

# Yan Fu

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/907592/publications.pdf>

Version: 2024-02-01

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	Ionic mitigation of CD4+ T cell metabolic fitness, Th1 central nervous system autoimmunity and Th2 asthmatic airway inflammation by therapeutic zinc. <i>Scientific Reports</i> , 2022, 12, 1943.	3.3	4
2	Null-free False Discovery Rate Control Using Decoy Permutations. <i>Acta Mathematicae Applicatae Sinica</i> , 2022, 38, 235-253.	0.7	5
3	DeepDigest: Prediction of Protein Proteolytic Digestion with Deep Learning. <i>Analytical Chemistry</i> , 2021, 93, 6094-6103.	6.5	23
4	Unambiguous Phosphosite Localization through the Combination of Trypsin and LysargiNase Mirror Spectra in a Large-Scale Phosphoproteome Study. <i>Journal of Proteome Research</i> , 2020, 19, 2185-2194.	3.7	7
5	Transfer posterior error probability estimation for peptide identification. <i>BMC Bioinformatics</i> , 2020, 21, 173.	2.6	13
6	Large-scale Identification of N-linked Intact Glycopeptides in Human Serum using HILIC Enrichment and Spectral Library Search. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 672-689.	3.8	42
7	AP3: An Advanced Proteotypic Peptide Predictor for Targeted Proteomics by Incorporating Peptide Digestibility. <i>Analytical Chemistry</i> , 2019, 91, 8705-8711.	6.5	29
8	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*. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 391-405.	3.8	38
9	LFAQ: Toward Unbiased Label-Free Absolute Protein Quantification by Predicting Peptide Quantitative Factors. <i>Analytical Chemistry</i> , 2019, 91, 1335-1343.	6.5	8
10	N-Linked Glycopeptide Identification Based on Open Mass Spectral Library Search. <i>BioMed Research International</i> , 2018, 2018, 1-11.	1.9	11
11	Quality control of single amino acid variations detected by tandem mass spectrometry. <i>Journal of Proteomics</i> , 2018, 187, 144-151.	2.4	10
12	Data Analysis Strategies for Protein Modification Identification. <i>Methods in Molecular Biology</i> , 2016, 1362, 265-275.	0.9	10
13	A note on the false discovery rate of novel peptides in proteogenomics. <i>Bioinformatics</i> , 2015, 31, 3249-3253.	4.1	27
14	Transferred Subgroup False Discovery Rate for Rare Post-translational Modifications Detected by Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 1359-1368.	3.8	77
15	pParse: A method for accurate determination of monoisotopic peaks in high-resolution mass spectra. <i>Proteomics</i> , 2012, 12, 226-235.	2.2	66
16	Bayesian false discovery rates for post-translational modification proteomics. <i>Statistics and Its Interface</i> , 2012, 5, 47-59.	0.3	23
17	Open MS/MS spectral library search to identify unanticipated post-translational modifications and increase spectral identification rate. <i>Bioinformatics</i> , 2010, 26, i399-i406.	4.1	74
18	pFind 2.0: a software package for peptide and protein identification via tandem mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2007, 21, 2985-2991.	1.5	194

#	ARTICLE	IF	CITATIONS
19	Exploiting the kernel trick to correlate fragment ions for peptide identification via tandem mass spectrometry. <i>Bioinformatics</i> , 2004, 20, 1948-1954.	4.1	103