

# Mingming Dong

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

29  
papers

542  
citations

11  
h-index

23  
g-index

30  
ext. papers

724  
ext. citations

7.4  
avg, IF

3.26  
L-index

#	Paper	IF	Citations
29	MS-Decipher: a user-friendly proteome database search software with an emphasis on deciphering the spectra of O-linked glycopeptides.. <i>Bioinformatics</i> , <b>2022</b> ,	7.2	1
28	Glyco-Decipher enables glycan database-independent peptide matching and in-depth characterization of site-specific N-glycosylation.. <i>Nature Communications</i> , <b>2022</b> , 13, 1900	17.4	2
27	Data-Independent Acquisition-Based Mass Spectrometry (DIA-MS) for Quantitative Analysis of Intact N-Linked Glycopeptides. <i>Analytical Chemistry</i> , <b>2021</b> , 93, 13774-13782	7.8	2
26	Development of Parallel Reaction Monitoring Assays for the Detection of Aggressive Prostate Cancer Using Urinary Glycoproteins. <i>Journal of Proteome Research</i> , <b>2021</b> , 20, 3590-3599	5.6	4
25	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> , <b>2020</b> , 13, 170	22.4	7
24	Glycans, Glycosite, and Intact Glycopeptide Analysis of N-Linked Glycoproteins Using Liquid Handling Systems. <i>Analytical Chemistry</i> , <b>2020</b> , 92, 1680-1686	7.8	16
23	Urinary glycoproteins associated with aggressive prostate cancer. <i>Theranostics</i> , <b>2020</b> , 10, 11892-11907	12.1	14
22	Proteomics analysis of site-specific glycoforms by a virtual multistage mass spectrometry method. <i>Analytica Chimica Acta</i> , <b>2019</b> , 1070, 60-68	6.6	10
21	A chemoenzymatic approach enables the site-specific conjugation of recombinant proteins. <i>Electrophoresis</i> , <b>2019</b> , 40, 2125-2128	3.6	
20	Highly Efficient Analysis of Glycoprotein Sialylation in Human Serum by Simultaneous Quantification of Glycosites and Site-Specific Glycoforms. <i>Journal of Proteome Research</i> , <b>2019</b> , 18, 3439-3446	5.6	8
19	SH2 Superbinder Modified Monolithic Capillary Column for the Sensitive Analysis of Protein Tyrosine Phosphorylation. <i>Journal of Proteome Research</i> , <b>2018</b> , 17, 243-251	5.6	7
18	Highly Efficient Identification of O-GalNAc Glycosylation by an Acid-Assisted Glycoform Simplification Approach. <i>Proteomics</i> , <b>2018</b> , 18, e1800042	4.8	6
17	The divide and conquer strategies for deep phosphoproteomics analysis. <i>TrAC - Trends in Analytical Chemistry</i> , <b>2018</b> , 105, 282-291	14.6	6
16	Biphasic Affinity Chromatographic Approach for Deep Tyrosine Phosphoproteome Analysis. <i>Analytical Chemistry</i> , <b>2017</b> , 89, 2405-2410	7.8	12
15	Analysis of therapeutic monoclonal antibody glycoforms by mass spectrometry for pharmacokinetics study. <i>Talanta</i> , <b>2017</b> , 165, 664-670	6.2	4
14	Sensitive Approaches for the Assay of the Global Protein Tyrosine Phosphorylation in Complex Samples Using a Mutated SH2 Domain. <i>Analytical Chemistry</i> , <b>2017</b> , 89, 2304-2311	7.8	7
13	An immobilized titanium (IV) ion affinity chromatography adsorbent for solid phase extraction of phosphopeptides for phosphoproteome analysis. <i>Journal of Chromatography A</i> , <b>2017</b> , 1498, 22-28	4.5	28

12	Proteomics Analysis of O-GalNAc Glycosylation in Human Serum by an Integrated Strategy. <i>Analytical Chemistry</i> , <b>2017</b> , 89, 1469-1476	7.8	29
11	Sensitive, Robust, and Cost-Effective Approach for Tyrosine Phosphoproteome Analysis. <i>Analytical Chemistry</i> , <b>2017</b> , 89, 9307-9314	7.8	16
10	Specific mixing facilitates the comparative quantification of phosphorylation sites with significant dysregulations. <i>Analytica Chimica Acta</i> , <b>2017</b> , 950, 129-137	6.6	4
9	Ultra-deep tyrosine phosphoproteomics enabled by a phosphotyrosine superbinder. <i>Nature Chemical Biology</i> , <b>2016</b> , 12, 959-966	11.7	88
8	Antibody-Free Approach for the Global Analysis of Protein Methylation. <i>Analytical Chemistry</i> , <b>2016</b> , 88, 11319-11327	7.8	29
7	Characterization of site-specific glycosylation of secreted proteins associated with multi-drug resistance of gastric cancer. <i>Oncotarget</i> , <b>2016</b> , 7, 25315-27	3.3	31
6	Selective Enrichment of Cysteine-Containing Phosphopeptides for Subphosphoproteome Analysis. <i>Journal of Proteome Research</i> , <b>2015</b> , 14, 5341-7	5.6	11
5	The proteomic analysis improved by cleavage kinetics-based fractionation of tryptic peptides. <i>Proteomics</i> , <b>2015</b> , 15, 3613-6	4.8	2
4	An enzyme assisted RP-RPLC approach for in-depth analysis of human liver phosphoproteome. <i>Journal of Proteomics</i> , <b>2014</b> , 96, 253-62	3.9	166
3	Identification of phosphopeptides with unknown cleavage specificity by a de novo sequencing assisted database search strategy. <i>Proteomics</i> , <b>2014</b> , 14, 2410-6	4.8	9
2	N-Terminal Labeling of Peptides by Trypsin-Catalyzed Ligation for Quantitative Proteomics. <i>Angewandte Chemie</i> , <b>2013</b> , 125, 9375-9379	3.6	
1	Depletion of acidic phosphopeptides by SAX to improve the coverage for the detection of basophilic kinase substrates. <i>Journal of Proteome Research</i> , <b>2012</b> , 11, 4673-81	5.6	22