Hendrik Weisser

List of Publications by Year in descending order

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