

Wen-Feng Zeng

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.

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	The structural context of posttranslational modifications at a proteome-wide scale.. <i>PLoS Biology</i> , 2022 , 20, e3001636	9.7	8
29	Accurate Proteoform Identification and Quantitation Using pTop 2.0. <i>Methods in Molecular Biology</i> , 2022 , 105-129	1.4	
28	Precise, fast and comprehensive analysis of intact glycopeptides and modified glycans with pGlyco3. <i>Nature Methods</i> , 2021 , 18, 1515-1523	21.6	12
27	Deep-Learning-Derived Evaluation Metrics Enable Effective Benchmarking of Computational Tools for Phosphopeptide Identification. <i>Molecular and Cellular Proteomics</i> , 2021 , 20, 100171	7.6	1
26	pDeep3: Toward More Accurate Spectrum Prediction with Fast Few-Shot Learning. <i>Analytical Chemistry</i> , 2021 , 93, 5815-5822	7.8	8
25	pDeepXL: MS/MS Spectrum Prediction for Cross-Linked Peptide Pairs by Deep Learning. <i>Journal of Proteome Research</i> , 2021 , 20, 2570-2582	5.6	1
24	Artificial intelligence for proteomics and biomarker discovery. <i>Cell Systems</i> , 2021 , 12, 759-770	10.6	22
23	A Deep Learning-Based Tumor Classifier Directly Using MS Raw Data. <i>Proteomics</i> , 2020 , 20, e1900344	4.8	3
22	Deep Learning in Proteomics. <i>Proteomics</i> , 2020 , 20, e1900335	4.8	27
21	MS/MS Spectrum Prediction for Modified Peptides Using pDeep2 Trained by Transfer Learning. <i>Analytical Chemistry</i> , 2019 , 91, 9724-9731	7.8	35
20	pValid: Validation Beyond the Target-Decoy Approach for Peptide Identification in Shotgun Proteomics. <i>Journal of Proteome Research</i> , 2019 , 18, 2747-2758	5.6	10
19	A high-speed search engine pLink 2 with systematic evaluation for proteome-scale identification of cross-linked peptides. <i>Nature Communications</i> , 2019 , 10, 3404	17.4	132
18	pNovo 3: precise de novo peptide sequencing using a learning-to-rank framework. <i>Bioinformatics</i> , 2019 , 35, i183-i190	7.2	24
17	N-glycopeptide Signatures of IgA in Serum from Patients with Hepatitis B Virus-related Liver Diseases. <i>Molecular and Cellular Proteomics</i> , 2019 , 18, 2262-2272	7.6	11
16	Precision Peptide Sequencing Using Mirror Proteases of Ac-LysargiNase and Trypsin for Large-scale Proteomics. <i>Molecular and Cellular Proteomics</i> , 2019 , 18, 773-785	7.6	19
15	pSite: Amino Acid Confidence Evaluation for Quality Control of De Novo Peptide Sequencing and Modification Site Localization. <i>Journal of Proteome Research</i> , 2018 , 17, 119-128	5.6	12
14	Comprehensive identification of peptides in tandem mass spectra using an efficient open search engine. <i>Nature Biotechnology</i> , 2018 ,	44.5	143

13	Open-pNovo: De Novo Peptide Sequencing with Thousands of Protein Modifications. <i>Journal of Proteome Research</i> , 2017 , 16, 645-654	5.6	23
12	pGlyco 2.0 enables precision N-glycoproteomics with comprehensive quality control and one-step mass spectrometry for intact glycopeptide identification. <i>Nature Communications</i> , 2017 , 8, 438	17.4	181
11	pDeep: Predicting MS/MS Spectra of Peptides with Deep Learning. <i>Analytical Chemistry</i> , 2017 , 89, 12690-12697	10.2	102
10	pGlyco: a pipeline for the identification of intact N-glycopeptides by using HCD- and CID-MS/MS and MS3. <i>Scientific Reports</i> , 2016 , 6, 25102	4.9	67
9	pTop 1.0: A High-Accuracy and High-Efficiency Search Engine for Intact Protein Identification. <i>Analytical Chemistry</i> , 2016 , 88, 3082-90	7.8	41
8	In-depth mapping of the mouse brain N-glycoproteome reveals widespread N-glycosylation of diverse brain proteins. <i>Oncotarget</i> , 2016 , 7, 38796-38809	3.3	24
7	A note on the false discovery rate of novel peptides in proteogenomics. <i>Bioinformatics</i> , 2015 , 31, 3249-53	2	20
6	pQuant improves quantitation by keeping out interfering signals and evaluating the accuracy of calculated ratios. <i>Analytical Chemistry</i> , 2014 , 86, 5286-94	7.8	58
5	pNovo+: de novo peptide sequencing using complementary HCD and ETD tandem mass spectra. <i>Journal of Proteome Research</i> , 2013 , 12, 615-25	5.6	72
4	Open-pFind enables precise, comprehensive and rapid peptide identification in shotgun proteomics		7
3	AlphaPept, a modern and open framework for MS-based proteomics		5
2	Precise, Fast and Comprehensive Analysis of Intact Glycopeptides and Monosaccharide-Modifications with pGlyco3		5
1	The structural context of PTMs at a proteome wide scale		1