

Timo Sachsenberg

List of Publications by Year in descending order

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Version: 2024-02-01

38
papers

10,017
citations

279798

23
h-index

302126

39
g-index

51
all docs

51
docs citations

51
times ranked

24777
citing authors

#	ARTICLE	IF	CITATIONS
1	Generation of ENSEMBL-based proteogenomics databases boosts the identification of non-canonical peptides. <i>Bioinformatics</i> , 2022, 38, 1470-1472.	4.1	16
2	A Comprehensive Evaluation of Consensus Spectrum Generation Methods in Proteomics. <i>Journal of Proteome Research</i> , 2022, 21, 1566-1574.	3.7	2
3	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
4	A proteomics sample metadata representation for multiomics integration and big data analysis. <i>Nature Communications</i> , 2021, 12, 5854.	12.8	45
5	ThermoRawFileParser: Modular, Scalable, and Cross-Platform RAW File Conversion. <i>Journal of Proteome Research</i> , 2020, 19, 537-542.	3.7	144
6	Analysis of protein-DNA interactions in chromatin by UV induced cross-linking and mass spectrometry. <i>Nature Communications</i> , 2020, 11, 5250.	12.8	22
7	SmartPeak Automates Targeted and Quantitative Metabolomics Data Processing. <i>Analytical Chemistry</i> , 2020, 92, 15968-15974.	6.5	23
8	EPIFANY: A Method for Efficient High-Confidence Protein Inference. <i>Journal of Proteome Research</i> , 2020, 19, 1060-1072.	3.7	20
9	Tracing incorporation of heavy water into proteins for species-specific metabolic activity in complex communities. <i>Journal of Proteomics</i> , 2020, 222, 103791.	2.4	7
10	A computational platform for high-throughput analysis of RNA sequences and modifications by mass spectrometry. <i>Nature Communications</i> , 2020, 11, 926.	12.8	54
11	OpenPepXL: An Open-Source Tool for Sensitive Identification of Cross-Linked Peptides in XL-MS. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 2157-2168.	3.8	10
12	MHCquant: Automated and Reproducible Data Analysis for Immunopeptidomics. <i>Journal of Proteome Research</i> , 2019, 18, 3876-3884.	3.7	35
13	mzTab-M: A Data Standard for Sharing Quantitative Results in Mass Spectrometry Metabolomics. <i>Analytical Chemistry</i> , 2019, 91, 3302-3310.	6.5	43
14	The PRIDE database and related tools and resources in 2019: improving support for quantification data. <i>Nucleic Acids Research</i> , 2019, 47, D442-D450.	14.5	6,449
15	Expanding the Use of Spectral Libraries in Proteomics. <i>Journal of Proteome Research</i> , 2018, 17, 4051-4060.	3.7	47
16	Comprehensive Analysis of Alternative Splicing Across Tumors from 8,705 Patients. <i>Cancer Cell</i> , 2018, 34, 211-224.e6.	16.8	623
17	Recommendations for the packaging and containerizing of bioinformatics software. <i>F1000Research</i> , 2018, 7, 742.	1.6	27
18	Recommendations for the packaging and containerizing of bioinformatics software. <i>F1000Research</i> , 2018, 7, 742.	1.6	29

#	ARTICLE	IF	CITATIONS
19	OpenMS â€“ A platform for reproducible analysis of mass spectrometry data. Journal of Biotechnology, 2017, 261, 142-148.	3.8	85
20	BioContainers: an open-source and community-driven framework for software standardization. Bioinformatics, 2017, 33, 2580-2582.	4.1	205
21	Differential Enzymatic ¹⁶ O/ ¹⁸ O Labeling for the Detection of Cross-Linked Nucleic Acidâ€“Protein Heteroconjugates. Analytical Chemistry, 2017, 89, 11208-11213.	6.5	1
22	In-depth analysis of protein inference algorithms using multiple search engines and well-defined metrics. Journal of Proteomics, 2017, 150, 170-182.	2.4	56
23	LFQProfiler and RNPxl: Open-Source Tools for Label-Free Quantification and Proteinâ€“RNA Cross-Linking Integrated into Proteome Discoverer. Journal of Proteome Research, 2016, 15, 3441-3448.	3.7	29
24	OpenMS: a flexible open-source software platform for mass spectrometry data analysis. Nature Methods, 2016, 13, 741-748.	19.0	537
25	Ten Simple Rules for Taking Advantage of Git and GitHub. PLoS Computational Biology, 2016, 12, e1004947.	3.2	96
26	Dithiothreitol (DTT) Acts as a Specific, UV-inducible Cross-linker in Elucidation of Proteinâ€“RNA Interactions*. Molecular and Cellular Proteomics, 2015, 14, 3196-3210.	3.8	10
27	Workflows for automated downstream data analysis and visualization in largeâ€“scale computational mass spectrometry. Proteomics, 2015, 15, 1443-1447.	2.2	32
28	Analysis of proteinâ€“RNA interactions in CRISPR proteins and effector complexes by UV-induced cross-linking and mass spectrometry. Methods, 2015, 89, 138-148.	3.8	25
29	MetaProSIP: Automated Inference of Stable Isotope Incorporation Rates in Proteins for Functional Metaproteomics. Journal of Proteome Research, 2015, 14, 619-627.	3.7	64
30	The mzTab Data Exchange Format: Communicating Mass-spectrometry-based Proteomics and Metabolomics Experimental Results to a Wider Audience. Molecular and Cellular Proteomics, 2014, 13, 2765-2775.	3.8	130
31	Photo-cross-linking and high-resolution mass spectrometry for assignment of RNA-binding sites in RNA-binding proteins. Nature Methods, 2014, 11, 1064-1070.	19.0	218
32	PTMeta: Increasing identification rates of modified peptides using modification prescanning and metaâ€“analysis. Proteomics, 2013, 13, 1042-1051.	2.2	5
33	The mzQuantML Data Standard for Mass Spectrometryâ€“based Quantitative Studies in Proteomics. Molecular and Cellular Proteomics, 2013, 12, 2332-2340.	3.8	66
34	On comparison of SimTandem with state-of-the-art peptide identification tools, efficiency of precursor mass filter and dealing with variable modifications. Journal of Integrative Bioinformatics, 2013, 10, 228.	1.5	1
35	Global effects of the small RNA biogenesis machinery on the <i>Arabidopsis thaliana</i> transcriptome. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 17466-17473.	7.1	66
36	Stressâ€“induced changes in the <i>Arabidopsis thaliana</i> transcriptome analyzed using wholeâ€“genome tiling arrays. Plant Journal, 2009, 58, 1068-1082.	5.7	273

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37	At-TAX: a whole genome tiling array resource for developmental expression analysis and transcript identification in <i>Arabidopsis thaliana</i> . <i>Genome Biology</i> , 2008, 9, R112.	9.6	91
38	Dual roles of the nuclear cap-binding complex and SERRATE in pre-mRNA splicing and microRNA processing in <i>Arabidopsis thaliana</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 8795-8800.	7.1	378