Timo Sachsenberg

List of Publications by Year
in descending order

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	The PRIDE database and related tools and resources in 2019: improving support for quantification data. Nucleic Acids Research, 2019, 47, D442-D450.	14.5	6,449
2	Comprehensive Analysis of Alternative Splicing Across Tumors from 8,705 Patients. Cancer Cell, 2018, 34, 211-224.e6.	16.8	623
3	OpenMS: a flexible open-source software platform for mass spectrometry data analysis. Nature Methods, 2016, 13, 741-748.	19.0	537
4	Dual roles of the nuclear cap-binding complex and SERRATE in pre-mRNA splicing and microRNA processing in <i>Arabidopsis thaliana</i>. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 8795-8800.	7.1	378
5	Stress‐induced changes in the <i>Arabidopsis thaliana</i> transcriptome analyzed using whole‐genome tiling arrays. Plant Journal, 2009, 58, 1068-1082.	5.7	273
6	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
7	BioContainers: an open-source and community-driven framework for software standardization. Bioinformatics, 2017, 33, 2580-2582.	4.1	205
8	ThermoRawFileParser: Modular, Scalable, and Cross-Platform RAW File Conversion. Journal of Proteome Research, 2020, 19, 537-542.	3.7	144
9	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
10	Ten Simple Rules for Taking Advantage of Git and GitHub. PLoS Computational Biology, 2016, 12, e1004947.	3.2	96
11	At-TAX: a whole genome tiling array resource for developmental expression analysis and transcript identification in Arabidopsis thaliana. Genome Biology, 2008, 9, R112.	9.6	91
12	OpenMS â€" A platform for reproducible analysis of mass spectrometry data. Journal of Biotechnology, 2017, 261, 142-148.	3.8	85
13	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
14	The mzQuantML Data Standard for Mass Spectrometryâ€"based Quantitative Studies in Proteomics. Molecular and Cellular Proteomics, 2013, 12, 2332-2340.	3.8	66
15	MetaProSIP: Automated Inference of Stable Isotope Incorporation Rates in Proteins for Functional Metaproteomics. Journal of Proteome Research, 2015, 14, 619-627.	3.7	64
16	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
17	A computational platform for high-throughput analysis of RNA sequences and modifications by mass spectrometry. Nature Communications, 2020, 11, 926.	12.8	54
18	Expanding the Use of Spectral Libraries in Proteomics. Journal of Proteome Research, 2018, 17, 4051-4060.	3.7	47

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19	A proteomics sample metadata representation for multiomics integration and big data analysis. Nature Communications, 2021, 12, 5854.	12.8	45
20	mzTab-M: A Data Standard for Sharing Quantitative Results in Mass Spectrometry Metabolomics. Analytical Chemistry, 2019, 91, 3302-3310.	6.5	43
21	MHCquant: Automated and Reproducible Data Analysis for Immunopeptidomics. Journal of Proteome Research, 2019, 18, 3876-3884.	3.7	35
22	Workflows for automated downstream data analysis and visualization in large-scale computational mass spectrometry. Proteomics, 2015, 15, 1443-1447.	2.2	32
23	LFQProfiler and RNPxl: Open-Source Tools for Label-Free Quantification and Protein–RNA Cross-Linking Integrated into Proteome Discoverer. Journal of Proteome Research, 2016, 15, 3441-3448.	3.7	29
24	Recommendations for the packaging and containerizing of bioinformatics software. F1000Research, 2018, 7, 742.	1.6	29
25	Recommendations for the packaging and containerizing of bioinformatics software. F1000Research, 2018, 7, 742.	1.6	27
26	Analysis of protein–RNA interactions in CRISPR proteins and effector complexes by UV-induced cross-linking and mass spectrometry. Methods, 2015, 89, 138-148.	3.8	25
27	SmartPeak Automates Targeted and Quantitative Metabolomics Data Processing. Analytical Chemistry, 2020, 92, 15968-15974.	6.5	23
28	Analysis of protein-DNA interactions in chromatin by UV induced cross-linking and mass spectrometry. Nature Communications, 2020, 11, 5250.	12.8	22
29	EPIFANY: A Method for Efficient High-Confidence Protein Inference. Journal of Proteome Research, 2020, 19, 1060-1072.	3.7	20
30	DIAproteomics: A Multifunctional Data Analysis Pipeline for Data-Independent Acquisition Proteomics and Peptidomics. Journal of Proteome Research, 2021, 20, 3758-3766.	3.7	17
31	Generation of ENSEMBL-based proteogenomics databases boosts the identification of non-canonical peptides. Bioinformatics, 2022, 38, 1470-1472.	4.1	16
32	Dithiothreitol (DTT) Acts as a Specific, UV-inducible Cross-linker in Elucidation of Protein–RNA Interactions*. Molecular and Cellular Proteomics, 2015, 14, 3196-3210.	3.8	10
33	OpenPepXL: An Open-Source Tool for Sensitive Identification of Cross-Linked Peptides in XL-MS. Molecular and Cellular Proteomics, 2020, 19, 2157-2168.	3.8	10
34	Tracing incorporation of heavy water into proteins for species-specific metabolic activity in complex communities. Journal of Proteomics, 2020, 222, 103791.	2.4	7
35	PTMeta: Increasing identification rates of modified peptides using modification prescanning and meta-analysis. Proteomics, 2013, 13, 1042-1051.	2.2	5
36	A Comprehensive Evaluation of Consensus Spectrum Generation Methods in Proteomics. Journal of Proteome Research, 2022, 21, 1566-1574.	3.7	2

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37	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
38	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