

Hao Chi

List of Publications by Year in descending order

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Version: 2024-02-01

26
papers

2,324
citations

430874

18
h-index

580821

25
g-index

29
all docs

29
docs citations

29
times ranked

3294
citing authors

#	ARTICLE	IF	CITATIONS
1	Identification of cross-linked peptides from complex samples. <i>Nature Methods</i> , 2012, 9, 904-906.	19.0	503
2	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.	12.8	298
3	Comprehensive identification of peptides in tandem mass spectra using an efficient open search engine. <i>Nature Biotechnology</i> , 2018, 36, 1059-1061.	17.5	275
4	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.	12.8	250
5	pDeep: Predicting MS/MS Spectra of Peptides with Deep Learning. <i>Analytical Chemistry</i> , 2017, 89, 12690-12697.	6.5	170
6	pNovo: <i>de novo</i> Peptide Sequencing and Identification Using HCD Spectra. <i>Journal of Proteome Research</i> , 2010, 9, 2713-2724.	3.7	144
7	pNovo+: <i>De Novo</i> Peptide Sequencing Using Complementary HCD and ETD Tandem Mass Spectra. <i>Journal of Proteome Research</i> , 2013, 12, 615-625.	3.7	91
8	pQuant Improves Quantitation by Keeping out Interfering Signals and Evaluating the Accuracy of Calculated Ratios. <i>Analytical Chemistry</i> , 2014, 86, 5286-5294.	6.5	78
9	MS/MS Spectrum Prediction for Modified Peptides Using pDeep2 Trained by Transfer Learning. <i>Analytical Chemistry</i> , 2019, 91, 9724-9731.	6.5	76
10	pParse: A method for accurate determination of monoisotopic peaks in high-resolution mass spectra. <i>Proteomics</i> , 2012, 12, 226-235.	2.2	66
11	pFind ^{Alioth} : A novel unrestricted database search algorithm to improve the interpretation of high-resolution MS/MS data. <i>Journal of Proteomics</i> , 2015, 125, 89-97.	2.4	54
12	pNovo 3: precise <i>de novo</i> peptide sequencing using a learning-to-rank framework. <i>Bioinformatics</i> , 2019, 35, i183-i190.	4.1	54
13	pTop 1.0: A High-Accuracy and High-Efficiency Search Engine for Intact Protein Identification. <i>Analytical Chemistry</i> , 2016, 88, 3082-3090.	6.5	53
14	Improved Peptide Identification for Proteomic Analysis Based on Comprehensive Characterization of Electron Transfer Dissociation Spectra. <i>Journal of Proteome Research</i> , 2010, 9, 6354-6367.	3.7	37
15	Precision <i>De Novo</i> Peptide Sequencing Using Mirror Proteases of Ac-LysargiNase and Trypsin for Large-scale Proteomics. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 773-785.	3.8	36
16	Assessing the Relationship Between Mass Window Width and Retention Time Scheduling on Protein Coverage for Data-Independent Acquisition. <i>Journal of the American Society for Mass Spectrometry</i> , 2019, 30, 1396-1405.	2.8	30
17	Open-pNovo: <i>De Novo</i> Peptide Sequencing with Thousands of Protein Modifications. <i>Journal of Proteome Research</i> , 2017, 16, 645-654.	3.7	27
18	N-glycopeptide Signatures of IgA2 in Serum from Patients with Hepatitis B Virus-related Liver Diseases. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 2262-2272.	3.8	23

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19	pValid: Validation Beyond the Target-Decoy Approach for Peptide Identification in Shotgun Proteomics. Journal of Proteome Research, 2019, 18, 2747-2758.	3.7	15
20	Reprint of "pFind" Alioth: A novel unrestricted database search algorithm to improve the interpretation of high-resolution MS/MS data. Journal of Proteomics, 2015, 129, 33-41.	2.4	6
21	Exploring the Microbiome-Wide Lysine Acetylation, Succinylation, and Propionylation in Human Gut Microbiota. Analytical Chemistry, 2021, 93, 6594-6598.	6.5	6
22	pValid 2: A deep learning based validation method for peptide identification in shotgun proteomics with increased discriminating power. Journal of Proteomics, 2022, 251, 104414.	2.4	5
23	pDeepXL: MS/MS Spectrum Prediction for Cross-Linked Peptide Pairs by Deep Learning. Journal of Proteome Research, 2021, 20, 2570-2582.	3.7	4
24	Open-pFind Verified Four Missing Proteins from Multi-Tissues. Journal of Proteome Research, 2020, 19, 4808-4814.	3.7	3
25	GameTag: A New Sequence Tag Generation Algorithm Based on Cooperative Game Theory. Proteomics, 2020, 20, 2000021.	2.2	1
26	Ac-LysargiNase efficiently helps genome reannotation of Mycolicibacterium smegmatis MC2 155. Journal of Proteomics, 2022, 264, 104622.	2.4	1