Yan Fu

List of Publications by Year
in descending order

19 papers	779 citations	759233 12 h-index	752698 20 g-index
22 all docs	22 docs citations	22 times ranked	1034 citing authors

#	Article	IF	Citations
1	pFind 2.0: a software package for peptide and protein identification via tandem mass spectrometry. Rapid Communications in Mass Spectrometry, 2007, 21, 2985-2991.	1.5	194
2	Exploiting the kernel trick to correlate fragment ions for peptide identification via tandem mass spectrometry. Bioinformatics, 2004, 20, 1948-1954.	4.1	103
3	Transferred Subgroup False Discovery Rate for Rare Post-translational Modifications Detected by Mass Spectrometry. Molecular and Cellular Proteomics, 2014, 13, 1359-1368.	3.8	77
4	Open MS/MS spectral library search to identify unanticipated post-translational modifications and increase spectral identification rate. Bioinformatics, 2010, 26, i399-i406.	4.1	74
5	pParse: A method for accurate determination of monoisotopic peaks in high-resolution mass spectra. Proteomics, 2012, 12, 226-235.	2.2	66
6	Large-scale Identification of N-linked Intact Glycopeptides in Human Serum using HILIC Enrichment and Spectral Library Search. Molecular and Cellular Proteomics, 2020, 19, 672-689.	3.8	42
7	PTMiner: Localization and Quality Control of Protein Modifications Detected in an Open Search and Its Application to Comprehensive Post-translational Modification Characterization in Human Proteome*. Molecular and Cellular Proteomics, 2019, 18, 391-405.	3.8	38
8	AP3: An Advanced Proteotypic Peptide Predictor for Targeted Proteomics by Incorporating Peptide Digestibility. Analytical Chemistry, 2019, 91, 8705-8711.	6.5	29
9	A note on the false discovery rate of novel peptides in proteogenomics. Bioinformatics, 2015, 31, 3249-3253.	4.1	27
10	DeepDigest: Prediction of Protein Proteolytic Digestion with Deep Learning. Analytical Chemistry, 2021, 93, 6094-6103.	6.5	23
11	Bayesian false discovery rates for post-translational modification proteomics. Statistics and Its Interface, 2012, 5, 47-59.	0.3	23
12	Transfer posterior error probability estimation for peptide identification. BMC Bioinformatics, 2020, 21, 173.	2.6	13
13	N-Linked Glycopeptide Identification Based on Open Mass Spectral Library Search. BioMed Research International, 2018, 2018, 1-11.	1.9	11
14	Data Analysis Strategies for Protein Modification Identification. Methods in Molecular Biology, 2016, 1362, 265-275.	0.9	10
15	Quality control of single amino acid variations detected by tandem mass spectrometry. Journal of Proteomics, 2018, 187, 144-151.	2.4	10
16	LFAQ: Toward Unbiased Label-Free Absolute Protein Quantification by Predicting Peptide Quantitative Factors. Analytical Chemistry, 2019, 91, 1335-1343.	6.5	8
17	Unambiguous Phosphosite Localization through the Combination of Trypsin and LysargiNase Mirror Spectra in a Large-Scale Phosphoproteome Study. Journal of Proteome Research, 2020, 19, 2185-2194.	3.7	7
18	Null-free False Discovery Rate Control Using Decoy Permutations. Acta Mathematicae Applicatae Sinica, 2022, 38, 235-253.	0.7	5

#	Article	IF	Citations
19	Ionic mitigation of CD4+ T cell metabolic fitness, Th1 central nervous system autoimmunity and Th2 asthmatic airway inflammation by therapeutic zinc. Scientific Reports, 2022, 12, 1943.	3.3	4