

# Magnus Palmblad

## List of Publications by Year in descending order

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125  
papers

3,741  
citations

101496

36  
h-index

155592

55  
g-index

131  
all docs

131  
docs citations

131  
times ranked

5117  
citing authors

#	ARTICLE	IF	CITATIONS
1	A high-stringency blueprint of the human proteome. <i>Nature Communications</i> , 2020, 11, 5301.	5.8	152
2	Fc specific IgG glycosylation profiling by robust nano-reverse phase HPLC-MS using a sheath-flow ESI sprayer interface. <i>Journal of Proteomics</i> , 2012, 75, 1318-1329.	1.2	141
3	Prediction of Chromatographic Retention and Protein Identification in Liquid Chromatography/Mass Spectrometry. <i>Analytical Chemistry</i> , 2002, 74, 5826-5830.	3.2	136
4	Peptide mapping of proteins in human body fluids using electrospray ionization Fourier transform ion cyclotron resonance mass spectrometry. <i>Mass Spectrometry Reviews</i> , 2002, 21, 2-15.	2.8	128
5	Scientific workflows for bibliometrics. <i>Scientometrics</i> , 2016, 107, 385-398.	1.6	125
6	Oxidation of Methionine 35 Attenuates Formation of Amyloid $\beta$ -Peptide 1-40 Oligomers. <i>Journal of Biological Chemistry</i> , 2002, 277, 19506-19510.	1.6	122
7	PeptidePicker: A scientific workflow with web interface for selecting appropriate peptides for targeted proteomics experiments. <i>Journal of Proteomics</i> , 2014, 106, 151-161.	1.2	117
8	Electron Donor-Acceptor Dyads Based on Ruthenium(II) Bipyridine and Terpyridine Complexes Bound to Naphthalenediimide. <i>Inorganic Chemistry</i> , 2003, 42, 2908-2918.	1.9	112
9	MassyTools: A High-Throughput Targeted Data Processing Tool for Relative Quantitation and Quality Control Developed for Glycomic and Glycoproteomic MALDI-MS. <i>Journal of Proteome Research</i> , 2015, 14, 5088-5098.	1.8	107
10	Immunoglobulin G Glycopeptide Profiling by Matrix-Assisted Laser Desorption Ionization Fourier Transform Ion Cyclotron Resonance Mass Spectrometry. <i>Analytical Chemistry</i> , 2010, 82, 1073-1081.	3.2	106
11	Hydroponic isotope labelling of entire plants (HILEP) for quantitative plant proteomics; an oxidative stress case study. <i>Phytochemistry</i> , 2008, 69, 1962-1972.	1.4	103
12	Identification of genetic variants influencing the human plasma proteome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 4673-4678.	3.3	78
13	Electron capture dissociation of substance P using a commercially available Fourier transform ion cyclotron resonance mass spectrometer. , 1999, 13, 474-477.		77
14	Fibronectin is a serum biomarker for Duchenne muscular dystrophy. <i>Proteomics - Clinical Applications</i> , 2014, 8, 269-278.	0.8	73
15	Mass spectrometry in clinical proteomics - from the present to the future. <i>Proteomics - Clinical Applications</i> , 2009, 3, 6-17.	0.8	71
16	A 9.4 T Fourier Transform Ion Cyclotron Resonance Mass Spectrometer: Description and Performance. <i>European Journal of Mass Spectrometry</i> , 2000, 6, 267-275.	0.5	66
17	Heat-Shock Response in <i>Arabidopsis thaliana</i> Explored by Multiplexed Quantitative Proteomics Using Differential Metabolic Labeling. <i>Journal of Proteome Research</i> , 2008, 7, 780-785.	1.8	66
18	Automatic analysis of hydrogen/deuterium exchange mass spectra of peptides and proteins using calculations of isotopic distributions. <i>Journal of the American Society for Mass Spectrometry</i> , 2001, 12, 1153-1162.	1.2	65

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19	Rapid Analysis of Tryptically Digested Cerebrospinal Fluid Using Capillary Electrophoresis-Electrospray Ionization-Fourier Transform Ion Cyclotron Resonance Mass Spectrometry. <i>Journal of Proteome Research</i> , 2002, 1, 361-366.	1.8	64
20	A full-body transcriptome and proteome resource for the European common carp. <i>BMC Genomics</i> , 2016, 17, 701.	1.2	55
21	Liquid chromatography and electron-capture dissociation in Fourier transform ion cyclotron resonance mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2002, 16, 988-992.	0.7	52
22	Mechanistic studies of multipole storage assisted dissociation. <i>Journal of the American Society for Mass Spectrometry</i> , 2000, 11, 210-217.	1.2	50
23	Alignment of capillary electrophoresis-mass spectrometry datasets using accurate mass information. <i>Analytical and Bioanalytical Chemistry</i> , 2009, 395, 2527-2533.	1.9	50
24	Top-Down MALDI-In-Source Decay-FTICR Mass Spectrometry of Isotopically Resolved Proteins. <i>Analytical Chemistry</i> , 2015, 87, 3429-3437.	3.2	50
25	Structural Analysis of an Intact Monoclonal Antibody by Online Electrochemical Reduction of Disulfide Bonds and Fourier Transform Ion Cyclotron Resonance Mass Spectrometry. <i>Analytical Chemistry</i> , 2014, 86, 5376-5382.	3.2	49
26	Protein identification by liquid chromatography-mass spectrometry using retention time prediction. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2004, 803, 131-135.	1.2	48
27	Proteomic analysis of <i>Taenia solium</i> metacestode excretion-secretion proteins. <i>Proteomics</i> , 2012, 12, 1860-1869.	1.3	46
28	Authentication of Fish Products by Large-Scale Comparison of Tandem Mass Spectra. <i>Journal of Proteome Research</i> , 2013, 12, 5253-5259.	1.8	46
29	Comparison of peptide and protein fractionation methods in proteomics. <i>EuPA Open Proteomics</i> , 2013, 1, 30-37.	2.5	45
30	Explorative Study of the Protein Composition of Amniotic Fluid by Liquid Chromatography Electrospray Ionization Fourier Transform Ion Cyclotron Resonance Mass Spectrometry. <i>Journal of Proteome Research</i> , 2004, 3, 884-889.	1.8	43
31	Assessing the translational landscape of myogenic differentiation by ribosome profiling. <i>Nucleic Acids Research</i> , 2015, 43, 4408-4428.	6.5	43
32	Chromatographic alignment of LC-MS and LC-MS/MS datasets by genetic algorithm feature extraction. <i>Journal of the American Society for Mass Spectrometry</i> , 2007, 18, 1835-1843.	1.2	42
33	ABRF Proteome Informatics Research Group (iPRG) 2015 Study: Detection of Differentially Abundant Proteins in Label-Free Quantitative LC-MS/MS Experiments. <i>Journal of Proteome Research</i> , 2017, 16, 945-957.	1.8	42
34	Quantitative proteomics using uniform <sup>15</sup> N-labeling, MASCOT, and the transproteomic pipeline. <i>Proteomics</i> , 2007, 7, 3462-3469.	1.3	41
35	Species-Specific Discrimination of Insect Meals for Aquafeeds by Direct Comparison of Tandem Mass Spectra. <i>Animals</i> , 2019, 9, 222.	1.0	41
36	Liquid matrix deposition on conductive hydrophobic surfaces for tuning and quantitation in UV-MALDI mass spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2007, 18, 693-697.	1.2	40

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37	Automated workflow composition in mass spectrometry-based proteomics. <i>Bioinformatics</i> , 2019, 35, 656-664.	1.8	39
38	Cloud Parallel Processing of Tandem Mass Spectrometry Based Proteomics Data. <i>Journal of Proteome Research</i> , 2012, 11, 5101-5108.	1.8	38
39	Analysis of enzymatically digested proteins and protein mixtures using a 9.4 Tesla Fourier transform ion cyclotron mass spectrometer. <i>Rapid Communications in Mass Spectrometry</i> , 2000, 14, 1029-1034.	0.7	37
40	Quantitation of binding, recovery and desalting efficiency of peptides and proteins in solid phase extraction micropipette tips. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2005, 814, 309-313.	1.2	37
41	Protein identification in cerebrospinal fluid using packed capillary liquid chromatography Fourier transform ion cyclotron resonance mass spectrometry. <i>Proteomics</i> , 2003, 3, 184-190.	1.3	35
42	Molecular phylogenetics by direct comparison of tandem mass spectra. <i>Rapid Communications in Mass Spectrometry</i> , 2012, 26, 728-732.	0.7	31
43	Identification of meat products by shotgun spectral matching. <i>Food Chemistry</i> , 2016, 203, 28-34.	4.2	31
44	Species and tissues specific differentiation of processed animal proteins in aquafeeds using proteomics tools. <i>Journal of Proteomics</i> , 2016, 147, 125-131.	1.2	30
45	Automating bibliometric analyses using Taverna scientific workflows: A tutorial on integrating Web Services. <i>Journal of Informetrics</i> , 2016, 10, 830-841.	1.4	25
46	Bibliometric Mapping: Eight Decades of Analytical Chemistry, With Special Focus on the Use of Mass Spectrometry. <i>Analytical Chemistry</i> , 2015, 87, 4588-4596.	3.2	24
47	Quality control based on isotopic distributions for high-throughput MALDI-TOF and MALDI-FTICR serum peptide profiling. <i>Journal of the American Society for Mass Spectrometry</i> , 2010, 21, 1515-1525.	1.2	23
48	Bibliometric Analyses Reveal Patterns of Collaboration between ASMS Members. <i>Journal of the American Society for Mass Spectrometry</i> , 2018, 29, 447-454.	1.2	23
49	A Protein Standard That Emulates Homology for the Characterization of Protein Inference Algorithms. <i>Journal of Proteome Research</i> , 2018, 17, 1879-1886.	1.8	22
50	Protein expression dynamics during <i>Escherichia Coli</i> glucose-lactose diauxie. <i>BMC Microbiology</i> , 2011, 11, 126.	1.3	20
51	Electron capture dissociation of peptide hormone changes upon opening of the tocin ring and complexation with transition metal cations. <i>Rapid Communications in Mass Spectrometry</i> , 2009, 23, 31-38.	0.7	19
52	Developments in FTICR-MS and Its Potential for Body Fluid Signatures. <i>International Journal of Molecular Sciences</i> , 2015, 16, 27133-27144.	1.8	19
53	Authentication of Closely Related Fish and Derived Fish Products Using Tandem Mass Spectrometry and Spectral Library Matching. <i>Journal of Agricultural and Food Chemistry</i> , 2016, 64, 3669-3677.	2.4	19
54	Scientific Workflow Management in Proteomics. <i>Molecular and Cellular Proteomics</i> , 2012, 11, M111.010595-1-M111.010595-10.	2.5	18

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55	Identifying Proteins in Zebrafish Embryos Using Spectral Libraries Generated from Dissected Adult Organs and Tissues. <i>Journal of Proteome Research</i> , 2014, 13, 1537-1544.	1.8	18
56	Autopiquer - a Robust and Reliable Peak Detection Algorithm for Mass Spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2017, 28, 253-262.	1.2	18
57	Multiplexed targeted proteomic assay to assess coagulation factor concentrations and thrombosis-associated cancer. <i>Blood Advances</i> , 2017, 1, 1080-1087.	2.5	18
58	One Thousand and One Software for Proteomics: Tales of the Toolmakers of Science. <i>Journal of Proteome Research</i> , 2019, 18, 3580-3585.	1.8	18
59	Automatic internal calibration in liquid chromatography/Fourier transform ion cyclotron resonance mass spectrometry of protein digests. <i>Rapid Communications in Mass Spectrometry</i> , 2006, 20, 3076-3080.	0.7	16
60	Improving mass measurement accuracy in mass spectrometry based proteomics by combining open source tools for chromatographic alignment and internal calibration. <i>Journal of Proteomics</i> , 2009, 72, 722-724.	1.2	16
61	Precision profiling and identification of human serum peptides using Fourier transform ion cyclotron resonance mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2011, 25, 3457-3463.	0.7	16
62	A new optimization phase for scientific workflow management systems. <i>Future Generation Computer Systems</i> , 2014, 36, 352-362.	4.9	16
63	Future feed control – Tracing banned bovine material in insect meal. <i>Food Control</i> , 2021, 128, 108183.	2.8	16
64	Investigation of Lignin Oligomers Using Electrospray Ionisation Mass Spectrometry. <i>Holzforschung</i> , 2003, 57, 37-43.	0.9	15
65	Neuroscience and accelerator mass spectrometry. <i>Journal of Mass Spectrometry</i> , 2005, 40, 154-159.	0.7	15
66	Targeted proteomics approach to species-level identification of <i>Bacillus thuringiensis</i> spores by AP-MALDI-MS. <i>Journal of the American Society for Mass Spectrometry</i> , 2010, 21, 993-1001.	1.2	15
67	Detection and Structural Elucidation of Esterified Oxylipids in Human Synovial Fluid by Electrospray Ionization-Fourier Transform Ion-Cyclotron Mass Spectrometry and Liquid Chromatography-Ion Trap-MS <sup>3</sup> : Detection of Esterified Hydroxylated Docosapentaenoic Acid Containing Phospholipids. <i>Analytical Chemistry</i> , 2013, 85, 6003-6010.	3.2	15
68	Palaeoproteomics of bird bones for taxonomic classification. <i>Zoological Journal of the Linnean Society</i> , 2019, 186, 650-665.	1.0	15
69	A Review of the Scientific Rigor, Reproducibility, and Transparency Studies Conducted by the ABRF Research Groups. <i>Journal of Biomolecular Techniques</i> , 2020, 31, 11-26.	0.8	15
70	Parallel deep transcriptome and proteome analysis of zebrafish larvae. <i>BMC Research Notes</i> , 2013, 6, 428.	0.6	14
71	Shotgun proteomics approaches for authentication, biological analyses, and allergen detection in feed and food-grade insect species. <i>Food Control</i> , 2022, 137, 108888.	2.8	14
72	A community proposal to integrate proteomics activities in ELIXIR. <i>F1000Research</i> , 2017, 6, 875.	0.8	13

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73	Counting Statistics and Ion Interval Density in AMS. <i>Radiocarbon</i> , 2004, 46, 1103-1109.	0.8	12
74	Biochemical paths in humans and cells: Frontiers of AMS bioanalysis. <i>Nuclear Instruments &amp; Methods in Physics Research B</i> , 2007, 259, 745-751.	0.6	12
75	A novel mass spectrometry cluster for high-throughput quantitative proteomics. <i>Journal of the American Society for Mass Spectrometry</i> , 2010, 21, 1002-1011.	1.2	12
76	Community curation of bioinformatics software and data resources. <i>Briefings in Bioinformatics</i> , 2020, 21, 1697-1705.	3.2	12
77	High Resolution Mass Spectrometry for Rapid Characterization of Combinatorial Peptide Libraries. <i>ACS Combinatorial Science</i> , 2010, 12, 65-68.	3.3	11
78	Scientific workflow optimization for improved peptide and protein identification. <i>BMC Bioinformatics</i> , 2015, 16, 284.	1.2	10
79	ARA290 Improves Insulin Release and Glucose Tolerance in Type 2 Diabetic Goto-Kakizaki Rats. <i>Molecular Medicine</i> , 2015, 21, 969-978.	1.9	10
80	A Pipeline for Differential Proteomics in Unsequenced Species. <i>Journal of Proteome Research</i> , 2016, 15, 1963-1970.	1.8	10
81	Spatiotemporal analysis of tropical disease research combining Europe PMC and affiliation mapping web services. <i>Tropical Medicine and Health</i> , 2017, 45, 33.	1.0	10
82	Isotopic Distributions. <i>Methods in Molecular Biology</i> , 2013, 1007, 65-99.	0.4	9
83	APE in the Wild: Automated Exploration of Proteomics Workflows in the bio.tools Registry. <i>Journal of Proteome Research</i> , 2021, 20, 2157-2165.	1.8	8
84	Comparing novel shotgun DNA sequencing and state-of-the-art proteomics approaches for authentication of fish species in mixed samples. <i>Food Control</i> , 2022, 131, 108417.	2.8	8
85	Insights from the First Phosphopeptide Challenge of the MS Resource Pillar of the HUPO Human Proteome Project. <i>Journal of Proteome Research</i> , 2020, 19, 4754-4765.	1.8	7
86	Perspectives on automated composition of workflows in the life sciences. <i>F1000Research</i> , 2021, 10, 897.	0.8	7
87	Semiautomated glycoproteomics data analysis workflow for maximized glycopeptide identification and reliable quantification. <i>Beilstein Journal of Organic Chemistry</i> , 2020, 16, 3038-3051.	1.3	7
88	Interpretation of the DOME Recommendations for Machine Learning in Proteomics and Metabolomics. <i>Journal of Proteome Research</i> , 2022, 21, 1204-1207.	1.8	7
89	A method to significantly lessen the sample contamination of the vacuum interface of an on-axis electrospray ion source by adding a mechanical shutter. , 1999, 13, 1550-1550.		6
90	$\hat{\pm}$ -Particle Energy Loss Measurement of Microgram Depositions of Biomolecules. <i>Analytical Chemistry</i> , 2003, 75, 4519-4524.	3.2	6

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91	ABRF Proteome Informatics Research Group (iPRG) 2016 Study: Inferring Proteoforms from Bottom-up Proteomics Data. <i>Journal of Biomolecular Techniques</i> , 2018, 29, 39-45.	0.8	6
92	Partially Sequenced Organisms, Decoy Searches and False Discovery Rates. <i>Journal of Proteome Research</i> , 2012, 11, 1991-1995.	1.8	5
93	Retention Time Prediction and Protein Identification. <i>Methods in Molecular Biology</i> , 2013, 1007, 101-118.	0.4	5
94	Human Dendritic Cells with Th2-Polarizing Capacity: Analysis Using Label-Free Quantitative Proteomics. <i>International Archives of Allergy and Immunology</i> , 2017, 174, 170-182.	0.9	5
95	Visualization and application of amino acid retention coefficients obtained from modeling of peptide retention. <i>Journal of Separation Science</i> , 2018, 41, 3644-3653.	1.3	5
96	Theoretical Considerations for Next-Generation Proteomics. <i>Journal of Proteome Research</i> , 2021, 20, 3395-3399.	1.8	5
97	Use of expressed sequence tags as an alternative approach for the identification of <i>Taenia solium</i> metacestode excretion/secretion proteins. <i>BMC Research Notes</i> , 2013, 6, 224.	0.6	4
98	Differentiating samples and experimental protocols by direct comparison of tandem mass spectra. <i>Rapid Communications in Mass Spectrometry</i> , 2016, 30, 731-738.	0.7	4
99	Protein Fractionation for Quantitative Plasma Proteomics by Semi-Selective Precipitation. <i>Journal of Proteomics and Bioinformatics</i> , 2012, 05, .	0.4	4
100	Identification and Characterization of Peptides and Proteins Using Fourier Transform Ion Cyclotron Resonance Mass Spectrometry. <i>Journal of Chromatography Library</i> , 2003, 68, 199-240.	0.1	3
101	SPE-MALDI Profiling of Serum Peptides and Proteins by Ultrahigh Resolution FTICR-MS. <i>Chromatographia</i> , 2015, 78, 445-449.	0.7	3
102	Visual and Semantic Enrichment of Analytical Chemistry Literature Searches by Combining Text Mining and Computational Chemistry. <i>Analytical Chemistry</i> , 2019, 91, 4312-4316.	3.2	3
103	Retention Time Prediction and Protein Identification. <i>Methods in Molecular Biology</i> , 2020, 2051, 115-132.	0.4	3
104	Retention Time Prediction and Protein Identification. , 2007, 367, 195-208.		2
105	Lossless-compression of high resolution mass spectra of small molecules. <i>Metabolomics</i> , 2010, 6, 335-340.	1.4	2
106	Data Decomposition in Biomedical e-Science Applications. , 2011, , .		2
107	Visualizing and comparing results of different peptide identification methods. <i>Briefings in Bioinformatics</i> , 2018, 19, bbw115.	3.2	2
108	mzRecal: universal MS1 recalibration in mzML using identified peptides in mzIdentML as internal calibrants. <i>Bioinformatics</i> , 2021, 37, 2768-2769.	1.8	2

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109	Using the Object-Oriented PowerShell for Simple Proteomics Data Analysis. <i>Methods in Molecular Biology</i> , 2020, 2051, 389-405.	0.4	2
110	Mass by Energy Loss Quantitation as a Practical Submicrogram Balance. <i>Analytical Chemistry</i> , 2005, 77, 952-953.	3.2	1
111	Quantitative metabolism using AMS: Choosing a labeled precursor. <i>Nuclear Instruments &amp; Methods in Physics Research B</i> , 2010, 268, 1309-1312.	0.6	1
112	Enhanced Resource Management Enabling Standard Parameter Sweep Jobs for Scientific Applications. , 2013, , .		1
113	COMICS: Cartoon Visualization of Omics Data in Spatial Context Using Anatomical Ontologies. <i>Journal of Proteome Research</i> , 2018, 17, 739-744.	1.8	1
114	Special Issue on Software Tools and Resources: Acknowledging the Toolmakers of Science. <i>Journal of Proteome Research</i> , 2019, 18, 575-575.	1.8	1
115	Rewinding the Molecular Clock: Looking at Pioneering Molecular Phylogenetics Experiments in the Light of Proteomics. <i>Journal of Proteome Research</i> , 2021, 20, 4640-4645.	1.8	1
116	Electron capture dissociation of substance P using a commercially available Fourier transform ion cyclotron resonance mass spectrometer. , 1999, 13, 474.		1
117	Simple Proteomics Data Analysis in the Object-Oriented PowerShell. <i>Methods in Molecular Biology</i> , 2013, 1007, 379-391.	0.4	1
118	Accelerator Mass Spectrometry in Protein Analysis. <i>Principles and Practice</i> , 2004, , 203-216.	0.3	1
119	Isotopic Distributions. <i>Methods in Molecular Biology</i> , 2020, 2051, 79-114.	0.4	1
120	Quantitative proteomics of Arabidopsis plants submitted to oxidative stress. <i>Comparative Biochemistry and Physiology Part A, Molecular &amp; Integrative Physiology</i> , 2007, 146, S256-S257.	0.8	0
121	P1.49 Mass spectrometry based clinical proteomics for biomarker discovery in Duchenne muscular dystrophy. <i>Neuromuscular Disorders</i> , 2011, 21, 656.	0.3	0
122	Automated Composition of Scientific Workflows in Mass Spectrometry-Based Proteomics. , 2018, , .		0
123	Semantically Enriched Literature Search Combining Text Mining, QSPR and Ontologies in Scientific Workflows. , 2018, , .		0
124	2021 Special Issue on Software Tools and Resources: Finding the Right Tools for the Job. <i>Journal of Proteome Research</i> , 2021, 20, 1819-1820.	1.8	0
125	Micro-capillary liquid chromatography Fourier transform ion cyclotron resonance mass spectrometry—a powerful tool for peptide and protein identification. <i>Acta Biochimica Polonica</i> , 2001, 48, 1101-4.	0.3	0