

List of Publications by Citations

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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.

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

| #  | Paper   | IF  | Citations |
|----|---|-----|-----------|
| 31 | 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        |
| 30 | 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        |
| 29 | 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        |
| 28 | 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        |
| 27 | Antibody-Free Approach for the Global Analysis of Protein Methylation. <i>Analytical Chemistry</i> , <b>2016</b> , 88, 11319-11327  | 7.8 | 29        |
| 26 | 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        |
| 25 | 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        |
| 24 | 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        |
| 23 | 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        |
| 22 | 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        |
| 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 | 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        |
| 19 | 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        |
| 18 | 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        |
| 17 | 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        |
| 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 | 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         |

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|----|---|------|---|
| 14 | 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 |
| 13 | 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 |
| 12 | 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 |
| 11 | 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 |
| 10 | 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 |
| 9  | 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 |
| 8  | 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 |
| 7  | 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 |
| 6  | The proteomic analysis improved by cleavage kinetics-based fractionation of tryptic peptides. <i>Proteomics</i> , <b>2015</b> , 15, 3613-6  | 4.8  | 2 |
| 5  | 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 |
| 4  | 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 |
| 3  | Rapid Enzyme-Mediated Biotinylation for Cell Surface Proteome Profiling. <i>Analytical Chemistry</i> , <b>2021</b> , 93, 4542-4551  | 7.8  | 1 |
| 2  | 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 |
| 1  | 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 |