

Chengjian Tu

List of Publications by Year in descending order

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33
papers

1,181
citations

394421

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395702

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36
docs citations

36
times ranked

1860
citing authors

#	ARTICLE	IF	CITATIONS
1	Proteomic Network Analysis of Bronchoalveolar Lavage Fluid in Ex-Smokers to Discover Implicated Protein Targets and Novel Drug Treatments for Chronic Obstructive Pulmonary Disease. <i>Pharmaceuticals</i> , 2022, 15, 566.	3.8	5
2	Surface hydrophobics mediate functional dimerization of CYP121A1 of <i>Mycobacterium tuberculosis</i> . <i>Scientific Reports</i> , 2021, 11, 394.	3.3	7
3	Improving retinal mitochondrial function as a treatment for age-related macular degeneration. <i>Redox Biology</i> , 2020, 34, 101552.	9.0	34
4	Evidence of Allosteric Coupling between Substrate Binding and Adx Recognition in the Vitamin D Carbon-24 Hydroxylase CYP24A1. <i>Biochemistry</i> , 2020, 59, 1537-1548.	2.5	11
5	Characterization and Proteomic-Transcriptomic Investigation of Monocarboxylate Transporter 6 Knockout Mice: Evidence of a Potential Role in Glucose and Lipid Metabolism. <i>Molecular Pharmacology</i> , 2019, 96, 364-376.	2.3	10
6	Regulator of G protein signaling 12 enhances osteoclastogenesis by suppressing Nrf2-dependent antioxidant proteins to promote the generation of reactive oxygen species. <i>ELife</i> , 2019, 8, .	6.0	33
7	Dynamics of Zebrafish Heart Regeneration Using an HPLC-ESI-MS/MS Approach. <i>Journal of Proteome Research</i> , 2018, 17, 1300-1308.	3.7	17
8	Mapping dynamic histone modification patterns during arsenic-induced malignant transformation of human bladder cells. <i>Toxicology and Applied Pharmacology</i> , 2018, 355, 164-173.	2.8	18
9	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
10	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
11	Comparative Characterization of Osteoclasts Derived From Murine Bone Marrow Macrophages and RAW 264.7 Cells Using Quantitative Proteomics. <i>JBMR Plus</i> , 2018, 2, 328-340.	2.7	35
12	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
13	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
14	Intrinsically Disordered Proteins as Important Players during Desiccation Stress of Soybean Radicles. <i>Journal of Proteome Research</i> , 2017, 16, 2393-2409.	3.7	13
15	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
16	A peptide-retrieval strategy enables significant improvement of quantitative performance without compromising confidence of identification. <i>Journal of Proteomics</i> , 2017, 152, 276-282.	2.4	3
17	Performance Investigation of Proteomic Identification by HCD/CID Fragmentations in Combination with High/Low-Resolution Detectors on a Tribrid, High-Field Orbitrap Instrument. <i>PLoS ONE</i> , 2016, 11, e0160160.	2.5	21
18	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

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19	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
20	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
21	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
22	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
23	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
24	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
25	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
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	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
29	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
30	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
31	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
32	Depletion of Abundant Plasma Proteins and Limitations of Plasma Proteomics. <i>Journal of Proteome Research</i> , 2010, 9, 4982-4991.	3.7	309
33	High-Sensitivity Analysis of Human Plasma Proteome by Immobilized Isoelectric Focusing Fractionation Coupled to Mass Spectrometry Identification. <i>Journal of Proteome Research</i> , 2005, 4, 1265-1273.	3.7	39