George Rosenberger

List of Publications by Year
in descending order

36 papers	**6,318** citations	186265 **28** h-index	345221 **36** g-index
47 all docs	**47** docs citations	**47** times ranked	**7624** citing authors

#	Article	IF	Citations
1	Data‐independent acquisition‐based <scp>SWATH</scp> ‐<scp>MS</scp> for quantitative proteomics: a tutorial. Molecular Systems Biology, 2018, 14, e8126.	7.2	701
2	OpenSWATH enables automated, targeted analysis of data-independent acquisition MS data. Nature Biotechnology, 2014, 32, 219-223.	17.5	692
3	OpenMS: a flexible open-source software platform for mass spectrometry data analysis. Nature Methods, 2016, 13, 741-748.	19.0	537
4	Multi-laboratory assessment of reproducibility, qualitative and quantitative performance of SWATH-mass spectrometry. Nature Communications, 2017, 8, 291.	12.8	423
5	A repository of assays to quantify 10,000 human proteins by SWATH-MS. Scientific Data, 2014, 1, 140031.	5.3	370
6	Rapid mass spectrometric conversion of tissue biopsy samples into permanent quantitative digital proteome maps. Nature Medicine, 2015, 21, 407-413.	30.7	358
7	A multicenter study benchmarks software tools for label-free proteome quantification. Nature Biotechnology, 2016, 34, 1130-1136.	17.5	321
8	Building high-quality assay libraries for targeted analysis of SWATH MS data. Nature Protocols, 2015, 10, 426-441.	12.0	319
9	Quantifying protein interaction dynamics by SWATH mass spectrometry: application to the 14-3-3 system. Nature Methods, 2013, 10, 1246-1253.	19.0	302
10	Absolute Proteome Composition and Dynamics during Dormancy and Resuscitation of Mycobacterium tuberculosis. Cell Host and Microbe, 2015, 18, 96-108.	11.0	229
11	Quantitative proteomics: challenges and opportunities in basic and applied research. Nature Protocols, 2017, 12, 1289-1294.	12.0	200
12	Statistical control of peptide and protein error rates in large-scale targeted data-independent acquisition analyses. Nature Methods, 2017, 14, 921-927.	19.0	189
13	TRIC: an automated alignment strategy for reproducible protein quantification in targeted proteomics. Nature Methods, 2016, 13, 777-783.	19.0	173
14	The Mtb Proteome Library: A Resource of Assays to Quantify the Complete Proteome of Mycobacterium tuberculosis. Cell Host and Microbe, 2013, 13, 602-612.	11.0	165
15	Cross-Link Guided Molecular Modeling with ROSETTA. PLoS ONE, 2013, 8, e73411.	2.5	144
16	Inference and quantification of peptidoforms in large sample cohorts by SWATH-MS. Nature Biotechnology, 2017, 35, 781-788.	17.5	122
17	dia-PASEF data analysis using FragPipe and DIA-NN for deep proteomics of low sample amounts. Nature Communications, 2022, 13, .	12.8	120
18	Complex‐centric proteome profiling by <scp>SEC</scp> ‐<scp>SWATH</scp> ‐<scp>MS</scp>. Molecular Systems Biology, 2019, 15, e8438.	7.2	109

#	Article	IF	Citations
19	DIANAâ€"algorithmic improvements for analysis of data-independent acquisition MS data. Bioinformatics, 2015, 31, 555-562.	4.1	95
20	xTract: software for characterizing conformational changes of protein complexes by quantitative cross-linking mass spectrometry. Nature Methods, 2015, 12, 1185-1190.	19.0	83
21	Identification of a Set of Conserved Eukaryotic Internal Retention Time Standards for Data-independent Acquisition Mass Spectrometry. Molecular and Cellular Proteomics, 2015, 14, 2800-2813.	3.8	76
22	Kinase Interaction Network Expands Functional and Disease Roles of Human Kinases. Molecular Cell, 2020, 79, 504-520.e9.	9.7	74
23	aLFQ: an R-package for estimating absolute protein quantities from label-free LC-MS/MS proteomics data. Bioinformatics, 2014, 30, 2511-2513.	4.1	63
24	Global and Site-Specific Effect of Phosphorylation on Protein Turnover. Developmental Cell, 2021, 56, 111-124.e6.	7.0	57
25	A Global Screen for Assembly State Changes of the Mitotic Proteome by SEC-SWATH-MS. Cell Systems, 2020, 10, 133-155.e6.	6.2	57
26	N-Glycoprotein SRMAtlas. Molecular and Cellular Proteomics, 2013, 12, 1005-1016.	3.8	48
27	Isoformâ€‹resolved correlation analysis between <scp>mRNA</scp> abundance regulation and protein level degradation. Molecular Systems Biology, 2020, 16, e9170.	7.2	42
28	Systematic detection of functional proteoform groups from bottom-up proteomic datasets. Nature Communications, 2021, 12, 3810.	12.8	40
29	Complex-centric proteome profiling by SEC-SWATH-MS for the parallel detection of hundreds of protein complexes. Nature Protocols, 2020, 15, 2341-2386.	12.0	34
30	Assessing the Relationship Between Mass Window Width and Retention Time Scheduling on Protein Coverage for Data-Independent Acquisition. Journal of the American Society for Mass Spectrometry, 2019, 30, 1396-1405.	2.8	30
31	SECAT: Quantifying Protein Complex Dynamics across Cell States by Network-Centric Analysis of SEC-SWATH-MS Profiles. Cell Systems, 2020, 11, 589-607.e8.	6.2	26
32	Automated Workflow for Large-Scale Selected Reaction Monitoring Experiments. Journal of Proteome Research, 2012, 11, 1644-1653.	3.7	20
33	Lysine and Arginine Protein Post-translational Modifications by Enhanced DIA Libraries: Quantification in Murine Liver Disease. Journal of Proteome Research, 2020, 19, 4163-4178.	3.7	18
34	DIAproteomics: A Multifunctional Data Analysis Pipeline for Data-Independent Acquisition Proteomics and Peptidomics. Journal of Proteome Research, 2021, 20, 3758-3766.	3.7	17
35	Efficient visualization of high-throughput targeted proteomics experiments: TAPIR. Bioinformatics, 2015, 31, 2415-2417.	4.1	14
36	Functional and Structural Properties of a Novel Protein and Virulence Factor (Protein sHIP) in Streptococcus pyogenes. Journal of Biological Chemistry, 2014, 289, 18175-18188.	3.4	6