

# The MaxQuant computational platform for mass spectrometry

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Citation Report

#	ARTICLE	IF	CITATIONS
6	Thermal proteome profiling: unbiased assessment of protein state through heat-induced stability changes. <i>Proteome Science</i> , 2016, 15, 13.	0.7	101
7	Deep Coverage of Global Protein Expression and Phosphorylation in Breast Tumor Cell Lines Using TMT 10-plex Isobaric Labeling. <i>Journal of Proteome Research</i> , 2017, 16, 1121-1132.	1.8	51
8	What computational non-targeted mass spectrometry-based metabolomics can gain from shotgun proteomics. <i>Current Opinion in Biotechnology</i> , 2017, 43, 141-146.	3.3	7
9	Assessment of Label-Free Quantification in Discovery Proteomics and Impact of Technological Factors and Natural Variability of Protein Abundance. <i>Journal of Proteome Research</i> , 2017, 16, 1410-1424.	1.8	91
10	Social network architecture of human immune cells unveiled by quantitative proteomics. <i>Nature Immunology</i> , 2017, 18, 583-593.	7.0	296
11	Expanding Proteome Coverage with CHarge Ordered Parallel Ion aNalysis (CHOPIN) Combined with Broad Specificity Proteolysis. <i>Journal of Proteome Research</i> , 2017, 16, 1288-1299.	1.8	92
12	CLUH regulates mitochondrial metabolism by controlling translation and decay of target mRNAs. <i>Journal of Cell Biology</i> , 2017, 216, 675-693.	2.3	73
13	Insights into autosomal dominant polycystic kidney disease by quantitative mass spectrometry-based proteomics. <i>Cell and Tissue Research</i> , 2017, 369, 41-51.	1.5	4
14	A comprehensive evaluation of popular proteomics software workflows for label-free proteome quantification and imputation. <i>Briefings in Bioinformatics</i> , 2018, 19, 1344-1355.	3.2	88
15	An Optimized Shotgun Strategy for the Rapid Generation of Comprehensive Human Proteomes. <i>Cell Systems</i> , 2017, 4, 587-599.e4.	2.9	413
16	Recent advances in applying mass spectrometry and systems biology to determine brain dynamics. <i>Expert Review of Proteomics</i> , 2017, 14, 545-559.	1.3	12
17	Inference and quantification of peptidofoms in large sample cohorts by SWATH-MS. <i>Nature Biotechnology</i> , 2017, 35, 781-788.	9.4	122
18	Improving data quality and preserving HCD-generated reporter ions with ETHcD for isobaric tag-based quantitative proteomics and proteome-wide PTM studies. <i>Analytica Chimica Acta</i> , 2017, 968, 40-49.	2.6	26
20	Sequential fragment ion filtering and endoglycosidase-assisted identification of intact glycopeptides. <i>Analytical and Bioanalytical Chemistry</i> , 2017, 409, 3077-3087.	1.9	8
21	Electrophilic probes for deciphering substrate recognition by O-GlcNAc transferase. <i>Nature Chemical Biology</i> , 2017, 13, 1267-1273.	3.9	28
22	Sample Preparation for Mass Spectrometry-based Identification of RNA-binding Regions. <i>Journal of Visualized Experiments</i> , 2017, , .	0.2	1
23	A Primer on Concepts and Applications of Proteomics in Neuroscience. <i>Neuron</i> , 2017, 96, 558-571.	3.8	65
24	Structural features of the TatC membrane protein that determine docking and insertion of a twin-arginine signal peptide. <i>Journal of Biological Chemistry</i> , 2017, 292, 21320-21329.	1.6	8

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25	Isobaric Labeling-Based LC-MS/MS Strategy for Comprehensive Profiling of Human Pancreatic Tissue Proteome. <i>Methods in Molecular Biology</i> , 2017, 1788, 215-224.	0.4	10
26	Multiplexed Temporal Quantification of the Exercise-regulated Plasma Peptidome. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 2055-2068.	2.5	56
27	Gel-based and gel-free proteome data associated with controlled deterioration treatment of Glycine max seeds. <i>Data in Brief</i> , 2017, 15, 449-453.	0.5	3
28	Target and identify: triazene linker helps identify azidation sites of labelled proteins via click and cleave strategy. <i>Chemical Communications</i> , 2017, 53, 11929-11932.	2.2	3
29	Collagenase treatment enhances proteomic coverage of low-abundance proteins in decellularized matrix bioscaffolds. <i>Biomaterials</i> , 2017, 144, 130-143.	5.7	39
30	Phosphoproteomic Analysis Reveals the Importance of Kinase Regulation During Orbivirus Infection. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 1990-2005.	2.5	12
31	Functional screening in human cardiac organoids reveals a metabolic mechanism for cardiomyocyte cell cycle arrest. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E8372-E8381.	3.3	361
32	Unrestricted Mass Spectrometric Data Analysis for Identification, Localization, and Quantification of Oxidative Protein Modifications. <i>Journal of Proteome Research</i> , 2017, 16, 3978-3988.	1.8	20
33	SOCS2 Binds to and Regulates EphA2 through Multiple Mechanisms. <i>Scientific Reports</i> , 2017, 7, 10838.	1.6	3
34	A Mass Spectrometry-Based Approach for Mapping Protein Subcellular Localization Reveals the Spatial Proteome of Mouse Primary Neurons. <i>Cell Reports</i> , 2017, 20, 2706-2718.	2.9	105
35	Lysine acetylation stoichiometry and proteomics analyses reveal pathways regulated by sirtuin 1 in human cells. <i>Journal of Biological Chemistry</i> , 2017, 292, 18129-18144.	1.6	36
36	Phosphoproteome-based kinase activity profiling reveals the critical role of MAP2K2 and PLK1 in neuronal autophagy. <i>Autophagy</i> , 2017, 13, 1969-1980.	4.3	48
37	PROCAL: A Set of 40 Peptide Standards for Retention Time Indexing, Column Performance Monitoring, and Collision Energy Calibration. <i>Proteomics</i> , 2017, 17, 1700263.	1.3	58
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40	Biallelic Mutations in MRPS34 Lead to Instability of the Small Mitochondrial Subunit and Leigh Syndrome. <i>American Journal of Human Genetics</i> , 2017, 101, 239-254.	2.6	83
41	MALDI Imaging Combined with Laser Microdissection-Based Microproteomics for Protein Identification: Application to Intratumor Heterogeneity Studies. <i>Methods in Molecular Biology</i> , 2017, 1788, 297-312.	0.4	5
42	The STUB1 RNF4 regulates protein group SUMOylation by targeting the SUMO conjugation machinery. <i>Nature Communications</i> , 2017, 8, 1809.	5.8	91

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43	Assessing species biomass contributions in microbial communities via metaproteomics. <i>Nature Communications</i> , 2017, 8, 1558.	5.8	211
44	Proteogenomics approaches for studying cancer biology and their potential in the identification of acute myeloid leukemia biomarkers. <i>Expert Review of Proteomics</i> , 2017, 14, 649-663.	1.3	7
45	In-depth proteomic analysis of <i>Glycine max</i> seeds during controlled deterioration treatment reveals a shift in seed metabolism. <i>Journal of Proteomics</i> , 2017, 169, 125-135.	1.2	61
46	Challenges and perspectives of metaproteomic data analysis. <i>Journal of Biotechnology</i> , 2017, 261, 24-36.	1.9	195
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50	Hydrogen Peroxide Is Involved in $\beta$ -Cyclodextrin-hemin Complex-Induced Lateral Root Formation in Tomato Seedlings. <i>Frontiers in Plant Science</i> , 2017, 8, 1445.	1.7	4
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52	Network-Driven Proteogenomics Unveils an Aging-Related Imbalance in the Olfactory $\beta$ -NF $\kappa$ B p65 Complex Functionality in Tg2576 Alzheimer's Disease Mouse Model. <i>International Journal of Molecular Sciences</i> , 2017, 18, 2260.	1.8	15
53	Direct Identification of Functional Amyloid Proteins by Label-Free Quantitative Mass Spectrometry. <i>Biomolecules</i> , 2017, 7, 58.	1.8	13
54	Label-Free Quantitative Proteomic Analysis of Harmless and Pathogenic Strains of Infectious Microalgae, <i>Prototheca</i> spp.. <i>International Journal of Molecular Sciences</i> , 2017, 18, 59.	1.8	27
55	Outer Membrane Proteome of <i>Veillonella parvula</i> : A Diderm Firmicute of the Human Microbiome. <i>Frontiers in Microbiology</i> , 2017, 8, 1215.	1.5	55
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60	Early cysteine-dependent inactivation of 26S proteasomes does not involve particle disassembly. <i>Redox Biology</i> , 2018, 16, 123-128.	3.9	6

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61	Quantitative mapping of RNA-mediated nuclear estrogen receptor $\hat{1}^2$ interactome in human breast cancer cells. <i>Scientific Data</i> , 2018, 5, 180031.	2.4	22
62	Three unrelated protease inhibitors enhance accumulation of pharmaceutical recombinant proteins in <i>Nicotiana benthamiana</i> . <i>Plant Biotechnology Journal</i> , 2018, 16, 1797-1810.	4.1	61
63	MUB40 Binds to Lactoferrin and Stands as a Specific Neutrophil Marker. <i>Cell Chemical Biology</i> , 2018, 25, 483-493.e9.	2.5	13
64	Proteogenomic Analysis to Identify Missing Proteins from Haploid Cell Lines. <i>Proteomics</i> , 2018, 18, e1700386.	1.3	13
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73	An Adaptive Pipeline To Maximize Isobaric Tagging Data in Large-Scale MS-Based Proteomics. <i>Journal of Proteome Research</i> , 2018, 17, 2165-2173.	1.8	11
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77	Proteome-Wide Evaluation of Two Common Protein Quantification Methods. <i>Journal of Proteome Research</i> , 2018, 17, 1934-1942.	1.8	143
78	Cysteine-reactive probes and their use in chemical proteomics. <i>Chemical Communications</i> , 2018, 54, 4501-4512.	2.2	50

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85	Comprehensive analysis of the lysine acetylome and its potential regulatory roles in the virulence of <i>Streptococcus pneumoniae</i> . <i>Journal of Proteomics</i> , 2018, 176, 46-55.	1.2	37
86	Widespread bacterial protein histidine phosphorylation revealed by mass spectrometry-based proteomics. <i>Nature Methods</i> , 2018, 15, 187-190.	9.0	140
87	Laser Microdissection-Based Microproteomics of Formalin-Fixed and Paraffin-Embedded (FFPE) Tissues. <i>Methods in Molecular Biology</i> , 2018, 1723, 19-31.	0.4	18
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96	Human disease glycomics: technology advances enabling protein glycosylation analysis - part 1. <i>Expert Review of Proteomics</i> , 2018, 15, 165-182.	1.3	32

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98	High-throughput and Sensitive Immunopeptidomics Platform Reveals Profound Interferon $\beta$ -Mediated Remodeling of the Human Leukocyte Antigen (HLA) Ligandome. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 533-548.	2.5	224
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118	Complement Activation in Peritoneal Dialysisâ€œInduced Arteriopathy. <i>Journal of the American Society of Nephrology: JASN</i> , 2018, 29, 268-282.	3.0	45
119	Histone H1 Purification and Post-Translational Modification Profiling by Highâ€œResolution Mass Spectrometry. <i>Methods in Molecular Biology</i> , 2018, 1675, 147-166.	0.4	1
120	The transcriptome, extracellular proteome and active secretome of agroinfiltrated <i>Nicotiana benthamiana</i> uncover a large, diverse protease repertoire. <i>Plant Biotechnology Journal</i> , 2018, 16, 1068-1084.	4.1	54
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131	Two-Dimensional Gel Electrophoresis as an Information Base for Human Proteome. , 2018, , .		0
132	Heterotrimeric Câ€œProteinâ€œDependent Proteome and Phosphoproteome in Unstimulated Arabidopsis Roots. <i>Proteomics</i> , 2018, 18, e1800323.	1.3	26



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149	Cell-Permeable Activity-Based Ubiquitin Probes Enable Intracellular Profiling of Human Deubiquitinases. <i>Journal of the American Chemical Society</i> , 2018, 140, 12424-12433.	6.6	61
150	Variant O89 O-Antigen of <i>E. coli</i> Is Associated With Group 1 Capsule Loci and Multidrug Resistance. <i>Frontiers in Microbiology</i> , 2018, 9, 2026.	1.5	8

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