022, 20, 648-656.	6.9	2
2	Global Quantification of Glutathione S-Transferases in Human Serum Using LC-MS/MS Coupled with Affinity Enrichment. <i>Journal of Proteome Research</i> , 2022, 21, 1311-1320.	3.7	1
3	Proteomic Profiling of Gastric Signet Ring Cell Carcinoma Tissues Reveals Characteristic Changes of the Complement Cascade Pathway. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100068.	3.8	4
4	The trans-omics landscape of COVID-19. <i>Nature Communications</i> , 2021, 12, 4543.	12.8	75
5	An increase of phosphatidylcholines in follicular fluid implies attenuation of embryo quality on day 3 post-fertilization. <i>BMC Biology</i> , 2021, 19, 200.	3.8	6
6	Prediction and Validation of Mouse Meiosis-Essential Genes Based on Spermatogenesis Proteome Dynamics. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100014.	3.8	18
7	Progress Identifying and Analyzing the Human Proteome: 2021 Metrics from the HUPO Human Proteome Project. <i>Journal of Proteome Research</i> , 2021, 20, 5227-5240.	3.7	30
8	Discovery of Missing Proteins from an Aneuploidy Cell Line Using a Proteogenomic Approach. <i>Journal of Proteome Research</i> , 2021, 20, 5329-5339.	3.7	2
9	Exploration of Missing Proteins by a Combination Approach to Enrich the Low-Abundance Hydrophobic Proteins from Four Cancer Cell Lines. <i>Journal of Proteome Research</i> , 2020, 19, 401-408.	3.7	9
10	Standardization and harmonization of distributed multi-center proteotype analysis supporting precision medicine studies. <i>Nature Communications</i> , 2020, 11, 5248.	12.8	49
11	D283 Med, a Cell Line Derived from Peritoneal Metastatic Medulloblastoma: A Good Choice for Missing Protein Discovery. <i>Journal of Proteome Research</i> , 2020, 19, 4857-4866.	3.7	5
12	Research on the Human Proteome Reaches a Major Milestone: >90% of Predicted Human Proteins Now Credibly Detected, According to the HUPO Human Proteome Project. <i>Journal of Proteome Research</i> , 2020, 19, 4735-4746.	3.7	38
13	Pathway attenuation of fatty acid beta-oxidation in the skeletal muscle of a type 2 diabetic mouse model. <i>Rapid Communications in Mass Spectrometry</i> , 2020, 34, e8869.	1.5	1
14	Evaluation and minimization of nonspecific tryptic cleavages in proteomic sample preparation. <i>Rapid Communications in Mass Spectrometry</i> , 2020, 34, e8733.	1.5	10
15	pClean: An Algorithm To Preprocess High-Resolution Tandem Mass Spectra for Database Searching. <i>Journal of Proteome Research</i> , 2019, 18, 3235-3244.	3.7	3
16	Progress on Identifying and Characterizing the Human Proteome: 2019 Metrics from the HUPO Human Proteome Project. <i>Journal of Proteome Research</i> , 2019, 18, 4098-4107.	3.7	41
17	Alternative Strategy To Explore Missing Proteins with Low Molecular Weight. <i>Journal of Proteome Research</i> , 2019, 18, 4180-4188.	3.7	7
18	Distinct gut metagenomics and metaproteomics signatures in prediabetics and treatment-naïve type 2 diabetics. <i>EBioMedicine</i> , 2019, 47, 373-383.	6.1	101

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19	Quantitative proteomics reveals the key molecular events occurring at different cell cycle phases of the in situ blooming dinoflagellate cells. <i>Science of the Total Environment</i> , 2019, 676, 62-71.	8.0	14
20	Rapid evolution of protein diversity by de novo origination in <i>Oryza</i> . <i>Nature Ecology and Evolution</i> , 2019, 3, 679-690.	7.8	121
21	Improvements to the Rice Genome Annotation Through Large-Scale Analysis of RNA-Seq and Proteomics Data Sets. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 86-98.	3.8	22
22	Reagents for Isobaric Labeling Peptides in Quantitative Proteomics. <i>Analytical Chemistry</i> , 2018, 90, 12366-12371.	6.5	33
23	Launching the C-HPP neXt-CP50 Pilot Project for Functional Characterization of Identified Proteins with No Known Function. <i>Journal of Proteome Research</i> , 2018, 17, 4042-4050.	3.7	41
24	Improvement of Peptide Separation for Exploring the Missing Proteins Localized on Membranes. <i>Journal of Proteome Research</i> , 2018, 17, 4152-4159.	3.7	12
25	Improved Peptide Retention Time Prediction in Liquid Chromatography through Deep Learning. <i>Analytical Chemistry</i> , 2018, 90, 10881-10888.	6.5	107
26	Progress on Identifying and Characterizing the Human Proteome: 2018 Metrics from the HUPO Human Proteome Project. <i>Journal of Proteome Research</i> , 2018, 17, 4031-4041.	3.7	59
27	Lowering Endogenous Cathepsin D Abundance Results in Reactive Oxygen Species Accumulation and Cell Senescence. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 1217-1232.	3.8	13
28	Lipidomic profiling reveals distinct differences in plasma lipid composition in healthy, prediabetic, and type 2 diabetic individuals. <i>GigaScience</i> , 2017, 6, 1-12.	6.4	49
29	metaX: a flexible and comprehensive software for processing metabolomics data. <i>BMC Bioinformatics</i> , 2017, 18, 183.	2.6	489
30	Digging More Missing Proteins Using an Enrichment Approach with ProteoMiner. <i>Journal of Proteome Research</i> , 2017, 16, 4330-4339.	3.7	26
31	Lipidomics profiling reveals the role of glycerophospholipid metabolism in psoriasis. <i>GigaScience</i> , 2017, 6, 1-11.	6.4	162
32	Multi-laboratory assessment of reproducibility, qualitative and quantitative performance of SWATH-mass spectrometry. <i>Nature Communications</i> , 2017, 8, 291.	12.8	423
33	Combination Strategy of Quantitative Proteomics Uncovers the Related Proteins of Colorectal Cancer in the Interstitial Fluid of Colonic Tissue from the AOM-DSS Mouse Model. <i>Methods in Molecular Biology</i> , 2017, 1788, 185-192.	0.9	3
34	Improvement of peptide identification with considering the abundance of mRNA and peptide. <i>BMC Bioinformatics</i> , 2017, 18, 109.	2.6	7
35	A Combinational Strategy upon RNA Sequencing and Peptidomics Unravels a Set of Novel Toxin Peptides in Scorpion <i>Mesobuthus martensii</i> . <i>Toxins</i> , 2016, 8, 286.	3.4	8
36	Peptide Biosynthesis with Stable Isotope Labeling from a Cell-free Expression System for Targeted Proteomics with Absolute Quantification. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 2819-2828.	3.8	9

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37	Drug Resistance in Colorectal Cancer Cell Lines is Partially Associated with Aneuploidy Status in Light of Profiling Gene Expression. <i>Journal of Proteome Research</i> , 2016, 15, 4047-4059.	3.7	14
38	PGA: an R/Bioconductor package for identification of novel peptides using a customized database derived from RNA-Seq. <i>BMC Bioinformatics</i> , 2016, 17, 244.	2.6	48
39	A Comprehensive Investigation toward the Indicative Proteins of Bladder Cancer in Urine: From Surveying Cell Secretomes to Verifying Urine Proteins. <i>Journal of Proteome Research</i> , 2016, 15, 2164-2177.	3.7	19
40	Discovery of potential colorectal cancer serum biomarkers through quantitative proteomics on the colonic tissue interstitial fluids from the AOM&DSS mouse model. <i>Journal of Proteomics</i> , 2016, 132, 31-40.	2.4	28
41	The levels of serine proteases in colon tissue interstitial fluid and serum serve as an indicator of colorectal cancer progression. <i>Oncotarget</i> , 2016, 7, 32592-32606.	1.8	22
42	Rapid Biosynthesis of Stable Isotope-Labeled Peptides from a Reconstituted In Vitro Translation System for Targeted Proteomics. <i>Methods in Enzymology</i> , 2015, 565, 347-366.	1.0	0
43	Biomarker Discovery and Verification of Esophageal Squamous Cell Carcinoma Using Integration of SWATH/MRM. <i>Journal of Proteome Research</i> , 2015, 14, 3793-3803.	3.7	41
44	Special Enrichment Strategies Greatly Increase the Efficiency of Missing Proteins Identification from Regular Proteome Samples. <i>Journal of Proteome Research</i> , 2015, 14, 3680-3692.	3.7	15
45	Insights from ENCODE on Missing Proteins: Why β -Defensin Expression Is Scarcely Detected. <i>Journal of Proteome Research</i> , 2015, 14, 3635-3644.	3.7	8
46	Tissue-Based Proteogenomics Reveals that Human Testis Endows Plentiful Missing Proteins. <i>Journal of Proteome Research</i> , 2015, 14, 3583-3594.	3.7	45
47	IQuant: An automated pipeline for quantitative proteomics based upon isobaric tags. <i>Proteomics</i> , 2014, 14, 2280-2285.	2.2	253
48	Prion-like Polymerization Underlies Signal Transduction in Antiviral Immune Defense and Inflammasome Activation. <i>Cell</i> , 2014, 156, 1207-1222.	28.9	489
49	Systematic Analyses of the Transcriptome, Translatome, and Proteome Provide a Global View and Potential Strategy for the C-HPP. <i>Journal of Proteome Research</i> , 2014, 13, 38-49.	3.7	60
50	sapFinder: an R/Bioconductor package for detection of variant peptides in shotgun proteomics experiments. <i>Bioinformatics</i> , 2014, 30, 3136-3138.	4.1	25
51	Quantitative Proteomics Reveals the Temperature-Dependent Proteins Encoded by a Series of Cluster Genes in <i>Thermoanaerobacter tengcongensis</i> . <i>Molecular and Cellular Proteomics</i> , 2013, 12, 2266-2277.	3.8	58
52	Quantitative Analysis of the Human AKR Family Members in Cancer Cell Lines Using the mTRAQ/MRM Approach. <i>Journal of Proteome Research</i> , 2013, 12, 2022-2033.	3.7	23
53	Stress Responsive Proteins Are Actively Regulated during Rice (<i>Oryza sativa</i>) Embryogenesis as Indicated by Quantitative Proteomics Analysis. <i>PLoS ONE</i> , 2013, 8, e74229.	2.5	38
54	Matrine, a novel autophagy inhibitor, blocks trafficking and the proteolytic activation of lysosomal proteases. <i>Carcinogenesis</i> , 2013, 34, 128-138.	2.8	64

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55	MAVS recruits multiple ubiquitin E3 ligases to activate antiviral signaling cascades. <i>ELife</i> , 2013, 2, e00785.	6.0	282
56	Proteolytic Characteristics of Cathepsin D Related to the Recognition and Cleavage of Its Target Proteins. <i>PLoS ONE</i> , 2013, 8, e65733.	2.5	36
57	A Draft Sequence of the Rice Genome (<i>Oryza sativa</i> L. ssp. <i>indica</i>). <i>Science</i> , 2002, 296, 79-92.	12.6	3,146