

# Neil L Kelleher

## List of Publications by Year in descending order

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392  
papers

33,645  
citations

3525

90  
h-index

5820

161  
g-index

452  
all docs

452  
docs citations

452  
times ranked

25401  
citing authors

#	ARTICLE	IF	CITATIONS
1	Electron Capture Dissociation of Multiply Charged Protein Cations. A Nonergodic Process. <i>Journal of the American Chemical Society</i> , 1998, 120, 3265-3266.	6.6	1,766
2	Proteoform: a single term describing protein complexity. <i>Nature Methods</i> , 2013, 10, 186-187.	9.0	1,180
3	Electron Capture Dissociation for Structural Characterization of Multiply Charged Protein Cations. <i>Analytical Chemistry</i> , 2000, 72, 563-573.	3.2	903
4	EZH2 Is Required for Germinal Center Formation and Somatic EZH2 Mutations Promote Lymphoid Transformation. <i>Cancer Cell</i> , 2013, 23, 677-692.	7.7	706
5	Mapping intact protein isoforms in discovery mode using top-down proteomics. <i>Nature</i> , 2011, 480, 254-258.	13.7	587
6	How many human proteoforms are there?. <i>Nature Chemical Biology</i> , 2018, 14, 206-214.	3.9	580
7	A computational framework to explore large-scale biosynthetic diversity. <i>Nature Chemical Biology</i> , 2020, 16, 60-68.	3.9	569
8	Top Down versus Bottom Up Protein Characterization by Tandem High-Resolution Mass Spectrometry. <i>Journal of the American Chemical Society</i> , 1999, 121, 806-812.	6.6	535
9	Peer Reviewed: Top-Down Proteomics. <i>Analytical Chemistry</i> , 2004, 76, 196 A-203 A.	3.2	472
10	Decoding protein modifications using top-down mass spectrometry. <i>Nature Methods</i> , 2007, 4, 817-821.	9.0	449
11	Progress in Top-Down Proteomics and the Analysis of Proteoforms. <i>Annual Review of Analytical Chemistry</i> , 2016, 9, 499-519.	2.8	427
12	A roadmap for natural product discovery based on large-scale genomics and metabolomics. <i>Nature Chemical Biology</i> , 2014, 10, 963-968.	3.9	416
13	Top Down proteomics: Facts and perspectives. <i>Biochemical and Biophysical Research Communications</i> , 2014, 445, 683-693.	1.0	393
14	Precision proteomics: The case for high resolution and high mass accuracy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 18132-18138.	3.3	388
15	Localization of Labile Posttranslational Modifications by Electron Capture Dissociation: The Case of <sup>13</sup> C-Carboxyglutamic Acid. <i>Analytical Chemistry</i> , 1999, 71, 4250-4253.	3.2	362
16	Genetically encoded short peptide tag for versatile protein labeling by Sfp phosphopantetheinyl transferase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 15815-15820.	3.3	362
17	A monovalent streptavidin with a single femtomolar biotin binding site. <i>Nature Methods</i> , 2006, 3, 267-273.	9.0	334
18	Therapeutic targeting of polycomb and BET bromodomain proteins in diffuse intrinsic pontine gliomas. <i>Nature Medicine</i> , 2017, 23, 493-500.	15.2	332

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19	The MMSET histone methyl transferase switches global histone methylation and alters gene expression in t(4;14) multiple myeloma cells. <i>Blood</i> , 2011, 117, 211-220.	0.6	300
20	Complete Protein Characterization Using Top-Down Mass Spectrometry and Ultraviolet Photodissociation. <i>Journal of the American Chemical Society</i> , 2013, 135, 12646-12651.	6.6	297
21	Loss of BAP1 function leads to EZH2-dependent transformation. <i>Nature Medicine</i> , 2015, 21, 1344-1349.	15.2	297
22	Certain and Progressive Methylation of Histone H4 at Lysine 20 during the Cell Cycle. <i>Molecular and Cellular Biology</i> , 2008, 28, 468-486.	1.1	264
23	Gaseous Conformational Structures of Cytochrome c. <i>Journal of the American Chemical Society</i> , 1998, 120, 4732-4740.	6.6	255
24	Best practices and benchmarks for intact protein analysis for top-down mass spectrometry. <i>Nature Methods</i> , 2019, 16, 587-594.	9.0	241
25	Evolution of translation machinery in recoded bacteria enables multi-site incorporation of nonstandard amino acids. <i>Nature Biotechnology</i> , 2015, 33, 1272-1279.	9.4	234
26	Quantitative Analysis of Modified Proteins and Their Positional Isomers by Tandem Mass Spectrometry: Human Histone H4. <i>Analytical Chemistry</i> , 2006, 78, 4271-4280.	3.2	223
27	ProSight PTM 2.0: improved protein identification and characterization for top down mass spectrometry. <i>Nucleic Acids Research</i> , 2007, 35, W701-W706.	6.5	222
28	Lactacin 481: In Vitro Reconstitution of Lantibiotic Synthetase Activity. <i>Science</i> , 2004, 303, 679-681.	6.0	221
29	Pervasive combinatorial modification of histone H3 in human cells. <i>Nature Methods</i> , 2007, 4, 487-489.	9.0	217
30	Discovery and in vitro biosynthesis of haloduracin, a two-component lantibiotic. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 17243-17248.	3.3	215
31	Attomole-Sensitivity Electrospray Source for Large-Molecule Mass Spectrometry. <i>Analytical Chemistry</i> , 1995, 67, 3802-3805.	3.2	214
32	Informatics and multiplexing of intact protein identification in bacteria and the archaea. <i>Nature Biotechnology</i> , 2001, 19, 952-957.	9.4	205
33	Proteoforms as the next proteomics currency. <i>Science</i> , 2018, 359, 1106-1107.	6.0	205
34	Deconstruction of Iterative Multidomain Polyketide Synthase Function. <i>Science</i> , 2008, 320, 243-246.	6.0	202
35	The emerging landscape of single-molecule protein sequencing technologies. <i>Nature Methods</i> , 2021, 18, 604-617.	9.0	198
36	Negative regulation of NF- $\kappa$ B action by Set9-mediated lysine methylation of the RelA subunit. <i>EMBO Journal</i> , 2009, 28, 1055-1066.	3.5	197

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37	ProSight Lite: Graphical software to analyze top-down mass spectrometry data. <i>Proteomics</i> , 2015, 15, 1235-1238.	1.3	196
38	Mass Spectrometric Characterization of Human Histone H3: A Bird's Eye View. <i>Journal of Proteome Research</i> , 2006, 5, 240-247.	1.8	179
39	Histone Methyltransferase MMSET/NSD2 Alters EZH2 Binding and Reprograms the Myeloma Epigenome through Global and Focal Changes in H3K36 and H3K27 Methylation. <i>PLoS Genetics</i> , 2014, 10, e1004566.	1.5	178
40	On the Scalability and Requirements of Whole Protein Mass Spectrometry. <i>Analytical Chemistry</i> , 2011, 83, 6868-6874.	3.2	177
41	Processing Complex Mixtures of Intact Proteins for Direct Analysis by Mass Spectrometry. <i>Analytical Chemistry</i> , 2002, 74, 2923-2929.	3.2	176
42	ProSight PTM: an integrated environment for protein identification and characterization by top-down mass spectrometry. <i>Nucleic Acids Research</i> , 2004, 32, W340-W345.	6.5	176
43	Rapid Sequencing of Oligonucleotides by High-Resolution Mass Spectrometry. <i>Journal of the American Chemical Society</i> , 1994, 116, 4893-4897.	6.6	169
44	Histone H3K4 monomethylation catalyzed by Trr and mammalian COMPASS-like proteins at enhancers is dispensable for development and viability. <i>Nature Genetics</i> , 2017, 49, 1647-1653.	9.4	168
45	Dichlorination of a pyrrolyl-S-carrier protein by FADH2-dependent halogenase PltA during pyoluteorin biosynthesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 13843-13848.	3.3	166
46	Cell-free protein synthesis from genomically recoded bacteria enables multisite incorporation of noncanonical amino acids. <i>Nature Communications</i> , 2018, 9, 1203.	5.8	165
47	Combinatorial Modification of Human Histone H4 Quantitated by Two-dimensional Liquid Chromatography Coupled with Top Down Mass Spectrometry. <i>Journal of Biological Chemistry</i> , 2008, 283, 14927-14937.	1.6	164
48	Convergence of isoprene and polyketide biosynthetic machinery: Isoprenyl-S-carrier proteins in the pksX pathway of <i>Bacillus subtilis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 8977-8982.	3.3	161
49	Spatial mapping of protein composition and tissue organization: a primer for multiplexed antibody-based imaging. <i>Nature Methods</i> , 2022, 19, 284-295.	9.0	156
50	Histone H1 loss drives lymphoma by disrupting 3D chromatin architecture. <i>Nature</i> , 2021, 589, 299-305.	13.7	155
51	Facile Detection of Acyl and Peptidyl Intermediates on Thio-template Carrier Domains via Phosphopantetheinyl Elimination Reactions during Tandem Mass Spectrometry. <i>Biochemistry</i> , 2006, 45, 12756-12766.	1.2	154
52	A scalable platform to identify fungal secondary metabolites and their gene clusters. <i>Nature Chemical Biology</i> , 2017, 13, 895-901.	3.9	154
53	Assembly line enzymology by multimodular nonribosomal peptide synthetases: the thioesterase domain of <i>E. coli</i> EntF catalyzes both elongation and cyclolactonization. <i>Chemistry and Biology</i> , 1999, 6, 385-400.	6.2	153
54	Shotgun Annotation of Histone Modifications: A New Approach for Streamlined Characterization of Proteins by Top Down Mass Spectrometry. <i>Journal of the American Chemical Society</i> , 2004, 126, 3386-3387.	6.6	150

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55	Precise Characterization of Human Histones in the H2A Gene Family by Top Down Mass Spectrometry. <i>Journal of Proteome Research</i> , 2006, 5, 248-253.	1.8	150
56	From Protein Complexes to Subunit Backbone Fragments: A Multi-stage Approach to Native Mass Spectrometry. <i>Analytical Chemistry</i> , 2013, 85, 11163-11173.	3.2	148
57	Identification and Quantification of Proteoforms by Mass Spectrometry. <i>Proteomics</i> , 2019, 19, e1800361.	1.3	147
58	Thiamin Biosynthesis in <i>Escherichia coli</i> . <i>Journal of Biological Chemistry</i> , 1998, 273, 16555-16560.	1.6	143
59	Analysis of Intact Monoclonal Antibody IgG1 by Electron Transfer Dissociation Orbitrap FTMS. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 1758-1767.	2.5	137
60	Mutant-IDH1-dependent chromatin state reprogramming, reversibility, and persistence. <i>Nature Genetics</i> , 2018, 50, 62-72.	9.4	137
61	Cell-free Protein Synthesis from a Release Factor 1 Deficient <i>Escherichia coli</i> Activates Efficient and Multiple Site-specific Nonstandard Amino Acid Incorporation. <i>ACS Synthetic Biology</i> , 2014, 3, 398-409.	1.9	133
62	Large-scale Top-down Proteomics of the Human Proteome: Membrane Proteins, Mitochondria, and Senescence. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 3465-3473.	2.5	132
63	Web and Database Software for Identification of Intact Proteins Using Top Down Mass Spectrometry. <i>Analytical Chemistry</i> , 2003, 75, 4081-4086.	3.2	130
64	Detection and localization of protein modifications by high resolution tandem mass spectrometry. <i>Mass Spectrometry Reviews</i> , 2005, 24, 126-134.	2.8	129
65	Total kinetic analysis reveals how combinatorial methylation patterns are established on lysines 27 and 36 of histone H3. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 13549-13554.	3.3	129
66	Biosynthesis of Pipecolic Acid by RapL, a Lysine Cyclodeaminase Encoded in the Rapamycin Gene Cluster. <i>Journal of the American Chemical Society</i> , 2006, 128, 3838-3847.	6.6	126
67	Unusual transformations in the biosynthesis of the antibiotic phosphinothricin tripeptide. <i>Nature Chemical Biology</i> , 2007, 3, 480-485.	3.9	126
68	A proteomics approach to discovering natural products and their biosynthetic pathways. <i>Nature Biotechnology</i> , 2009, 27, 951-956.	9.4	125
69	Diversity of Amyloid-beta Proteoforms in the Alzheimer's Disease Brain. <i>Scientific Reports</i> , 2017, 7, 9520.	1.6	125
70	Unit resolution mass spectra of 112 kDa molecules with 3 Da accuracy. <i>Journal of the American Society for Mass Spectrometry</i> , 1997, 8, 380-383.	1.2	123
71	Hydroxymalonyl-acyl carrier protein (ACP) and aminomalonyl-ACP are two additional type I polyketide synthase extender units. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 14349-14354.	3.3	123
72	Lacticin 481 Synthetase Phosphorylates its Substrate during Lantibiotic Production. <i>Journal of the American Chemical Society</i> , 2005, 127, 15332-15333.	6.6	120

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73	Directed Evolution of the Nonribosomal Peptide Synthetase AdmK Generates New Andrimid Derivatives In Vivo. <i>Chemistry and Biology</i> , 2011, 18, 601-607.	6.2	119
74	Cover Picture: Proteomics 7'15. <i>Proteomics</i> , 2015, 15, NA-NA.	1.3	119
75	Heterologous Production of Fosfomycin and Identification of the Minimal Biosynthetic Gene Cluster. <i>Chemistry and Biology</i> , 2006, 13, 1171-1182.	6.2	116
76	Top-Down Proteomics on a Chromatographic Time Scale Using Linear Ion Trap Fourier Transform Hybrid Mass Spectrometers. <i>Analytical Chemistry</i> , 2007, 79, 7984-7991.	3.2	116
77	Preferential Dimethylation of Histone H4 Lysine 20 by Suv4-20. <i>Journal of Biological Chemistry</i> , 2008, 283, 12085-12092.	1.6	115
78	Top-down characterization of endogenous protein complexes with native proteomics. <i>Nature Chemical Biology</i> , 2018, 14, 36-41.	3.9	115
79	Multiplexed mass spectrometry of individual ions improves measurement of proteoforms and their complexes. <i>Nature Methods</i> , 2020, 17, 391-394.	9.0	110
80	Facile synthesis of site-specifically acetylated and methylated histone proteins: Reagents for evaluation of the histone code hypothesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 12033-12038.	3.3	109
81	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.	1.2	107
82	UTX/KDM6A Loss Enhances the Malignant Phenotype of Multiple Myeloma and Sensitizes Cells to EZH2 inhibition. <i>Cell Reports</i> , 2017, 21, 628-640.	2.9	106
83	The Human Proteoform Project: Defining the human proteome. <i>Science Advances</i> , 2021, 7, eabk0734.	4.7	106
84	A protease for 'middle-down' proteomics. <i>Nature Methods</i> , 2012, 9, 822-824.	9.0	103
85	Efficient sequence analysis of the six gene products (74 kDa) from the escherichia coli thiamin biosynthetic operon by tandem high-resolution mass spectrometry. <i>Protein Science</i> , 1998, 7, 1796-1801.	3.1	101
86	Gene-Specific Characterization of Human Histone H2B by Electron Capture Dissociation. <i>Journal of Proteome Research</i> , 2006, 5, 233-239.	1.8	101
87	Mass spectrometry-based discovery of circadian peptides. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 12527-12532.	3.3	101
88	The biosynthesis of methanobactin. <i>Science</i> , 2018, 359, 1411-1416.	6.0	101
89	Measurement of acetylation turnover at distinct lysines in human histones identifies long-lived acetylation sites. <i>Nature Communications</i> , 2013, 4, 2203.	5.8	100
90	Accurate Sequence Analysis of a Monoclonal Antibody by Top-Down and Middle-Down Orbitrap Mass Spectrometry Applying Multiple Ion Activation Techniques. <i>Analytical Chemistry</i> , 2018, 90, 8421-8429.	3.2	100

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91	Nine Enzymes Are Required for Assembly of the Pacidamycin Group of Peptidyl Nucleoside Antibiotics. <i>Journal of the American Chemical Society</i> , 2011, 133, 5240-5243.	6.6	99
92	Metabologenomics: Correlation of Microbial Gene Clusters with Metabolites Drives Discovery of a Nonribosomal Peptide with an Unusual Amino Acid Monomer. <i>ACS Central Science</i> , 2016, 2, 99-108.	5.3	99
93	Mo-, V-, and Fe-Nitrogenases Use a Universal Eight-Electron Reductive-Elimination Mechanism To Achieve N <sub>2</sub> Reduction. <i>Biochemistry</i> , 2019, 58, 3293-3301.	1.2	99
94	Precise and Parallel Characterization of Coding Polymorphisms, Alternative Splicing, and Modifications in Human Proteins by Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2005, 4, 1002-1008.	2.5	95
95	An interpreted atlas of biosynthetic gene clusters from 1,000 fungal genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	94
96	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.	3.3	93
97	Top Down Proteomics. <i>Analytical Chemistry</i> , 2013, 85, 6151-6151.	3.2	93
98	Mutant EZH2 Induces a Pre-malignant Lymphoma Niche by Reprogramming the Immune Response. <i>Cancer Cell</i> , 2020, 37, 655-673.e11.	7.7	93
99	The emerging process of Top Down mass spectrometry for protein analysis: biomarkers, protein-therapeutics, and achieving high throughput. <i>Molecular BioSystems</i> , 2010, 6, 1532.	2.9	92
100	A robust two-dimensional separation for top-down tandem mass spectrometry of the low-mass proteome. <i>Journal of the American Society for Mass Spectrometry</i> , 2009, 20, 2183-2191.	1.2	91
101	Size-Sorting Combined with Improved Nanocapillary Liquid Chromatography~Mass Spectrometry for Identification of Intact Proteins up to 80 kDa. <i>Analytical Chemistry</i> , 2010, 82, 1234-1244.	3.2	91
102	The first pilot project of the consortium for top-down proteomics: <scp>A</scp> status report. <i>Proteomics</i> , 2014, 14, 1130-1140.	1.3	90
103	Large-Scale Metabolomics Reveals a Complex Response of <i>Aspergillus nidulans</i> to Epigenetic Perturbation. <i>ACS Chemical Biology</i> , 2015, 10, 1535-1541.	1.6	90
104	The emergence of top-down proteomics in clinical research. <i>Genome Medicine</i> , 2013, 5, 53.	3.6	89
105	Quantitation and Identification of Thousands of Human Proteoforms below 30 kDa. <i>Journal of Proteome Research</i> , 2016, 15, 976-982.	1.8	89
106	Cloning, Expression, and Biochemical Characterization of <i>Streptomyces rubellomurinus</i> Genes Required for Biosynthesis of Antimalarial Compound FR900098. <i>Chemistry and Biology</i> , 2008, 15, 765-770.	6.2	88
107	Histone H1 phosphorylation is associated with transcription by RNA polymerases I and II. <i>Journal of Cell Biology</i> , 2010, 189, 407-415.	2.3	88
108	Analysis of Intact Protein Isoforms by Mass Spectrometry. <i>Journal of Biological Chemistry</i> , 2011, 286, 25451-25458.	1.6	88

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109	Applying Label-Free Quantitation to Top Down Proteomics. <i>Analytical Chemistry</i> , 2014, 86, 4961-4968.	3.2	88
110	A phosphopantetheinylating polyketide synthase producing a linear polyene to initiate enediyne antitumor antibiotic biosynthesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 1460-1465.	3.3	87
111	Evaluation of the Compact High-Field Orbitrap for Top-Down Proteomics of Human Cells. <i>Journal of Proteome Research</i> , 2012, 11, 4308-4314.	1.8	84
112	Endogenous Peptide Discovery of the Rat Circadian Clock. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 285-297.	2.5	83
113	Ultraviolet Photodissociation for Characterization of Whole Proteins on a Chromatographic Time Scale. <i>Analytical Chemistry</i> , 2014, 86, 2185-2192.	3.2	81
114	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.	1.8	81
115	A community resource for paired genomic and metabolomic data mining. <i>Nature Chemical Biology</i> , 2021, 17, 363-368.	3.9	81
116	tRNA-dependent peptide bond formation by the transferase PacB in biosynthesis of the pacidamycin group of pentapeptidyl nucleoside antibiotics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 12249-12253.	3.3	80
117	Expansion for the <i>Brachylophosaurus canadensis</i> Collagen I Sequence and Additional Evidence of the Preservation of Cretaceous Protein. <i>Journal of Proteome Research</i> , 2017, 16, 920-932.	1.8	80
118	<i>In Vitro</i> Reconstruction of Nonribosomal Peptide Biosynthesis Directly from DNA Using Cell-Free Protein Synthesis. <i>ACS Synthetic Biology</i> , 2017, 6, 39-44.	1.9	80
119	Mechanism of $N_2$ Reduction Catalyzed by Fe-Nitrogenase Involves Reductive Elimination of $H_2$ . <i>Biochemistry</i> , 2018, 57, 701-710.	1.2	80
120	Structure Determination and Interception of Biosynthetic Intermediates for the Plantazolicin Class of Highly Discriminating Antibiotics. <i>ACS Chemical Biology</i> , 2011, 6, 1307-1313.	1.6	79
121	Global Assessment of Combinatorial Post-translational Modification of Core Histones in Yeast Using Contemporary Mass Spectrometry. <i>Journal of Biological Chemistry</i> , 2007, 282, 27923-27934.	1.6	77
122	Improving Cell-Free Protein Synthesis through Genome Engineering of <i>Escherichia coli</i> Lacking Release Factor 1. <i>ChemBioChem</i> , 2015, 16, 844-853.	1.3	77
123	Top-Down Approaches for Measuring Expression Ratios of Intact Yeast Proteins Using Fourier Transform Mass Spectrometry. <i>Analytical Chemistry</i> , 2006, 78, 686-694.	3.2	76
124	Optimizing capillary electrophoresis for top-down proteomics of 30-80 kDa proteins. <i>Proteomics</i> , 2014, 14, 1158-1164.	1.3	76
125	The C-Score: A Bayesian Framework to Sharply Improve Proteoform Scoring in High-Throughput Top Down Proteomics. <i>Journal of Proteome Research</i> , 2014, 13, 3231-3240.	1.8	76
126	Fungal artificial chromosomes for mining of the fungal secondary metabolome. <i>BMC Genomics</i> , 2015, 16, 343.	1.2	76



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127	Kinetic and Mass Spectrometric Analysis of p300 Histone Acetyltransferase Domain Autoacetylation. <i>Journal of Biological Chemistry</i> , 2006, 281, 40292-40301.	1.6	75
128	Precise characterization of KRAS4b proteoforms in human colorectal cells and tumors reveals mutation/modification cross-talk. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 4140-4145.	3.3	74
129	Native top-down mass spectrometry provides insights into the copper centers of membrane-bound methane monooxygenase. <i>Nature Communications</i> , 2019, 10, 2675.	5.8	74
130	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.	3.2	72
131	Top Down Proteomics of Human Membrane Proteins from Enriched Mitochondrial Fractions. <i>Analytical Chemistry</i> , 2013, 85, 1880-1888.	3.2	72
132	Incorporation of Nonmethyl Branches by Isoprenoid-like Logic: Multiple $\beta^2$ -Alkylation Events in the Biosynthesis of Myxovirescin A1. <i>Chemistry and Biology</i> , 2007, 14, 835-846.	6.2	71
133	Interpreting Top-Down Mass Spectra Using Spectral Alignment. <i>Analytical Chemistry</i> , 2008, 80, 2499-2505.	3.2	71
134	New and automated MSn approaches for top-down identification of modified proteins. <i>Journal of the American Society for Mass Spectrometry</i> , 2005, 16, 2027-2038.	1.2	70
135	The Loading Module of Mycosubtilin: An Adenylation Domain with Fatty Acid Selectivity. <i>Journal of the American Chemical Society</i> , 2007, 129, 6366-6367.	6.6	70
136	Redox Metabolites Signal Polymicrobial Biofilm Development via the NapA Oxidative Stress Cascade in <i>Aspergillus</i> . <i>Current Biology</i> , 2015, 25, 29-37.	1.8	70
137	Mapping Proteoforms and Protein Complexes From King Cobra Venom Using Both Denaturing and Native Top-down Proteomics. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 2423-2434.	2.5	69
138	High-Throughput Analysis of Intact Human Proteins Using UVPD and HCD on an Orbitrap Mass Spectrometer. <i>Journal of Proteome Research</i> , 2017, 16, 2072-2079.	1.8	69
139	Integrated Bottom-Up and Top-Down Proteomics of Patient-Derived Breast Tumor Xenografts. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 45-56.	2.5	68
140	Advancing Top-down Analysis of the Human Proteome Using a Benchtop Quadrupole-Orbitrap Mass Spectrometer. <i>Journal of Proteome Research</i> , 2017, 16, 609-618.	1.8	68
141	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.	1.2	67
142	USP7 Cooperates with NOTCH1 to Drive the Oncogenic Transcriptional Program in T-Cell Leukemia. <i>Clinical Cancer Research</i> , 2019, 25, 222-239.	3.2	66
143	A Mutation in Histone H2B Represents a New Class of Oncogenic Driver. <i>Cancer Discovery</i> , 2019, 9, 1438-1451.	7.7	65
144	Protein Assembly Line Components in Prodigiosin Biosynthesis: Characterization of PigA,C,H,I,J. <i>Journal of the American Chemical Society</i> , 2006, 128, 12600-12601.	6.6	64

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145	The Blood Proteoform Atlas: A reference map of proteoforms in human hematopoietic cells. <i>Science</i> , 2022, 375, 411-418.	6.0	64
146	Dissecting non-ribosomal and polyketide biosynthetic machineries using electrospray ionization Fourier-Transform mass spectrometry. <i>Natural Product Reports</i> , 2006, 23, 893.	5.2	63
147	Tissue-Specific Expression and Post-Translational Modification of Histone H3 Variants. <i>Journal of Proteome Research</i> , 2008, 7, 4225-4236.	1.8	63
148	Top Down Mass Spectrometry of <60-kDa Proteins from <i>Methanosarcina acetivorans</i> Using Quadrupole FTMS with Automated Octopole Collisionally Activated Dissociation. <i>Molecular and Cellular Proteomics</i> , 2006, 5, 14-25.	2.5	62
149	Robust Analysis of the Yeast Proteome under 50 kDa by Molecular-Mass-Based Fractionation and Top-Down Mass Spectrometry. <i>Analytical Chemistry</i> , 2012, 84, 209-215.	3.2	62
150	Epiproteomics: quantitative analysis of histone marks and codes by mass spectrometry. <i>Current Opinion in Chemical Biology</i> , 2016, 33, 142-150.	2.8	62
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