

Wout Bittremieux

List of Publications by Year in Descending Order

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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	Physicochemical properties determining drug detection in skin. <i>Clinical and Translational Science</i> , 2021 ,	4.9	1
45	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
44	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
43	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
42	Universal Spectrum Identifier for mass spectra. <i>Nature Methods</i> , 2021 , 18, 768-770	21.6	9
41	Large-scale tandem mass spectrum clustering using fast nearest neighbor searching. <i>Rapid Communications in Mass Spectrometry</i> , 2021 , e9153	2.2	4
40	Auto-deconvolution and molecular networking of gas chromatography-mass spectrometry data. <i>Nature Biotechnology</i> , 2021 , 39, 169-173	44.5	36
39	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
38	ppx: Programmatic Access to Proteomics Data Repositories. <i>Journal of Proteome Research</i> , 2021 , 20, 4621-4624	5.6	4
37	MESSAR: Automated recommendation of metabolite substructures from tandem mass spectra. <i>PLoS ONE</i> , 2020 , 15, e0226770	3.7	10
36	Identification of Epitope-Specific T Cells in T-Cell Receptor Repertoires. <i>Methods in Molecular Biology</i> , 2020 , 2120, 183-195	1.4	1
35	spectrum_utils: A Python Package for Mass Spectrometry Data Processing and Visualization. <i>Analytical Chemistry</i> , 2020 , 92, 659-661	7.8	17
34	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
33	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
32	Using Expert Driven Machine Learning to Enhance Dynamic Metabolomics Data Analysis. <i>Metabolites</i> , 2019 , 9,	5.6	11
31	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
30	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

29	On the feasibility of mining CD8+ T cell receptor patterns underlying immunogenic peptide recognition. <i>Immunogenetics</i> , 2018 , 70, 159-168	3.2	30
28	Quality control in mass spectrometry-based proteomics. <i>Mass Spectrometry Reviews</i> , 2018 , 37, 697-711	11	44
27	Fast Open Modification Spectral Library Searching through Approximate Nearest Neighbor Indexing. <i>Journal of Proteome Research</i> , 2018 , 17, 3463-3474	5.6	42
26	Grasping frequent subgraph mining for bioinformatics applications. <i>BioData Mining</i> , 2018 , 11, 20	4.3	13
25	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
24	Proteomics Standards Initiative: Fifteen Years of Progress and Future Work. <i>Journal of Proteome Research</i> , 2017 , 16, 4288-4298	5.6	61
23	Computational quality control tools for mass spectrometry proteomics. <i>Proteomics</i> , 2017 , 17, 1600159	4.8	23
22	A community proposal to integrate proteomics activities in ELIXIR. <i>F1000Research</i> , 2017 , 6,	3.6	10
21	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
20	Designing biomedical proteomics experiments: state-of-the-art and future perspectives. <i>Expert Review of Proteomics</i> , 2016 , 13, 495-511	4.2	9
19	iMonDB: Mass Spectrometry Quality Control through Instrument Monitoring. <i>Journal of Proteome Research</i> , 2015 , 14, 2360-6	5.6	18
18	A primer to frequent itemset mining for bioinformatics. <i>Briefings in Bioinformatics</i> , 2015 , 16, 216-31	13.4	71
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	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
15	Machine learning applications in proteomics research: how the past can boost the future. <i>Proteomics</i> , 2014 , 14, 353-66	4.8	43
14	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
13	On the feasibility of mining CD8+ T-cell receptor patterns underlying immunogenic peptide recognition		1
12	Current challenges for epitope-agnostic TCR interaction prediction and a new perspective derived from image classification		7

11	Universal MS/MS Visualization and Retrieval with the Metabolomics Spectrum Resolver Web Service	6
10	Reference data based insights expand understanding of human metabolomes	4
9	Universal Spectrum Identifier for mass spectra	5
8	TCRex: detection of enriched T cell epitope specificity in full T cell receptor sequence repertoires	7
7	A learned embedding for efficient joint analysis of millions of mass spectra	3
6	spectrum_utils: A Python package for mass spectrometry data processing and visualization	3
5	Multi-omics profiling of Earth's biomes reveals that microbial and metabolite composition are shaped by the environment	3
4	Large-scale tandem mass spectrum clustering using fast nearest neighbor searching	1
3	Native Metabolomics Identifies the Rivulariapeptolide Family of Protease Inhibitors	1
2	Four layer multi-omics reveals molecular responses to aneuploidy in Leishmania	1
1	A learned embedding for efficient joint analysis of millions of mass spectra. <i>Nature Methods</i> ,	21.6 3