Gerhard Mayer

List of Publications by Year
in descending order

19 papers	13,133 citations	706676 14 h-index	889612 19 g-index
20 all docs	20 docs citations	20 times ranked	35237 citing authors

#	Article	IF	Citations
1	A Current Encyclopedia of Bioinformatics Tools, Data Formats and Resources for Mass Spectrometry Lipidomics. Metabolites, 2022, 12, 584.	1.3	10
2	Implementing FAIR data management within the German Network for Bioinformatics Infrastructure (de.NBI) exemplified by selected use cases. Briefings in Bioinformatics, 2021, 22, .	3.2	18
3	mzTab-M: A Data Standard for Sharing Quantitative Results in Mass Spectrometry Metabolomics. Analytical Chemistry, 2019, 91, 3302-3310.	3.2	43
4	Proteomics Standards Initiative Extended FASTA Format. Journal of Proteome Research, 2019, 18, 2686-2692.	1.8	22
5	The PRIDE database and related tools and resources in 2019: improving support for quantification data. Nucleic Acids Research, 2019, 47, D442-D450.	6.5	6,449
6	A generally applicable lightweight method for calculating a value structure for tools and services in bioinformatics infrastructure projects. Briefings in Bioinformatics, 2019, 20, 1215-1221.	3.2	1
7	BioInfra.Prot: A comprehensive proteomics workflow including data standardization, protein inference, expression analysis and data publication. Journal of Biotechnology, 2017, 261, 116-125.	1.9	21
8	Proteomics Standards Initiative: Fifteen Years of Progress and Future Work. Journal of Proteome Research, 2017, 16, 4288-4298.	1.8	87
9	The mzIdentML Data Standard Version 1.2, Supporting Advances in Proteome Informatics. Molecular and Cellular Proteomics, 2017, 16, 1275-1285.	2.5	55
10	Boolean modeling techniques for protein co-expression networks in systems medicine. Expert Review of Proteomics, 2016, 13, 555-569.	1.3	3
11	2016 update of the PRIDE database and its related tools. Nucleic Acids Research, 2016, 44, D447-D456.	6.5	3,451
12	ProCon â€" PROteomics CONversion tool. Journal of Proteomics, 2015, 129, 56-62.	1.2	14
13	Development of data representation standards by the human proteome organization proteomics standards initiative. Journal of the American Medical Informatics Association: JAMIA, 2015, 22, 495-506.	2.2	54
14	ProteomeXchange provides globally coordinated proteomics data submission and dissemination. Nature Biotechnology, 2014, 32, 223-226.	9.4	2,505
15	Controlled vocabularies and ontologies in proteomics: Overview, principles and practice. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2014, 1844, 98-107.	1.1	36
16	Guidelines for reporting quantitative mass spectrometry based experiments in proteomics. Journal of Proteomics, 2013, 95, 84-88.	1.2	46
17	The mzQuantML Data Standard for Mass Spectrometryâ€"based Quantitative Studies in Proteomics. Molecular and Cellular Proteomics, 2013, 12, 2332-2340.	2.5	66
18	The HUPO proteomics standards initiative- mass spectrometry controlled vocabulary. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat009-bat009.	1.4	76

#	Article	IF	Citations
19	The mzIdentML Data Standard for Mass Spectrometry-Based Proteomics Results. Molecular and Cellular Proteomics, 2012, 11, M111.014381-1-M111.014381-10.	2.5	175