

Yan Ren

List of Publications by Year in descending order

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Version: 2024-02-01

26
papers

573
citations

840776

11
h-index

677142

22
g-index

30
all docs

30
docs citations

30
times ranked

888
citing authors

#	ARTICLE	IF	CITATIONS
1	Improved Peptide Retention Time Prediction in Liquid Chromatography through Deep Learning. <i>Analytical Chemistry</i> , 2018, 90, 10881-10888.	6.5	107
2	The trans-omics landscape of COVID-19. <i>Nature Communications</i> , 2021, 12, 4543.	12.8	75
3	Multi-platform omics analysis reveals molecular signature for COVID-19 pathogenesis, prognosis and drug target discovery. <i>Signal Transduction and Targeted Therapy</i> , 2021, 6, 155.	17.1	49
4	Evaluation of the Effect of Trypsin Digestion Buffers on Artificial Deamidation. <i>Journal of Proteome Research</i> , 2015, 14, 1308-1314.	3.7	46
5	Systematic evaluation of IgG responses to SARS-CoV-2 spike protein-derived peptides for monitoring COVID-19 patients. <i>Cellular and Molecular Immunology</i> , 2021, 18, 621-631.	10.5	43
6	Reagents for Isobaric Labeling Peptides in Quantitative Proteomics. <i>Analytical Chemistry</i> , 2018, 90, 12366-12371.	6.5	33
7	Digging More Missing Proteins Using an Enrichment Approach with ProteoMiner. <i>Journal of Proteome Research</i> , 2017, 16, 4330-4339.	3.7	26
8	Comparative evaluation of electrostatic repulsion and hydrophilic interaction chromatography (ERLIC) and high-pH reversed phase (Hp-RP) chromatography in profiling of rat kidney proteome. <i>Journal of Proteomics</i> , 2013, 82, 254-262.	2.4	25
9	Proteomic profiling and genome-wide mapping of O-GlcNAc chromatin-associated proteins reveal an O-GlcNAc-regulated genotoxic stress response. <i>Nature Communications</i> , 2020, 11, 5898.	12.8	19
10	Accurate classification of COVID-19 patients with different severity via machine learning. <i>Clinical and Translational Medicine</i> , 2021, 11, e323.	4.0	17
11	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
12	Lipidomic Biomarkers of Extracellular Vesicles for the Prediction of Preterm Birth in the Early Second Trimester. <i>Journal of Proteome Research</i> , 2020, 19, 4104-4113.	3.7	14
13	Systematic profiling of SARS-CoV-2-specific IgG epitopes at amino acid resolution. <i>Cellular and Molecular Immunology</i> , 2021, 18, 1067-1069.	10.5	14
14	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
15	Evaluation and minimization of nonspecific tryptic cleavages in proteomic sample preparation. <i>Rapid Communications in Mass Spectrometry</i> , 2020, 34, e8733.	1.5	10
16	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
17	A preliminary analysis of LncRNA biomarkers for schizophrenia. <i>Epigenomics</i> , 2021, 13, 1443-1458.	2.1	9
18	Multiparameter Optimization of Two Common Proteomics Quantification Methods for Quantifying Low-Abundance Proteins. <i>Journal of Proteome Research</i> , 2019, 18, 461-468.	3.7	8

#	ARTICLE	IF	CITATIONS
19	Alternative Strategy To Explore Missing Proteins with Low Molecular Weight. <i>Journal of Proteome Research</i> , 2019, 18, 4180-4188.	3.7	7
20	The tRNA discriminator base defines the mutual orthogonality of two distinct pyrrolysyl-tRNA synthetase/tRNAPyl pairs in the same organism. <i>Nucleic Acids Research</i> , 2022, 50, 4601-4615.	14.5	7
21	The defensive system of tree frog skin identified by peptidomics and RNA sequencing analysis. <i>Amino Acids</i> , 2019, 51, 345-353.	2.7	6
22	Pre- and Post-treatment Levels of Plasma Metabolites in Patients With Bipolar Depression. <i>Frontiers in Psychiatry</i> , 2021, 12, 747595.	2.6	6
23	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
24	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
25	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
26	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