Ralf Gabriels

List of Publications by Year
in descending order

15 papers	**523** citations	840585 **11** h-index	940416 **16** g-index
31 all docs	**31** docs citations	**31** times ranked	**555** citing authors

#	ARTICLE	IF	CITATIONS
1	Proteomics Standards Initiative's ProForma 2.0: Unifying the Encoding of Proteoforms and Peptidoforms. Journal of Proteome Research, 2022, 21, 1189-1195.	1.8	14
2	A comprehensive LFQ benchmark dataset on modern day acquisition strategies in proteomics. Scientific Data, 2022, 9, 126.	2.4	20
3	Sensitive and Specific Spectral Library Searching with CompOmics Spectral Library Searching Tool and Percolator. Journal of Proteome Research, 2022, 21, 1365-1370.	1.8	6
4	A Comprehensive Evaluation of Consensus Spectrum Generation Methods in Proteomics. Journal of Proteome Research, 2022, 21, 1566-1574.	1.8	2
5	MS2Rescore: Data-Driven Rescoring Dramatically Boosts Immunopeptide Identification Rates. Molecular and Cellular Proteomics, 2022, 21, 100266.	2.5	34
6	Personalized Proteome: Comparing Proteogenomics and Open Variant Search Approaches for Single Amino Acid Variant Detection. Journal of Proteome Research, 2021, 20, 3353-3364.	1.8	10
7	Cov-MS: A Community-Based Template Assay for Mass-Spectrometry-Based Protein Detection in SARS-CoV-2 Patients. Jacs Au, 2021, 1, 750-765.	3.6	29
8	Universal Spectrum Identifier for mass spectra. Nature Methods, 2021, 18, 768-770.	9.0	47
9	Ion Mobility Coupled to a Time-of-Flight Mass Analyzer Combined With Fragment Intensity Predictions Improves Identification of Classical Bioactive Peptides and Small Open Reading Frame-Encoded Peptides. Frontiers in Cell and Developmental Biology, 2021, 9, 720570.	1.8	8
10	Spectral Prediction Features as a Solution for the Search Space Size Problem in Proteogenomics. Molecular and Cellular Proteomics, 2021, 20, 100076.	2.5	31
11	DeepLC can predict retention times for peptides that carry as-yet unseen modifications. Nature Methods, 2021, 18, 1363-1369.	9.0	95
12	Removing the Hidden Data Dependency of DIA with Predicted Spectral Libraries. Proteomics, 2020, 20, e1900306.	1.3	38
13	COSS: A Fast and User-Friendly Tool for Spectral Library Searching. Journal of Proteome Research, 2020, 19, 2786-2793.	1.8	18
14	The Age of Data-Driven Proteomics: How Machine Learning Enables Novel Workflows. Proteomics, 2020, 20, e1900351.	1.3	34
15	Updated MS²PIP web server delivers fast and accurate MS² peak intensity prediction for multiple fragmentation methods, instruments and labeling techniques. Nucleic Acids Research, 2019, 47, W295-W299.	6.5	77