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List of Publications by Year in descending order

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36
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citing authors

#	ARTICLE	IF	CITATIONS
1	An Essential Role for Alzheimer's-Linked Amyloid Beta Oligomers in Neurodevelopment: Transient Expression of Multiple Proteoforms during Retina Histogenesis. <i>International Journal of Molecular Sciences</i> , 2022, 23, 2208.	4.1	5
2	ProSight Annotator: Complete control and customization of protein entries in UniProt XML files. <i>Proteomics</i> , 2022, 22, e2100209.	2.2	6
3	Robustness and Ruggedness of Isoelectric Focusing and Superficially Porous Liquid Chromatography with Fourier Transform Mass Spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2021, 32, 346-354.	2.8	5
4	Reassembling protein complexes after controlled disassembly by top-down mass spectrometry in native mode. <i>International Journal of Mass Spectrometry</i> , 2021, 465, 116591.	1.5	8
5	Online 1/4SEC ² -nRPLC-MS for Improved Sensitivity of Intact Protein Detection of IEF-Separated Nonhuman Primate Cerebrospinal Fluid Proteins. <i>Analytical Chemistry</i> , 2021, 93, 16741-16750.	6.5	6
6	Top-down mass spectrometry for protein molecular diagnostics, structure analysis, and biomarker discovery. , 2020, , 313-326.		5
7	Native vs Denatured: An in Depth Investigation of Charge State and Isotope Distributions. <i>Journal of the American Society for Mass Spectrometry</i> , 2020, 31, 574-581.	2.8	27
8	Using 10,000 Fragment Ions to Inform Scoring in Native Top-down Proteomics. <i>Journal of the American Society for Mass Spectrometry</i> , 2020, 31, 1398-1409.	2.8	18
9	Multidimensional Top-Down Proteomics of Brain-Region-Specific Mouse Brain Proteoforms Responsive to Cocaine and Estradiol. <i>Journal of Proteome Research</i> , 2019, 18, 3999-4012.	3.7	12
10	Native top-down mass spectrometry provides insights into the copper centers of membrane-bound methane monooxygenase. <i>Nature Communications</i> , 2019, 10, 2675.	12.8	74
11	Standard Proteoforms and Their Complexes for Native Mass Spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2019, 30, 1190-1198.	2.8	33
12	Top-Down Proteomics Enables Comparative Analysis of Brain Proteoforms Between Mouse Strains. <i>Analytical Chemistry</i> , 2018, 90, 3802-3810.	6.5	27
13	How many human proteoforms are there?. <i>Nature Chemical Biology</i> , 2018, 14, 206-214.	8.0	580
14	Exploring bioactive peptides from bacterial secretomes using PepSAVI-MS: identification and characterization of Bac ²¹ from <i>Enterococcus faecalis</i> pPD ¹ . <i>Microbial Biotechnology</i> , 2018, 11, 943-951.	4.2	7
15	Continuous Elution Proteoform Identification of Myelin Basic Protein by Superficially Porous Reversed-Phase Liquid Chromatography and Fourier Transform Mass Spectrometry. <i>Analytical Chemistry</i> , 2017, 89, 12030-12038.	6.5	13
16	Top-Down Mass Spectrometry: Proteomics to Proteoforms. <i>Advances in Experimental Medicine and Biology</i> , 2016, 919, 171-200.	1.6	24
17	Methyl labeling and TROSY NMR spectroscopy of proteins expressed in the eukaryote <i>Pichia pastoris</i> . <i>Journal of Biomolecular NMR</i> , 2015, 62, 239-245.	2.8	42
18	Proteoform analysis of lipocalin-type prostaglandin synthase from human cerebrospinal fluid by isoelectric focusing and superficially porous liquid chromatography with Fourier transform mass spectrometry. <i>Proteomics</i> , 2014, 14, 1223-1231.	2.2	9

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19	Top-Down Mass Spectrometry on Tissue Extracts and Biofluids with Isoelectric Focusing and Superficially Porous Silica Liquid Chromatography. <i>Analytical Chemistry</i> , 2013, 85, 10377-10384.	6.5	23
20	Introduction to Glycosylation and Mass Spectrometry. <i>Methods in Molecular Biology</i> , 2013, 951, 1-17.	0.9	16
21	Measurement of Blood Protease Kinetic Parameters with Self-Assembled Monolayer Ligand Binding Assays and Label-Free MALDI-TOF MS. <i>Analytical Chemistry</i> , 2013, 85, 10597-10604.	6.5	11
22	Surface Preparation Strategies for Improved Parallelization and Reproducible MALDI-TOF MS Ligand Binding Assays. <i>ACS Applied Materials & Interfaces</i> , 2013, 5, 6-10.	8.0	11
23	Proteolytic elimination of N-myristoyl modifications by the Shigella virulence factor IpaJ. <i>Nature</i> , 2013, 496, 106-109.	27.8	139
24	MS-based ligand binding assays with speed, sensitivity, and specificity. <i>Proteomics</i> , 2012, 12, 3143-3146.	2.2	3
25	Thin-Layer Matrix Sublimation with Vapor-Sorption Induced Co-Crystallization for Sensitive and Reproducible SAMDI-TOF MS Analysis of Protein Biosensors. <i>Journal of the American Society for Mass Spectrometry</i> , 2012, 23, 1661-1669.	2.8	12
26	Metabolism of Diazirine-Modified N-Acetylmannosamine Analogues to Photo-Cross-Linking Sialosides. <i>Bioconjugate Chemistry</i> , 2011, 22, 1811-1823.	3.6	51
27	Sensitive and Reproducible Intact Mass Analysis of Complex Protein Mixtures with Superficially Porous Capillary Reversed-Phase Liquid Chromatography Mass Spectrometry. <i>Analytical Chemistry</i> , 2011, 83, 9586-9592.	6.5	39
28	Self-Assembled Monolayers for MALDI-TOF Mass Spectrometry for Immunoassays of Human Protein Antigens. <i>Analytical Chemistry</i> , 2007, 79, 5878-5887.	6.5	56
29	Top Down Mass Spectrometry of <60-kDa Proteins from Methanosarcina acetivorans Using Quadrupole FTMS with Automated Octopole Collisionally Activated Dissociation. <i>Molecular and Cellular Proteomics</i> , 2006, 5, 14-25.	3.8	62
30	Targeted analysis and discovery of posttranslational modifications in proteins from methanogenic archaea by top-down MS. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 2678-2683.	7.1	93
31	Strategies for automating top-down protein analysis with Q-FTICR MS. <i>International Journal of Mass Spectrometry</i> , 2004, 234, 175-184.	1.5	20
32	Construction of a hybrid quadrupole/fourier transform ion cyclotron resonance mass spectrometer for versatile MS/MS above 10 kDa. <i>Journal of the American Society for Mass Spectrometry</i> , 2004, 15, 1099-1108.	2.8	107
33	Improved Molecular Weight-Based Processing of Intact Proteins for Interrogation by Quadrupole-Enhanced FT MS/MS. <i>Journal of Proteome Research</i> , 2004, 3, 801-806.	3.7	28
34	Molecular-Level Description of Proteins from <i>Saccharomyces cerevisiae</i> Using Quadrupole FT Hybrid Mass Spectrometry for Top Down Proteomics. <i>Analytical Chemistry</i> , 2004, 76, 2852-2858.	6.5	72
35	Electron Capture Dissociation and ¹³ C, ¹⁵ N Depletion for Deuterium Localization in Intact Proteins after Solution-Phase Exchange. <i>Analytical Chemistry</i> , 2003, 75, 3263-3266.	6.5	32
36	Processing Complex Mixtures of Intact Proteins for Direct Analysis by Mass Spectrometry. <i>Analytical Chemistry</i> , 2002, 74, 2923-2929.	6.5	176