

# Jiawei Mao

## 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.

31 papers	444 citations	13 h-index	20 g-index
32 ext. papers	562 ext. citations	6.6 avg, IF	3.35 L-index

#	Paper	IF	Citations
31	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
30	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
29	Rapid Enzyme-Mediated Biotinylation for Cell Surface Proteome Profiling. <i>Analytical Chemistry</i> , <b>2021</b> , 93, 4542-4551	7.8	1
28	Selective enrichment of N-terminal proline peptides via hydrazide chemistry for proteomics analysis. <i>Analytica Chimica Acta</i> , <b>2021</b> , 1142, 48-55	6.6	4
27	Profiling of Endogenously Intact N-Linked and O-Linked Glycopeptides from Human Serum Using an Integrated Platform. <i>Journal of Proteome Research</i> , <b>2020</b> , 19, 1423-1434	5.6	4
26	Comparative proteomic analysis of protein methylation provides insight into the resistance of hepatocellular carcinoma to 5-fluorouracil. <i>Journal of Proteomics</i> , <b>2020</b> , 219, 103738	3.9	1
25	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
24	One-Step SH2 Superbinder-Based Approach for Sensitive Analysis of Tyrosine Phosphoproteome. <i>Journal of Proteome Research</i> , <b>2019</b> , 18, 1870-1879	5.6	8
23	Sensitive profiling of cell surface proteome by using an optimized biotinylation method. <i>Journal of Proteomics</i> , <b>2019</b> , 196, 33-41	3.9	10
22	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
21	A New Searching Strategy for the Identification of O-Linked Glycopeptides. <i>Analytical Chemistry</i> , <b>2019</b> , 91, 3852-3859	7.8	20
20	Pseudotargeted MS Method for the Sensitive Analysis of Protein Phosphorylation in Protein Complexes. <i>Analytical Chemistry</i> , <b>2018</b> , 90, 6214-6221	7.8	8
19	Highly Porous Metal-Free Graphitic Carbon Derived from Metal-Organic Framework for Profiling of N-Linked Glycans. <i>ACS Applied Materials &amp; Interfaces</i> , <b>2018</b> , 10, 11896-11906	9.5	26
18	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
17	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
16	Chemoenzymatic Approach for the Proteomics Analysis of Mucin-Type Core-1 O-Glycosylation in Human Serum. <i>Analytical Chemistry</i> , <b>2018</b> , 90, 12714-12722	7.8	10
15	In-Depth Analysis of Glycoprotein Sialylation in Serum Using a Dual-Functional Material with Superior Hydrophilicity and Switchable Surface Charge. <i>Analytical Chemistry</i> , <b>2017</b> , 89, 3966-3972	7.8	33

14	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
13	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
12	Investigating the Relationship between the Substrates\Consumption and Their Abundances in a Complex Enzymatic System. <i>Analytical Chemistry</i> , <b>2017</b> , 89, 10644-10648	7.8	0
11	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
10	Enzyme Kinetics for Complex System Enables Accurate Determination of Specificity Constants of Numerous Substrates in a Mixture by Proteomics Platform. <i>Molecular and Cellular Proteomics</i> , <b>2017</b> , 16, 135-145	7.6	7
9	Salinity-Induced Palmella Formation Mechanism in Halotolerant Algae Revealed by Quantitative Proteomics and Phosphoproteomics. <i>Frontiers in Plant Science</i> , <b>2017</b> , 8, 810	6.2	28
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	Preparation of Polypropylene Spin Tips Filled with Immobilized Titanium(IV) Ion Monolithic Adsorbent for Robust Phosphoproteome Analysis. <i>Analytical Chemistry</i> , <b>2016</b> , 88, 5058-64	7.8	31
6	Amine Chemistry Method for Selective Enrichment of N-Linked Glycopeptides for Glycoproteomics Analysis. <i>Journal of Proteome Research</i> , <b>2015</b> , 14, 3892-9	5.6	13
5	A peptide N-terminal protection strategy for comprehensive glycoproteome analysis using hydrazide chemistry based method. <i>Scientific Reports</i> , <b>2015</b> , 5, 10164	4.9	28
4	Highly Efficient Release of Glycopeptides from Hydrazide Beads by Hydroxylamine Assisted PNGase F Deglycosylation for N-Glycoproteome Analysis. <i>Analytical Chemistry</i> , <b>2015</b> , 87, 10199-204	7.8	39
3	Proteomic analysis of protein methylation in the yeast <i>Saccharomyces cerevisiae</i> . <i>Journal of Proteomics</i> , <b>2015</b> , 114, 226-33	3.9	27
2	The proteomic analysis improved by cleavage kinetics-based fractionation of tryptic peptides. <i>Proteomics</i> , <b>2015</b> , 15, 3613-6	4.8	2
1	Quantitative proteomics reveals the kinetics of trypsin-catalyzed protein digestion. <i>Analytical and Bioanalytical Chemistry</i> , <b>2014</b> , 406, 6247-56	4.4	19