

# Wen-Feng Zeng

## 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.

30  
papers

1,075  
citations

16  
h-index

32  
g-index

35  
ext. papers

1,603  
ext. citations

8.6  
avg, IF

4.31  
L-index

#	Paper	IF	Citations
30	pGlyco 2.0 enables precision N-glycoproteomics with comprehensive quality control and one-step mass spectrometry for intact glycopeptide identification. <i>Nature Communications</i> , <b>2017</b> , 8, 438	17.4	181
29	Comprehensive identification of peptides in tandem mass spectra using an efficient open search engine. <i>Nature Biotechnology</i> , <b>2018</b> ,	44.5	143
28	A high-speed search engine pLink 2 with systematic evaluation for proteome-scale identification of cross-linked peptides. <i>Nature Communications</i> , <b>2019</b> , 10, 3404	17.4	132
27	pDeep: Predicting MS/MS Spectra of Peptides with Deep Learning. <i>Analytical Chemistry</i> , <b>2017</b> , 89, 12690-12697	12.69	102
26	pNovo+: de novo peptide sequencing using complementary HCD and ETD tandem mass spectra. <i>Journal of Proteome Research</i> , <b>2013</b> , 12, 615-25	5.6	72
25	pGlyco: a pipeline for the identification of intact N-glycopeptides by using HCD- and CID-MS/MS and MS3. <i>Scientific Reports</i> , <b>2016</b> , 6, 25102	4.9	67
24	pQuant improves quantitation by keeping out interfering signals and evaluating the accuracy of calculated ratios. <i>Analytical Chemistry</i> , <b>2014</b> , 86, 5286-94	7.8	58
23	pTop 1.0: A High-Accuracy and High-Efficiency Search Engine for Intact Protein Identification. <i>Analytical Chemistry</i> , <b>2016</b> , 88, 3082-90	7.8	41
22	MS/MS Spectrum Prediction for Modified Peptides Using pDeep2 Trained by Transfer Learning. <i>Analytical Chemistry</i> , <b>2019</b> , 91, 9724-9731	7.8	35
21	Deep Learning in Proteomics. <i>Proteomics</i> , <b>2020</b> , 20, e1900335	4.8	27
20	pNovo 3: precise de novo peptide sequencing using a learning-to-rank framework. <i>Bioinformatics</i> , <b>2019</b> , 35, i183-i190	7.2	24
19	In-depth mapping of the mouse brain N-glycoproteome reveals widespread N-glycosylation of diverse brain proteins. <i>Oncotarget</i> , <b>2016</b> , 7, 38796-38809	3.3	24
18	Open-pNovo: De Novo Peptide Sequencing with Thousands of Protein Modifications. <i>Journal of Proteome Research</i> , <b>2017</b> , 16, 645-654	5.6	23
17	Artificial intelligence for proteomics and biomarker discovery. <i>Cell Systems</i> , <b>2021</b> , 12, 759-770	10.6	22
16	A note on the false discovery rate of novel peptides in proteogenomics. <i>Bioinformatics</i> , <b>2015</b> , 31, 3249-53	5.2	20
15	Precision Peptide Sequencing Using Mirror Proteases of Ac-LysargiNase and Trypsin for Large-scale Proteomics. <i>Molecular and Cellular Proteomics</i> , <b>2019</b> , 18, 773-785	7.6	19
14	Precise, fast and comprehensive analysis of intact glycopeptides and modified glycans with pGlyco3. <i>Nature Methods</i> , <b>2021</b> , 18, 1515-1523	21.6	12

13	pSite: Amino Acid Confidence Evaluation for Quality Control of De Novo Peptide Sequencing and Modification Site Localization. <i>Journal of Proteome Research</i> , <b>2018</b> , 17, 119-128	5.6	12
12	N-glycopeptide Signatures of IgA in Serum from Patients with Hepatitis B Virus-related Liver Diseases. <i>Molecular and Cellular Proteomics</i> , <b>2019</b> , 18, 2262-2272	7.6	11
11	pValid: Validation Beyond the Target-Decoy Approach for Peptide Identification in Shotgun Proteomics. <i>Journal of Proteome Research</i> , <b>2019</b> , 18, 2747-2758	5.6	10
10	pDeep3: Toward More Accurate Spectrum Prediction with Fast Few-Shot Learning. <i>Analytical Chemistry</i> , <b>2021</b> , 93, 5815-5822	7.8	8
9	The structural context of posttranslational modifications at a proteome-wide scale.. <i>PLoS Biology</i> , <b>2022</b> , 20, e3001636	9.7	8
8	Open-pFind enables precise, comprehensive and rapid peptide identification in shotgun proteomics		7
7	AlphaPept, a modern and open framework for MS-based proteomics		5
6	Precise, Fast and Comprehensive Analysis of Intact Glycopeptides and Monosaccharide-Modifications with pGlyco3		5
5	A Deep Learning-Based Tumor Classifier Directly Using MS Raw Data. <i>Proteomics</i> , <b>2020</b> , 20, e1900344	4.8	3
4	Deep-Learning-Derived Evaluation Metrics Enable Effective Benchmarking of Computational Tools for Phosphopeptide Identification. <i>Molecular and Cellular Proteomics</i> , <b>2021</b> , 20, 100171	7.6	1
3	pDeepXL: MS/MS Spectrum Prediction for Cross-Linked Peptide Pairs by Deep Learning. <i>Journal of Proteome Research</i> , <b>2021</b> , 20, 2570-2582	5.6	1
2	The structural context of PTMs at a proteome wide scale		1
1	Accurate Proteoform Identification and Quantitation Using pTop 2.0. <i>Methods in Molecular Biology</i> , <b>2022</b> , 105-129	1.4	