

George Rosenberger

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3187965/publications.pdf>

Version: 2024-02-01

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	dia-PASEF data analysis using FragPipe and DIA-NN for deep proteomics of low sample amounts. Nature Communications, 2022, 13, .	12.8	120
2	Global and Site-Specific Effect of Phosphorylation on Protein Turnover. Developmental Cell, 2021, 56, 111-124.e6.	7.0	57
3	DIAproteomics: A Multifunctional Data Analysis Pipeline for Data-Independent Acquisition Proteomics and Peptidomics. Journal of Proteome Research, 2021, 20, 3758-3766.	3.7	17
4	Systematic detection of functional proteoform groups from bottom-up proteomic datasets. Nature Communications, 2021, 12, 3810.	12.8	40
5	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
6	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
7	Kinase Interaction Network Expands Functional and Disease Roles of Human Kinases. Molecular Cell, 2020, 79, 504-520.e9.	9.7	74
8	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
9	Isoformâ€resolved correlation analysis between <sc>mRNA</sc> abundance regulation and protein level degradation. Molecular Systems Biology, 2020, 16, e9170.	7.2	42
10	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
11	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
12	Complexâ€centric proteome profiling by <sc>SEC</sc> â€•<sc>SWATH</sc> â€•<sc>MS</sc>. Molecular Systems Biology, 2019, 15, e8438.	7.2	109
13	Dataâ€independent acquisitionâ€based <sc>SWATH</sc> â€•<sc>MS</sc> for quantitative proteomics: a tutorial. Molecular Systems Biology, 2018, 14, e8126.	7.2	701
14	Quantitative proteomics: challenges and opportunities in basic and applied research. Nature Protocols, 2017, 12, 1289-1294.	12.0	200
15	Inference and quantification of peptidofoms in large sample cohorts by SWATH-MS. Nature Biotechnology, 2017, 35, 781-788.	17.5	122
16	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
17	Multi-laboratory assessment of reproducibility, qualitative and quantitative performance of SWATH-mass spectrometry. Nature Communications, 2017, 8, 291.	12.8	423
18	A multicenter study benchmarks software tools for label-free proteome quantification. Nature Biotechnology, 2016, 34, 1130-1136.	17.5	321

#	ARTICLE	IF	CITATIONS
19	TRIC: an automated alignment strategy for reproducible protein quantification in targeted proteomics. <i>Nature Methods</i> , 2016, 13, 777-783.	19.0	173
20	OpenMS: a flexible open-source software platform for mass spectrometry data analysis. <i>Nature Methods</i> , 2016, 13, 741-748.	19.0	537
21	Building high-quality assay libraries for targeted analysis of SWATH MS data. <i>Nature Protocols</i> , 2015, 10, 426-441.	12.0	319
22	Rapid mass spectrometric conversion of tissue biopsy samples into permanent quantitative digital proteome maps. <i>Nature Medicine</i> , 2015, 21, 407-413.	30.7	358
23	Absolute Proteome Composition and Dynamics during Dormancy and Resuscitation of <i>Mycobacterium tuberculosis</i> . <i>Cell Host and Microbe</i> , 2015, 18, 96-108.	11.0	229
24	Efficient visualization of high-throughput targeted proteomics experiments: TAPIR. <i>Bioinformatics</i> , 2015, 31, 2415-2417.	4.1	14
25	Identification of a Set of Conserved Eukaryotic Internal Retention Time Standards for Data-independent Acquisition Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 2800-2813.	3.8	76
26	xTract: software for characterizing conformational changes of protein complexes by quantitative cross-linking mass spectrometry. <i>Nature Methods</i> , 2015, 12, 1185-1190.	19.0	83
27	DIANA algorithmic improvements for analysis of data-independent acquisition MS data. <i>Bioinformatics</i> , 2015, 31, 555-562.	4.1	95
28	aLFQ: an R-package for estimating absolute protein quantities from label-free LC-MS/MS proteomics data. <i>Bioinformatics</i> , 2014, 30, 2511-2513.	4.1	63
29	OpenSWATH enables automated, targeted analysis of data-independent acquisition MS data. <i>Nature Biotechnology</i> , 2014, 32, 219-223.	17.5	692
30	Functional and Structural Properties of a Novel Protein and Virulence Factor (Protein sHIP) in <i>Streptococcus pyogenes</i> . <i>Journal of Biological Chemistry</i> , 2014, 289, 18175-18188.	3.4	6
31	A repository of assays to quantify 10,000 human proteins by SWATH-MS. <i>Scientific Data</i> , 2014, 1, 140031.	5.3	370
32	Quantifying protein interaction dynamics by SWATH mass spectrometry: application to the 14-3-3 system. <i>Nature Methods</i> , 2013, 10, 1246-1253.	19.0	302
33	The Mtb Proteome Library: A Resource of Assays to Quantify the Complete Proteome of <i>Mycobacterium tuberculosis</i> . <i>Cell Host and Microbe</i> , 2013, 13, 602-612.	11.0	165
34	N-Glycoprotein SRMATlas. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 1005-1016.	3.8	48
35	Cross-Link Guided Molecular Modeling with ROSETTA. <i>PLoS ONE</i> , 2013, 8, e73411.	2.5	144
36	Automated Workflow for Large-Scale Selected Reaction Monitoring Experiments. <i>Journal of Proteome Research</i> , 2012, 11, 1644-1653.	3.7	20