

Lin He

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9548586/publications.pdf>

Version: 2024-02-01

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