Lin He

List of Publications by Year
in descending order

17 papers	1,185 citations	687363 13 h-index	940533 16 g-index
17 all docs	17 docs citations	17 times ranked	2765 citing authors

#	Article	IF	Citations
1	Activity-Based Hydrazine Probes for Protein Profiling of Electrophilic Functionality in Therapeutic Targets. ACS Central Science, 2021, 7, 1524-1534.	11.3	21
2	Discovery of Electrophiles and Profiling of Enzyme Cofactors. Current Protocols in Chemical Biology, 2020, 12, e86.	1.7	9
3	Quantitative InÂVivo Proteomics of Metformin Response in Liver Reveals AMPK-Dependent and -Independent Signaling Networks. Cell Reports, 2019, 29, 3331-3348.e7.	6.4	30
4	Differential processing of HIV envelope glycans on the virus and soluble recombinant trimer. Nature Communications, 2018, 9, 3693.	12.8	124
5	Expanding Proteome Coverage with CHarge Ordered Parallel Ion aNalysis (CHOPIN) Combined with Broad Specificity Proteolysis. Journal of Proteome Research, 2017, 16, 1288-1299.	3.7	92
6	Global site-specific N-glycosylation analysis of HIV envelope glycoprotein. Nature Communications, 2017, 8, 14954.	12.8	176
7	Chemoproteomic profiling and discovery of protein electrophiles in human cells. Nature Chemistry, 2017, 9, 234-243.	13.6	68
8	Complete De Novo Assembly of Monoclonal Antibody Sequences. Scientific Reports, 2016, 6, 31730.	3.3	85
9	From Raw Data to Biological Discoveries: A Computational Analysis Pipeline for Mass Spectrometry-Based Proteomics. Journal of the American Society for Mass Spectrometry, 2015, 26, 1820-1826.	2.8	17
10	Extracting Accurate Precursor Information for Tandem Mass Spectra by RawConverter. Analytical Chemistry, 2015, 87, 11361-11367.	6.5	241
11	Fingerprinting protein structures effectively and efficiently. Bioinformatics, 2014, 30, 949-955.	4.1	9
12	GlycoMaster DB: Software To Assist the Automated Identification of N-Linked Glycopeptides by Tandem Mass Spectrometry. Journal of Proteome Research, 2014, 13, 3881-3895.	3.7	80
13	*DE NOVO* SEQUENCING WITH LIMITED NUMBER OF POST-TRANSLATIONAL MODIFICATIONS PER PEPTIDE. Journal of Bioinformatics and Computational Biology, 2013, 11, 1350007.	0.8	9
14	A combinatorial approach to the peptide feature matching problem for label-free quantification. Bioinformatics, 2013, 29, 1768-1775.	4.1	49
15	PeaksPTM: Mass Spectrometry-Based Identification of Peptides with Unspecified Modifications. Journal of Proteome Research, 2011, 10, 2930-2936.	3.7	145
16	ADEPTS: ADVANCED PEPTIDE *DE NOVO* SEQUENCING WITH A PAIR OF TANDEM MASS SPECTRA. Journal of Bioinformatics and Computational Biology, 2010, 08, 981-994.	0.8	30
17	Applying Application Level Gateways for Real-Time Service. Information Technology Journal, 2006, 5, 1088-1092.	0.3	0