

Hendrik Weisser

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2262023/publications.pdf>

Version: 2024-02-01

10
papers

965
citations

1163117

8
h-index

1372567

10
g-index

10
all docs

10
docs citations

10
times ranked

2162
citing authors

#	ARTICLE	IF	CITATIONS
1	Novel Insights into Quantitative Proteomics from an Innovative Bottom-Up Simple Light Isotope Metabolic (bSLIM) Labeling Data Processing Strategy. <i>Journal of Proteome Research</i> , 2021, 20, 1476-1487.	3.7	7
2	Genome-wide investigation of gene-cancer associations for the prediction of novel therapeutic targets in oncology. <i>Scientific Reports</i> , 2020, 10, 10787.	3.3	13
3	A computational platform for high-throughput analysis of RNA sequences and modifications by mass spectrometry. <i>Nature Communications</i> , 2020, 11, 926.	12.8	54
4	Evaluation of a Dual Isolation Width Acquisition Method for Isobaric Labeling Ratio Decompression. <i>Journal of Proteome Research</i> , 2019, 18, 1433-1440.	3.7	13
5	Targeted Feature Detection for Data-Dependent Shotgun Proteomics. <i>Journal of Proteome Research</i> , 2017, 16, 2964-2974.	3.7	43
6	OpenMS: a flexible open-source software platform for mass spectrometry data analysis. <i>Nature Methods</i> , 2016, 13, 741-748.	19.0	537
7	Prediction of colorectal cancer diagnosis based on circulating plasma proteins. <i>EMBO Molecular Medicine</i> , 2015, 7, 1166-1178.	6.9	80
8	Dynamic phosphoproteomics reveals TORC1-dependent regulation of yeast nucleotide and amino acid biosynthesis. <i>Science Signaling</i> , 2015, 8, rs4.	3.6	64
9	Using synthetic peptides to benchmark peptide identification software and search parameters for MS/MS data analysis. <i>EuPA Open Proteomics</i> , 2014, 5, 21-31.	2.5	8
10	An Automated Pipeline for High-Throughput Label-Free Quantitative Proteomics. <i>Journal of Proteome Research</i> , 2013, 12, 1628-1644.	3.7	146