

Wout Bittremieux

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

46
papers

671
citations

13
h-index

24
g-index

68
ext. papers

1,091
ext. citations

8.2
avg, IF

4.3
L-index

#	Paper	IF	Citations
46	A primer to frequent itemset mining for bioinformatics. <i>Briefings in Bioinformatics</i> , 2015 , 16, 216-31	13.4	71
45	Proteomics Standards Initiative: Fifteen Years of Progress and Future Work. <i>Journal of Proteome Research</i> , 2017 , 16, 4288-4298	5.6	61
44	Quality control in mass spectrometry-based proteomics. <i>Mass Spectrometry Reviews</i> , 2018 , 37, 697-711	11	44
43	Machine learning applications in proteomics research: how the past can boost the future. <i>Proteomics</i> , 2014 , 14, 353-66	4.8	43
42	Fast Open Modification Spectral Library Searching through Approximate Nearest Neighbor Indexing. <i>Journal of Proteome Research</i> , 2018 , 17, 3463-3474	5.6	42
41	qcML: an exchange format for quality control metrics from mass spectrometry experiments. <i>Molecular and Cellular Proteomics</i> , 2014 , 13, 1905-13	7.6	36
40	Auto-deconvolution and molecular networking of gas chromatography-mass spectrometry data. <i>Nature Biotechnology</i> , 2021 , 39, 169-173	44.5	36
39	Detection of Enriched T Cell Epitope Specificity in Full T Cell Receptor Sequence Repertoires. <i>Frontiers in Immunology</i> , 2019 , 10, 2820	8.4	31
38	On the feasibility of mining CD8+ T cell receptor patterns underlying immunogenic peptide recognition. <i>Immunogenetics</i> , 2018 , 70, 159-168	3.2	30
37	Computational quality control tools for mass spectrometry proteomics. <i>Proteomics</i> , 2017 , 17, 1600159	4.8	23
36	Extremely Fast and Accurate Open Modification Spectral Library Searching of High-Resolution Mass Spectra Using Feature Hashing and Graphics Processing Units. <i>Journal of Proteome Research</i> , 2019 , 18, 3792-3799	5.6	19
35	iMonDB: Mass Spectrometry Quality Control through Instrument Monitoring. <i>Journal of Proteome Research</i> , 2015 , 14, 2360-6	5.6	18
34	spectrum_utils: A Python Package for Mass Spectrometry Data Processing and Visualization. <i>Analytical Chemistry</i> , 2020 , 92, 659-661	7.8	17
33	Grasping frequent subgraph mining for bioinformatics applications. <i>BioData Mining</i> , 2018 , 11, 20	4.3	13
32	The Human Proteome Organization-Proteomics Standards Initiative Quality Control Working Group: Making Quality Control More Accessible for Biological Mass Spectrometry. <i>Analytical Chemistry</i> , 2017 , 89, 4474-4479	7.8	12
31	Unsupervised Quality Assessment of Mass Spectrometry Proteomics Experiments by Multivariate Quality Control Metrics. <i>Journal of Proteome Research</i> , 2016 , 15, 1300-7	5.6	12
30	Current challenges for unseen-epitope TCR interaction prediction and a new perspective derived from image classification. <i>Briefings in Bioinformatics</i> , 2021 , 22,	13.4	12

29	Using Expert Driven Machine Learning to Enhance Dynamic Metabolomics Data Analysis. <i>Metabolites</i> , 2019 , 9,	5.6	11
28	A community proposal to integrate proteomics activities in ELIXIR. <i>F1000Research</i> , 2017 , 6,	3.6	10
27	MESSAR: Automated recommendation of metabolite substructures from tandem mass spectra. <i>PLoS ONE</i> , 2020 , 15, e0226770	3.7	10
26	jqcML: an open-source java API for mass spectrometry quality control data in the qcML format. <i>Journal of Proteome Research</i> , 2014 , 13, 3484-7	5.6	9
25	Universal Spectrum Identifier for mass spectra. <i>Nature Methods</i> , 2021 , 18, 768-770	21.6	9
24	Designing biomedical proteomics experiments: state-of-the-art and future perspectives. <i>Expert Review of Proteomics</i> , 2016 , 13, 495-511	4.2	9
23	Current challenges for epitope-agnostic TCR interaction prediction and a new perspective derived from image classification		7
22	TCRex: detection of enriched T cell epitope specificity in full T cell receptor sequence repertoires		7
21	Universal MS/MS Visualization and Retrieval with the Metabolomics Spectrum Resolver Web Service		6
20	Universal Spectrum Identifier for mass spectra		5
19	Current and future deep learning algorithms for tandem mass spectrometry (MS/MS)-based small molecule structure elucidation. <i>Rapid Communications in Mass Spectrometry</i> , 2021 , e9120	2.2	5
18	2018 YPIC Challenge: A Case Study in Characterizing an Unknown Protein Sample. <i>Journal of Proteome Research</i> , 2019 , 18, 3936-3943	5.6	4
17	Efficient reduction of candidate matches in peptide spectrum library searching using the top k most intense peaks. <i>Journal of Proteome Research</i> , 2014 , 13, 4175-83	5.6	4
16	Reference data based insights expand understanding of human metabolomes		4
15	Large-scale tandem mass spectrum clustering using fast nearest neighbor searching. <i>Rapid Communications in Mass Spectrometry</i> , 2021 , e9153	2.2	4
14	Open Science Resources for the Mass Spectrometry-Based Analysis of SARS-CoV-2. <i>Journal of Proteome Research</i> , 2021 , 20, 1464-1475	5.6	4
13	ppx: Programmatic Access to Proteomics Data Repositories. <i>Journal of Proteome Research</i> , 2021 , 20, 4621-4624	5.6	4
12	A learned embedding for efficient joint analysis of millions of mass spectra		3

11	spectrum_utils: A Python package for mass spectrometry data processing and visualization		3
10	Multi-omics profiling of Earth's biomes reveals that microbial and metabolite composition are shaped by the environment		3
9	A learned embedding for efficient joint analysis of millions of mass spectra. <i>Nature Methods</i> ,	21.6	3
8	The European Bioinformatics Community for Mass Spectrometry (EuBIC-MS): an open community for bioinformatics training and research. <i>Rapid Communications in Mass Spectrometry</i> , 2021 , e9087	2.2	2
7	Physicochemical properties determining drug detection in skin. <i>Clinical and Translational Science</i> , 2021 ,	4.9	1
6	Identification of Epitope-Specific T Cells in T-Cell Receptor Repertoires. <i>Methods in Molecular Biology</i> , 2020 , 2120, 183-195	1.4	1
5	On the feasibility of mining CD8+ T-cell receptor patterns underlying immunogenic peptide recognition		1
4	Mining the Enriched Subgraphs for Specific Vertices in a Biological Graph. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019 , 16, 1496-1507	3	1
3	Large-scale tandem mass spectrum clustering using fast nearest neighbor searching		1
2	Native Metabolomics Identifies the Rivulariapeptolide Family of Protease Inhibitors		1
1	Four layer multi-omics reveals molecular responses to aneuploidy in Leishmania		1