

Jun Li

List of Publications by Year in descending order

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44
papers

1,674
citations

279798

23
h-index

302126

39
g-index

45
all docs

45
docs citations

45
times ranked

2389
citing authors

#	ARTICLE	IF	CITATIONS
1	Phosphorylation of guanosine monophosphate reductase triggers a GTP-dependent switch from pro- to anti-oncogenic function of EPHA4. <i>Cell Chemical Biology</i> , 2022, 29, 970-984.e6.	5.2	4
2	Glucose Drives Growth Factor-Independent Esophageal Cancer Proliferation via Phosphohistidine-Focal Adhesion Kinase Signaling. <i>Cellular and Molecular Gastroenterology and Hepatology</i> , 2019, 8, 37-60.	4.5	10
3	Temporal Effects of Combined Birinapant and Paclitaxel on Pancreatic Cancer Cells Investigated via Large-Scale, Ion-Current-Based Quantitative Proteomics (IonStar). <i>Molecular and Cellular Proteomics</i> , 2018, 17, 655-671.	3.8	16
4	Phe71 in Type III Trypanosomal Protein Arginine Methyltransferase 7 (TbPRMT7) Restricts the Enzyme to Monomethylation. <i>Biochemistry</i> , 2018, 57, 1349-1359.	2.5	21
5	GPR56/ADGRG1 regulates development and maintenance of peripheral myelin. <i>Journal of Experimental Medicine</i> , 2018, 215, 941-961.	8.5	51
6	Surfactant Cocktail-Aided Extraction/Precipitation/On-Pellet Digestion Strategy Enables Efficient and Reproducible Sample Preparation for Large-Scale Quantitative Proteomics. <i>Analytical Chemistry</i> , 2018, 90, 10350-10359.	6.5	37
7	Proteomic Analysis of Charcoal-Stripped Fetal Bovine Serum Reveals Changes in the Insulin-like Growth Factor Signaling Pathway. <i>Journal of Proteome Research</i> , 2018, 17, 2963-2977.	3.7	26
8	IonStar enables high-precision, low-missing-data proteomics quantification in large biological cohorts. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E4767-E4776.	7.1	76
9	An IonStar Experimental Strategy for MS1 Ion Current-Based Quantification Using Ultrahigh-Field Orbitrap: Reproducible, In-Depth, and Accurate Protein Measurement in Large Cohorts. <i>Journal of Proteome Research</i> , 2017, 16, 2445-2456.	3.7	74
10	Quantitative proteomic profiling of paired cancerous and normal colon epithelial cells isolated freshly from colorectal cancer patients. <i>Proteomics - Clinical Applications</i> , 2017, 11, 1600155.	1.6	6
11	A Comprehensive, Open-source Platform for Mass Spectrometry-based Glycoproteomics Data Analysis. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 2032-2047.	3.8	44
12	Comparative Proteomic Analysis of the Mitochondria-associated ER Membrane (MAM) in a Long-term Type 2 Diabetic Rodent Model. <i>Scientific Reports</i> , 2017, 7, 2062.	3.3	63
13	Ion Current-Based Proteomic Profiling for Understanding the Inhibitory Effect of Tumor Necrosis Factor Alpha on Myogenic Differentiation. <i>Journal of Proteome Research</i> , 2016, 15, 3147-3157.	3.7	5
14	Phosphorylation of Tyr188 in the WW domain of YAP1 plays an essential role in YAP1-induced cellular transformation. <i>Cell Cycle</i> , 2016, 15, 2497-2505.	2.6	13
15	Ion-Current-Based Temporal Proteomic Profiling of Influenza-A-Virus-Infected Mouse Lungs Revealed Underlying Mechanisms of Altered Integrity of the Lung Microvascular Barrier. <i>Journal of Proteome Research</i> , 2016, 15, 540-553.	3.7	11
16	Large-Scale, Ion-Current-Based Proteomic Investigation of the Rat Striatal Proteome in a Model of Short- and Long-Term Cocaine Withdrawal. <i>Journal of Proteome Research</i> , 2016, 15, 1702-1716.	3.7	11
17	Arginine methylation of DRBD18 differentially impacts its opposing effects on the trypanosome transcriptome. <i>Nucleic Acids Research</i> , 2015, 43, 5501-5523.	14.5	33
18	Proteomic Profiling of the Retinas in a Neonatal Rat Model of Oxygen-Induced Retinopathy with a Reproducible Ion-Current-Based MS1 Approach. <i>Journal of Proteome Research</i> , 2015, 14, 2109-2120.	3.7	29

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19	Tandem Analysis of Transcriptome and Proteome Changes after a Single Dose of Corticosteroid: A Systems Approach to Liver Function in Pharmacogenomics. <i>OMICS A Journal of Integrative Biology</i> , 2015, 19, 80-91.	2.0	18
20	Optimization of Search Engines and Postprocessing Approaches to Maximize Peptide and Protein Identification for High-Resolution Mass Data. <i>Journal of Proteome Research</i> , 2015, 14, 4662-4673.	3.7	30
21	New Insights into the Disease Progression Control Mechanisms by Comparing Long-Term-Nonprogressors versus Normal-Progressors among HIV-1-Positive Patients Using an Ion Current-Based MS1 Proteomic Profiling. <i>Journal of Proteome Research</i> , 2015, 14, 5225-5239.	3.7	7
22	Experimental Null Method to Guide the Development of Technical Procedures and to Control False-Positive Discovery in Quantitative Proteomics. <i>Journal of Proteome Research</i> , 2015, 14, 4147-4157.	3.7	23
23	Kinetics of Precursor Labeling in Stable Isotope Labeling in Cell Cultures (SILAC) Experiments. <i>Analytical Chemistry</i> , 2014, 86, 11334-11341.	6.5	15
24	ICan: An Optimized Ion-Current-Based Quantification Procedure with Enhanced Quantitative Accuracy and Sensitivity in Biomarker Discovery. <i>Journal of Proteome Research</i> , 2014, 13, 5888-5897.	3.7	22
25	A Remodeled Protein Arginine Methyltransferase 1 (PRMT1) Generates Symmetric Dimethylarginine. <i>Journal of Biological Chemistry</i> , 2014, 289, 9320-9327.	3.4	24
26	Highly Multiplexed and Reproducible Ion-Current-Based Strategy for Large-Scale Quantitative Proteomics and the Application to Protein Expression Dynamics Induced by Methylprednisolone in 60 Rats. <i>Analytical Chemistry</i> , 2014, 86, 8149-8157.	6.5	44
27	Systematic Assessment of Survey Scan and MS2-Based Abundance Strategies for Label-Free Quantitative Proteomics Using High-Resolution MS Data. <i>Journal of Proteome Research</i> , 2014, 13, 2069-2079.	3.7	41
28	Reproducible Ion-Current-Based Approach for 24-Plex Comparison of the Tissue Proteomes of Hibernating versus Normal Myocardium in Swine Models. <i>Journal of Proteome Research</i> , 2014, 13, 2571-2584.	3.7	20
29	Large-Scale, Ion-Current-Based Proteomics Investigation of Bronchoalveolar Lavage Fluid in Chronic Obstructive Pulmonary Disease Patients. <i>Journal of Proteome Research</i> , 2014, 13, 627-639.	3.7	59
30	Global proteomic analysis in trypanosomes reveals unique proteins and conserved cellular processes impacted by arginine methylation. <i>Journal of Proteomics</i> , 2013, 91, 210-225.	2.4	59
31	Ion-current-based Proteomic Profiling of the Retina in a Rat Model of Smith-Lemli-Opitz Syndrome. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 3583-3598.	3.8	49
32	Proteomic Analysis Reveals Diverse Classes of Arginine Methylproteins in Mitochondria of Trypanosomes. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 302-311.	3.8	71
33	Proteomic analysis of interactors for yeast protein arginine methyltransferase Hmt1 reveals novel substrate and insights into additional biological roles. <i>Proteomics</i> , 2012, 12, 3304-3314.	2.2	10
34	An ion-current-based, comprehensive and reproducible proteomic strategy for comparative characterization of the cellular responses to novel anti-cancer agents in a prostate cell model. <i>Journal of Proteomics</i> , 2012, 77, 187-201.	2.4	29
35	Cisplatin-induced Ototoxicity Is Mediated by Nitroxidative Modification of Cochlear Proteins Characterized by Nitration of Lmo4. <i>Journal of Biological Chemistry</i> , 2012, 287, 18674-18686.	3.4	51
36	Combinatorial Peptide Ligand Library Treatment Followed by a Dual-Enzyme, Dual-Activation Approach on a Nanoflow Liquid Chromatography/Orbitrap/Electron Transfer Dissociation System for Comprehensive Analysis of Swine Plasma Proteome. <i>Analytical Chemistry</i> , 2011, 83, 4802-4813.	6.5	49

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37	A Novel Member of the RNase D Exoribonuclease Family Functions in Mitochondrial Guide RNA Metabolism in <i>Trypanosoma brucei</i> . <i>Journal of Biological Chemistry</i> , 2011, 286, 10329-10340.	3.4	22
38	Ultrasensitive Quantification of Serum Vitamin D Metabolites Using Selective Solid-Phase Extraction Coupled to Microflow Liquid Chromatography and Isotope-Dilution Mass Spectrometry. <i>Analytical Chemistry</i> , 2010, 82, 2488-2497.	6.5	98
39	Enhanced detection of thiol peptides by matrix-assisted laser desorption/ionization mass spectrometry after selective derivatization with a tailor-made quaternary ammonium tag containing maleimidyl group. <i>Rapid Communications in Mass Spectrometry</i> , 2007, 21, 2608-2612.	1.5	21
40	Direct determination of reduced glutathione in biological fluids by Ce(IV)-quinine chemiluminescence. <i>Talanta</i> , 2006, 70, 518-521.	5.5	67
41	Direct Identification of Tryptophan in a Mixture of Amino Acids by the Naked Eye. <i>Angewandte Chemie - International Edition</i> , 2006, 45, 6723-6725.	13.8	16
42	Detection of Local Polarity of β -Lactalbumin by N-Terminal Specific Labeling with a New Tailor-Made Fluorescent Probe. <i>Journal of Proteome Research</i> , 2005, 4, 161-166.	3.7	28
43	4,5-Dimethylthio-4'-[2-(9-anthryloxy)ethylthio]tetrathiafulvalene, a Highly Selective and Sensitive Chemiluminescence Probe for Singlet Oxygen. <i>Journal of the American Chemical Society</i> , 2004, 126, 11543-11548.	13.7	233
44	A selective and sensitive chemiluminescence reaction of 4,4'-bis[2-(9-anthryloxy)ethylthio]tetrathiafulvalene with singlet oxygen. <i>Chemical Communications</i> , 2004, , 2072-2073.	4.1	37