

Lissa C Anderson

List of Publications by Year in descending order

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Version: 2024-02-01

23
papers

841
citations

567281

15
h-index

642732

23
g-index

23
all docs

23
docs citations

23
times ranked

872
citing authors

#	ARTICLE	IF	CITATIONS
1	Identification and Quantification of Proteoforms by Mass Spectrometry. <i>Proteomics</i> , 2019, 19, e1800361.	2.2	147
2	Identification and Characterization of Human Proteoforms by Top-Down LC-21 Tesla FT-ICR Mass Spectrometry. <i>Journal of Proteome Research</i> , 2017, 16, 1087-1096.	3.7	81
3	Interlaboratory Study for Characterizing Monoclonal Antibodies by Top-Down and Middle-Down Mass Spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2020, 31, 1783-1802.	2.8	67
4	The Blood Proteoform Atlas: A reference map of proteoforms in human hematopoietic cells. <i>Science</i> , 2022, 375, 411-418.	12.6	64
5	Front-End Electron Transfer Dissociation: A New Ionization Source. <i>Analytical Chemistry</i> , 2013, 85, 8385-8390.	6.5	56
6	A five-level classification system for proteoform identifications. <i>Nature Methods</i> , 2019, 16, 939-940.	19.0	55
7	Analysis of Monoclonal Antibodies in Human Serum as a Model for Clinical Monoclonal Gammopathy by Use of 21 Tesla FT-ICR Top-Down and Middle-Down MS/MS. <i>Journal of the American Society for Mass Spectrometry</i> , 2017, 28, 827-838.	2.8	49
8	PEPPI-MS: Polyacrylamide-Gel-Based Prefractionation for Analysis of Intact Proteoforms and Protein Complexes by Mass Spectrometry. <i>Journal of Proteome Research</i> , 2020, 19, 3779-3791.	3.7	49
9	Analyses of Histone Proteoforms Using Front-end Electron Transfer Dissociation-enabled Orbitrap Instruments. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 975-988.	3.8	43
10	Front-End Electron Transfer Dissociation Coupled to a 21 Tesla FT-ICR Mass Spectrometer for Intact Protein Sequence Analysis. <i>Journal of the American Society for Mass Spectrometry</i> , 2017, 28, 1787-1795.	2.8	33
11	Diagnosis of Hemoglobinopathy and β^2 -Thalassemia by 21 Tesla Fourier Transform Ion Cyclotron Resonance Mass Spectrometry and Tandem Mass Spectrometry of Hemoglobin from Blood. <i>Clinical Chemistry</i> , 2019, 65, 986-994.	3.2	30
12	Protein derivatization and sequential ion/ion reactions to enhance sequence coverage produced by electron transfer dissociation mass spectrometry. <i>International Journal of Mass Spectrometry</i> , 2015, 377, 617-624.	1.5	27
13	Ion-Ion Proton Transfer and Parallel Ion Parking for the Analysis of Mixtures of Intact Proteins on a Modified Orbitrap Mass Analyzer. <i>Journal of the American Society for Mass Spectrometry</i> , 2019, 30, 2163-2173.	2.8	27
14	Phosphorylation and arginine methylation mark histone H2A prior to deposition during <i>Xenopus laevis</i> development. <i>Epigenetics and Chromatin</i> , 2014, 7, 22.	3.9	26
15	Classification of Plasma Cell Disorders by 21 Tesla Fourier Transform Ion Cyclotron Resonance Top-Down and Middle-Down MS/MS Analysis of Monoclonal Immunoglobulin Light Chains in Human Serum. <i>Analytical Chemistry</i> , 2019, 91, 3263-3269.	6.5	21
16	Ultrahigh Resolution Ion Isolation by Stored Waveform Inverse Fourier Transform 21 T Fourier Transform Ion Cyclotron Resonance Mass Spectrometry. <i>Analytical Chemistry</i> , 2020, 92, 3213-3219.	6.5	15
17	Advanced Strategies for Proton-Transfer Reactions Coupled with Parallel Ion Parking on a 21 T FT-ICR MS for Intact Protein Analysis. <i>Analytical Chemistry</i> , 2021, 93, 9119-9128.	6.5	10
18	Back Cover: Identification and Quantification of Proteoforms by Mass Spectrometry. <i>Proteomics</i> , 2019, 19, 1970085.	2.2	9

#	ARTICLE	IF	CITATIONS
19	Intact Protein Analysis at 21 Tesla and X-Ray Crystallography Define Structural Differences in Single Amino Acid Variants of Human Mitochondrial Branched-Chain Amino Acid Aminotransferase 2 (BCAT2). <i>Journal of the American Society for Mass Spectrometry</i> , 2017, 28, 1796-1804.	2.8	8
20	Construction of Human Proteoform Families from 21 Tesla Fourier Transform Ion Cyclotron Resonance Mass Spectrometry Top-Down Proteomic Data. <i>Journal of Proteome Research</i> , 2021, 20, 317-325.	3.7	8
21	Development of novel methods for non-canonical myeloma protein analysis with an innovative adaptation of immunofixation electrophoresis, native top-down mass spectrometry, and middle-down <i>de novo</i> sequencing. <i>Clinical Chemistry and Laboratory Medicine</i> , 2021, 59, 653-661.	2.3	7
22	Increased Single-Spectrum Top-Down Protein Sequence Coverage in Trapping Mass Spectrometers with Chimeric Ion Loading. <i>Analytical Chemistry</i> , 2020, 92, 12193-12200.	6.5	5
23	Characterization of Structural Hemoglobin Variants by Top-Down Mass Spectrometry and R Programming Tools for Rapid Identification. <i>Journal of the American Society for Mass Spectrometry</i> , 2022, 33, 123-130.	2.8	4