

Hannes L RÃ¶st

List of Publications by Year in descending order

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Version: 2024-02-01

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	Democratizing data-independent acquisition proteomics analysis on public cloud infrastructures via the Galaxy framework. <i>GigaScience</i> , 2022, 11, .	6.4	13
2	DIAMetAlyzer allows automated false-discovery rate-controlled analysis for data-independent acquisition in metabolomics. <i>Nature Communications</i> , 2022, 13, 1347.	12.8	11
3	Automated Workflow for Peptide-Level Quantitation from DIA/ Data. <i>Methods in Molecular Biology</i> , 2021, 2228, 453-468.	0.9	4
4	PRMT5 inhibition disrupts splicing and stemness in glioblastoma. <i>Nature Communications</i> , 2021, 12, 979.	12.8	77
5	DIAProteomics: A Multifunctional Data Analysis Pipeline for Data-Independent Acquisition Proteomics and Peptidomics. <i>Journal of Proteome Research</i> , 2021, 20, 3758-3766.	3.7	17
6	Cell size homeostasis is maintained by CDK4-dependent activation of p38 MAPK. <i>Developmental Cell</i> , 2021, 56, 1756-1769.e7.	7.0	35
7	Systematic detection of functional proteoform groups from bottom-up proteomic datasets. <i>Nature Communications</i> , 2021, 12, 3810.	12.8	40
8	Analyzing Assay Specificity in Metabolomics Using Unique Ion Signature Simulations. <i>Analytical Chemistry</i> , 2021, 93, 11415-11423.	6.5	1
9	mSPACK: efficient lossless and lossy mass spectrometry data compression. <i>Bioinformatics</i> , 2021, 37, 3923-3925.	4.1	3
10	Intensive lactation among women with recent gestational diabetes significantly alters the early postpartum circulating lipid profile: the SWIFT study. <i>BMC Medicine</i> , 2021, 19, 241.	5.5	17
11	Trapped Ion Mobility Spectrometry Reduces Spectral Complexity in Mass Spectrometry-Based Proteomics. <i>Analytical Chemistry</i> , 2021, 93, 16751-16758.	6.5	24
12	diaPASEF: parallel accumulation-serial fragmentation combined with data-independent acquisition. <i>Nature Methods</i> , 2020, 17, 1229-1236.	19.0	387
13	SmartPeak Automates Targeted and Quantitative Metabolomics Data Processing. <i>Analytical Chemistry</i> , 2020, 92, 15968-15974.	6.5	23
14	Metabolic Dynamics and Prediction of Gestational Age and Time to Delivery in Pregnant Women. <i>Obstetrical and Gynecological Survey</i> , 2020, 75, 649-651.	0.4	2
15	DrawAlignR: An Interactive Tool for Across Run Chromatogram Alignment Visualization. <i>Proteomics</i> , 2020, 20, e1900353.	2.2	6
16	Amino acid and lipid metabolism in post-gestational diabetes and progression to type 2 diabetes: A metabolic profiling study. <i>PLoS Medicine</i> , 2020, 17, e1003112.	8.4	63
17	Metabolic Dynamics and Prediction of Gestational Age and Time to Delivery in Pregnant Women. <i>Cell</i> , 2020, 181, 1680-1692.e15.	28.9	154
18	Machine Learning in Mass Spectrometric Analysis of DIA Data. <i>Proteomics</i> , 2020, 20, e1900352.	2.2	22

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19	Underlying dyslipidemia postpartum in women with a recent GDM pregnancy who develop type 2 diabetes. <i>ELife</i> , 2020, 9, .	6.0	24
20	DIAAlignR Provides Precise Retention Time Alignment Across Distant Runs in DIA and Targeted Proteomics. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 806-817.	3.8	23
21	Longitudinal multi-omics of host-microbe dynamics in prediabetes. <i>Nature</i> , 2019, 569, 663-671.	27.8	391
22	Deep learning adds an extra dimension to peptide fragmentation. <i>Nature Methods</i> , 2019, 16, 469-470.	19.0	7
23	Initial Guidelines for Manuscripts Employing Data-independent Acquisition Mass Spectrometry for Proteomic Analysis. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 1-2.	3.8	11
24	Integrative Personal Omics Profiles during Periods of Weight Gain and Loss. <i>Cell Systems</i> , 2018, 6, 157-170.e8.	6.2	183
25	High-frequency actionable pathogenic exome variants in an average-risk cohort. <i>Journal of Physical Education and Sports Management</i> , 2018, 4, a003178.	1.2	23
26	Expanding the Use of Spectral Libraries in Proteomics. <i>Journal of Proteome Research</i> , 2018, 17, 4051-4060.	3.7	47
27	From hype to reality: data science enabling personalized medicine. <i>BMC Medicine</i> , 2018, 16, 150.	5.5	278
28	Recommendations for the packaging and containerizing of bioinformatics software. <i>F1000Research</i> , 2018, 7, 742.	1.6	27
29	Recommendations for the packaging and containerizing of bioinformatics software. <i>F1000Research</i> , 2018, 7, 742.	1.6	29
30	Automated SWATH Data Analysis Using Targeted Extraction of Ion Chromatograms. <i>Methods in Molecular Biology</i> , 2017, 1550, 289-307.	0.9	33
31	Heterogeneous Ribosomes Preferentially Translate Distinct Subpools of mRNAs Genome-wide. <i>Molecular Cell</i> , 2017, 67, 71-83.e7.	9.7	480
32	Quantitative proteomics: challenges and opportunities in basic and applied research. <i>Nature Protocols</i> , 2017, 12, 1289-1294.	12.0	200
33	Inference and quantification of peptidofoms in large sample cohorts by SWATH-MS. <i>Nature Biotechnology</i> , 2017, 35, 781-788.	17.5	122
34	BioContainers: an open-source and community-driven framework for software standardization. <i>Bioinformatics</i> , 2017, 33, 2580-2582.	4.1	205
35	Statistical control of peptide and protein error rates in large-scale targeted data-independent acquisition analyses. <i>Nature Methods</i> , 2017, 14, 921-927.	19.0	189
36	A multicenter study benchmarks software tools for label-free proteome quantification. <i>Nature Biotechnology</i> , 2016, 34, 1130-1136.	17.5	321

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37	TRIC: an automated alignment strategy for reproducible protein quantification in targeted proteomics. <i>Nature Methods</i> , 2016, 13, 777-783.	19.0	173
38	Systems-level Proteomics of Two Ubiquitous Leaf Commensals Reveals Complementary Adaptive Traits for Phyllosphere Colonization. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 3256-3269.	3.8	48
39	OpenMS: a flexible open-source software platform for mass spectrometry data analysis. <i>Nature Methods</i> , 2016, 13, 741-748.	19.0	537
40	Chapter 10. Data Analysis for Data Independent Acquisition. <i>New Developments in Mass Spectrometry</i> , 2016, , 200-228.	0.2	0
41	Statistical elimination of spectral features with large between-run variation enhances quantitative protein-level conclusions in experiments with data-independent spectral acquisition. <i>BMC Bioinformatics</i> , 2015, 16, .	2.6	1
42	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
43	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
44	Efficient visualization of high-throughput targeted proteomics experiments: TAPIR. <i>Bioinformatics</i> , 2015, 31, 2415-2417.	4.1	14
45	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
46	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
47	Reproducible quantitative proteotype data matrices for systems biology. <i>Molecular Biology of the Cell</i> , 2015, 26, 3926-3931.	2.1	46
48	DIANAâ€”algorithmic improvements for analysis of data-independent acquisition MS data. <i>Bioinformatics</i> , 2015, 31, 555-562.	4.1	95
49	Fast and Efficient XML Data Access for Next-Generation Mass Spectrometry. <i>PLoS ONE</i> , 2015, 10, e0125108.	2.5	17
50	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
51	pyOpenMS: A Pythonâ€”based interface to the OpenMS massâ€”spectrometry algorithm library. <i>Proteomics</i> , 2014, 14, 74-77.	2.2	109
52	Numerical Compression Schemes for Proteomics Mass Spectrometry Data. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 1537-1542.	3.8	53
53	OpenSWATH enables automated, targeted analysis of data-independent acquisition MS data. <i>Nature Biotechnology</i> , 2014, 32, 219-223.	17.5	692
54	A repository of assays to quantify 10,000 human proteins by SWATH-MS. <i>Scientific Data</i> , 2014, 1, 140031.	5.3	370

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55	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
56	A complete mass-spectrometric map of the yeast proteome applied to quantitative trait analysis. <i>Nature</i> , 2013, 494, 266-270.	27.8	307
57	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
58	A Computational Tool to Detect and Avoid Redundancy in Selected Reaction Monitoring. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 540-549.	3.8	90
59	Reproducible Quantification of Cancer-Associated Proteins in Body Fluids Using Targeted Proteomics. <i>Science Translational Medicine</i> , 2012, 4, 142ra94.	12.4	236
60	Targeted Data Extraction of the MS/MS Spectra Generated by Data-independent Acquisition: A New Concept for Consistent and Accurate Proteome Analysis. <i>Molecular and Cellular Proteomics</i> , 2012, 11, O111.016717.	3.8	2,285