

Mathias Wilhelm

List of Publications by Year in descending order

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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	ProteomicsDB: toward a FAIR open-source resource for life-science research. <i>Nucleic Acids Research</i> , 2022, 50, D1541-D1552.	14.5	35
2	Linking post-translational modifications and protein turnover by site-resolved protein turnover profiling. <i>Nature Communications</i> , 2022, 13, 165.	12.8	33
3	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
4	High temporal resolution proteome and phosphoproteome profiling of stem cell-derived hepatocyte development. <i>Cell Reports</i> , 2022, 38, 110604.	6.4	8
5	Prosit Transformer: A transformer for Prediction of MS2 Spectrum Intensities. <i>Journal of Proteome Research</i> , 2022, 21, 1359-1364.	3.7	10
6	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
7	Prosit-TMT: Deep Learning Boosts Identification of TMT-Labeled Peptides. <i>Analytical Chemistry</i> , 2022, 94, 7181-7190.	6.5	8
8	Target deconvolution of HDAC pharmacopoeia reveals MBLAC2 as common off-target. <i>Nature Chemical Biology</i> , 2022, 18, 812-820.	8.0	36
9	Predicting fragment intensities and retention time of iTRAQ- and TMTPro-labeled peptides with Prosit-TMT. <i>Proteomics</i> , 2022, , 2100257.	2.2	5
10	Mass spectrometry-based draft of the mouse proteome. <i>Nature Methods</i> , 2022, 19, 803-811.	19.0	19
11	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
12	Deep learning boosts sensitivity of mass spectrometry-based immunopeptidomics. <i>Nature Communications</i> , 2021, 12, 3346.	12.8	90
13	The emerging landscape of single-molecule protein sequencing technologies. <i>Nature Methods</i> , 2021, 18, 604-617.	19.0	198
14	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
15	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
16	A proteomics sample metadata representation for multiomics integration and big data analysis. <i>Nature Communications</i> , 2021, 12, 5854.	12.8	45
17	ProteomicsDB: a multi-omics and multi-organism resource for life science research. <i>Nucleic Acids Research</i> , 2020, 48, D1153-D1163.	14.5	126
18	Proteome activity landscapes of tumor cell lines determine drug responses. <i>Nature Communications</i> , 2020, 11, 3639.	12.8	47

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19	Proteomic and transcriptomic profiling of aerial organ development in Arabidopsis. <i>Scientific Data</i> , 2020, 7, 334.	5.3	20
20	Mass-spectrometry-based draft of the Arabidopsis proteome. <i>Nature</i> , 2020, 579, 409-414.	27.8	328
21	Generating high quality libraries for DIA MS with empirically corrected peptide predictions. <i>Nature Communications</i> , 2020, 11, 1548.	12.8	148
22	Meltome atlas—thermal proteome stability across the tree of life. <i>Nature Methods</i> , 2020, 17, 495-503.	19.0	152
23	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
24	Prosit: proteome-wide prediction of peptide tandem mass spectra by deep learning. <i>Nature Methods</i> , 2019, 16, 509-518.	19.0	539
25	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
26	Chemoproteomic Selectivity Profiling of PIKK and PI3K Kinase Inhibitors. <i>ACS Chemical Biology</i> , 2019, 14, 655-664.	3.4	21
27	CiRCus: A Framework to Enable Classification of Complex High-Throughput Experiments. <i>Journal of Proteome Research</i> , 2019, 18, 1486-1493.	3.7	3
28	A deep proteome and transcriptome abundance atlas of 29 healthy human tissues. <i>Molecular Systems Biology</i> , 2019, 15, e8503.	7.2	576
29	Mining the Human Tissue Proteome for Protein Citrullination. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 1378-1391.	3.8	93
30	ProteomicsDB. <i>Nucleic Acids Research</i> , 2018, 46, D1271-D1281.	14.5	197
31	Peptide Level Turnover Measurements Enable the Study of Proteoform Dynamics. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 974-992.	3.8	98
32	Expanding the Use of Spectral Libraries in Proteomics. <i>Journal of Proteome Research</i> , 2018, 17, 4051-4060.	3.7	47
33	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
34	Building ProteomeTools based on a complete synthetic human proteome. <i>Nature Methods</i> , 2017, 14, 259-262.	19.0	182
35	Chemoproteomics-Aided Medicinal Chemistry for the Discovery of EPHA2 Inhibitors. <i>ChemMedChem</i> , 2017, 12, 999-1011.	3.2	23
36	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

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37	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
38	The target landscape of clinical kinase drugs. <i>Science</i> , 2017, 358, .	12.6	609
39	Pharmacoproteomic characterisation of human colon and rectal cancer. <i>Molecular Systems Biology</i> , 2017, 13, 951.	7.2	44
40	Ethylene glycol improves electrospray ionization efficiency in bottom-up proteomics. <i>Analytical and Bioanalytical Chemistry</i> , 2017, 409, 1049-1057.	3.7	14
41	Wilhelm et al. reply. <i>Nature</i> , 2017, 547, E23-E23.	27.8	7
42	Chemical Proteomics and Structural Biology Define EPHA2 Inhibition by Clinical Kinase Drugs. <i>ACS Chemical Biology</i> , 2016, 11, 3400-3411.	3.4	42
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	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
45	Optimized Chemical Proteomics Assay for Kinase Inhibitor Profiling. <i>Journal of Proteome Research</i> , 2015, 14, 1574-1586.	3.7	104
46	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
47	BiPACE 2D graph-based multiple alignment for comprehensive 2D gas chromatography-mass spectrometry. <i>Bioinformatics</i> , 2014, 30, 988-995.	4.1	14
48	Ion Mobility Tandem Mass Spectrometry Enhances Performance of Bottom-up Proteomics. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 3709-3715.	3.8	98
49	Mass-spectrometry-based draft of the human proteome. <i>Nature</i> , 2014, 509, 582-587.	27.8	1,697
50	Global Proteome Analysis of the NCI-60 Cell Line Panel. <i>Cell Reports</i> , 2013, 4, 609-620.	6.4	276
51	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
52	mz5: Space- and Time-efficient Storage of Mass Spectrometry Data Sets. <i>Molecular and Cellular Proteomics</i> , 2012, 11, O111.011379.	3.8	56
53	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