Hannes L Röst

List of Publications by Year
in descending order

60 papers	9,881 citations	117625 34 h-index	133252 59 g-index
78 all docs	78 docs citations	78 times ranked	13261 citing authors

#	Article	IF	Citations
1	Targeted Data Extraction of the MS/MS Spectra Generated by Data-independent Acquisition: A New Concept for Consistent and Accurate Proteome Analysis. Molecular and Cellular Proteomics, 2012, 11, O111.016717.	3.8	2,285
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	Heterogeneous Ribosomes Preferentially Translate Distinct Subpools of mRNAs Genome-wide. Molecular Cell, 2017, 67, 71-83.e7.	9.7	480
5	Longitudinal multi-omics of host–microbe dynamics in prediabetes. Nature, 2019, 569, 663-671.	27.8	391
6	diaPASEF: parallel accumulation–serial fragmentation combined with data-independent acquisition. Nature Methods, 2020, 17, 1229-1236.	19.0	387
7	A repository of assays to quantify 10,000 human proteins by SWATH-MS. Scientific Data, 2014, 1, 140031.	5.3	370
8	Rapid mass spectrometric conversion of tissue biopsy samples into permanent quantitative digital proteome maps. Nature Medicine, 2015, 21, 407-413.	30.7	358
9	A multicenter study benchmarks software tools for label-free proteome quantification. Nature Biotechnology, 2016, 34, 1130-1136.	17.5	321
10	A complete mass-spectrometric map of the yeast proteome applied to quantitative trait analysis. Nature, 2013, 494, 266-270.	27.8	307
11	Quantifying protein interaction dynamics by SWATH mass spectrometry: application to the 14-3-3 system. Nature Methods, 2013, 10, 1246-1253.	19.0	302
12	From hype to reality: data science enabling personalized medicine. BMC Medicine, 2018, 16, 150.	5.5	278
13	Reproducible Quantification of Cancer-Associated Proteins in Body Fluids Using Targeted Proteomics. Science Translational Medicine, 2012, 4, 142ra94.	12.4	236
14	Absolute Proteome Composition and Dynamics during Dormancy and Resuscitation of Mycobacterium tuberculosis. Cell Host and Microbe, 2015, 18, 96-108.	11.0	229
15	BioContainers: an open-source and community-driven framework for software standardization. Bioinformatics, 2017, 33, 2580-2582.	4.1	205
16	Quantitative proteomics: challenges and opportunities in basic and applied research. Nature Protocols, 2017, 12, 1289-1294.	12.0	200
17	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
18	Integrative Personal Omics Profiles during Periods of Weight Gain and Loss. Cell Systems, 2018, 6, 157-170.e8.	6.2	183

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19	TRIC: an automated alignment strategy for reproducible protein quantification in targeted proteomics. Nature Methods, 2016, 13, 777-783.	19.0	173
20	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
21	Metabolic Dynamics and Prediction of Gestational Age and Time to Delivery in Pregnant Women. Cell, 2020, 181, 1680-1692.e15.	28.9	154
22	Inference and quantification of peptidoforms in large sample cohorts by SWATH-MS. Nature Biotechnology, 2017, 35, 781-788.	17.5	122
23	pyOpenMS: A Python€based interface to the OpenMS mass€spectrometry algorithm library. Proteomics, 2014, 14, 74-77.	2.2	109
24	DIANA€"algorithmic improvements for analysis of data-independent acquisition MS data. Bioinformatics, 2015, 31, 555-562.	4.1	95
25	A Computational Tool to Detect and Avoid Redundancy in Selected Reaction Monitoring. Molecular and Cellular Proteomics, 2012, 11, 540-549.	3.8	90
26	xTract: software for characterizing conformational changes of protein complexes by quantitative cross-linking mass spectrometry. Nature Methods, 2015, 12, 1185-1190.	19.0	83
27	PRMT5 inhibition disrupts splicing and stemness in glioblastoma. Nature Communications, 2021, 12, 979.	12.8	77
28	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
29	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
30	Amino acid and lipid metabolism in post-gestational diabetes and progression to type 2 diabetes: A metabolic profiling study. PLoS Medicine, 2020, 17, e1003112.	8.4	63
31	Numerical Compression Schemes for Proteomics Mass Spectrometry Data. Molecular and Cellular Proteomics, 2014, 13, 1537-1542.	3.8	53
32	Systems-level Proteomics of Two Ubiquitous Leaf Commensals Reveals Complementary Adaptive Traits for Phyllosphere Colonization. Molecular and Cellular Proteomics, 2016, 15, 3256-3269.	3.8	48
33	Expanding the Use of Spectral Libraries in Proteomics. Journal of Proteome Research, 2018, 17, 4051-4060.	3.7	47
34	Reproducible quantitative proteotype data matrices for systems biology. Molecular Biology of the Cell, 2015, 26, 3926-3931.	2.1	46
35	Systematic detection of functional proteoform groups from bottom-up proteomic datasets. Nature Communications, 2021, 12, 3810.	12.8	40
36	Cell size homeostasis is maintained by CDK4-dependent activation of p38 MAPK. Developmental Cell, 2021, 56, 1756-1769.e7.	7.0	35

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37	Automated SWATH Data Analysis Using Targeted Extraction of Ion Chromatograms. Methods in Molecular Biology, 2017, 1550, 289-307.	0.9	33
38	Recommendations for the packaging and containerizing of bioinformatics software. F1000Research, 2018, 7, 742.	1.6	29
39	Recommendations for the packaging and containerizing of bioinformatics software. F1000Research, 2018, 7, 742.	1.6	27
40	Underlying dyslipidemia postpartum in women with a recent GDM pregnancy who develop type 2 diabetes. ELife, 2020, 9, .	6.0	24
41	Trapped Ion Mobility Spectrometry Reduces Spectral Complexity in Mass Spectrometry-Based Proteomics. Analytical Chemistry, 2021, 93, 16751-16758.	6.5	24
42	High-frequency actionable pathogenic exome variants in an average-risk cohort. Journal of Physical Education and Sports Management, 2018, 4, a003178.	1.2	23
43	DIAlignR Provides Precise Retention Time Alignment Across Distant Runs in DIA and Targeted Proteomics. Molecular and Cellular Proteomics, 2019, 18, 806-817.	3.8	23
44	SmartPeak Automates Targeted and Quantitative Metabolomics Data Processing. Analytical Chemistry, 2020, 92, 15968-15974.	6.5	23
45	Machine Learning in Mass Spectrometric Analysis of DIA Data. Proteomics, 2020, 20, e1900352.	2.2	22
46	DIAproteomics: A Multifunctional Data Analysis Pipeline for Data-Independent Acquisition Proteomics and Peptidomics. Journal of Proteome Research, 2021, 20, 3758-3766.	3.7	17
47	Fast and Efficient XML Data Access for Next-Generation Mass Spectrometry. PLoS ONE, 2015, 10, e0125108.	2.5	17
48	Intensive lactation among women with recent gestational diabetes significantly alters the early postpartum circulating lipid profile: the SWIFT study. BMC Medicine, 2021, 19, 241.	5.5	17
49	Efficient visualization of high-throughput targeted proteomics experiments: TAPIR. Bioinformatics, 2015, 31, 2415-2417.	4.1	14
50	Democratizing data-independent acquisition proteomics analysis on public cloud infrastructures via the Galaxy framework. GigaScience, 2022, 11, .	6.4	13
51	Initial Guidelines for Manuscripts Employing Data-independent Acquisition Mass Spectrometry for Proteomic Analysis. Molecular and Cellular Proteomics, 2019, 18, 1-2.	3.8	11
52	DIAMetAlyzer allows automated false-discovery rate-controlled analysis for data-independent acquisition in metabolomics. Nature Communications, 2022, 13, 1347.	12.8	11
53	Deep learning adds an extra dimension to peptide fragmentation. Nature Methods, 2019, 16, 469-470.	19.0	7
54	DrawAlignR: An Interactive Tool for Across Run Chromatogram Alignment Visualization. Proteomics, 2020, 20, e1900353.	2.2	6

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55	Automated Workflow for Peptide-Level Quantitation from DIA/ Data. Methods in Molecular Biology, 2021, 2228, 453-468.	0.9	4
56	mspack: efficient lossless and lossy mass spectrometry data compression. Bioinformatics, 2021, 37, 3923-3925.	4.1	3
57	Metabolic Dynamics and Prediction of Gestational Age and Time to Delivery in Pregnant Women. Obstetrical and Gynecological Survey, 2020, 75, 649-651.	0.4	2
58	Statistical elimination of spectral features with large between-run variation enhances quantitative protein-level conclusions in experiments with data-independent spectral acquisition. BMC Bioinformatics, 2015, 16, .	2.6	1
59	Analyzing Assay Specificity in Metabolomics Using Unique Ion Signature Simulations. Analytical Chemistry, 2021, 93, 11415-11423.	6.5	1
60	Chapter 10. Data Analysis for Data Independent Acquisition. New Developments in Mass Spectrometry, 2016, , 200-228.	0.2	0