

Mingming Dong

List of Publications by Year in descending order

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Version: 2024-02-01

29
papers

836
citations

623574

14
h-index

501076

28
g-index

30
all docs

30
docs citations

30
times ranked

1376
citing authors

#	ARTICLE	IF	CITATIONS
1	An enzyme assisted RP-RPLC approach for in-depth analysis of human liver phosphoproteome. <i>Journal of Proteomics</i> , 2014, 96, 253-262.	1.2	209
2	Ultra-deep tyrosine phosphoproteomics enabled by a phosphotyrosine superbinder. <i>Nature Chemical Biology</i> , 2016, 12, 959-966.	3.9	141
3	An immobilized titanium (IV) ion affinity chromatography adsorbent for solid phase extraction of phosphopeptides for phosphoproteome analysis. <i>Journal of Chromatography A</i> , 2017, 1498, 22-28.	1.8	42
4	Characterization of site-specific glycosylation of secreted proteins associated with multi-drug resistance of gastric cancer. <i>Oncotarget</i> , 2016, 7, 25315-25327.	0.8	40
5	Antibody-Free Approach for the Global Analysis of Protein Methylation. <i>Analytical Chemistry</i> , 2016, 88, 11319-11327.	3.2	38
6	Proteomics Analysis of O-GalNAc Glycosylation in Human Serum by an Integrated Strategy. <i>Analytical Chemistry</i> , 2017, 89, 1469-1476.	3.2	38
7	Glyco-Decipher enables glycan database-independent peptide matching and in-depth characterization of site-specific N-glycosylation. <i>Nature Communications</i> , 2022, 13, 1900.	5.8	34
8	Sensitive, Robust, and Cost-Effective Approach for Tyrosine Phosphoproteome Analysis. <i>Analytical Chemistry</i> , 2017, 89, 9307-9314.	3.2	27
9	Glycans, Glycosite, and Intact Glycopeptide Analysis of N-Linked Glycoproteins Using Liquid Handling Systems. <i>Analytical Chemistry</i> , 2020, 92, 1680-1686.	3.2	27
10	Proteomic signatures of 16 major types of human cancer reveal universal and cancer-type-specific proteins for the identification of potential therapeutic targets. <i>Journal of Hematology and Oncology</i> , 2020, 13, 170.	6.9	25
11	Depletion of Acidic Phosphopeptides by SAX To Improve the Coverage for the Detection of Basophilic Kinase Substrates. <i>Journal of Proteome Research</i> , 2012, 11, 4673-4681.	1.8	23
12	Urinary glycoproteins associated with aggressive prostate cancer. <i>Theranostics</i> , 2020, 10, 11892-11907.	4.6	22
13	Proteomics analysis of site-specific glycoforms by a virtual multistage mass spectrometry method. <i>Analytica Chimica Acta</i> , 2019, 1070, 60-68.	2.6	19
14	Highly Efficient Analysis of Glycoprotein Sialylation in Human Serum by Simultaneous Quantification of Glycosites and Site-Specific Glycoforms. <i>Journal of Proteome Research</i> , 2019, 18, 3439-3446.	1.8	16
15	Biphasic Affinity Chromatographic Approach for Deep Tyrosine Phosphoproteome Analysis. <i>Analytical Chemistry</i> , 2017, 89, 2405-2410.	3.2	15
16	Sensitive Approaches for the Assay of the Global Protein Tyrosine Phosphorylation in Complex Samples Using a Mutated SH2 Domain. <i>Analytical Chemistry</i> , 2017, 89, 2304-2311.	3.2	14
17	Data-Independent Acquisition-Based Mass Spectrometry (DIA-MS) for Quantitative Analysis of Intact N-Linked Glycopeptides. <i>Analytical Chemistry</i> , 2021, 93, 13774-13782.	3.2	14
18	SH2 Superbinder Modified Monolithic Capillary Column for the Sensitive Analysis of Protein Tyrosine Phosphorylation. <i>Journal of Proteome Research</i> , 2018, 17, 243-251.	1.8	13

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19	Identification of phosphopeptides with unknown cleavage specificity by a de novo sequencing assisted database search strategy. <i>Proteomics</i> , 2014, 14, 2410-2416.	1.3	12
20	Selective Enrichment of Cysteine-Containing Phosphopeptides for Subphosphoproteome Analysis. <i>Journal of Proteome Research</i> , 2015, 14, 5341-5347.	1.8	12
21	Development of Parallel Reaction Monitoring Assays for the Detection of Aggressive Prostate Cancer Using Urinary Glycoproteins. <i>Journal of Proteome Research</i> , 2021, 20, 3590-3599.	1.8	12
22	The divide and conquer strategies for deep phosphoproteomics analysis. <i>TrAC - Trends in Analytical Chemistry</i> , 2018, 105, 282-291.	5.8	9
23	Highly Efficient Identification of O-GalNAc Glycosylation by an Acid-Assisted Glycoform Simplification Approach. <i>Proteomics</i> , 2018, 18, e1800042.	1.3	9
24	Analysis of therapeutic monoclonal antibody glycoforms by mass spectrometry for pharmacokinetics study. <i>Talanta</i> , 2017, 165, 664-670.	2.9	8
25	MS-Decipher: a user-friendly proteome database search software with an emphasis on deciphering the spectra of O-linked glycopeptides. <i>Bioinformatics</i> , 2022, 38, 1911-1919.	1.8	6
26	Specific mixing facilitates the comparative quantification of phosphorylation sites with significant dysregulations. <i>Analytica Chimica Acta</i> , 2017, 950, 129-137.	2.6	4
27	A Tyrosine Phosphoproteome Analysis Approach Enabled by Selective Dephosphorylation with Protein Tyrosine Phosphatase. <i>Analytical Chemistry</i> , 2022, 94, 4155-4164.	3.2	4
28	The proteomic analysis improved by cleavage kinetics-based fractionation of tryptic peptides. <i>Proteomics</i> , 2015, 15, 3613-3616.	1.3	3
29	A chemoenzymatic approach enables the site-specific conjugation of recombinant proteins. <i>Electrophoresis</i> , 2019, 40, 2125-2128.	1.3	0