

Joshua J Coon

List of Publications by Year in descending order

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284
papers

23,069
citations

10986

71
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10734

138
g-index

306
all docs

306
docs citations

306
times ranked

25584
citing authors

#	ARTICLE	IF	CITATIONS
1	Peptide and protein sequence analysis by electron transfer dissociation mass spectrometry. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 9528-9533.	7.1	2,174
2	Parallel Reaction Monitoring for High Resolution and High Mass Accuracy Quantitative, Targeted Proteomics. Molecular and Cellular Proteomics, 2012, 11, 1475-1488.	3.8	1,023
3	Formic-acid-induced depolymerization of oxidized lignin to aromatics. Nature, 2014, 515, 249-252.	27.8	955
4	Calorie Restriction and SIRT3 Trigger Global Reprogramming of the Mitochondrial Protein Acetylome. Molecular Cell, 2013, 49, 186-199.	9.7	584
5	Analysis of phosphorylation sites on proteins from Saccharomyces cerevisiae by electron transfer dissociation (ETD) mass spectrometry. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 2193-2198.	7.1	541
6	The One Hour Yeast Proteome. Molecular and Cellular Proteomics, 2014, 13, 339-347.	3.8	489
7	Large-Scale Multi-omic Analysis of COVID-19 Severity. Cell Systems, 2021, 12, 23-40.e7.	6.2	438
8	Naturally Occurring Human Urinary Peptides for Use in Diagnosis of Chronic Kidney Disease. Molecular and Cellular Proteomics, 2010, 9, 2424-2437.	3.8	434
9	Value of Using Multiple Proteases for Large-Scale Mass Spectrometry-Based Proteomics. Journal of Proteome Research, 2010, 9, 1323-1329.	3.7	398
10	A Neutral Loss Activation Method for Improved Phosphopeptide Sequence Analysis by Quadrupole Ion Trap Mass Spectrometry. Analytical Chemistry, 2004, 76, 3590-3598.	6.5	389
11	Protein identification using sequential ion/ion reactions and tandem mass spectrometry. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 9463-9468.	7.1	362
12	Performance Characteristics of Electron Transfer Dissociation Mass Spectrometry. Molecular and Cellular Proteomics, 2007, 6, 1942-1951.	3.8	356
13	Supplemental Activation Method for High-Efficiency Electron-Transfer Dissociation of Doubly Protonated Peptide Precursors. Analytical Chemistry, 2007, 79, 477-485.	6.5	341
14	Probing the dynamics of O-GlcNAc glycosylation in the brain using quantitative proteomics. Nature Chemical Biology, 2007, 3, 339-348.	8.0	302
15	Decision tree-driven tandem mass spectrometry for shotgun proteomics. Nature Methods, 2008, 5, 959-964.	19.0	289
16	A dynamic model of proteome changes reveals new roles for transcript alteration in yeast. Molecular Systems Biology, 2011, 7, 514.	7.2	273
17	A Single Kinase Generates the Majority of the Secreted Phosphoproteome. Cell, 2015, 161, 1619-1632.	28.9	264
18	Proteomic and phosphoproteomic comparison of human ES and iPS cells. Nature Methods, 2011, 8, 821-827.	19.0	254

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19	Mitochondrial Protein Interaction Mapping Identifies Regulators of Respiratory Chain Function. <i>Molecular Cell</i> , 2016, 63, 621-632.	9.7	241
20	Gas-phase purification enables accurate, multiplexed proteome quantification with isobaric tagging. <i>Nature Methods</i> , 2011, 8, 933-935.	19.0	229
21	Electron transfer dissociation of peptide anions. <i>Journal of the American Society for Mass Spectrometry</i> , 2005, 16, 880-882.	2.8	227
22	Comprehensive Single-Shot Proteomics with FAIMS on a Hybrid Orbitrap Mass Spectrometer. <i>Analytical Chemistry</i> , 2018, 90, 9529-9537.	6.5	218
23	Phosphoproteomics in the Age of Rapid and Deep Proteome Profiling. <i>Analytical Chemistry</i> , 2016, 88, 74-94.	6.5	217
24	Anion dependence in the partitioning between proton and electron transfer in ion/ion reactions. <i>International Journal of Mass Spectrometry</i> , 2004, 236, 33-42.	1.5	188
25	Human embryonic stem cell phosphoproteome revealed by electron transfer dissociation tandem mass spectrometry. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 995-1000.	7.1	186
26	Capturing site-specific heterogeneity with large-scale N-glycoproteome analysis. <i>Nature Communications</i> , 2019, 10, 1311.	12.8	180
27	CE-MS analysis of the human urinary proteome for biomarker discovery and disease diagnostics. <i>Proteomics - Clinical Applications</i> , 2008, 2, 964-973.	1.6	178
28	Mass spectrometry identifies and quantifies 74 unique histone H4 isoforms in differentiating human embryonic stem cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 4093-4098.	7.1	167
29	Implementation of Electron-Transfer Dissociation on a Hybrid Linear Ion Trap Orbitrap Mass Spectrometer. <i>Analytical Chemistry</i> , 2007, 79, 3525-3534.	6.5	166
30	Human Pumilio Proteins Recruit Multiple Deadenylation Factors to Efficiently Repress Messenger RNAs. <i>Journal of Biological Chemistry</i> , 2012, 287, 36370-36383.	3.4	165
31	Neutron-encoded mass signatures for multiplexed proteome quantification. <i>Nature Methods</i> , 2013, 10, 332-334.	19.0	165
32	Maximal Oxidative Capacity during Exercise Is Associated with Skeletal Muscle Fuel Selection and Dynamic Changes in Mitochondrial Protein Acetylation. <i>Cell Metabolism</i> , 2015, 21, 468-478.	16.2	165
33	Deterministic HOX Patterning in Human Pluripotent Stem Cell-Derived Neuroectoderm. <i>Stem Cell Reports</i> , 2015, 4, 632-644.	4.8	162
34	SIRT3 Mediates Multi-Tissue Coupling for Metabolic Fuel Switching. <i>Cell Metabolism</i> , 2015, 21, 637-646.	16.2	154
35	Phosphoproteomics for the Masses. <i>ACS Chemical Biology</i> , 2010, 5, 105-119.	3.4	150
36	A Proteomics Search Algorithm Specifically Designed for High-Resolution Tandem Mass Spectra. <i>Journal of Proteome Research</i> , 2013, 12, 1377-1386.	3.7	147

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37	COMPASS: A suite of pre- and post-search proteomics software tools for OMSSA. <i>Proteomics</i> , 2011, 11, 1064-1074.	2.2	146
38	A Quantitative Map of the Liver Mitochondrial Phosphoproteome Reveals Posttranslational Control of Ketogenesis. <i>Cell Metabolism</i> , 2012, 16, 672-683.	16.2	141
39	Collisions or Electrons? Protein Sequence Analysis in the 21st Century. <i>Analytical Chemistry</i> , 2009, 81, 3208-3215.	6.5	138
40	A Proteomics Grade Electron Transfer Dissociation-Enabled Hybrid Linear Ion Trap-Orbitrap Mass Spectrometer. <i>Journal of Proteome Research</i> , 2008, 7, 3127-3136.	3.7	137
41	Large-Scale Phosphoprotein Analysis in <i>Medicago truncatula</i> Roots Provides Insight into in Vivo Kinase Activity in Legumes. <i>Plant Physiology</i> , 2009, 152, 19-28.	4.8	133
42	A proteomic atlas of the legume <i>Medicago truncatula</i> and its nitrogen-fixing endosymbiont <i>Sinorhizobium meliloti</i> . <i>Nature Biotechnology</i> , 2016, 34, 1198-1205.	17.5	133
43	Mitochondrial protein hyperacetylation in the failing heart. <i>JCI Insight</i> , 2016, 1, .	5.0	133
44	Dual-Pressure Linear Ion Trap Mass Spectrometer Improving the Analysis of Complex Protein Mixtures. <i>Analytical Chemistry</i> , 2009, 81, 7757-7765.	6.5	130
45	The Role of Electron Transfer Dissociation in Modern Proteomics. <i>Analytical Chemistry</i> , 2018, 90, 40-64.	6.5	124
46	Mitochondrial protein functions elucidated by multi-omic mass spectrometry profiling. <i>Nature Biotechnology</i> , 2016, 34, 1191-1197.	17.5	122
47	Lignin Conversion to Low-Molecular-Weight Aromatics via an Aerobic Oxidation-Hydrolysis Sequence: Comparison of Different Lignin Sources. <i>ACS Sustainable Chemistry and Engineering</i> , 2018, 6, 3367-3374.	6.7	118
48	Now, More Than Ever, Proteomics Needs Better Chromatography. <i>Cell Systems</i> , 2016, 3, 321-324.	6.2	117
49	Mitochondrial COQ9 is a lipid-binding protein that associates with COQ7 to enable coenzyme Q biosynthesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E4697-705.	7.1	113
50	Rapid Phosphoproteomic and Transcriptomic Changes in the Rhizobia-legume Symbiosis. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 724-744.	3.8	112
51	A role for the mevalonate pathway in early plant symbiotic signaling. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 9781-9786.	7.1	111
52	Tandem Phosphorylation of Ser-911 and Thr-912 at the C Terminus of Yeast Plasma Membrane H ⁺ -ATPase Leads to Glucose-dependent Activation. <i>Journal of Biological Chemistry</i> , 2007, 282, 35471-35481.	3.4	110
53	LipiDex: An Integrated Software Package for High-Confidence Lipid Identification. <i>Cell Systems</i> , 2018, 6, 621-625.e5.	6.2	108
54	Quantification of Mitochondrial Acetylation Dynamics Highlights Prominent Sites of Metabolic Regulation. <i>Journal of Biological Chemistry</i> , 2013, 288, 26209-26219.	3.4	105

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55	One-hour proteome analysis in yeast. <i>Nature Protocols</i> , 2015, 10, 701-714.	12.0	105
56	Mitochondrial ADCK3 Employs an Atypical Protein Kinase-like Fold to Enable Coenzyme Q Biosynthesis. <i>Molecular Cell</i> , 2015, 57, 83-94.	9.7	104
57	Cerebellar Ataxia and Coenzyme Q Deficiency through Loss of Unorthodox Kinase Activity. <i>Molecular Cell</i> , 2016, 63, 608-620.	9.7	101
58	Global mapping of CARM1 substrates defines enzyme specificity and substrate recognition. <i>Nature Communications</i> , 2017, 8, 15571.	12.8	100
59	Tandem Mass Spectrometry for Peptide and Protein Sequence Analysis. <i>BioTechniques</i> , 2005, 38, 519-523.	1.8	99
60	Interactive Peptide Spectral Annotator: A Versatile Web-based Tool for Proteomic Applications. <i>Molecular and Cellular Proteomics</i> , 2019, 18, S193-S201.	3.8	97
61	NeuCode Labels for Relative Protein Quantification. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 2503-2512.	3.8	94
62	Proteome sequencing goes deep. <i>Current Opinion in Chemical Biology</i> , 2015, 24, 11-17.	6.1	94
63	Metabolic Remodeling during Biofilm Development of <i>Bacillus subtilis</i> . <i>MBio</i> , 2019, 10, .	4.1	93
64	Plant-derived antifungal agent poacic acid targets β -1,3-glucan. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E1490-7.	7.1	91
65	Engineering and Two-Stage Evolution of a Lignocellulosic Hydrolysate-Tolerant <i>Saccharomyces cerevisiae</i> Strain for Anaerobic Fermentation of Xylose from AFEX Pretreated Corn Stover. <i>PLoS ONE</i> , 2014, 9, e107499.	2.5	91
66	Infrared Photoactivation Reduces Peptide Folding and Hydrogen-Atom Migration following ETD Tandem Mass Spectrometry. <i>Angewandte Chemie - International Edition</i> , 2009, 48, 8526-8528.	13.8	90
67	Phosphorylation regulates human OCT4. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 7162-7168.	7.1	87
68	ATM directs DNA damage responses and proteostasis via genetically separable pathways. <i>Science Signaling</i> , 2018, 11, .	3.6	87
69	Pathway connectivity and signaling coordination in the yeast stress-activated signaling network. <i>Molecular Systems Biology</i> , 2014, 10, 759.	7.2	83
70	Over 10 ⁶ Peptide Identifications from the HeLa Proteome by Using Single-Shot Capillary Zone Electrophoresis Combined with Tandem Mass Spectrometry. <i>Angewandte Chemie - International Edition</i> , 2014, 53, 13931-13933.	13.8	82
71	Development of a GC/Quadrupole-Orbitrap Mass Spectrometer, Part I: Design and Characterization. <i>Analytical Chemistry</i> , 2014, 86, 10036-10043.	6.5	82
72	Multi-omics Reveal Specific Targets of the RNA-Binding Protein Puf3p and Its Orchestration of Mitochondrial Biogenesis. <i>Cell Systems</i> , 2018, 6, 125-135.e6.	6.2	80

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73	The Peripheral Blood Eosinophil Proteome. <i>Journal of Proteome Research</i> , 2016, 15, 1524-1533.	3.7	79
74	Complete genome sequence and the expression pattern of plasmids of the model ethanologen <i>Zymomonas mobilis</i> ZM4 and its xylose-utilizing derivatives 8b and 2032. <i>Biotechnology for Biofuels</i> , 2018, 11, 125.	6.2	79
75	Genetic determinants of gut microbiota composition and bile acid profiles in mice. <i>PLoS Genetics</i> , 2019, 15, e1008073.	3.5	75
76	Mapping Physiological ADP-Ribosylation Using Activated Ion Electron Transfer Dissociation. <i>Cell Reports</i> , 2020, 32, 108176.	6.4	75
77	A map of the phosphoproteomic alterations that occur after a bout of maximal intensity contractions. <i>Journal of Physiology</i> , 2017, 595, 5209-5226.	2.9	70
78	Coenzyme Q biosynthetic proteins assemble in a substrate-dependent manner into domains at ER-mitochondria contacts. <i>Journal of Cell Biology</i> , 2019, 218, 1353-1369.	5.2	69
79	Mechanism of imidazolium ionic liquids toxicity in <i>Saccharomyces cerevisiae</i> and rational engineering of a tolerant, xylose-fermenting strain. <i>Microbial Cell Factories</i> , 2016, 15, 17.	4.0	67
80	The cellular economy of the <i>Saccharomyces cerevisiae</i> zinc proteome. <i>Metallomics</i> , 2018, 10, 1755-1776.	2.4	66
81	Activated-Ion Electron Transfer Dissociation Improves the Ability of Electron Transfer Dissociation to Identify Peptides in a Complex Mixture. <i>Analytical Chemistry</i> , 2010, 82, 10068-10074.	6.5	65
82	Improved Precursor Characterization for Data-Dependent Mass Spectrometry. <i>Analytical Chemistry</i> , 2018, 90, 2333-2340.	6.5	65
83	Activated Ion Electron Transfer Dissociation for Improved Fragmentation of Intact Proteins. <i>Analytical Chemistry</i> , 2015, 87, 7109-7116.	6.5	64
84	Conserved Lipid and Small-Molecule Modulation of COQ8 Reveals Regulation of the Ancient Kinase-like UbiB Family. <i>Cell Chemical Biology</i> , 2018, 25, 154-165.e11.	5.2	63
85	Peptide Quantification Using 8-Plex Isobaric Tags and Electron Transfer Dissociation Tandem Mass Spectrometry. <i>Analytical Chemistry</i> , 2009, 81, 1693-1698.	6.5	62
86	Ultra-High Pressure (>30,000 psi) Packing of Capillary Columns Enhancing Depth of Shotgun Proteomic Analyses. <i>Analytical Chemistry</i> , 2018, 90, 11503-11508.	6.5	62
87	Post-acquisition ETD spectral processing for increased peptide identifications. <i>Journal of the American Society for Mass Spectrometry</i> , 2009, 20, 1435-1440.	2.8	61
88	Genome Sequence and Analysis of a Stress-Tolerant, Wild-Derived Strain of <i>Saccharomyces cerevisiae</i> Used in Biofuels Research. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 1757-1766.	1.8	61
89	Learning Drug Functions from Chemical Structures with Convolutional Neural Networks and Random Forests. <i>Journal of Chemical Information and Modeling</i> , 2019, 59, 4438-4449.	5.4	61
90	The genetic basis of aneuploidy tolerance in wild yeast. <i>ELife</i> , 2020, 9, .	6.0	61

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91	Activated Ion-Electron Transfer Dissociation Enables Comprehensive Top-Down Protein Fragmentation. <i>Journal of Proteome Research</i> , 2017, 16, 2653-2659.	3.7	60
92	Analysis of the Acidic Proteome with Negative Electron-Transfer Dissociation Mass Spectrometry. <i>Analytical Chemistry</i> , 2012, 84, 2875-2882.	6.5	57
93	Amine-reactive Neutron-encoded Labels for Highly Plexed Proteomic Quantitation. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 3360-3369.	3.8	57
94	NeuCode Proteomics Reveals Bap1 Regulation of Metabolism. <i>Cell Reports</i> , 2016, 16, 583-595.	6.4	57
95	Influenza virus recruits host protein kinase C to control assembly and activity of its replication machinery. <i>ELife</i> , 2017, 6, .	6.0	57
96	Caloric Restriction Engages Hepatic RNA Processing Mechanisms in Rhesus Monkeys. <i>Cell Metabolism</i> , 2018, 27, 677-688.e5.	16.2	56
97	S-adenosylmethionine biosynthesis is a targetable metabolic vulnerability of cancer stem cells. <i>Breast Cancer Research and Treatment</i> , 2019, 175, 39-50.	2.5	55
98	Systems Analyses Reveal Physiological Roles and Genetic Regulators of Liver Lipid Species. <i>Cell Systems</i> , 2018, 6, 722-733.e6.	6.2	54
99	Assessing the Viability of Recovery of Hydroxycinnamic Acids from Lignocellulosic Biorefinery Alkaline Pretreatment Waste Streams. <i>ChemSusChem</i> , 2020, 13, 2012-2024.	6.8	54
100	Broad and thematic remodeling of the surfaceome and glycoproteome on isogenic cells transformed with driving proliferative oncogenes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 7764-7775.	7.1	54
101	Phosphorylation at the Homotypic Interface Regulates Nucleoprotein Oligomerization and Assembly of the Influenza Virus Replication Machinery. <i>PLoS Pathogens</i> , 2015, 11, e1004826.	4.7	53
102	Peptide and Protein Quantification Using iTRAQ with Electron Transfer Dissociation. <i>Journal of the American Society for Mass Spectrometry</i> , 2008, 19, 1255-1262.	2.8	52
103	The Negative Mode Proteome with Activated Ion Negative Electron Transfer Dissociation (AI-NETD). <i>Molecular and Cellular Proteomics</i> , 2015, 14, 2644-2660.	3.8	52
104	Genetic Regulation of Plasma Lipid Species and Their Association with Metabolic Phenotypes. <i>Cell Systems</i> , 2018, 6, 709-721.e6.	6.2	52
105	Metabolism of Multiple Aromatic Compounds in Corn Stover Hydrolysate by <i>Rhodospseudomonas palustris</i> . <i>Environmental Science & Technology</i> , 2015, 49, 8914-8922.	10.0	51
106	Coupling Capillary Zone Electrophoresis with Electron Transfer Dissociation and Activated Ion Electron Transfer Dissociation for Top-Down Proteomics. <i>Analytical Chemistry</i> , 2015, 87, 5422-5429.	6.5	51
107	Enhanced Dissociation of Intact Proteins with High Capacity Electron Transfer Dissociation. <i>Journal of the American Society for Mass Spectrometry</i> , 2016, 27, 520-531.	2.8	51
108	Sequencing Larger Intact Proteins (30-70 kDa) with Activated Ion Electron Transfer Dissociation. <i>Journal of the American Society for Mass Spectrometry</i> , 2018, 29, 140-149.	2.8	51

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109	Synthesis and scavenging role of furan fatty acids. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E3450-7.	7.1	49
110	Mitochondrial DNA Variant in COX1 Subunit Significantly Alters Energy Metabolism of Geographically Divergent Wild Isolates in <i>Caenorhabditis elegans</i> . Journal of Molecular Biology, 2014, 426, 2199-2216.	4.2	49
111	Development of a GC/Quadrupole-Orbitrap Mass Spectrometer, Part II: New Approaches for Discovery Metabolomics. Analytical Chemistry, 2014, 86, 10044-10051.	6.5	49
112	Defining mitochondrial protein functions through deep multiomic profiling. Nature, 2022, 606, 382-388.	27.8	49
113	A Calibration Routine for Efficient ETD in Large-Scale Proteomics. Journal of the American Society for Mass Spectrometry, 2015, 26, 1848-1857.	2.8	48
114	Quantitative shotgun proteome analysis by direct infusion. Nature Methods, 2020, 17, 1222-1228.	19.0	48
115	Comprehensive Mass Spectrometric Mapping of the Hydroxylated Amino Acid residues of the $\hat{I}\pm 1$ (V) Collagen Chain. Journal of Biological Chemistry, 2012, 287, 40598-40610.	3.4	47
116	NANOG Is Multiply Phosphorylated and Directly Modified by ERK2 and CDK1 In Vitro. Stem Cell Reports, 2014, 2, 18-25.	4.8	47
117	Advancing proteomics with ion/ion chemistry. BioTechniques, 2006, 40, 783-789.	1.8	46
118	Instant spectral assignment for advanced decision tree-driven mass spectrometry. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 8411-8416.	7.1	46
119	Aromatic inhibitors derived from ammonia-pretreated lignocellulose hinder bacterial ethanologenesis by activating regulatory circuits controlling inhibitor efflux and detoxification. Frontiers in Microbiology, 2014, 5, 402.	3.5	46
120	Inhibition of microbial biofuel production in drought-stressed switchgrass hydrolysate. Biotechnology for Biofuels, 2016, 9, 237.	6.2	46
121	Neutron-Encoded Mass Signatures for Quantitative Top-Down Proteomics. Analytical Chemistry, 2014, 86, 2314-2319.	6.5	45
122	Ptc7p Dephosphorylates Select Mitochondrial Proteins to Enhance Metabolic Function. Cell Reports, 2017, 18, 307-313.	6.4	45
123	Multi-omic Mitoprotease Profiling Defines a Role for Oct1p in Coenzyme Q Production. Molecular Cell, 2017, 68, 970-977.e11.	9.7	45
124	Pptc7 is an essential phosphatase for promoting mammalian mitochondrial metabolism and biogenesis. Nature Communications, 2019, 10, 3197.	12.8	45
125	Negative Electron Transfer Dissociation Sequencing of Increasingly Sulfated Glycosaminoglycan Oligosaccharides on an Orbitrap Mass Spectrometer. Journal of the American Society for Mass Spectrometry, 2017, 28, 1844-1854.	2.8	44
126	Phosphoproteomics with Activated Ion Electron Transfer Dissociation. Analytical Chemistry, 2017, 89, 6367-6376.	6.5	44

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127	The dental calculus metabolome in modern and historic samples. <i>Metabolomics</i> , 2017, 13, 134.	3.0	44
128	Infrared Multiphoton Dissociation of Peptide Cations in a Dual Pressure Linear Ion Trap Mass Spectrometer. <i>Analytical Chemistry</i> , 2009, 81, 8109-8118.	6.5	43
129	Multiplexed Quantification for Data-Independent Acquisition. <i>Analytical Chemistry</i> , 2015, 87, 2570-2575.	6.5	43
130	High-Resolution Filtering for Improved Small Molecule Identification via GC/MS. <i>Analytical Chemistry</i> , 2015, 87, 8328-8335.	6.5	43
131	Islet proteomics reveals genetic variation in dopamine production resulting in altered insulin secretion. <i>Journal of Biological Chemistry</i> , 2018, 293, 5860-5877.	3.4	43
132	A large-scale genome-wide lipid association map guides lipid identification. <i>Nature Metabolism</i> , 2020, 2, 1149-1162.	11.9	43
133	Neutron Encoded Labeling for Peptide Identification. <i>Analytical Chemistry</i> , 2013, 85, 5129-5137.	6.5	42
134	Valosin-containing protein (VCP) Adaptor Interactions are Exceptionally Dynamic and Subject to Differential Modulation by a VCP Inhibitor. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 2970-2986.	3.8	42
135	Decoupling Yeast Cell Division and Stress Defense Implicates mRNA Repression in Translational Reallocation during Stress. <i>Current Biology</i> , 2018, 28, 2673-2680.e4.	3.9	42
136	Proteomic Atlas of the Human Brain in Alzheimer's Disease. <i>Journal of Proteome Research</i> , 2019, 18, 1380-1391.	3.7	42
137	Implementation of Activated Ion Electron Transfer Dissociation on a Quadrupole-Orbitrap-Linear Ion Trap Hybrid Mass Spectrometer. <i>Analytical Chemistry</i> , 2017, 89, 6358-6366.	6.5	41
138	Decoding Polo-like kinase 1 signaling along the kinetochore-centromere axis. <i>Nature Chemical Biology</i> , 2016, 12, 411-418.	8.0	40
139	Intelligent Data Acquisition Blends Targeted and Discovery Methods. <i>Journal of Proteome Research</i> , 2014, 13, 2152-2161.	3.7	39
140	Real-time health monitoring through urine metabolomics. <i>Npj Digital Medicine</i> , 2019, 2, 109.	10.9	39
141	Chemical Derivatization of Peptide Carboxyl Groups for Highly Efficient Electron Transfer Dissociation. <i>Journal of the American Society for Mass Spectrometry</i> , 2013, 24, 1710-1721.	2.8	37
142	Proteomics Moves into the Fast Lane. <i>Cell Systems</i> , 2016, 2, 142-143.	6.2	37
143	An Isoprene Lipid-Binding Protein Promotes Eukaryotic Coenzyme Q Biosynthesis. <i>Molecular Cell</i> , 2019, 73, 763-774.e10.	9.7	37
144	Phosphoproteome Response to Dithiothreitol Reveals Unique Versus Shared Features of <i>Saccharomyces cerevisiae</i> Stress Responses. <i>Journal of Proteome Research</i> , 2020, 19, 3405-3417.	3.7	37

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145	Mass spectrometry proteomics reveals a function for mammalian CALCOCO1 in MTOR-regulated selective autophagy. <i>Autophagy</i> , 2020, 16, 2219-2237.	9.1	37
146	Characterization and Diagnostic Value of Amino Acid Side Chain Neutral Losses Following Electron-Transfer Dissociation. <i>Journal of the American Society for Mass Spectrometry</i> , 2011, 22, 255-264.	2.8	36
147	Erythropoietin signaling regulates heme biosynthesis. <i>ELife</i> , 2017, 6, .	6.0	36
148	OptSSeq explores enzyme expression and function landscapes to maximize isobutanol production rate. <i>Metabolic Engineering</i> , 2019, 52, 324-340.	7.0	36
149	Mapping of the contraction-induced phosphoproteome identifies TRIM28 as a significant regulator of skeletal muscle size and function. <i>Cell Reports</i> , 2021, 34, 108796.	6.4	36
150	The effect of interfering ions on search algorithm performance for electron-transfer dissociation data. <i>Proteomics</i> , 2010, 10, 164-167.	2.2	35
151	Multiplexed proteome analysis with neutron-encoded stable isotope labeling in cells and mice. <i>Nature Protocols</i> , 2018, 13, 293-306.	12.0	35
152	The Value of Activated Ion Electron Transfer Dissociation for High-Throughput Top-Down Characterization of Intact Proteins. <i>Analytical Chemistry</i> , 2018, 90, 8553-8560.	6.5	35
153	Proteomic and transcriptomic analyses of early and late-chronic <i>Toxoplasma gondii</i> infection shows novel and stage specific transcripts. <i>BMC Genomics</i> , 2019, 20, 859.	2.8	35
154	A New Probabilistic Database Search Algorithm for ETD Spectra. <i>Journal of Proteome Research</i> , 2009, 8, 3198-3205.	3.7	33
155	Top-Down Protein Fragmentation by Infrared Multiphoton Dissociation in a Dual Pressure Linear Ion Trap. <i>Analytical Chemistry</i> , 2009, 81, 8677-8686.	6.5	33
156	Dual Electrospray Ion Source for Electron-Transfer Dissociation on a Hybrid Linear Ion Trap Orbitrap Mass Spectrometer. <i>Analytical Chemistry</i> , 2007, 79, 7916-7919.	6.5	32
157	Statistical Analysis of Electron Transfer Dissociation Pairwise Fragmentation Patterns. <i>Analytical Chemistry</i> , 2011, 83, 9540-9545.	6.5	32
158	Implementing Photodissociation in an Orbitrap Mass Spectrometer. <i>Journal of the American Society for Mass Spectrometry</i> , 2011, 22, 1105-1108.	2.8	32
159	Higher-energy Collision-activated Dissociation Without a Dedicated Collision Cell. <i>Molecular and Cellular Proteomics</i> , 2011, 10, O111.009456.	3.8	31
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