Neil Kelleher

List of Articles by Year
in descending order

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417 peer-reviewed articles	28,996 peer-reviewed citations	4998 82 peer-reviewed h-index	91036 6.27 score
467 documents	38909 doc citations	3409 96 h-index	44985 citing authors

#	Article	IF	Citations
1	A Robust and Automated Platform for Charge Detection Mass Spectrometry of Megadalton Biotherapeutics. Analytical Chemistry, 2025, 97, 4549-4555.	5.2	8
2	Proteoform-predictor: Increasing the Phylogenetic Reach of Top-Down Proteomics. Journal of Proteome Research, 2025, 24, 1861-1870.	2.2	3
3	Capillary Zone Electrophoresis-Mass Spectrometry of Intact G Protein-Coupled Receptors Enables Proteoform Profiling. Analytical Chemistry, 2025, 97, 7307-7316.	5.2	5
4	Blocking C-terminal processing of KRAS4b via a direct covalent attack on the CaaX-box cysteine. Proceedings of the National Academy of Sciences of the United States of America, 2025, 122, .	5.2	7
5	The Proteoform Landscape of Tau from the Human Brain. Journal of Proteome Research, 2025, 24, 2916-2925.	2.2	19
6	Wavelength Dependence of Intact Protein Extraction Using Femtosecond Laser Ablation. Journal of Physical Chemistry Letters, 2025, 16, 8785-8791.	2.9	2
7	Improved Signal Processing for Mass Shifting Ions in Charge Detection Mass Spectrometry. Journal of the American Society for Mass Spectrometry, 2024, 35, 658-662.	1.8	13
8	Terpenoid balance in *Aspergillus nidulans* unveiled by heterologous squalene synthase expression. Science Advances, 2024, 10, .	8.1	8
9	Precise Readout of MEK1 Proteoforms upon MAPK Pathway Modulation by Individual Ion Mass Spectrometry. Analytical Chemistry, 2024, 96, 4455-4462.	5.2	11
10	Single Cell Analysis of Proteoforms. Journal of Proteome Research, 2024, 23, 1883-1893.	2.2	27
11	Design, Synthesis, and Mechanistic Studies of (R)-3-Amino-5,5-difluorocyclohex-1-ene-1-carboxylic Acid as an Inactivator of Human Ornithine Aminotransferase. ACS Chemical Biology, 2024, 19, 1066-1081.	2.5	7
12	MSModDetector: a tool for detecting mass shifts and post-translational modifications in individual ion mass spectrometry data. Bioinformatics, 2024, 40, .	3.2	2
13	Top-down mass spectrometry of native proteoforms and their complexes: a community study. Nature Methods, 2024, 21, 2388-2396.	13.1	40
14	A multi-iron enzyme installs copper-binding oxazolone/thioamide pairs on a nontypeable *Haemophilus influenzae* virulence factor. Proceedings of the National Academy of Sciences of the United States of America, 2024, 121, .	5.2	27
15	Bioactivity-driven fungal metabologenomics identifies antiproliferative stemphone analogs and their biosynthetic gene cluster. Metabolomics, 2024, 20, .	1.9	12
16	Characterization of the Antibody Response to SARS-CoV-2 Infection in COVID-19 Transplant versus Nontransplant Recipients by Ig-MS. Journal of Proteome Research, 2024, 23, 3944-3957.	2.2	2
17	Deep Profiling of Plasma Proteoforms with Engineered Nanoparticles for Top-Down Proteomics. Journal of Proteome Research, 2024, 23, 4694-4703.	2.2	34
18	Temporal regulation of gene expression through integration of p53 dynamics and modifications. Science Advances, 2024, 10, .	8.1	8

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19	Top-Down Proteomics Identifies Plasma Proteoform Signatures of Liver Cirrhosis Progression. Molecular and Cellular Proteomics, 2024, 23, 100876.	3.2	17
20	Top-Down Stability of Proteins from Rates of Oxidation (TD-SPROX) Approach for Measuring Proteoform-Specific Folding Stability. Analytical Chemistry, 2024, 96, 19597-19604.	5.2	9
21	Preparative Electrophoresis for HDL Particle Size Separation and Intact-Mass Apolipoprotein Proteoform Analysis. Journal of Proteome Research, 2023, 22, 1455-1465.	2.2	9
22	Correlative metabologenomics of 110 fungi reveals metabolite–gene cluster pairs. Nature Chemical Biology, 2023, 19, 846-854.	9.1	56
23	ProSight Native: Defining Protein Complex Composition from Native Top-Down Mass Spectrometry Data. Journal of Proteome Research, 2023, 22, 2660-2668.	2.2	41
24	Sperm chromatin structure and reproductive fitness are altered by substitution of a single amino acid in mouse protamine 1. Nature Structural and Molecular Biology, 2023, 30, 1077-1091.	5.8	28
25	Organ Mapping Antibody Panels: a community resource for standardized multiplexed tissue imaging. Nature Methods, 2023, 20, 1174-1178.	13.1	47
26	Identification of Splice Variants and Isoforms in Transcriptomics and Proteomics. Annual Review of Biomedical Data Science, 2023, 6, 357-376.	4.4	36
27	Automated imaging and identification of proteoforms directly from ovarian cancer tissue. Nature Communications, 2023, 14, .	10.8	31
28	Advancing Intact Protein Quantitation with Updated Deconvolution Routines. Analytical Chemistry, 2023, 95, 14954-14962.	5.2	7
29	Immunocomplexed Antigen Capture and Identification by Native Top-Down Mass Spectrometry. Journal of the American Society for Mass Spectrometry, 2023, 34, 2093-2097.	1.8	3
30	Amyloid β Proteoforms Elucidated by Quantitative LC/MS in the 5xFAD Mouse Model of Alzheimer's Disease. Journal of Proteome Research, 2023, 22, 3475-3488.	2.2	6
31	Mass spectrometry-based proteomics for advancing solid organ transplantation research. Frontiers in Transplantation, 2023, 2, .	1.3	11
32	Determining Collisional Cross Sections from Ion Decay with Individual Ion Mass Spectrometry. Journal of the American Society for Mass Spectrometry, 2023, 34, 2625-2629.	1.8	2
33	Determining Collisional Cross Sections from Ion Decay with Individual Ion Mass Spectrometry. Journal of the American Society for Mass Spectrometry, 2023, 34, 2625-2629.	1.8	7
34	The Blood Proteoform Atlas: A reference map of proteoforms in human hematopoietic cells. Science, 2022, 375, 411-418.	26.1	141
35	Next-Generation Serology by Mass Spectrometry: Readout of the SARS-CoV-2 Antibody Repertoire. Journal of Proteome Research, 2022, 21, 274-288.	2.2	25
36	Rational Design, Synthesis, and Mechanism of (3S,4R)-3-Amino-4-(difluoromethyl)cyclopent-1-ene-1-carboxylic Acid: Employing a Second-Deprotonation Strategy for Selectivity of Human Ornithine Aminotransferase over GABA Aminotransferase. Journal of the American Chemical Society, 2022, 144, 5629-5642.	11.7	15

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37	A mixed-valent Fe(II)Fe(III) species converts cysteine to an oxazolone/thioamide pair in methanobactin biosynthesis. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	5.2	48
38	ProSight Annotator: Complete control and customization of protein entries in UniProt XML files. Proteomics, 2022, 22, .	2.1	8
39	The Human Proteoform Atlas: a FAIR community resource for experimentally derived proteoforms. Nucleic Acids Research, 2022, 50, D526-D533.	10.7	36
40	Mapping the Proteoform Landscape of Five Human Tissues. Journal of Proteome Research, 2022, 21, 1299-1310.	2.2	56
41	SETD2 Haploinsufficiency Enhances Germinal Center–Associated AICDA Somatic Hypermutation to Drive B-cell Lymphomagenesis. Cancer Discovery, 2022, 12, 1782-1803.	6.8	30
42	Proteoform-Selective Imaging of Tissues Using Mass Spectrometry**. Angewandte Chemie - International Edition, 2022, 61, .	11.6	48
43	An efficient cell-free protein synthesis platform for producing proteins with pyrrolysine-based noncanonical amino acids. Biotechnology Journal, 2022, 17, .	2.4	16
44	Innenrücktitelbild: Proteoform-Selective Imaging of Tissues Using Mass Spectrometry (Angew. Chem. 29/2022). Angewandte Chemie, 2022, 134, .	0.9	0
45	Native Mass Spectrometry at the Convergence of Structural Biology and Compositional Proteomics. Accounts of Chemical Research, 2022, 55, 1928-1937.	11.6	29
46	C16orf72/HAPSTR1 is a molecular rheostat in an integrated network of stress response pathways. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	5.2	25
47	Revving an Engine of Human Metabolism: Activity Enhancement of Triosephosphate Isomerase via Hemi-Phosphorylation. ACS Chemical Biology, 2022, 17, 2769-2780.	2.5	14
48	Highly multiplexed, label-free proteoform imaging of tissues by individual ion mass spectrometry. Science Advances, 2022, 8, .	8.1	69
49	SPT6 functions in transcriptional pause/release via PAF1C recruitment. Molecular Cell, 2022, 82, 3412-3423.e5.	8.6	73
50	Venom characterization of the Brazilian Pampa snake Bothrops pubescens by top-down and bottom-up proteomics. Toxicon, 2022, 220, 106937.	1.2	6
51	Divergent Antibody Repertoires Found for Omicron versus Wuhan SARS-CoV-2 Strains Using Ig-MS. Journal of Proteome Research, 2022, 21, 2987-2997.	2.2	9
52	Middle-Down Mass Spectrometry Reveals Activity-Modifying Phosphorylation Barcode in a Class C G Protein-Coupled Receptor. Journal of the American Chemical Society, 2022, 144, 23104-23114.	11.7	20
53	Isotopic Resolution of Protein Complexes up to 466 kDa Using Individual Ion Mass Spectrometry. Analytical Chemistry, 2021, 93, 2723-2727.	5.2	56
54	Standard procedures for native CZE-MS of proteins and protein complexes up to 800 kDa. Electrophoresis, 2021, 42, 1050-1059.	1.7	39

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55	Metabolomics and genomics in natural products research: complementary tools for targeting new chemical entities. Natural Product Reports, 2021, 38, 2041-2065.	8.6	158
56	In vitro-Constructed Ribosomes Enable Multi-site Incorporation of Noncanonical Amino Acids into Proteins. Biochemistry, 2021, 60, 161-169.	1.5	17
57	Decoding the protein composition of whole nucleosomes with Nuc-MS. Nature Methods, 2021, 18, 303-308.	13.1	68
58	Separation and Characterization of Endogenous Nucleosomes by Native Capillary Zone Electrophoresis–Top-Down Mass Spectrometry. Analytical Chemistry, 2021, 93, 5151-5160.	5.2	42
59	Deeper Protein Identification Using Field Asymmetric Ion Mobility Spectrometry in Top-Down Proteomics. Analytical Chemistry, 2021, 93, 6323-6328.	5.2	58
60	Remarkable and Unexpected Mechanism for (S)-3-Amino-4-(difluoromethylenyl)cyclohex-1-ene-1-carboxylic Acid as a Selective Inactivator of Human Ornithine Aminotransferase. Journal of the American Chemical Society, 2021, 143, 8193-8207.	11.7	16
61	New Interface for Faster Proteoform Analysis: Immunoprecipitation Coupled with SampleStream-Mass Spectrometry. Journal of the American Society for Mass Spectrometry, 2021, 32, 1659-1670.	1.8	24
62	An interpreted atlas of biosynthetic gene clusters from 1,000 fungal genomes. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	5.2	177
63	Turnover and Inactivation Mechanisms for (S)-3-Amino-4,4-difluorocyclopent-1-enecarboxylic Acid, a Selective Mechanism-Based Inactivator of Human Ornithine Aminotransferase. Journal of the American Chemical Society, 2021, 143, 8689-8703.	11.7	12
64	Oncogenic KRAS creates an aspartate metabolism signature in colorectal cancer cells. FEBS Journal, 2021, 288, 6683-6699.	3.3	22
65	Reassembling protein complexes after controlled disassembly by top-down mass spectrometry in native mode. International Journal of Mass Spectrometry, 2021, 465, 116591.	1.1	16
66	Spectrum of Apolipoprotein AI and Apolipoprotein AII Proteoforms and Their Associations With Indices of Cardiometabolic Health: The CARDIA Study. Journal of the American Heart Association, 2021, 10, .	3.1	29
67	Characterization of a Copper-Chelating Natural Product from the Methanotroph Methylosinus sp. LW3. Biochemistry, 2021, 60, 2845-2850.	1.5	11
68	SPT5 stabilization of promoter-proximal RNA polymerase II. Molecular Cell, 2021, 81, 4413-4424.e5.	8.6	113
69	Should LC-MS/MS Be the Reference Measurement Procedure to Determine Protein Concentrations in Human Samples?. Clinical Chemistry, 2021, 67, 466-471.	0.6	23
70	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 de novo sequencing. Clinical Chemistry and Laboratory Medicine, 2021, 59, 653-661.	2.0	8
71	The Human Proteoform Project: Defining the human proteome. Science Advances, 2021, 7, .	8.1	239
72	Novel Interface for High-Throughput Analysis of Biotherapeutics by Electrospray Mass Spectrometry. Analytical Chemistry, 2020, 92, 2186-2193.	5.2	47

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73	Discovery of the Biosynthetic Machinery for Stravidins, Biotin Antimetabolites. ACS Chemical Biology, 2020, 15, 1134-1140.	2.5	15
74	In the fungus where it happens: History and future propelling Aspergillus nidulans as the archetype of natural products research. Fungal Genetics and Biology, 2020, 144, 103477.	1.8	64
75	Streptomyces buecherae sp. nov., an actinomycete isolated from multiple bat species. Antonie Van Leeuwenhoek, 2020, 113, 2213-2221.	1.2	14
76	Histone tail analysis reveals H3K36me2 and H4K16ac as epigenetic signatures of diffuse intrinsic pontine glioma. Journal of Experimental and Clinical Cancer Research, 2020, 39, .	7.6	33
77	Interlaboratory Study for Characterizing Monoclonal Antibodies by Top-Down and Middle-Down Mass Spectrometry. Journal of the American Society for Mass Spectrometry, 2020, 31, 1783-1802.	1.8	106
78	Heterologous Expression of the Unusual Terreazepine Biosynthetic Gene Cluster Reveals a Promising Approach for Identifying New Chemical Scaffolds. MBio, 2020, 11, .	3.1	20
79	Genome Mining and Metabolomics Uncover a Rare d-Capreomycidine Containing Natural Product and Its Biosynthetic Gene Cluster. ACS Chemical Biology, 2020, 15, 3013-3020.	2.5	11
80	Mutant EZH2 Induces a Pre-malignant Lymphoma Niche by Reprogramming the Immune Response. Cancer Cell, 2020, 37, 655-673.e11.	28.4	154
81	The serine hydroxymethyltransferase-2 (SHMT2) initiates lymphoma development through epigenetic tumor suppressor silencing. Nature Cancer, 2020, 1, 653-664.	15.2	65
82	Individual Ion Mass Spectrometry Enhances the Sensitivity and Sequence Coverage of Top-Down Mass Spectrometry. Journal of Proteome Research, 2020, 19, 1346-1350.	2.2	74
83	Voltage Rollercoaster Filtering of Low-Mass Contaminants During Native Protein Analysis. Journal of the American Society for Mass Spectrometry, 2020, 31, 763-767.	1.8	23
84	NMT1 and NMT2 are lysine myristoyltransferases regulating the ARF6 GTPase cycle. Nature Communications, 2020, 11, .	10.8	106
85	A Remarkable Difference That One Fluorine Atom Confers on the Mechanisms of Inactivation of Human Ornithine Aminotransferase by Two Cyclohexene Analogues of γ-Aminobutyric Acid. Journal of the American Chemical Society, 2020, 142, 4892-4903.	11.7	30
86	Multiplexed mass spectrometry of individual ions improves measurement of proteoforms and their complexes. Nature Methods, 2020, 17, 391-394.	13.1	190
87	Thorough Performance Evaluation of 213 nm Ultraviolet Photodissociation for Top-down Proteomics. Molecular and Cellular Proteomics, 2020, 19, 405-420.	3.2	71
88	Elucidating Proteoform Dynamics Underlying the Senescence Associated Secretory Phenotype. Journal of Proteome Research, 2020, 19, 938-948.	2.2	13
89	Native vs Denatured: An in Depth Investigation of Charge State and Isotope Distributions. Journal of the American Society for Mass Spectrometry, 2020, 31, 574-581.	1.8	51
90	A MUC16 IgG Binding Activity Selects for a Restricted Subset of IgG Enriched for Certain Simian Immunodeficiency Virus Epitope Specificities. Journal of Virology, 2020, 94, .	2.4	6

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91	Histone H1 loss drives lymphoma by disrupting 3D chromatin architecture. Nature, 2020, 589, 299-305.	30.7	256
92	Mechanism-Based Design of 3-Amino-4-Halocyclopentenecarboxylic Acids as Inactivators of GABA Aminotransferase. ACS Medicinal Chemistry Letters, 2020, 11, 1949-1955.	2.1	12
93	Using 10,000 Fragment Ions to Inform Scoring in Native Top-down Proteomics. Journal of the American Society for Mass Spectrometry, 2020, 31, 1398-1409.	1.8	29
94	Targeted detection and quantitation of histone modifications from 1,000 cells. PLoS ONE, 2020, 15, e0240829.	1.5	5
95	Coupling Fluorescence-Activated Cell Sorting and Targeted Analysis of Histone Modification Profiles in Primary Human Leukocytes. Journal of the American Society for Mass Spectrometry, 2019, 30, 2526-2534.	1.8	16
96	Mo-, V-, and Fe-Nitrogenases Use a Universal Eight-Electron Reductive-Elimination Mechanism To Achieve N_2 Reduction. Biochemistry, 2019, 58, 3293-3301.	1.5	146
97	A Mutation in Histone H2B Represents a New Class of Oncogenic Driver. Cancer Discovery, 2019, 9, 1438-1451.	6.8	108
98	Mechanism of Inactivation of Ornithine Aminotransferase by (1S,3S)-3-Amino-4-(hexafluoropropan-2-ylidenyl)cyclopentane-1-carboxylic Acid. Journal of the American Chemical Society, 2019, 141, 10711-10721.	11.7	28
99	Defining the NSD2 interactome: PARP1 PARylation reduces NSD2 histone methyltransferase activity and impedes chromatin binding. Journal of Biological Chemistry, 2019, 294, 12459-12471.	1.3	19
100	Direct measurement of light and heavy antibody chains using ion mobility and middle-down mass spectrometry. MAbs, 2019, 11, 1351-1357.	8.9	31
101	A Highly Productive, One-Pot Cell-Free Protein Synthesis Platform Based on Genomically Recoded Escherichia coli. Cell Chemical Biology, 2019, 26, 1743-1754.e9.	4.5	85
102	A five-level classification system for proteoform identifications. Nature Methods, 2019, 16, 939-940.	13.1	89
103	Multidimensional Top-Down Proteomics of Brain-Region-Specific Mouse Brain Proteoforms Responsive to Cocaine and Estradiol. Journal of Proteome Research, 2019, 18, 3999-4012.	2.2	17
104	Native top-down mass spectrometry provides insights into the copper centers of membrane-bound methane monooxygenase. Nature Communications, 2019, 10, .	10.8	101
105	Identification and Quantification of Proteoforms by Mass Spectrometry. Proteomics, 2019, 19, .	2.1	192
106	Standard Proteoforms and Their Complexes for Native Mass Spectrometry. Journal of the American Society for Mass Spectrometry, 2019, 30, 1190-1198.	1.8	52
107	Precision Targeting with EZH2 and HDAC Inhibitors in Epigenetically Dysregulated Lymphomas. Clinical Cancer Research, 2019, 25, 5271-5283.	4.5	78
108	Chromatin occupancy and epigenetic analysis reveal new insights into the function of the GATA1 N terminus in erythropoiesis. Blood, 2019, 134, 1619-1631.	3.6	55

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109	Proton Transfer Charge Reduction Enables High-Throughput Top-Down Analysis of Large Proteoforms. Analytical Chemistry, 2019, 91, 15732-15739.	5.2	96
110	USP7 Cooperates with NOTCH1 to Drive the Oncogenic Transcriptional Program in T-Cell Leukemia. Clinical Cancer Research, 2019, 25, 222-239.	4.5	92
111	A novel crosslinking protocol stabilizes amyloid β oligomers capable of inducing Alzheimer's-associated pathologies. Journal of Neurochemistry, 2019, 148, 822-836.	2.7	26
112	Accurate Estimation of Context-Dependent False Discovery Rates in Top-Down Proteomics. Molecular and Cellular Proteomics, 2019, 18, 796-805.	3.2	43
113	Measurement of Individual Ions Sharply Increases the Resolution of Orbitrap Mass Spectra of Proteins. Analytical Chemistry, 2019, 91, 2776-2783.	5.2	87
114	A computational framework to explore large-scale biosynthetic diversity. Nature Chemical Biology, 2019, 16, 60-68.	9.1	1,087
115	Discovery of the Tyrobetaine Natural Products and Their Biosynthetic Gene Cluster via Metabologenomics. ACS Chemical Biology, 2018, 13, 1029-1037.	2.5	49
116	Top-Down Proteomics Enables Comparative Analysis of Brain Proteoforms Between Mouse Strains. Analytical Chemistry, 2018, 90, 3802-3810.	5.2	35
117	β-Glucocerebrosidase Modulators Promote Dimerization of β-Glucocerebrosidase and Reveal an Allosteric Binding Site. Journal of the American Chemical Society, 2018, 140, 5914-5924.	11.7	49
118	Repurposed HisC Aminotransferases Complete the Biosynthesis of Some Methanobactins. Biochemistry, 2018, 57, 3515-3523.	1.5	21
119	Precise characterization of KRAS4b proteoforms in human colorectal cells and tumors reveals mutation/modification cross-talk. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 4140-4145.	5.2	98
120	Identification of the First Diketomorpholine Biosynthetic Pathway Using FAC-MS Technology. ACS Chemical Biology, 2018, 13, 1142-1147.	2.5	34
121	A Targeted, Differential Top-Down Proteomic Methodology for Comparison of ApoA-I Proteoforms in Individuals with High and Low HDL Efflux Capacity. Journal of Proteome Research, 2018, 17, 2156-2164.	2.2	41
122	Mechanism of N2 Reduction Catalyzed by Fe-Nitrogenase Involves Reductive Elimination of H2. Biochemistry, 2018, 57, 701-710.	1.5	111
123	Total Synthesis of Tambromycin Enabled by Indole C–H Functionalization. Organic Letters, 2018, 20, 2369-2373.	3.2	34
124	Cell-free protein synthesis from genomically recoded bacteria enables multisite incorporation of noncanonical amino acids. Nature Communications, 2018, 9, .	10.8	221
125	Interrogation of Benzomalvin Biosynthesis Using Fungal Artificial Chromosomes with Metabolomic Scoring (FAC-MS): Discovery of a Benzodiazepine Synthase Activity. Biochemistry, 2018, 57, 3237-3243.	1.5	27
126	Characterization of a long overlooked copper protein from methane- and ammonia-oxidizing bacteria. Nature Communications, 2018, 9, .	10.8	64

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127	Stability of histone post-translational modifications in samples derived from liver tissue and primary hepatic cells. PLoS ONE, 2018, 13, e0203351.	1.5	4
128	The unique biomineralization transcriptome and proteome of Lytechinus variegatus teeth. Connective Tissue Research, 2018, 59, 20-29.	1.2	3
129	Estimating the Distribution of Protein Post-Translational Modification States by Mass Spectrometry. Journal of Proteome Research, 2018, 17, 2727-2734.	2.2	36
130	The Value of Activated Ion Electron Transfer Dissociation for High-Throughput Top-Down Characterization of Intact Proteins. Analytical Chemistry, 2018, 90, 8553-8560.	5.2	43
131	Accurate Sequence Analysis of a Monoclonal Antibody by Top-Down and Middle-Down Orbitrap Mass Spectrometry Applying Multiple Ion Activation Techniques. Analytical Chemistry, 2018, 90, 8421-8429.	5.2	149
132	Natural products from thioester reductase containing biosynthetic pathways. Natural Product Reports, 2018, 35, 847-878.	8.6	94
133	An activating mutation of the NSD2 histone methyltransferase drives oncogenic reprogramming in acute lymphocytic leukemia. Oncogene, 2018, 38, 671-686.	5.2	57
134	Coupling Fluorescence-Activated Cell Sorting and Targeted LC-MS/MS for Epi-Proteomic Analysis of Normal Leukocytes. FASEB Journal, 2018, 32, .	2.3	0
135	Expansion for theBrachylophosaurus canadensisCollagen I Sequence and Additional Evidence of the Preservation of Cretaceous Protein. Journal of Proteome Research, 2017, 16, 920-932.	2.2	93
136	Chromatographic efficiency and selectivity in top-down proteomics of histones. Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences, 2017, 1044-1045, 47-53.	1.7	9
137	Therapeutic targeting of polycomb and BET bromodomain proteins in diffuse intrinsic pontine gliomas. Nature Medicine, 2017, 23, 493-500.	22.6	415
138	Characterizing the Structure and Oligomerization of Major Royal Jelly Protein 1 (MRJP1) by Mass Spectrometry and Complementary Biophysical Tools. Biochemistry, 2017, 56, 1645-1655.	1.5	32
139	Substrate Trapping in the Siderophore Tailoring Enzyme PvdQ. ACS Chemical Biology, 2017, 12, 643-647.	2.5	6
140	High-Throughput Analysis of Intact Human Proteins Using UVPD and HCD on an Orbitrap Mass Spectrometer. Journal of Proteome Research, 2017, 16, 2072-2079.	2.2	87
141	A scalable platform to identify fungal secondary metabolites and their gene clusters. Nature Chemical Biology, 2017, 13, 895-901.	9.1	193
142	Defining Gas-Phase Fragmentation Propensities of Intact Proteins During Native Top-Down Mass Spectrometry. Journal of the American Society for Mass Spectrometry, 2017, 28, 1203-1215.	1.8	60
143	Modulation of Protein Fragmentation Through Carbamylation of Primary Amines. Journal of the American Society for Mass Spectrometry, 2017, 28, 1587-1599.	1.8	21
144	Translation system engineering in Escherichia coli enhances non-canonical amino acid incorporation into proteins. Biotechnology and Bioengineering, 2017, 114, 1074-1086.	2.7	58

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145	A cryptic Tudor domain links BRWD2/PHIP to COMPASS-mediated histone H3K4 methylation. Genes and Development, 2017, 31, 2003-2014.	2.8	69
146	Histone H3K4 monomethylation catalyzed by Trr and mammalian COMPASS-like proteins at enhancers is dispensable for development and viability. Nature Genetics, 2017, 49, 1647-1653.	14.1	226
147	UTX/KDM6A Loss Enhances the Malignant Phenotype of Multiple Myeloma and Sensitizes Cells to EZH2 inhibition. Cell Reports, 2017, 21, 628-640.	4.4	129
148	Native Electron Capture Dissociation Maps to Iron-Binding Channels in Horse Spleen Ferritin. Analytical Chemistry, 2017, 89, 10711-10716.	5.2	18
149	Selective Targeting by a Mechanism-Based Inactivator against Pyridoxal 5'-Phosphate-Dependent Enzymes: Mechanisms of Inactivation and Alternative Turnover. Biochemistry, 2017, 56, 4951-4961.	1.5	18
150	Diversity of Amyloid-beta Proteoforms in the Alzheimer's Disease Brain. Scientific Reports, 2017, 7, .	2.7	157
151	Colibactin assembly line enzymes use S-adenosylmethionine to build a cyclopropane ring. Nature Chemical Biology, 2017, 13, 1063-1065.	9.1	65
152	Advancing Top-down Analysis of the Human Proteome Using a Benchtop Quadrupole-Orbitrap Mass Spectrometer. Journal of Proteome Research, 2017, 16, 609-618.	2.2	84
153	In Vitro Reconstruction of Nonribosomal Peptide Biosynthesis Directly from DNA Using Cell-Free Protein Synthesis. ACS Synthetic Biology, 2017, 6, 39-44.	3.0	96
154	Top-down characterization of endogenous protein complexes with native proteomics. Nature Chemical Biology, 2017, 14, 36-41.	9.1	161
155	Mutant-IDH1-dependent chromatin state reprogramming, reversibility, and persistence. Nature Genetics, 2017, 50, 62-72.	14.1	195
156	High-Throughput Natural Products Discovery in Fungi Using FAC-MS Technology. FASEB Journal, 2017, 31, .	2.3	0
157	Native Proteomics: A New Approach to Protein Complex Discovery and Characterization. FASEB Journal, 2017, 31, .	2.3	2
158	GENT-51. EPIGENETIC PROFILING REVEALS A UNIQUE HISTONE CODE IN CHORDOMA. Neuro-Oncology, 2016, 18, vi85-vi85.	0.9	0
159	Comparative top down proteomics of peripheral blood mononuclear cells from kidney transplant recipients with normal kidney biopsies or acute rejection. Proteomics, 2016, 16, 2048-2058.	2.1	24
160	The Search Engine for Multi-Proteoform Complexes: An Online Tool for the Identification and Stoichiometry Determination of Protein Complexes. Current Protocols in Bioinformatics, 2016, 56, .	3.3	7
161	Mass Spectrometry Imaging and Identification of Peptides Associated with Cephalic Ganglia Regeneration in Schmidtea mediterranea. Journal of Biological Chemistry, 2016, 291, 8109-8120.	1.3	30
162	A researcher's guide to mass spectrometry-based proteomics. Proteomics, 2016, 16, 2435-2443.	2.1	43

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163	Characterization of Methanobactin from Methylosinus sp. LW4. Journal of the American Chemical Society, 2016, 138, 11124-11127.	11.7	43
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