# Gerhard Mayer

## List of Publications by Citations

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|---|---|
| **19** papers | **8,889** citations |
| **13** h-index | **20** g-index |
| **20** ext. papers | **12,013** ext. citations |
| **9.7** avg, IF | **5.61** L-index |

| # | Paper | IF | Citations |
|---|-------|----|-----------|
| 19 | The PRIDE database and related tools and resources in 2019: improving support for quantification data. *Nucleic Acids Research*, **2019**, 47, D442-D450 | 20.1 | 3856 |
| 18 | 2016 update of the PRIDE database and its related tools. *Nucleic Acids Research*, **2016**, 44, D447-56 | 20.1 | 2440 |
| 17 | ProteomeXchange provides globally coordinated proteomics data submission and dissemination. *Nature Biotechnology*, **2014**, 32, 223-6 | 44.5 | 2053 |
| 16 | The mzIdentML data standard for mass spectrometry-based proteomics results. *Molecular and Cellular Proteomics*, **2012**, 11, M111.014381 | 7.6 | 150 |
| 15 | Proteomics Standards Initiative: Fifteen Years of Progress and Future Work. *Journal of Proteome Research*, **2017**, 16, 4288-4298 | 5.6 | 61 |
| 14 | The HUPO proteomics standards initiative- mass spectrometry controlled vocabulary. *Database: the Journal of Biological Databases and Curation*, **2013**, 2013, bat009 | 5 | 56 |
| 13 | The mzQuantML data standard for mass spectrometry-based quantitative studies in proteomics. *Molecular and Cellular Proteomics*, **2013**, 12, 2332-40 | 7.6 | 55 |
| 12 | 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 | 8.6 | 42 |
| 11 | Guidelines for reporting quantitative mass spectrometry based experiments in proteomics. *Journal of Proteomics*, **2013**, 95, 84-8 | 3.9 | 37 |
| 10 | The mzIdentML Data Standard Version 1.2, Supporting Advances in Proteome Informatics. *Molecular and Cellular Proteomics*, **2017**, 16, 1275-1285 | 7.6 | 37 |
| 9 | mzTab-M: A Data Standard for Sharing Quantitative Results in Mass Spectrometry Metabolomics. *Analytical Chemistry*, **2019**, 91, 3302-3310 | 7.8 | 27 |
| 8 | Controlled vocabularies and ontologies in proteomics: overview, principles and practice. *Biochimica Et Biophysica Acta - Proteins and Proteomics*, **2014**, 1844, 98-107 | 4 | 26 |
| 7 | BioInfra.Prot: A comprehensive proteomics workflow including data standardization, protein inference, expression analysis and data publication. *Journal of Biotechnology*, **2017**, 261, 116-125 | 3.7 | 17 |
| 6 | ProCon - PROteomics CONversion tool. *Journal of Proteomics*, **2015**, 129, 56-62 | 3.9 | 12 |
| 5 | Proteomics Standards Initiative Extended FASTA Format. *Journal of Proteome Research*, **2019**, 18, 2686-2692 | 5.6 | 11 |
| 4 | Implementing FAIR data management within the German Network for Bioinformatics Infrastructure (de.NBI) exemplified by selected use cases. *Briefings in Bioinformatics*, **2021**, 22, | 13.4 | 4 |
| 3 | Proteomics Standards Initiative Extended FASTA Format (PEFF) | | 1 |

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|---|---|---|---|
| 2 | Boolean modeling techniques for protein co-expression networks in systems medicine. *Expert Review of Proteomics*, **2016**, 13, 555-69 | 4.2 | 1 |
| 1 | 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 | 13.4 | 0 |