

# Mathias Wilhelm

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6809261/publications.pdf>

Version: 2024-02-01

53  
papers

6,894  
citations

159585

30  
h-index

155660

55  
g-index

61  
all docs

61  
docs citations

61  
times ranked

11260  
citing authors

| #  | ARTICLE   | IF   | CITATIONS |
|----|---|------|-----------|
| 1  | Mass-spectrometry-based draft of the human proteome. <i>Nature</i> , 2014, 509, 582-587.  | 27.8 | 1,697     |
| 2  | The target landscape of clinical kinase drugs. <i>Science</i> , 2017, 358, .  | 12.6 | 609       |
| 3  | A deep proteome and transcriptome abundance atlas of 29 healthy human tissues. <i>Molecular Systems Biology</i> , 2019, 15, e8503.                            | 7.2  | 576       |
| 4  | Prosit: proteome-wide prediction of peptide tandem mass spectra by deep learning. <i>Nature Methods</i> , 2019, 16, 509-518.                                  | 19.0 | 539       |
| 5  | A Scalable Approach for Protein False Discovery Rate Estimation in Large Proteomic Data Sets. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 2394-2404. | 3.8  | 350       |
| 6  | Mass-spectrometry-based draft of the Arabidopsis proteome. <i>Nature</i> , 2020, 579, 409-414.  | 27.8 | 328       |
| 7  | Global Proteome Analysis of the NCI-60 Cell Line Panel. <i>Cell Reports</i> , 2013, 4, 609-620.   | 6.4  | 276       |
| 8  | The emerging landscape of single-molecule protein sequencing technologies. <i>Nature Methods</i> , 2021, 18, 604-617.   | 19.0 | 198       |
| 9  | ProteomicsDB. <i>Nucleic Acids Research</i> , 2018, 46, D1271-D1281.  | 14.5 | 197       |
| 10 | Building ProteomeTools based on a complete synthetic human proteome. <i>Nature Methods</i> , 2017, 14, 259-262.   | 19.0 | 182       |
| 11 | Meltome atlas <sup>™</sup> thermal proteome stability across the tree of life. <i>Nature Methods</i> , 2020, 17, 495-503.                                     | 19.0 | 152       |
| 12 | Generating high quality libraries for DIA MS with empirically corrected peptide predictions. <i>Nature Communications</i> , 2020, 11, 1548.                   | 12.8 | 148       |
| 13 | ProteomicsDB: a multi-omics and multi-organism resource for life science research. <i>Nucleic Acids Research</i> , 2020, 48, D1153-D1163.                     | 14.5 | 126       |
| 14 | Optimized Chemical Proteomics Assay for Kinase Inhibitor Profiling. <i>Journal of Proteome Research</i> , 2015, 14, 1574-1586.                                | 3.7  | 104       |
| 15 | Ion Mobility Tandem Mass Spectrometry Enhances Performance of Bottom-up Proteomics. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 3709-3715.           | 3.8  | 98        |
| 16 | Peptide Level Turnover Measurements Enable the Study of Proteoform Dynamics. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 974-992.                    | 3.8  | 98        |
| 17 | Mining the Human Tissue Proteome for Protein Citrullination. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 1378-1391.                                  | 3.8  | 93        |
| 18 | Deep learning boosts sensitivity of mass spectrometry-based immunopeptidomics. <i>Nature Communications</i> , 2021, 12, 3346.                                 | 12.8 | 90        |

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|----|--|------|-----------|
| 19 | ProteomeTools: Systematic Characterization of 21 Post-translational Protein Modifications by Liquid Chromatography Tandem Mass Spectrometry (LC-MS/MS) Using Synthetic Peptides. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 1850-1863. | 3.8  | 78        |
| 20 | Challenges in Clinical Metaproteomics Highlighted by the Analysis of Acute Leukemia Patients with Gut Colonization by Multidrug-Resistant Enterobacteriaceae. <i>Proteomes</i> , 2019, 7, 2.   | 3.5  | 71        |
| 21 | PROCAL: A Set of 40 Peptide Standards for Retention Time Indexing, Column Performance Monitoring, and Collision Energy Calibration. <i>Proteomics</i> , 2017, 17, 1700263.   | 2.2  | 58        |
| 22 | mz5: Space- and Time-efficient Storage of Mass Spectrometry Data Sets. <i>Molecular and Cellular Proteomics</i> , 2012, 11, O111.011379.   | 3.8  | 56        |
| 23 | Expanding the Use of Spectral Libraries in Proteomics. <i>Journal of Proteome Research</i> , 2018, 17, 4051-4060.  | 3.7  | 47        |
| 24 | Proteome activity landscapes of tumor cell lines determine drug responses. <i>Nature Communications</i> , 2020, 11, 3639.  | 12.8 | 47        |
| 25 | A proteomics sample metadata representation for multiomics integration and big data analysis. <i>Nature Communications</i> , 2021, 12, 5854.   | 12.8 | 45        |
| 26 | Pharmacoproteomic characterisation of human colon and rectal cancer. <i>Molecular Systems Biology</i> , 2017, 13, 951.   | 7.2  | 44        |
| 27 | PROTEOFORMER 2.0: Further Developments in the Ribosome Profiling-assisted Proteogenomic Hunt for New Proteoforms. <i>Molecular and Cellular Proteomics</i> , 2019, 18, S126-S140.  | 3.8  | 43        |
| 28 | Chemical Proteomics and Structural Biology Define EPHA2 Inhibition by Clinical Kinase Drugs. <i>ACS Chemical Biology</i> , 2016, 11, 3400-3411.  | 3.4  | 42        |
| 29 | Target deconvolution of HDAC pharmacopoeia reveals MBLAC2 as common off-target. <i>Nature Chemical Biology</i> , 2022, 18, 812-820.  | 8.0  | 36        |
| 30 | ProteomicsDB: toward a FAIR open-source resource for life-science research. <i>Nucleic Acids Research</i> , 2022, 50, D1541-D1552.   | 14.5 | 35        |
| 31 | Combining peak- and chromatogram-based retention time alignment algorithms for multiple chromatography-mass spectrometry datasets. <i>BMC Bioinformatics</i> , 2012, 13, 214.  | 2.6  | 33        |
| 32 | Linking post-translational modifications and protein turnover by site-resolved protein turnover profiling. <i>Nature Communications</i> , 2022, 13, 165.   | 12.8 | 33        |
| 33 | Spectral Prediction Features as a Solution for the Search Space Size Problem in Proteogenomics. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100076.   | 3.8  | 31        |
| 34 | Identification of 7â€000â€9â€000 Proteins from Cell Lines and Tissues by Single-Shot Microflow LCâ€MS/MS. <i>Analytical Chemistry</i> , 2021, 93, 8687-8692.   | 6.5  | 25        |
| 35 | A Classifier Based on Accurate Mass Measurements to Aid Large Scale, Unbiased Glycoproteomics. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 1017-1025.   | 3.8  | 23        |
| 36 | Chemoproteomicsâ€Aided Medicinal Chemistry for the Discovery of EPHA2 Inhibitors. <i>ChemMedChem</i> , 2017, 12, 999-1011.  | 3.2  | 23        |

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|----|--|------|-----------|
| 37 | Semi-supervised Learning Predicts Approximately One Third of the Alternative Splicing Isoforms as Functional Proteins. <i>Cell Reports</i> , 2015, 12, 183-189.  | 6.4  | 22        |
| 38 | Trimodal Mixed Mode Chromatography That Enables Efficient Offline Two-Dimensional Peptide Fractionation for Proteome Analysis. <i>Analytical Chemistry</i> , 2017, 89, 8884-8891.  | 6.5  | 22        |
| 39 | Universal Spectrum Explorer: A Standalone (Web-)Application for Cross-Resource Spectrum Comparison. <i>Journal of Proteome Research</i> , 2021, 20, 3388-3394.   | 3.7  | 22        |
| 40 | Chemoproteomic Selectivity Profiling of PIKK and PI3K Kinase Inhibitors. <i>ACS Chemical Biology</i> , 2019, 14, 655-664.  | 3.4  | 21        |
| 41 | Proteomic and transcriptomic profiling of aerial organ development in Arabidopsis. <i>Scientific Data</i> , 2020, 7, 334.  | 5.3  | 20        |
| 42 | Mass spectrometry-based draft of the mouse proteome. <i>Nature Methods</i> , 2022, 19, 803-811.  | 19.0 | 19        |
| 43 | Phosphoproteome Profiling Reveals Molecular Mechanisms of Growth-Factor-Mediated Kinase Inhibitor Resistance in EGFR-Overexpressing Cancer Cells. <i>Journal of Proteome Research</i> , 2016, 15, 4490-4504.               | 3.7  | 18        |
| 44 | BiPACE 2D graph-based multiple alignment for comprehensive 2D gas chromatography-mass spectrometry. <i>Bioinformatics</i> , 2014, 30, 988-995.   | 4.1  | 14        |
| 45 | Ethylene glycol improves electrospray ionization efficiency in bottom-up proteomics. <i>Analytical and Bioanalytical Chemistry</i> , 2017, 409, 1049-1057.   | 3.7  | 14        |
| 46 | Prosit Transformer: A transformer for Prediction of MS2 Spectrum Intensities. <i>Journal of Proteome Research</i> , 2022, 21, 1359-1364.   | 3.7  | 10        |
| 47 | SIMSI-Transfer: Software-Assisted Reduction of Missing Values in Phosphoproteomic and Proteomic Isobaric Labeling Data Using Tandem Mass Spectrum Clustering. <i>Molecular and Cellular Proteomics</i> , 2022, 21, 100238. | 3.8  | 9         |
| 48 | High temporal resolution proteome and phosphoproteome profiling of stem cell-derived hepatocyte development. <i>Cell Reports</i> , 2022, 38, 110604.   | 6.4  | 8         |
| 49 | Prosit-TMT: Deep Learning Boosts Identification of TMT-Labeled Peptides. <i>Analytical Chemistry</i> , 2022, 94, 7181-7190.  | 6.5  | 8         |
| 50 | Wilhelm et al. reply. <i>Nature</i> , 2017, 547, E23-E23.  | 27.8 | 7         |
| 51 | Interpretation of the DOME Recommendations for Machine Learning in Proteomics and Metabolomics. <i>Journal of Proteome Research</i> , 2022, 21, 1204-1207.   | 3.7  | 7         |
| 52 | Predicting fragment intensities and retention time of iTRAQ- and TMTPro-labeled peptides with ProsiTMT. <i>Proteomics</i> , 2022, , 2100257.   | 2.2  | 5         |
| 53 | CiRCus: A Framework to Enable Classification of Complex High-Throughput Experiments. <i>Journal of Proteome Research</i> , 2019, 18, 1486-1493.  | 3.7  | 3         |