

Helen J Cooper

List of Publications by Year in descending order

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137
papers

5,755
citations

71102

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91884

69
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139
all docs

139
docs citations

139
times ranked

5150
citing authors

#	ARTICLE	IF	CITATIONS
1	Native Ambient Mass Spectrometry Imaging of Ligand-Bound and Metal-Bound Proteins in Rat Brain. <i>Journal of the American Chemical Society</i> , 2022, 144, 2120-2128.	13.7	26
2	Native Ambient Mass Spectrometry Enables Analysis of Intact Endogenous Protein Assemblies up to 145 kDa Directly from Tissue. <i>Analytical Chemistry</i> , 2022, 94, 5608-5614.	6.5	20
3	Discovery, validation, and diagnostic ability of multiple protein-based biomarkers in saliva and gingival crevicular fluid to distinguish between health and periodontal diseases. <i>Journal of Clinical Periodontology</i> , 2022, 49, 622-632.	4.9	21
4	Native ambient mass spectrometry of intact protein assemblies directly from <i>Escherichia coli</i> colonies. <i>Chemical Communications</i> , 2022, 58, 6857-6860.	4.1	4
5	Native Ambient Mass Spectrometry of an Intact Membrane Protein Assembly and Soluble Protein Assemblies Directly from Lens Tissue. <i>Angewandte Chemie - International Edition</i> , 2022, 61, .	13.8	7
6	Quantitative Characterization of Three Carbonic Anhydrase Inhibitors by LESA Mass Spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2022, 33, 1168-1175.	2.8	2
7	Mass Spectrometry Detection and Imaging of a Non-covalent Protein-Drug Complex in Tissue from Orally Dosed Rats. <i>Angewandte Chemie</i> , 2022, 134, .	2.0	1
8	Mass Spectrometry Detection and Imaging of a Non-covalent Protein-Drug Complex in Tissue from Orally Dosed Rats. <i>Angewandte Chemie - International Edition</i> , 2022, 61, .	13.8	7
9	Native Mass Spectrometry Imaging of Proteins and Protein Complexes by Nano-DESI. <i>Analytical Chemistry</i> , 2021, 93, 4619-4627.	6.5	63
10	Liquid Extraction Surface Analysis Mass Spectrometry of ESKAPE Pathogens. <i>Journal of the American Society for Mass Spectrometry</i> , 2021, 32, 1345-1351.	2.8	8
11	Simultaneous spatial, conformational, and mass analysis of intact proteins and protein assemblies by nano-DESI travelling wave ion mobility mass spectrometry imaging. <i>International Journal of Mass Spectrometry</i> , 2021, 468, 116656.	1.5	13
12	Structural proteomics and protein complexes – special issue. <i>Proteomics</i> , 2021, 21, e2000286.	2.2	0
13	In situ analysis of intact proteins by ion mobility mass spectrometry. <i>TrAC - Trends in Analytical Chemistry</i> , 2020, 124, 115534.	11.4	9
14	Electroporation and Mass Spectrometry: A New Paradigm for In Situ Analysis of Intact Proteins Direct from Living Yeast Colonies. <i>Analytical Chemistry</i> , 2020, 92, 2605-2611.	6.5	8
15	Structural Analysis of 14-3-3- η -Derived Phosphopeptides Using Electron Capture Dissociation Mass Spectrometry, Traveling Wave Ion Mobility Spectrometry, and Molecular Modeling. <i>Journal of Physical Chemistry B</i> , 2020, 124, 461-469.	2.6	5
16	Direct identification of bacterial and human proteins from infected wounds in living 3D skin models. <i>Scientific Reports</i> , 2020, 10, 11900.	3.3	15
17	Native Mass Spectrometry Imaging and <i>In Situ</i> Top-Down Identification of Intact Proteins Directly from Tissue. <i>Journal of the American Society for Mass Spectrometry</i> , 2020, 31, 2531-2537.	2.8	25
18	Self-Incompatibility Triggers Irreversible Oxidative Modification of Proteins in Incompatible Pollen. <i>Plant Physiology</i> , 2020, 183, 1391-1404.	4.8	13

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19	Differential responses to kinase inhibition in FGFR2-addicted triple negative breast cancer cells: a quantitative phosphoproteomics study. <i>Scientific Reports</i> , 2020, 10, 7950.	3.3	10
20	Native LESA TWIMS-MSI: Spatial, Conformational, and Mass Analysis of Proteins and Protein Complexes. <i>Journal of the American Society for Mass Spectrometry</i> , 2020, 31, 873-879.	2.8	28
21	Comprehensive LESA Mass Spectrometry Imaging of Intact Proteins by Integration of Cylindrical FAIMS. <i>Analytical Chemistry</i> , 2020, 92, 2885-2890.	6.5	37
22	High-Field Asymmetric Waveform Ion Mobility Spectrometry and Native Mass Spectrometry: Analysis of Intact Protein Assemblies and Protein Complexes. <i>Analytical Chemistry</i> , 2020, 92, 6811-6816.	6.5	37
23	LESA Cyclic Ion Mobility Mass Spectrometry of Intact Proteins from Thin Tissue Sections. <i>Analytical Chemistry</i> , 2020, 92, 6321-6326.	6.5	23
24	Liquid Extraction Surface Analysis (LESA) High-Field Asymmetric Waveform Ion Mobility Spectrometry (FAIMS) Mass Spectrometry for In Situ Analysis of Intact Proteins. <i>Methods in Molecular Biology</i> , 2020, 2084, 191-201.	0.9	3
25	In situ mass spectrometry analysis of intact proteins and protein complexes from biological substrates. <i>Biochemical Society Transactions</i> , 2020, 48, 317-326.	3.4	14
26	Investigation of the 12-Month Stability of Dried Blood and Urine Spots Applying Untargeted UHPLC-MS Metabolomic Assays. <i>Analytical Chemistry</i> , 2019, 91, 14306-14313.	6.5	43
27	Quantitative Imaging of Proteins in Tissue by Stable Isotope Labeled Mimetic Liquid Extraction Surface Analysis Mass Spectrometry. <i>Analytical Chemistry</i> , 2019, 91, 14198-14202.	6.5	21
28	Probing the Fundamentals of Native Liquid Extraction Surface Analysis Mass Spectrometry of Proteins: Can Proteins Refold during Extraction?. <i>Analytical Chemistry</i> , 2019, 91, 12246-12254.	6.5	8
29	Direct Mass Spectrometry Analysis of Protein Complexes and Intact Proteins up to >70 kDa from Tissue. <i>Analytical Chemistry</i> , 2019, 91, 6962-6966.	6.5	29
30	Application of High-Field Asymmetric Waveform Ion Mobility Separation to LESA Mass Spectrometry of Bacteria. <i>Analytical Chemistry</i> , 2019, 91, 4755-4761.	6.5	12
31	Workflow for fast lipid tissue screening using LESA-FT-ICR-MS. <i>Analytical Methods</i> , 2019, 11, 2385-2395.	2.7	7
32	Native mass spectrometry imaging of intact proteins and protein complexes in thin tissue sections. <i>International Journal of Mass Spectrometry</i> , 2019, 437, 23-29.	1.5	50
33	Ambient ionisation mass spectrometry for in situ analysis of intact proteins. <i>Journal of Mass Spectrometry</i> , 2018, 53, 565-578.	1.6	15
34	Ambient surface mass spectrometry-ion mobility spectrometry of intact proteins. <i>Current Opinion in Chemical Biology</i> , 2018, 42, 67-75.	6.1	12
35	High Field Asymmetric Waveform Ion Mobility Spectrometry in Nontargeted Bottom-up Proteomics of Dried Blood Spots. <i>Journal of Proteome Research</i> , 2018, 17, 1997-2004.	3.7	25
36	LESA MS Imaging of Heat-Preserved and Frozen Tissue: Benefits of Multistep Static FAIMS. <i>Analytical Chemistry</i> , 2018, 90, 13306-13314.	6.5	22

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37	Liquid Extraction Surface Analysis (LESA) Electron-Induced Dissociation and Collision-Induced Dissociation Mass Spectrometry of Small Molecule Drug Compounds. <i>Journal of the American Society for Mass Spectrometry</i> , 2018, 29, 2218-2226.	2.8	12
38	Brain Targeting Delivery Facilitated by Ligand-Functionalized Layered Double Hydroxide Nanoparticles. <i>ACS Applied Materials & Interfaces</i> , 2018, 10, 20326-20333.	8.0	45
39	Identification of Phosphorylation Sites Altering Pollen Soluble Inorganic Pyrophosphatase Activity. <i>Plant Physiology</i> , 2017, 173, 1606-1616.	4.8	10
40	Raster-Mode Continuous-Flow Liquid Microjunction Mass Spectrometry Imaging of Proteins in Thin Tissue Sections. <i>Analytical Chemistry</i> , 2017, 89, 5683-5687.	6.5	33
41	Subcritical Water Hydrolysis of Peptides: Amino Acid Side-Chain Modifications. <i>Journal of the American Society for Mass Spectrometry</i> , 2017, 28, 1775-1786.	2.8	14
42	MnAl Layered Double Hydroxide Nanoparticles as a Dual-Functional Platform for Magnetic Resonance Imaging and siRNA Delivery. <i>Chemistry - A European Journal</i> , 2017, 23, 14299-14306.	3.3	55
43	Top-Down LESA Mass Spectrometry Protein Analysis of Gram-Positive and Gram-Negative Bacteria. <i>Journal of the American Society for Mass Spectrometry</i> , 2017, 28, 2066-2077.	2.8	32
44	Liquid extraction surface analysis for native mass spectrometry: Protein complexes and ligand binding. <i>International Journal of Mass Spectrometry</i> , 2017, 420, 43-50.	1.5	33
45	Separation of <i>cis</i> and <i>trans</i> Isomers of Polyproline by FAIMS Mass Spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2016, 27, 2071-2074.	2.8	9
46	Direct Tissue Profiling of Protein Complexes: Toward Native Mass Spectrometry Imaging. <i>Analytical Chemistry</i> , 2016, 88, 606-609.	6.5	30
47	LESA FAIMS Mass Spectrometry for the Spatial Profiling of Proteins from Tissue. <i>Analytical Chemistry</i> , 2016, 88, 6758-6766.	6.5	66
48	Subcritical Water Processing of Proteins: An Alternative to Enzymatic Digestion?. <i>Analytical Chemistry</i> , 2016, 88, 6425-6432.	6.5	57
49	MALDI Imaging of Liquid Extraction Surface Analysis Sampled Tissue. <i>Analytical Chemistry</i> , 2016, 88, 8433-8440.	6.5	25
50	To What Extent is FAIMS Beneficial in the Analysis of Proteins?. <i>Journal of the American Society for Mass Spectrometry</i> , 2016, 27, 566-577.	2.8	54
51	Online LC-FAIMS-MS/MS for the Analysis of Phosphorylation in Proteins. <i>Methods in Molecular Biology</i> , 2016, 1355, 241-250.	0.9	8
52	Electron capture dissociation mass spectrometry of phosphopeptides: Arginine and phosphoserine. <i>International Journal of Mass Spectrometry</i> , 2015, 390, 63-70.	1.5	6
53	Liquid Extraction Surface Analysis Mass Spectrometry Coupled with Field Asymmetric Waveform Ion Mobility Spectrometry for Analysis of Intact Proteins from Biological Substrates. <i>Analytical Chemistry</i> , 2015, 87, 6794-6800.	6.5	75
54	Liquid extraction surface analysis field asymmetric waveform ion mobility spectrometry mass spectrometry for the analysis of dried blood spots. <i>Analyst</i> , 2015, 140, 6879-6885.	3.5	53

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55	Probing the Electron Capture Dissociation Mass Spectrometry of Phosphopeptides with Traveling Wave Ion Mobility Spectrometry and Molecular Dynamics Simulations. <i>Journal of the American Society for Mass Spectrometry</i> , 2015, 26, 1004-1013.	2.8	14
56	FAIMS and Phosphoproteomics of Fibroblast Growth Factor Signaling: Enhanced Identification of Multiply Phosphorylated Peptides. <i>Journal of Proteome Research</i> , 2015, 14, 5077-5087.	3.7	23
57	Comprehensive mapping of O-glycosylation in flagellin from <i>Campylobacter jejuni</i> 11168: A multienzyme differential ion mobility mass spectrometry approach. <i>Proteomics</i> , 2015, 15, 2733-2745.	2.2	33
58	Native Liquid Extraction Surface Analysis Mass Spectrometry: Analysis of Noncovalent Protein Complexes Directly from Dried Substrates. <i>Journal of the American Society for Mass Spectrometry</i> , 2015, 26, 1320-1327.	2.8	43
59	Robust twin boosting for feature selection from high-dimensional omics data with label noise. <i>Information Sciences</i> , 2015, 291, 1-18.	6.9	32
60	Challenges and opportunities in mass spectrometric analysis of proteins from dried blood spots. <i>Expert Review of Proteomics</i> , 2014, 11, 685-695.	3.0	23
61	Top-Down and Bottom-Up Identification of Proteins by Liquid Extraction Surface Analysis Mass Spectrometry of Healthy and Diseased Human Liver Tissue. <i>Journal of the American Society for Mass Spectrometry</i> , 2014, 25, 1953-1961.	2.8	78
62	De Novo Design of Ln(III) Coiled Coils for Imaging Applications. <i>Journal of the American Chemical Society</i> , 2014, 136, 1166-1169.	13.7	55
63	Direct Analysis of Intact Proteins from <i>Escherichia coli</i> Colonies by Liquid Extraction Surface Analysis Mass Spectrometry. <i>Analytical Chemistry</i> , 2014, 86, 10504-10510.	6.5	66
64	Compound heterozygotes and beta-thalassemia: Top-down mass spectrometry for detection of hemoglobinopathies. <i>Proteomics</i> , 2014, 14, 1232-1238.	2.2	40
65	Unusual ECD fragmentation attributed to gas-phase helix formation in a conformationally dynamic peptide. <i>Chemical Communications</i> , 2014, 50, 198-200.	4.1	14
66	Electron Capture Dissociation and Collision Induced Dissociation of S-Dipalmitoylated Peptides. <i>Journal of the American Society for Mass Spectrometry</i> , 2013, 24, 1224-1227.	2.8	5
67	Dried Blood Spot Proteomics: Surface Extraction of Endogenous Proteins Coupled with Automated Sample Preparation and Mass Spectrometry Analysis. <i>Journal of the American Society for Mass Spectrometry</i> , 2013, 24, 1242-1249.	2.8	61
68	Probing the Complementarity of FAIMS and Strong Cation Exchange Chromatography in Shotgun Proteomics. <i>Journal of the American Society for Mass Spectrometry</i> , 2013, 24, 431-443.	2.8	30
69	Large-Scale Analysis of Peptide Sequence Variants: The Case for High-Field Asymmetric Waveform Ion Mobility Spectrometry. <i>Analytical Chemistry</i> , 2013, 85, 4836-4843.	6.5	23
70	Hemoglobin variant analysis of whole blood and dried blood spots by MS. <i>Bioanalysis</i> , 2013, 5, 2043-2052.	1.5	7
71	Analysis of premalignant pancreatic cancer mass spectrometry data for biomarker selection using a group search optimizer. <i>Transactions of the Institute of Measurement and Control</i> , 2012, 34, 668-676.	1.7	13
72	Plasma Levels of Complement 4a Protein are Increased in Alzheimer's Disease. <i>Alzheimer Disease and Associated Disorders</i> , 2012, 26, 329-334.	1.3	33

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73	Higher Energy Collision Dissociation (HCD) Product Ion-Triggered Electron Transfer Dissociation (ETD) Mass Spectrometry for the Analysis of <i>N</i> -Linked Glycoproteins. <i>Journal of Proteome Research</i> , 2012, 11, 4517-4525.	3.7	150
74	Top-Down Proteomics and Direct Surface Sampling of Neonatal Dried Blood Spots: Diagnosis of Unknown Hemoglobin Variants. <i>Journal of the American Society for Mass Spectrometry</i> , 2012, 23, 1921-1930.	2.8	71
75	The Radical Ion Chemistry of <i>S</i> -Nitrosylated Peptides. <i>Journal of the American Society for Mass Spectrometry</i> , 2012, 23, 2063-2074.	2.8	7
76	Separation and Identification of Isomeric Glycopeptides by High Field Asymmetric Waveform Ion Mobility Spectrometry. <i>Analytical Chemistry</i> , 2012, 84, 2597-2601.	6.5	105
77	Dissociation techniques in mass spectrometry-based proteomics. <i>Analyst</i> , 2011, 136, 3419.	3.5	37
78	Electron induced dissociation (EID) tandem mass spectrometry of octaethylporphyrin and its iron(<i>iii</i>) complex. <i>Chemical Communications</i> , 2011, 47, 418-420.	4.1	19
79	On-line liquid chromatography neutral loss-triggered electron transfer dissociation mass spectrometry for the targeted analysis of citrullinated peptides. <i>Analytical Methods</i> , 2011, 3, 259-266.	2.7	12
80	Novel Glycosylation Sites Localized in <i>Campylobacter jejuni</i> Flagellin FlaA by Liquid Chromatography Electron Capture Dissociation Tandem Mass Spectrometry. <i>Journal of Proteome Research</i> , 2011, 10, 1238-1245.	3.7	26
81	Hemoglobin Variant Analysis via Direct Surface Sampling of Dried Blood Spots Coupled with High-Resolution Mass Spectrometry. <i>Analytical Chemistry</i> , 2011, 83, 2265-2270.	6.5	109
82	Separation of a Set of Peptide Sequence Isomers Using Differential Ion Mobility Spectrometry. <i>Analytical Chemistry</i> , 2011, 83, 6918-6923.	6.5	53
83	Manipulation of quorum sensing regulation in <i>Pseudomonas fluorescens</i> NCIMB 10586 to increase mupirocin production. <i>Applied Microbiology and Biotechnology</i> , 2011, 90, 1017-1026.	3.6	13
84	Nitration of lysozyme by ultrasonic waves; demonstration by immunochemistry and mass spectrometry. <i>Ultrasonics Sonochemistry</i> , 2011, 18, 334-344.	8.2	0
85	Electron capture dissociation mass spectrometry of metallo-supramolecular complexes. <i>Journal of the American Society for Mass Spectrometry</i> , 2010, 21, 300-309.	2.8	17
86	Can museum egg specimens be used for proteomic analyses?. <i>Proteome Science</i> , 2010, 8, 40.	1.7	10
87	Electron capture dissociation mass spectrometry of tyrosine nitrated peptides. <i>Journal of the American Society for Mass Spectrometry</i> , 2010, 21, 268-277.	2.8	42
88	Electron induced dissociation: A mass spectrometry technique for the structural analysis of trinuclear oxo-centred carboxylate-bridged iron complexes. <i>Journal of the American Society for Mass Spectrometry</i> , 2010, 21, 1398-1403.	2.8	14
89	Retention of enzyme activity with a boron-doped diamond electrode in the electro-oxidative nitration of lysozyme. <i>Enzyme and Microbial Technology</i> , 2010, 46, 472-478.	3.2	8
90	Differential Phosphoproteomics of Fibroblast Growth Factor Signaling: Identification of Src Family Kinase-Mediated Phosphorylation Events. <i>Journal of Proteome Research</i> , 2010, 9, 2317-2328.	3.7	46

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91	Proteomic Analysis of a Noninvasive Human Model of Acute Inflammation and Its Resolution: The Twenty-one Day Gingivitis Model. <i>Journal of Proteome Research</i> , 2010, 9, 4732-4744.	3.7	72
92	Top-Down Mass Analysis of Protein Tyrosine Nitration: Comparison of Electron Capture Dissociation with Slow-Heating Tandem Mass Spectrometry Methods. <i>Analytical Chemistry</i> , 2010, 82, 7283-7292.	6.5	25
93	Separation of Peptide Isomers with Variant Modified Sites by High-Resolution Differential Ion Mobility Spectrometry. <i>Analytical Chemistry</i> , 2010, 82, 8327-8334.	6.5	74
94	Probing the mechanisms of electron capture dissociation mass spectrometry with nitrated peptides. <i>Physical Chemistry Chemical Physics</i> , 2010, 12, 13394.	2.8	16
95	Large Scale Localization of Protein Phosphorylation by Use of Electron Capture Dissociation Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 904-912.	3.8	79
96	Hot electron capture dissociation distinguishes leucine from isoleucine in a novel hemoglobin variant, Hb Askew, $\beta^{254}(D5)Val \rightarrow Ile$. <i>Journal of the American Society for Mass Spectrometry</i> , 2009, 20, 1707-1713.	2.8	22
97	Characterization of polyphosphoesters by fourier transform ion cyclotron resonance mass spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2009, 20, 2238-2247.	2.8	18
98	High-field asymmetric waveform ion mobility spectrometry (FAIMS) coupled with high-resolution electron transfer dissociation mass spectrometry for the analysis of isobaric phosphopeptides. <i>Rapid Communications in Mass Spectrometry</i> , 2009, 23, 1963-1969.	1.5	75
99	Electron capture dissociation and collision-induced dissociation of metal ion (Ag^{+} , Tj ETQq1 1 0.784314 rgBT /Overlock) polyamidoamine (PAMAM) dendrimers. <i>Journal of the American Society for Mass Spectrometry</i> , 2009, 20, 674-681.	2.8	39
100	Activated ion electron capture dissociation (AI ECD) of proteins: Synchronization of infrared and electron irradiation with ion magnetron motion. <i>Journal of the American Society for Mass Spectrometry</i> , 2009, 20, 763-771.	2.8	33
101	Database Search Strategies for Proteomic Data Sets Generated by Electron Capture Dissociation Mass Spectrometry. <i>Journal of Proteome Research</i> , 2009, 8, 5475-5484.	3.7	14
102	SLoMo: Automated Site Localization of Modifications from ETD/ECD Mass Spectra. <i>Journal of Proteome Research</i> , 2009, 8, 1965-1971.	3.7	92
103	On-Line Liquid Chromatography Electron Capture Dissociation for the Characterization of Phosphorylation Sites in Proteins. <i>Methods in Molecular Biology</i> , 2009, 527, 191-199.	0.9	2
104	Fourier Transform Ion Cyclotron Resonance Mass Spectrometry in the Analysis of Peptides and Proteins. , 2009, , 121-152.		1
105	The effect of phosphorylation on the electron capture dissociation of peptide ions. <i>Journal of the American Society for Mass Spectrometry</i> , 2008, 19, 1263-1274.	2.8	46
106	Electron capture dissociation, electron detachment dissociation, and collision-induced dissociation of polyamidoamine (PAMAM) dendrimer ions with amino, amidoethanol, and sodium carboxylate surface groups. <i>Journal of the American Society for Mass Spectrometry</i> , 2008, 19, 1312-1319.	2.8	28
107	Specific electrochemical iodination of horse heart myoglobin at tyrosine 103 as determined by Fourier transform ion cyclotron resonance mass spectrometry. <i>Archives of Biochemistry and Biophysics</i> , 2008, 474, 1-7.	3.0	16
108	Targeted Online Liquid Chromatography Electron Capture Dissociation Mass Spectrometry for the Localization of Sites of in Vivo Phosphorylation in Human Sprouty2. <i>Analytical Chemistry</i> , 2008, 80, 6650-6657.	6.5	30

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109	Electron capture dissociation in the analysis of protein phosphorylation. <i>Expert Review of Proteomics</i> , 2007, 4, 149-159.	3.0	31
110	Dynamic Range and Mass Accuracy of Wide-Scan Direct Infusion Nanoelectrospray Fourier Transform Ion Cyclotron Resonance Mass Spectrometry-Based Metabolomics Increased by the Spectral Stitching Method. <i>Analytical Chemistry</i> , 2007, 79, 4595-4602.	6.5	170
111	Liquid chromatography electron capture dissociation tandem mass spectrometry (LC-ECD-MS/MS) versus liquid chromatography collision-induced dissociation tandem mass spectrometry (LC-CID-MS/MS) for the identification of proteins. <i>Journal of the American Society for Mass Spectrometry</i> , 2007, 18, 891-897.	2.8	41
112	Protein partners in the life history of activated fibroblast growth factor receptors. <i>Proteomics</i> , 2007, 7, 4565-4578.	2.2	19
113	Strategy for the Identification of Sites of Phosphorylation in Proteins: Neutral Loss Triggered Electron Capture Dissociation. <i>Analytical Chemistry</i> , 2006, 78, 7563-7569.	6.5	56
114	Mass spectrometry in demonstrating the site-specific nitration of hen egg white lysozyme by an improved electrochemical method. <i>Analytical Biochemistry</i> , 2006, 356, 171-181.	2.4	15
115	Investigation of the presence of b ions in electron capture dissociation mass spectra. <i>Journal of the American Society for Mass Spectrometry</i> , 2005, 16, 1932-1940.	2.8	60
116	The role of electron capture dissociation in biomolecular analysis. <i>Mass Spectrometry Reviews</i> , 2005, 24, 201-222.	5.4	453
117	Liver Tumors in Wild Flatfish: A Histopathological, Proteomic, and Metabolomic Study. <i>OMICS A Journal of Integrative Biology</i> , 2005, 9, 281-299.	2.0	82
118	Determination of Aberrant O-Glycosylation in the IgA1 Hinge Region by Electron Capture Dissociation Fourier Transform-Ion Cyclotron Resonance Mass Spectrometry. <i>Journal of Biological Chemistry</i> , 2005, 280, 19136-19145.	3.4	125
119	Fourier Transform Ion Cyclotron Resonance Mass Spectrometry for the Analysis of Small Ubiquitin-like Modifier (SUMO) Modification: Identification of Lysines in RanBP2 and SUMO Targeted for Modification during the E3 AutoSUMOylation Reaction. <i>Analytical Chemistry</i> , 2005, 77, 6310-6319.	6.5	51
120	Data-Dependent Electron Capture Dissociation FT ² ICR Mass Spectrometry for Proteomic Analyses. <i>Journal of Proteome Research</i> , 2005, 4, 1538-1544.	3.7	132
121	Electron capture dissociation Fourier transform ion cyclotron resonance mass spectrometry of cyclodepsipeptides, branched peptides, and μ -peptides. <i>International Journal of Mass Spectrometry</i> , 2004, 234, 23-35.	1.5	27
122	Identification of Sites of Ubiquitination in Proteins: A Fourier Transform Ion Cyclotron Resonance Mass Spectrometry Approach. <i>Analytical Chemistry</i> , 2004, 76, 6982-6988.	6.5	50
123	Determination of the activation energy for unimolecular dissociation of a non-covalent gas-phase peptide: Substrate complex by infrared multiphoton dissociation fourier transform ion cyclotron resonance mass spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2003, 14, 1282-1289.	2.8	14
124	Secondary fragmentation of linear peptides in electron capture dissociation. <i>International Journal of Mass Spectrometry</i> , 2003, 228, 723-728.	1.5	81
125	Electrospray Ionization Fourier Transform Ion Cyclotron Resonance Mass Spectrometric Analysis of Metal-Ion Selected Dynamic Protein Libraries. <i>Journal of the American Chemical Society</i> , 2003, 125, 5331-5339.	13.7	36
126	Letter: The Diagnostic Value of Amino Acid Side-Chain Losses in Electron Capture Dissociation of Polypeptides. Comment on: "Can the (M, Δ X) Region in Electron Capture Dissociation Provide Reliable Information on Amino Acid Composition of Polypeptides?" Eur. J. Mass Spectrom. 8, 461-469 (2002). <i>European Journal of Mass Spectrometry</i> , 2003, 9, 221-222.	1.0	36

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127	High Resolution Tandem Mass Spectrometry for Structural Biochemistry. <i>Current Organic Chemistry</i> , 2003, 7, 1503-1525.	1.6	38
128	Supramolecular Organization of $\hat{I}\pm, \hat{I}\pm\hat{e}^-$ -Disubstituted Sexithiophenes. <i>Journal of the American Chemical Society</i> , 2002, 124, 1269-1275.	13.7	211
129	Characterization of amino acid side chain losses in electron capture dissociation. <i>Journal of the American Society for Mass Spectrometry</i> , 2002, 13, 241-249.	2.8	146
130	Characterization of the P13 membrane protein of <i>Borrelia burgdorferi</i> by mass spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2002, 13, 295-299.	2.8	20
131	Direct detection and quantitation of He@C60 by ultrahigh-resolution Fourier transform ion cyclotron resonance mass spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2002, 13, 1349-1355.	2.8	9
132	Electron Capture Dissociation and Infrared Multiphoton Dissociation MS/MS of an N-Glycosylated Tryptic Peptide To Yield Complementary Sequence Information. <i>Analytical Chemistry</i> , 2001, 73, 4530-4536.	6.5	362
133	Specific Electrochemical Nitration of Horse Heart Myoglobin. <i>Archives of Biochemistry and Biophysics</i> , 2001, 392, 169-179.	3.0	24
134	Electrospray Ionization Fourier Transform Mass Spectrometric Analysis of Wine. <i>Journal of Agricultural and Food Chemistry</i> , 2001, 49, 5710-5718.	5.2	117
135	A 9.4 T Fourier Transform Ion Cyclotron Resonance Mass Spectrometer: Description and Performance. <i>European Journal of Mass Spectrometry</i> , 2000, 6, 267-275.	1.0	66
136	Letter: Target capture of argon by fullerene radical cations in high- energy collisions. <i>European Journal of Mass Spectrometry</i> , 1995, 1, 501.	0.7	5
137	Native Ambient Mass Spectrometry of an Intact Membrane Protein Assembly and Soluble Protein Assemblies Directly from Lens Tissue. <i>Angewandte Chemie</i> , 0, , .	2.0	2