

Tim Van Den Bossche

List of Publications by Year in descending order

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Version: 2024-02-01

19
papers

452
citations

933264

10
h-index

839398

18
g-index

28
all docs

28
docs citations

28
times ranked

582
citing authors

#	ARTICLE	IF	CITATIONS
1	<i><i>Pout2Prot</i></i> : An Efficient Tool to Create Protein (Sub)groups from Percolator Output Files. <i>Journal of Proteome Research</i> , 2022, 21, 1175-1180.	1.8	4
2	Proteomics Standards Initiative's ProForma 2.0: Unifying the Encoding of Proteoforms and Peptidoforms. <i>Journal of Proteome Research</i> , 2022, 21, 1189-1195.	1.8	14
3	Sensitive and Specific Spectral Library Searching with CompOmics Spectral Library Searching Tool and Percolator. <i>Journal of Proteome Research</i> , 2022, 21, 1365-1370.	1.8	6
4	Unipept Desktop: A Faster, More Powerful Metaproteomics Results Analysis Tool. <i>Journal of Proteome Research</i> , 2021, 20, 2005-2009.	1.8	17
5	MegaGO: A Fast Yet Powerful Approach to Assess Functional Gene Ontology Similarity across Meta-Omics Data Sets. <i>Journal of Proteome Research</i> , 2021, 20, 2083-2088.	1.8	8
6	The European Bioinformatics Community for Mass Spectrometry (EuBICâ€MS): an open community for bioinformatics training and research. <i>Rapid Communications in Mass Spectrometry</i> , 2021, , e9087.	0.7	3
7	Cov-MS: A Community-Based Template Assay for Mass-Spectrometry-Based Protein Detection in SARS-CoV-2 Patients. <i>Jacs Au</i> , 2021, 1, 750-765.	3.6	29
8	Universal Spectrum Identifier for mass spectra. <i>Nature Methods</i> , 2021, 18, 768-770.	9.0	47
9	Research culture: science from bench to society. <i>Biology Open</i> , 2021, 10, .	0.6	4
10	A proteomics sample metadata representation for multiomics integration and big data analysis. <i>Nature Communications</i> , 2021, 12, 5854.	5.8	45
11	Critical Assessment of MetaProteome Investigation (CAMPI): a multi-laboratory comparison of established workflows. <i>Nature Communications</i> , 2021, 12, 7305.	5.8	34
12	The Metaproteomics Initiative: a coordinated approach for propelling the functional characterization of microbiomes. <i>Microbiome</i> , 2021, 9, 243.	4.9	36
13	gNOMO: a multi-omics pipeline for integrated host and microbiome analysis of non-model organisms. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqaa058.	1.5	5
14	Connecting MetaProteomeAnalyzer and PeptideShaker to Unipept for Seamless End-to-End Metaproteomics Data Analysis. <i>Journal of Proteome Research</i> , 2020, 19, 3562-3566.	1.8	11
15	Unipept CLI 2.0: adding support for visualizations and functional annotations. <i>Bioinformatics</i> , 2020, 36, 4220-4221.	1.8	9
16	The Age of Dataâ€Driven Proteomics: How Machine Learning Enables Novel Workflows. <i>Proteomics</i> , 2020, 20, e1900351.	1.3	34
17	Extracellular vesicles in patients in the acute phase of psychosis and after clinical improvement: an explorative study. <i>PeerJ</i> , 2020, 8, e9714.	0.9	6
18	Proteomics Standards Initiative Extended FASTA Format. <i>Journal of Proteome Research</i> , 2019, 18, 2686-2692.	1.8	22

#	ARTICLE	IF	CITATIONS
19	Challenges and promise at the interface of metaproteomics and genomics: an overview of recent progress in metaproteogenomic data analysis. Expert Review of Proteomics, 2019, 16, 375-390.	1.3	86