List of Publications by Year in descending order

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293 papers	18,407 citations	¹⁶⁴⁵¹ 64 h-index	16650 123 g-index
321	321	321	14772
all docs	docs citations	times ranked	citing authors

#	Article	IF	CITATIONS
1	Electron Capture Dissociation of Multiply Charged Protein Cations. A Nonergodic Process. Journal of the American Chemical Society, 1998, 120, 3265-3266.	13.7	1,766
2	Electron Capture Dissociation for Structural Characterization of Multiply Charged Protein Cations. Analytical Chemistry, 2000, 72, 563-573.	6.5	903
3	Electron Capture Dissociation of Gaseous Multiply-Charged Proteins Is Favored at Disulfide Bonds and Other Sites of High Hydrogen Atom Affinity. Journal of the American Chemical Society, 1999, 121, 2857-2862.	13.7	539
4	Automated reduction and interpretation of. Journal of the American Society for Mass Spectrometry, 2000, 11, 320-332.	2.8	500
5	Orbitrap Mass Spectrometry. Analytical Chemistry, 2013, 85, 5288-5296.	6.5	454
6	Reactions of polypeptide ions with electrons in the gas phase. Mass Spectrometry Reviews, 2003, 22, 57-77.	5.4	407
7	Localization of O-Glycosylation Sites in Peptides by Electron Capture Dissociation in a Fourier Transform Mass Spectrometer. Analytical Chemistry, 1999, 71, 4431-4436.	6.5	379
8	Localization of Labile Posttranslational Modifications by Electron Capture Dissociation:Â The Case of Î ³ -Carboxyglutamic Acid. Analytical Chemistry, 1999, 71, 4250-4253.	6.5	362
9	Electron capture dissociation of singly and multiply phosphorylated peptides. Rapid Communications in Mass Spectrometry, 2000, 14, 1793-1800.	1.5	341
10	Electron-capture dissociation tandem mass spectrometry. Current Opinion in Biotechnology, 2004, 15, 12-16.	6.6	328
11	Low-mass ions observed in plasma desorption mass spectrometry of high explosives. , 2000, 35, 337-346.		280
12	Automated de novo sequencing of proteins by tandem high-resolution mass spectrometry. Proceedings of the National Academy of Sciences of the United States of America, 2000, 97, 10313-10317.	7.1	243
13	Electron detachment dissociation of peptide di-anions: an electron–hole recombination phenomenon. Chemical Physics Letters, 2001, 342, 299-302.	2.6	228
14	Towards An Understanding of the Mechanism of Electron-Capture Dissociation: A Historical Perspective and Modern Ideas. European Journal of Mass Spectrometry, 2002, 8, 337-349.	1.0	227
15	Electron capture dissociation of gaseous multiply charged ions by Fourier-transform ion cyclotron resonance. Journal of the American Society for Mass Spectrometry, 2001, 12, 245-249.	2.8	226
16	Release of Active Peptidyl Arginine Deiminases by Neutrophils Can Explain Production of Extracellular Citrullinated Autoantigens in Rheumatoid Arthritis Synovial Fluid. Arthritis and Rheumatology, 2015, 67, 3135-3145.	5.6	193
17	De Novo Peptide Sequencing and Identification with Precision Mass Spectrometry. Journal of Proteome Research, 2007, 6, 114-123.	3.7	185
18	Dissociative capture of hot $(3\hat{a} \in 13 \text{ eV})$ electrons by polypeptide polycations: an efficient process accompanied by secondary fragmentation. Chemical Physics Letters, 2002, 356, 201-206.	2.6	184

#	Article	IF	CITATIONS
19	ModifiComb, a New Proteomic Tool for Mapping Substoichiometric Post-translational Modifications, Finding Novel Types of Modifications, and Fingerprinting Complex Protein Mixtures. Molecular and Cellular Proteomics, 2006, 5, 935-948.	3.8	178
20	BIOCHEMISTRY:Biomolecule Mass Spectrometry. Science, 1999, 284, 1289-1290.	12.6	177
21	Heightened immune response to autocitrullinated <i>Porphyromonas gingivalis</i> peptidylarginine deiminase: a potential mechanism for breaching immunologic tolerance in rheumatoid arthritis. Annals of the Rheumatic Diseases, 2014, 73, 263-269.	0.9	171
22	Functional Conservation of Subfamilies of Putative UDP-N-acetylgalactosamine:Polypeptide N-Acetylgalactosaminyltransferases inDrosophila, Caenorhabditis elegans, and Mammals. Journal of Biological Chemistry, 2002, 277, 22623-22638.	3.4	168
23	Electron Capture Dissociation Proceeds with a Low Degree of Intramolecular Migration of Peptide Amide Hydrogens. Journal of the American Chemical Society, 2008, 130, 1341-1349.	13.7	167
24	The challenge of the proteome dynamic range and its implications for in-depth proteomics. Proteomics, 2013, 13, 723-726.	2.2	160
25	Small-molecule inhibitor of OGG1 suppresses proinflammatory gene expression and inflammation. Science, 2018, 362, 834-839.	12.6	156
26	Mass spectrometric analysis of asparagine deamidation and aspartate isomerization in polypeptides. Electrophoresis, 2010, 31, 1764-1772.	2.4	150
27	Proteome Integral Solubility Alteration: A High-Throughput Proteomics Assay for Target Deconvolution. Journal of Proteome Research, 2019, 18, 4027-4037.	3.7	148
28	Proteomics-Grade de Novo Sequencing Approach. Journal of Proteome Research, 2005, 4, 2348-2354.	3.7	147
29	On the Proper Use of Mass Accuracy in Proteomics. Molecular and Cellular Proteomics, 2007, 6, 377-381.	3.8	144
30	Myeloid-derived suppressor cells express the death receptor Fas and apoptose in response to T cell–expressed FasL. Blood, 2011, 117, 5381-5390.	1.4	140
31	Electron capture/transfer versus collisionally activated/induced dissociations: Solo or duet?. Journal of the American Society for Mass Spectrometry, 2008, 19, 753-761.	2.8	136
32	Improving Protein Identification Using Complementary Fragmentation Techniques in Fourier Transform Mass Spectrometry. Molecular and Cellular Proteomics, 2005, 4, 835-845.	3.8	128
33	Complete Characterization of Posttranslational Modification Sites in the Bovine Milk Protein PP3 by Tandem Mass Spectrometry with Electron Capture Dissociation as the Last Stage. Analytical Chemistry, 2003, 75, 2355-2361.	6.5	126
34	Distinguishing of Ile/Leu Amino Acid Residues in the PP3 Protein by (Hot) Electron Capture Dissociation in Fourier Transform Ion Cyclotron Resonance Mass Spectrometry. Analytical Chemistry, 2003, 75, 1267-1274.	6.5	126
35	Fragmentation of Peptides in MALDI In-Source Decay Mediated by Hydrogen Radicals. Analytical Chemistry, 2005, 77, 172-177.	6.5	125
36	Rapid and Deep Human Proteome Analysis by Single-dimension Shotgun Proteomics. Molecular and Cellular Proteomics, 2013, 12, 3330-3338.	3.8	123

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37	Hydrogen rearrangement to and from radical z fragments in electron capture dissociation of peptides. Journal of the American Society for Mass Spectrometry, 2007, 18, 113-120.	2.8	120
38	The SysteMHC Atlas project. Nucleic Acids Research, 2018, 46, D1237-D1247.	14.5	119
39	Accuracy Requirements for Peptide Characterization by Monoisotopic Molecular Mass Measurements. Analytical Chemistry, 1996, 68, 4060-4063.	6.5	117
40	Optimizing heterologous protein production in the periplasm of E. coli by regulating gene expression levels. Microbial Cell Factories, 2013, 12, 24.	4.0	114
41	Repurposing of auranofin: Thioredoxin reductase remains a primary target of the drug. Biochimie, 2019, 162, 46-54.	2.6	113
42	Improved low-energy electron injection systems for high rate electron capture dissociation in Fourier transform ion cyclotron resonance mass spectrometry. Rapid Communications in Mass Spectrometry, 2001, 15, 1849-1854.	1.5	112
43	C??C Backbone Fragmentation Dominates in Electron Detachment Dissociation of Gas-Phase Polypeptide Polyanions. Chemistry - A European Journal, 2005, 11, 1803-1812.	3.3	112
44	Shared immunological targets in the lungs and joints of patients with rheumatoid arthritis: identification and validation. Annals of the Rheumatic Diseases, 2015, 74, 1772-1777.	0.9	112
45	Validation and development of MTH1 inhibitors for treatment of cancer. Annals of Oncology, 2016, 27, 2275-2283.	1.2	111
46	Molecular profiling of prostate cancer derived exosomes may reveal a predictive signature for response to docetaxel. Oncotarget, 2015, 6, 21740-21754.	1.8	109
47	Advantages of External Accumulation for Electron Capture Dissociation in Fourier Transform Mass Spectrometry. Analytical Chemistry, 2001, 73, 2998-3005.	6.5	106
48	Facile Disulfide Bond Cleavage in Gaseous Peptide and Protein Cations by Ultraviolet Photodissociation at 157 nm. Angewandte Chemie - International Edition, 2005, 44, 6399-6403.	13.8	99
49	Prodynorphin Mutations Cause the Neurodegenerative Disorder Spinocerebellar Ataxia Type 23. American Journal of Human Genetics, 2010, 87, 593-603.	6.2	99
50	The RBCC GeneRFP2(Leu5) Encodes a Novel Transmembrane E3 Ubiquitin Ligase Involved in ERAD. Molecular Biology of the Cell, 2007, 18, 1670-1682.	2.1	97
51	Electron capture dissociation distinguishes a single D-amino acid in a protein and probes the tertiary structure. Journal of the American Society for Mass Spectrometry, 2004, 15, 1087-1098.	2.8	93
52	Extent of Modifications in Human Proteome Samples and Their Effect on Dynamic Range of Analysis in Shotgun Proteomics. Molecular and Cellular Proteomics, 2006, 5, 2384-2391.	3.8	93
53	New Data Base-independent, Sequence Tag-based Scoring of Peptide MS/MS Data Validates Mowse Scores, Recovers Below Threshold Data, Singles Out Modified Peptides, and Assesses the Quality of MS/MS Techniques. Molecular and Cellular Proteomics, 2005, 4, 1180-1188.	3.8	88
54	Electron capture dissociation of multiply charged peptide cations. International Journal of Mass Spectrometry, 1999, 185-187, 787-793.	1.5	85

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55	Proteomic analysis of urinary biomarker candidates for nonmuscle invasive bladder cancer. Proteomics, 2012, 12, 135-144.	2.2	83
56	Electron Ionization Dissociation of Singly and Multiply Charged Peptides. Journal of the American Chemical Society, 2009, 131, 9977-9985.	13.7	81
57	In Silico Instrumental Response Correction Improves Precision of Label-free Proteomics and Accuracy of Proteomics-based Predictive Models. Molecular and Cellular Proteomics, 2013, 12, 2324-2331.	3.8	81
58	Applications of Electronâ^'lon Dissociation Reactions for Analysis of Polycationic Chitooligosaccharides in Fourier Transform Mass Spectrometry. Analytical Chemistry, 2003, 75, 5994-6001.	6.5	80
59	Electron capture dissociation of polypeptides in a three-dimensional quadrupole ion trap: Implementation and first results. Journal of the American Society for Mass Spectrometry, 2005, 16, 22-27.	2.8	79
60	Complementary Sequence Preferences of Electron-Capture Dissociation and Vibrational Excitation in Fragmentation of Polypeptide Polycations. Angewandte Chemie - International Edition, 2006, 45, 5301-5303.	13.8	79
61	Electron capture versus energetic dissociation of protein ions. International Journal of Mass Spectrometry, 1999, 182-183, 1-5.	1.5	75
62	Liquid Chromatography at Critical Conditions:Â Comprehensive Approach to Sequence-Dependent Retention Time Prediction. Analytical Chemistry, 2006, 78, 7770-7777.	6.5	73
63	Urinary Prognostic Biomarkers and Classification of IgA Nephropathy by High Resolution Mass Spectrometry Coupled with Liquid Chromatography. PLoS ONE, 2013, 8, e80830.	2.5	73
64	Functional and Structural Characterization of a Novel HLA-DRB1*04:01-Restricted α-Enolase T Cell Epitope in Rheumatoid Arthritis. Frontiers in Immunology, 2016, 7, 494.	4.8	73
65	Distinguishing and Quantifying Peptides and Proteins Containingd-Amino Acids by Tandem Mass Spectrometry. Analytical Chemistry, 2005, 77, 4571-4580.	6.5	70
66	De novo sequencing of antimicrobial peptides isolated from the venom glands of the wolf spiderLycosa singoriensis. Journal of Mass Spectrometry, 2004, 39, 193-201.	1.6	68
67	Side-Chain Losses in Electron Capture Dissociation To Improve Peptide Identification. Analytical Chemistry, 2007, 79, 2296-2302.	6.5	68
68	Blood Plasma IgG Fc Glycans are Significantly Altered in Alzheimer's Disease and Progressive Mild Cognitive Impairment. Journal of Alzheimer's Disease, 2013, 38, 567-579.	2.6	66
69	Tetrathiafulvaleno-Annelated Porphyrins. Angewandte Chemie - International Edition, 2001, 40, 2497-2500.	13.8	64
70	Electron capture dissociation of weakly bound polypeptide polycationic complexes. Rapid Communications in Mass Spectrometry, 2002, 16, 2260-2265.	1.5	64
71	Cerebrospinal fluid protein patterns in neurodegenerative disease revealed by liquid chromatographyâ€Fourier transform ion cyclotron resonance mass spectrometry. Proteomics, 2004, 4, 4010-4018.	2.2	64
72	Covariation of Peptide Abundances Accurately Reflects Protein Concentration Differences. Molecular and Cellular Proteomics, 2017, 16, 936-948.	3.8	64

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73	Structural Basis of Crossâ€Reactivity of Anti–Citrullinated Protein Antibodies. Arthritis and Rheumatology, 2019, 71, 210-221.	5.6	64
74	DeMix-Q: Quantification-Centered Data Processing Workflow. Molecular and Cellular Proteomics, 2016, 15, 1467-1478.	3.8	63
75	Proteomic Pathway Analysis Reveals Inflammation Increases Myeloid-Derived Suppressor Cell Resistance to Apoptosis. Molecular and Cellular Proteomics, 2011, 10, M110.002980.	3.8	60
76	Prediction of NCα bond cleavage frequencies in electron capture dissociation of Trp-cage dications by force-field molecular dynamics simulations. International Journal of Mass Spectrometry, 2006, 248, 124-135.	1.5	59
77	MS analysis of rheumatoid arthritic synovial tissue identifies specific citrullination sites on fibrinogen. Proteomics - Clinical Applications, 2010, 4, 511-518.	1.6	59
78	High levels of the adhesion molecule CD44 on leukemic cells generate acute myeloid leukemia relapse after withdrawal of the initial transforming event. Leukemia, 2011, 25, 515-526.	7.2	59
79	Intramolecular hydrogen atom transfer in hydrogen-deficient polypeptide radical cations. Chemical Physics Letters, 2000, 330, 558-562.	2.6	58
80	Comprehensive chemical proteomics for target deconvolution of the redox active drug auranofin. Redox Biology, 2020, 32, 101491.	9.0	58
81	Can the (M• — X) Region in Electron Capture Dissociation Provide Reliable Information on Amino Acid Composition of Polypeptides?. European Journal of Mass Spectrometry, 2002, 8, 461-469.	1.0	55
82	Bifurcating Fragmentation Behavior of Gas-Phase Tryptic Peptide Dications in Collisional Activation. Journal of the American Society for Mass Spectrometry, 2008, 19, 1755-1763.	2.8	55
83	Zwitterionic States in Gas-Phase Polypeptide Ions Revealed by 157-nm Ultra-Violet Photodissociation. Chemistry - A European Journal, 2006, 12, 7920-7928.	3.3	54
84	Structural basis of SUFU–GLI interaction in human Hedgehog signalling regulation. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 2563-2579.	2.5	54
85	Cationic gold nanoparticles elicit mitochondrial dysfunction: a multi-omics study. Scientific Reports, 2019, 9, 4366.	3.3	54
86	Approaches and Limits for Accurate Mass Characterization of Large Biomolecules. Analytical Chemistry, 1995, 67, 3793-3798.	6.5	53
87	MH2+â‹ ion production from protonated polypeptides by electron impact: observation and determination of ionization energies and a cross-section. Chemical Physics Letters, 2000, 316, 19-23.	2.6	53
88	Immunoaffinity Enrichments Followed by Mass Spectrometric Detection for Studying Global Protein Tyrosine Phosphorylation. Journal of Proteome Research, 2008, 7, 2897-2910.	3.7	52
89	DeMix Workflow for Efficient Identification of Cofragmented Peptides in High Resolution Data-dependent Tandem Mass Spectrometry. Molecular and Cellular Proteomics, 2014, 13, 3211-3223.	3.8	52
90	Binding of Pro-Gly-Pro at the active site of leukotriene A ₄ hydrolase/aminopeptidase and development of an epoxide hydrolase selective inhibitor. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 4227-4232.	7.1	50

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91	Cell line profiling to improve monoclonal antibody production. Biotechnology and Bioengineering, 2014, 111, 748-760.	3.3	50
92	<i>De novo</i> sequencing of peptides secreted by the skin glands of the Caucasian Green Frog <i>Rana ridibunda</i> . Rapid Communications in Mass Spectrometry, 2008, 22, 3517-3525.	1.5	48
93	Sequence Scrambling in Shotgun Proteomics is Negligible. Journal of the American Society for Mass Spectrometry, 2011, 22, 1121-1124.	2.8	48
94	Autoreactivity to malondialdehyde-modifications in rheumatoid arthritis is linked to disease activity and synovial pathogenesis. Journal of Autoimmunity, 2017, 84, 29-45.	6.5	48
95	ProTargetMiner as a proteome signature library of anticancer molecules for functional discovery. Nature Communications, 2019, 10, 5715.	12.8	47
96	A Direct Comparison of Protein Structure in the Gas and Solution Phase:  The Trp-cage. Journal of Physical Chemistry B, 2007, 111, 13147-13150.	2.6	46
97	Approach for Identifying Human Leukocyte Antigen (HLA)-DR Bound Peptides from Scarce Clinical Samples. Molecular and Cellular Proteomics, 2016, 15, 3017-3029.	3.8	46
98	Prognostic Polypeptide Blood Plasma Biomarkers of Alzheimer's Disease Progression. Journal of Alzheimer's Disease, 2014, 40, 659-666.	2.6	44
99	Functional Identification of Target by Expression Proteomics (FITExP) reveals protein targets and highlights mechanisms of action of small molecule drugs. Scientific Reports, 2015, 5, 11176.	3.3	44
100	System-wide identification and prioritization of enzyme substrates by thermal analysis. Nature Communications, 2021, 12, 1296.	12.8	44
101	lonization energies of multiply protonated polypeptides obtained by tandem ionization in Fourier transform mass spectrometers. Journal of Mass Spectrometry, 2002, 37, 1141-1144.	1.6	43
102	Can relative cleavage frequencies in peptides provide additional sequence information?. International Journal of Mass Spectrometry, 2002, 219, 283-294.	1.5	42
103	Analytical Utility of Small Neutral Losses from Reduced Species in Electron Capture Dissociation Studied Using SwedECD Database. Analytical Chemistry, 2008, 80, 8089-8094.	6.5	42
104	Conformational Selection in Biocatalytic Plastic Degradation by PETase. ACS Catalysis, 2022, 12, 3397-3409.	11.2	42
105	Secondary Losses via γ-Lactam Formation in Hot Electron Capture Dissociation:  A Missing Link to Complete de Novo Sequencing of Proteins?. Journal of the American Chemical Society, 2003, 125, 6628-6629.	13.7	41
106	Dissociation of peptide ions by fast atom bombardment in a quadrupole ion trap. Rapid Communications in Mass Spectrometry, 2005, 19, 2163-2171.	1.5	41
107	Variable domain Nâ€linked glycosylation and negative surface charge are key features of monoclonal ACPA: Implications for Bâ€cell selection. European Journal of Immunology, 2018, 48, 1030-1045.	2.9	41
108	Optimizing Recombinant Protein Production in the Escherichia coli Periplasm Alleviates Stress. Applied and Environmental Microbiology, 2018, 84, .	3.1	41

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109	C57BL/6 mice need MHC class II Aq to develop collagen-induced arthritis dependent on autoreactive T cells. Annals of the Rheumatic Diseases, 2013, 72, 1225-1232.	0.9	40
110	PhosTShunter:Â A Fast and Reliable Tool to Detect Phosphorylated Peptides in Liquid Chromatography Fourier Transform Tandem Mass Spectrometry Data Sets. Journal of Proteome Research, 2006, 5, 659-668.	3.7	39
111	Toward Proteome-Scale Identification and Quantification of Isoaspartyl Residues in Biological Samples. Journal of Proteome Research, 2009, 8, 4615-4621.	3.7	39
112	The Effects of 5-Fluorouracil on the Proteome of Colon Cancer Cells. Journal of Proteome Research, 2013, 12, 1969-1979.	3.7	39
113	Two-dimensional mass spectrometry of biomolecules at the subfemtomole level. Current Opinion in Chemical Biology, 1998, 2, 571-578.	6.1	38
114	Chemosensory proteins, major salivary factors in caterpillar mandibular glands. Insect Biochemistry and Molecular Biology, 2012, 42, 796-805.	2.7	38
115	Protein primary structure using orthogonal fragmentation techniques in Fourier transform mass spectrometry. Expert Review of Proteomics, 2006, 3, 251-261.	3.0	37
116	Lysine-specific demethylase 1A restricts ex vivo propagation of human HSCs and is a target of UM171. Blood, 2020, 136, 2151-2161.	1.4	37
117	Letter: The Diagnostic Value of Amino Acid Side-Chain Losses in Electron Capture Dissociation of Polypeptides. Comment on: "Can the (M.â^X) Region in Electron Capture Dissociation Provide Reliable Information on Amino Acid Composition of Polypeptides?â€9 Eur. J. Mass Spectrom. 8, 461–469 (2002). European Journal of Mass Spectrometry. 2003. 9. 221-222.	1.0	36
118	Calibration function for the orbitrap FTMS accounting for the space charge effect. Journal of the American Society for Mass Spectrometry, 2010, 21, 1846-1851.	2.8	36
119	Impact of Temperature Dependent Sampling Procedures in Proteomics and Peptidomics – A Characterization of the Liver and Pancreas Post Mortem Degradome. Molecular and Cellular Proteomics, 2011, 10, M900229-MCP200.	3.8	35
120	IgG Fc galactosylation predicts response to methotrexate in early rheumatoid arthritis. Arthritis Research and Therapy, 2017, 19, 182.	3.5	35
121	Determination of the location of positive charges in gas-phase polypeptide polycations by tandem mass spectrometry. International Journal of Mass Spectrometry, 2006, 252, 204-212.	1.5	34
122	Cytotoxic and Proinflammatory Effects of Metal-Based Nanoparticles on THP-1 Monocytes Characterized by Combined Proteomics Approaches. Journal of Proteome Research, 2017, 16, 689-697.	3.7	34
123	IgM antibodies against phosphorylcholine promote polarization of T regulatory cells from patients with atherosclerotic plaques, systemic lupus erythematosus and healthy donors. Atherosclerosis, 2018, 268, 36-48.	0.8	34
124	Anticancer Effect of Deuterium Depleted Water - Redox Disbalance Leads to Oxidative Stress. Molecular and Cellular Proteomics, 2019, 18, 2373-2387.	3.8	34
125	Probing Combinatorial Library Diversity by Mass Spectrometry. Analytical Chemistry, 1997, 69, 2893-2900.	6.5	33
126	Tandem MALDI/EI ionization for tandem Fourier transform ion cyclotron resonance mass spectrometry of polypeptides. International Journal of Mass Spectrometry, 2003, 226, 181-187.	1.5	33

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127	On studying protein phosphorylation patterns using bottom-up LC–MS/MS: the case of human α-casein. Analyst, The, 2007, 132, 768-776.	3.5	33
128	Identification of dominant signaling pathways from proteomics expression data. Journal of Proteomics, 2008, 71, 89-96.	2.4	33
129	The Exosome Associates Cotranscriptionally with the Nascent Pre-mRNP through Interactions with Heterogeneous Nuclear Ribonucleoproteins. Molecular Biology of the Cell, 2009, 20, 3459-3470.	2.1	33
130	Proteomic Analysis of Mouse Brain Subjected to Spaceflight. International Journal of Molecular Sciences, 2019, 20, 7.	4.1	33
131	Development of autoantibodies against muscle-specific FHL1 in severe inflammatory myopathies. Journal of Clinical Investigation, 2015, 125, 4612-4624.	8.2	33
132	Comparison of electron capture dissociation and collisionally activated dissociation of polycations of peptide nucleic acids. Rapid Communications in Mass Spectrometry, 2001, 15, 969-974.	1.5	32
133	Apoptotic, Regenerative, And Immune-Related Signaling in Human Islets from Type 2 Diabetes Individuals. Journal of Proteome Research, 2009, 8, 5650-5656.	3.7	32
134	Probing solution- and gas-phase structures of Trp-cage cations by chiral substitution and spectroscopic techniques. International Journal of Mass Spectrometry, 2006, 253, 263-273.	1.5	31
135	Roomâ€Temperature Infrared Spectroscopy Combined with Mass Spectrometry Distinguishes Gasâ€Phase Protein Isomers. Angewandte Chemie - International Edition, 2009, 48, 8340-8342.	13.8	31
136	IgG Antibodies to Cyclic Citrullinated Peptides Exhibit Profiles Specific in Terms of IgG Subclasses, Fc-Glycans and a Fab-Peptide Sequence. PLoS ONE, 2014, 9, e113924.	2.5	31
137	Tetrathiafulvalene–phenanthroline macrocycles as redox responsive sensors for metal ions. Chemical Communications, 2000, , 215-216.	4.1	30
138	Predictive urinary biomarkers for steroid-resistant and steroid-sensitive focal segmental glomerulosclerosis using high resolution mass spectrometry and multivariate statistical analysis. BMC Nephrology, 2014, 15, 141.	1.8	30
139	Bacterial citrullinated epitopes generated by <i>Porphyromonas gingivalis</i> infection—a missing link for ACPA production. Annals of the Rheumatic Diseases, 2020, 79, 1194-1202.	0.9	30
140	DAF-16/FOXO requires Protein Phosphatase 4 to initiate transcription of stress resistance and longevity promoting genes. Nature Communications, 2020, 11, 138.	12.8	30
141	SwedCAD, a Database of Annotated High-Mass Accuracy MS/MS Spectra of Tryptic Peptides. Journal of Proteome Research, 2007, 6, 4063-4067.	3.7	28
142	Alzheimer's Disease and Mild Cognitive Impairment are Associated with Elevated Levels of Isoaspartyl Residues in Blood Plasma Proteins. Journal of Alzheimer's Disease, 2011, 27, 113-118.	2.6	28
143	Isotopic Resonance Hypothesis: Experimental Verification by Escherichia coli Growth Measurements. Scientific Reports, 2015, 5, 9215.	3.3	28
144	SpotLight Proteomics: uncovering the hidden blood proteome improves diagnostic power of proteomics. Scientific Reports, 2017, 7, 41929.	3.3	27

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145	Isotope depletion of large biomolecules: Implications for molecular mass measurements. Journal of the American Society for Mass Spectrometry, 1998, 9, 149-156.	2.8	26
146	Two Dimensional Mass Mapping as a General Method of Data Representation in Comprehensive Analysis of Complex Molecular Mixtures. Analytical Chemistry, 2009, 81, 3738-3745.	6.5	26
147	The PredictAD project: development of novel biomarkers and analysis software for early diagnosis of the Alzheimer's disease. Interface Focus, 2013, 3, 20120072.	3.0	26
148	Electron capture dissociation ofb2+ peptide fragments reveals the presence of the acylium ion structure. Rapid Communications in Mass Spectrometry, 2000, 14, 2242-2246.	1.5	25
149	Synthesis of linear oligo-TTFs and their [2]rotaxanes with cyclobis(paraquat-p-phenylene). Journal of Materials Chemistry, 2000, 10, 2249-2258.	6.7	25
150	Backbone Carbonyl Group Basicities Are Related to Gas-Phase Fragmentation of Peptides and Protein Folding. Angewandte Chemie - International Edition, 2007, 46, 1481-1484.	13.8	25
151	Comparative Proteomics of Dying and Surviving Cancer Cells Improves the Identification of Drug Targets and Sheds Light on Cell Life/Death Decisions. Molecular and Cellular Proteomics, 2018, 17, 1144-1155.	3.8	25
152	Combination of nozzle-skimmer fragmentation and partial acid hydrolysis in electrospray ionization time-of-flight mass spectrometry of synthetic peptides. Rapid Communications in Mass Spectrometry, 1998, 12, 705-711.	1.5	24
153	Electron capture dissociation of polypeptides using a 3 Tesla Fourier transform ion cyclotron resonance mass spectrometer. Rapid Communications in Mass Spectrometry, 2002, 16, 936-943.	1.5	24
154	Urinary Prognostic Biomarkers in Patients With Focal Segmental Glomerulosclerosis. Nephro-Urology Monthly, 2014, 6, e16806.	0.1	24
155	Fragmentation of Positively-Charged Biological lons Activated with a Beam of High-Energy Cations. Analytical Chemistry, 2014, 86, 372-379.	6.5	24
156	Multiparametric Profiling of Engineered Nanomaterials: Unmasking the Surface Coating Effect. Advanced Science, 2020, 7, 2002221.	11.2	24
157	High-performance liquid chromatography–mass spectrometry and electron-capture dissociation tandem mass spectrometry of osteocalcin. Journal of Chromatography A, 2002, 962, 95-103.	3.7	23
158	Relative Specificities of Water and Ammonia Losses from Backbone Fragments in Collision-Activated Dissociation. Journal of Proteome Research, 2007, 6, 2669-2673.	3.7	23
159	Effects of Low-Level Deuterium Enrichment on Bacterial Growth. PLoS ONE, 2014, 9, e102071.	2.5	23
160	The Novel Diagnostic Biomarkers for Focal Segmental Clomerulosclerosis. International Journal of Nephrology, 2014, 2014, 1-10.	1.3	23
161	Benefits of 2.94?i¿½m infrared matrix-assisted laser desorption/ionization for analysis of labile molecules by Fourier transform mass spectrometry. , 2000, 14, 578-584.		22
162	Systems biology to battle vascular disease. Nephrology Dialysis Transplantation, 2010, 25, 1019-1022.	0.7	22

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163	The deubiquitinase inhibitor b-AP15 induces strong proteotoxic stress and mitochondrial damage. Biochemical Pharmacology, 2018, 156, 291-301.	4.4	22
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