

Joseph A Loo

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

299
papers

20,879
citations

82
h-index

136
g-index

458
ext. papers

23,170
ext. citations

7.1
avg, IF

6.75
L-index

#	Paper	IF	Citations
299	Towards understanding the formation of internal fragments generated by collisionally activated dissociation for top-down mass spectrometry.. <i>Analytica Chimica Acta</i> , 2022 , 1194, 339400	6.6	1
298	Amyloid fibrils in disease FTLD-TDP are composed of TMEM106B not TDP-43.. <i>Nature</i> , 2022 ,	50.4	5
297	The acyl-proteome of <i>Syntrophus aciditrophicus</i> reveals metabolic relationships in benzoate degradation.. <i>Molecular and Cellular Proteomics</i> , 2022 , 100215	7.6	1
296	Three-repeat and four-repeat Tau isoforms form different oligomers.. <i>Protein Science</i> , 2021 ,	6.3	1
295	Insight into the molecular basis of substrate recognition by the wall teichoic acid glycosyltransferase TagA. <i>Journal of Biological Chemistry</i> , 2021 , 101464	5.4	0
294	The Human Proteoform Project: Defining the human proteome. <i>Science Advances</i> , 2021 , 7, eabk0734	14.3	19
293	ClipsMS: An Algorithm for Analyzing Internal Fragments Resulting from Top-Down Mass Spectrometry. <i>Journal of Proteome Research</i> , 2021 , 20, 1928-1935	5.6	7
292	Internal Fragments Generated from Different Top-Down Mass Spectrometry Fragmentation Methods Extend Protein Sequence Coverage. <i>Journal of the American Society for Mass Spectrometry</i> , 2021 , 32, 1752-1758	3.5	4
291	Leveraging Immonium Ions for Targeting Acyl-Lysine Modifications in Proteomic Datasets. <i>Proteomics</i> , 2021 , 21, e2000111	4.8	3
290	Unequivocal Identification of Aspartic Acid and Aspartic Acid by MALDI-TOF/TOF: From Peptide Standards to a Therapeutic Antibody. <i>Journal of the American Society for Mass Spectrometry</i> , 2021 , 32, 1901-1909	3.5	1
289	Characterization of protein-ligand binding interactions of enoyl-ACP reductase (FabI) by native MS reveals allosteric effects of coenzymes and the inhibitor triclosan. <i>Protein Science</i> , 2021 ,	6.3	2
288	Kinetics and Optimization of the Lysine-Isopeptide Bond Forming Sortase Enzyme from. <i>Bioconjugate Chemistry</i> , 2020 , 31, 1624-1634	6.3	3
287	PEPPI-MS: Polyacrylamide-Gel-Based Prefractionation for Analysis of Intact Proteoforms and Protein Complexes by Mass Spectrometry. <i>Journal of Proteome Research</i> , 2020 , 19, 3779-3791	5.6	23
286	Confronting Racism in Chemistry Journals. <i>ACS Applied Nano Materials</i> , 2020 , 3, 6131-6133	5.6	
285	Confronting Racism in Chemistry Journals. <i>ACS Applied Polymer Materials</i> , 2020 , 2, 2496-2498	4.3	
284	Confronting Racism in Chemistry Journals. <i>Organometallics</i> , 2020 , 39, 2331-2333	3.8	
283	High Mass Analysis with a Fourier Transform Ion Cyclotron Resonance Mass Spectrometer: From Inorganic Salt Clusters to Antibody Conjugates and Beyond. <i>Journal of the American Society for Mass Spectrometry</i> , 2020 , 31, 1155-1162	3.5	10

282	Update to Our Reader, Reviewer, and Author Communities April 2020. <i>Energy & Fuels</i> , 2020 , 34, 5107-5108	4.1	
281	Update to Our Reader, Reviewer, and Author Communities April 2020. <i>Organometallics</i> , 2020 , 39, 1665-1666	3.6	
280	Confronting Racism in Chemistry Journals. <i>Journal of Chemical Health and Safety</i> , 2020 , 27, 198-200	1.7	
279	Higher-order structural characterisation of native proteins and complexes by top-down mass spectrometry. <i>Chemical Science</i> , 2020 , 11, 12918-12936	9.4	30
278	N-terminal autoprocessing and acetylation of multifunctional-autoprocessing repeats-in-toxins (MARTX) Makes Caterpillars Floppy-like effector is stimulated by adenosine diphosphate (ADP)-Ribosylation Factor 1 in advance of Golgi fragmentation. <i>Cellular Microbiology</i> , 2020 , 22, e13133	3.9	5
277	Interlaboratory Study for Characterizing Monoclonal Antibodies by Top-Down and Middle-Down Mass Spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2020 , 31, 1783-1802	3.5	32
276	Internal Fragments Generated by Electron Ionization Dissociation Enhance Protein Top-Down Mass Spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2020 , 31, 1896-1902	3.5	16
275	A five-level classification system for proteoform identifications. <i>Nature Methods</i> , 2019 , 16, 939-940	21.6	25
274	The l-isoaspartate modification within protein fragments in the aging lens can promote protein aggregation. <i>Journal of Biological Chemistry</i> , 2019 , 294, 12203-12219	5.4	12
273	Best practices and benchmarks for intact protein analysis for top-down mass spectrometry. <i>Nature Methods</i> , 2019 , 16, 587-594	21.6	137
272	Top or Middle? Up or Down? Toward a Standard Lexicon for Protein Top-Down and Allied Mass Spectrometry Approaches. <i>Journal of the American Society for Mass Spectrometry</i> , 2019 , 30, 1149-1157	3.5	59
271	Native and Denaturing MS Protein Deconvolution for Biopharma: Monoclonal Antibodies and Antibody-Drug Conjugates to Polydisperse Membrane Proteins and Beyond. <i>Analytical Chemistry</i> , 2019 , 91, 9472-9480	7.8	17
270	Syntrophus aciditrophicus uses the same enzymes in a reversible manner to degrade and synthesize aromatic and alicyclic acids. <i>Environmental Microbiology</i> , 2019 , 21, 1833-1846	5.2	6
269	Native Top-Down Mass Spectrometry and Ion Mobility Spectrometry of the Interaction of Tau Protein with a Molecular Tweezer Assembly Modulator. <i>Journal of the American Society for Mass Spectrometry</i> , 2019 , 30, 16-23	3.5	30
268	Time-Dependent Measurement of Nrf2-Regulated Antioxidant Response to Ionizing Radiation Toward Identifying Potential Protein Biomarkers for Acute Radiation Injury. <i>Proteomics - Clinical Applications</i> , 2019 , 13, e1900035	3.1	6
267	Mass Spectrometry-Based Tissue Imaging of Small Molecules. <i>Advances in Experimental Medicine and Biology</i> , 2019 , 1140, 99-109	3.6	6
266	The molecular tweezer CLR01 inhibits aberrant superoxide dismutase 1 (SOD1) self-assembly and in the G93A-SOD1 mouse model of ALS. <i>Journal of Biological Chemistry</i> , 2019 , 294, 3501-3513	5.4	18
265	Top-Down Protein Identification using a Time-of-Flight Mass Spectrometer and Data Independent Acquisition. <i>International Journal of Mass Spectrometry</i> , 2019 , 435, 136-144	1.9	4

264	ProForma: A Standard Proteoform Notation. <i>Journal of Proteome Research</i> , 2018 , 17, 1321-1325	5.6	27
263	How many human proteoforms are there?. <i>Nature Chemical Biology</i> , 2018 , 14, 206-214	11.7	324
262	Supramolecular Modulation of Structural Polymorphism in Pathogenic β Synuclein Fibrils Using Copper(II) Coordination. <i>Angewandte Chemie</i> , 2018 , 130, 3153-3157	3.6	1
261	Fixed-Charge Trimethyl Pyrylium Modification for Enabling Enhanced Top-Down Mass Spectrometry Sequencing of Intact Protein Complexes. <i>Analytical Chemistry</i> , 2018 , 90, 2756-2764	7.8	13
260	Fourier Transform-Ion Cyclotron Resonance Mass Spectrometry as a Platform for Characterizing Multimeric Membrane Protein Complexes. <i>Journal of the American Society for Mass Spectrometry</i> , 2018 , 29, 183-193	3.5	23
259	Radical solutions: Principles and application of electron-based dissociation in mass spectrometry-based analysis of protein structure. <i>Mass Spectrometry Reviews</i> , 2018 , 37, 750-771	11	46
258	Supramolecular Modulation of Structural Polymorphism in Pathogenic β Synuclein Fibrils Using Copper(II) Coordination. <i>Angewandte Chemie - International Edition</i> , 2018 , 57, 3099-3103	16.4	17
257	Enhancing Sensitivity of Liquid Chromatography-Mass Spectrometry of Peptides and Proteins Using Supercharging Agents. <i>International Journal of Mass Spectrometry</i> , 2018 , 427, 157-164	1.9	34
256	An integrated native mass spectrometry and top-down proteomics method that connects sequence to structure and function of macromolecular complexes. <i>Nature Chemistry</i> , 2018 , 10, 139-148	17.6	119
255	To Improve is to Change. <i>Journal of the American Society for Mass Spectrometry</i> , 2018 , 29, 1-3	3.5	0
254	Submicrometer Emitter ESI Tips for Native Mass Spectrometry of Membrane Proteins in Ionic and Nonionic Detergents. <i>Journal of the American Society for Mass Spectrometry</i> , 2018 , 29, 203-206	3.5	24
253	Protein Labeling via a Specific Lysine-Isopeptide Bond Using the Pilin Polymerizing Sortase from <i>Corynebacterium diphtheriae</i> . <i>Journal of the American Chemical Society</i> , 2018 , 140, 8420-8423	16.4	20
252	Focus on Application of Photons and Radicals for Mass Spectrometry, Honoring Dr. Ryan Julian, Recipient of the 2017 ASMS Biemann Medal. <i>Journal of the American Society for Mass Spectrometry</i> , 2018 , 29, 1757-1759	3.5	
251	Extracting Charge and Mass Information from Highly Congested Mass Spectra Using Fourier-Domain Harmonics. <i>Journal of the American Society for Mass Spectrometry</i> , 2018 , 29, 2067-2080	3.5	15
250	Native-MS Analysis of Monoclonal Antibody Conjugates by Fourier Transform Ion Cyclotron Resonance Mass Spectrometry. <i>Analytical Chemistry</i> , 2018 , 90, 745-751	7.8	27
249	Proteomics identification of radiation-induced changes of membrane proteins in the rat model of arteriovenous malformation in pursuit of targets for brain AVM molecular therapy. <i>Clinical Proteomics</i> , 2018 , 15, 43	5	3
248	Rapid LC-MS Method for Accurate Molecular Weight Determination of Membrane and Hydrophobic Proteins. <i>Analytical Chemistry</i> , 2018 , 90, 13616-13623	7.8	5
247	In vitro reconstitution of sortase-catalyzed pilus polymerization reveals structural elements involved in pilin cross-linking. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, E5477-E5486	11.5	11

246	Native Top-Down Mass Spectrometry and Ion Mobility MS for Characterizing the Cobalt and Manganese Metal Binding of Synuclein Protein. <i>Journal of the American Society for Mass Spectrometry</i> , 2018 , 29, 1870-1880	3.5	38
245	Improving Proteome Coverage and Sample Recovery with Enhanced FASP (eFASP) for Quantitative Proteomic Experiments. <i>Methods in Molecular Biology</i> , 2017 , 1550, 11-18	1.4	18
244	Structural Characterization of Native Proteins and Protein Complexes by Electron Ionization Dissociation-Mass Spectrometry. <i>Analytical Chemistry</i> , 2017 , 89, 2731-2738	7.8	41
243	Inhibition of Huntingtin Exon-1 Aggregation by the Molecular Tweezer CLR01. <i>Journal of the American Chemical Society</i> , 2017 , 139, 5640-5643	16.4	34
242	Keystone predation and molecules of keystone significance. <i>Ecology</i> , 2017 , 98, 1710-1721	4.6	6
241	Top-down/Bottom-up Mass Spectrometry Workflow Using Dissolvable Polyacrylamide Gels. <i>Analytical Chemistry</i> , 2017 , 89, 8244-8250	7.8	14
240	Structural Characterization of a Thrombin-Aptamer Complex by High Resolution Native Top-Down Mass Spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2017 , 28, 1815-1822	3.5	19
239	New astroglial injury-defined biomarkers for neurotrauma assessment. <i>Journal of Cerebral Blood Flow and Metabolism</i> , 2017 , 37, 3278-3299	7.3	36
238	Identification of protein targets in cerebral endothelial cells for brain arteriovenous malformation (AVMs) molecular therapies. <i>Clinical Proteomics</i> , 2017 , 14, 17	5	5
237	4-(Nitrophenylsulfonyl)piperazines mitigate radiation damage to multiple tissues. <i>PLoS ONE</i> , 2017 , 12, e0181577	3.7	11
236	Characterization of <i>Saccharomyces cerevisiae</i> Coenzyme Q Biosynthetic Protein Coq11. <i>FASEB Journal</i> , 2017 , 31, 781.9	0.9	
235	Pyrophosphate-Dependent ATP Formation from Acetyl Coenzyme A in <i>Syntrophus aciditrophicus</i> , a New Twist on ATP Formation. <i>MBio</i> , 2016 , 7,	7.8	21
234	Native MS Analysis of Bacteriorhodopsin and an Empty Nanodisc by Orthogonal Acceleration Time-of-Flight, Orbitrap and Ion Cyclotron Resonance. <i>Analytical Chemistry</i> , 2016 , 88, 12427-12436	7.8	36
233	Fibroblast growth factor 2 dimer with superagonist <i>in vitro</i> activity improves granulation tissue formation during wound healing. <i>Biomaterials</i> , 2016 , 81, 157-168	15.6	43
232	Combining high-throughput MALDI-TOF mass spectrometry and isoelectric focusing gel electrophoresis for virtual 2D gel-based proteomics. <i>Methods</i> , 2016 , 104, 163-9	4.6	12
231	Simultaneously Revealing All Lysine Acylations in an Organism to Elucidate Substrate Metabolism. <i>FASEB Journal</i> , 2016 , 30, 831.1	0.9	
230	Metabolite-Driven Modifications: Protein Acylations Elucidate Substrate Metabolism in Syntrophic Bacteria. <i>FASEB Journal</i> , 2016 , 30, 864.1	0.9	
229	Traumatically injured astrocytes release a proteomic signature modulated by STAT3-dependent cell survival. <i>Glia</i> , 2016 , 64, 668-94	9	36

228	MULTIFUNCin: A Multifunctional Protein Cue Induces Habitat Selection by, and Predation on, Barnacles. <i>Integrative and Comparative Biology</i> , 2016 , 56, 901-913	2.8	19
227	A multifunctional chemical cue drives opposing demographic processes and structures ecological communities. <i>Ecology</i> , 2016 , 97, 2232-2239	4.6	18
226	Salt Bridge Rearrangement (SaBRe) Explains the Dissociation Behavior of Noncovalent Complexes. <i>Journal of the American Society for Mass Spectrometry</i> , 2016 , 27, 975-90	3.5	56
225	Enhancing Protein Disulfide Bond Cleavage by UV Excitation and Electron Capture Dissociation for Top-Down Mass Spectrometry. <i>International Journal of Mass Spectrometry</i> , 2015 , 390, 137-145	1.9	28
224	Increasing Fragmentation of Disulfide-Bonded Proteins for Top-Down Mass Spectrometry by Supercharging. <i>International Journal of Mass Spectrometry</i> , 2015 , 377, 546-556	1.9	18
223	Surface induced dissociation yields substructure of 20S proteasome complexes. <i>International Journal of Mass Spectrometry</i> , 2015 , 377, 201-204	1.9	12
222	Mining proteomic data to expose protein modifications in <i>Methanosarcina mazei</i> strain G11. <i>Frontiers in Microbiology</i> , 2015 , 6, 149	5.7	6
221	Investigation of the Mechanism of Electron Capture and Electron Transfer Dissociation of Peptides with a Covalently Attached Free Radical Hydrogen Atom Scavenger. <i>International Journal of Mass Spectrometry</i> , 2015 , 390, 49-55	1.9	11
220	Structure of <i>Tetrahymena</i> telomerase reveals previously unknown subunits, functions, and interactions. <i>Science</i> , 2015 , 350, aab4070	33.3	105
219	Enhancing Performance of Liquid Sample Desorption Electrospray Ionization Mass Spectrometry Using Trap and Capillary Columns. <i>International Journal of Mass Spectrometry</i> , 2015 , 392, 73-79	1.9	8
218	Native top-down mass spectrometry for the structural characterization of human hemoglobin. <i>European Journal of Mass Spectrometry</i> , 2015 , 21, 221-31	1.1	25
217	Integration of electrochemistry with ultra-performance liquid chromatography/mass spectrometry. <i>European Journal of Mass Spectrometry</i> , 2015 , 21, 341-51	1.1	10
216	Focus on Mass Spectrometry-Based Strategies for Neuroproteomics and Peptidomics, Honoring Dr. Lingjun Li, Recipient of the 2014 ASMS Biemann Medal. <i>Journal of the American Society for Mass Spectrometry</i> , 2015 , 26, 1967-9	3.5	
215	Significance of filamin A in mTORC2 function in glioblastoma. <i>Molecular Cancer</i> , 2015 , 14, 127	42.1	31
214	Conserved SMP domains of the ERMES complex bind phospholipids and mediate tether assembly. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, E3179-88	11.5	140
213	Identification of Coq11, a new coenzyme Q biosynthetic protein in the CoQ-synthome in <i>Saccharomyces cerevisiae</i> . <i>Journal of Biological Chemistry</i> , 2015 , 290, 7517-34	5.4	53
212	Characterization of Proteins Associated with the Coenzyme Q Biosynthetic Complex and Analyses of Phosphorylated Coq Proteins in Yeast Mitochondria. <i>FASEB Journal</i> , 2015 , 29, 568.29	0.9	
211	Enhanced FASP (eFASP) to increase proteome coverage and sample recovery for quantitative proteomic experiments. <i>Journal of Proteome Research</i> , 2014 , 13, 1885-95	5.6	202

210	Molecular basis for preventing β -synuclein aggregation by a molecular tweezer. <i>Journal of Biological Chemistry</i> , 2014 , 289, 10727-10737	5.4	70
209	Translational roles of elongation factor 2 protein lysine methylation. <i>Journal of Biological Chemistry</i> , 2014 , 289, 30511-30524	5.4	17
208	Top-down protein identification of proteasome proteins with nanoLC-FT-ICR-MS employing data-independent fragmentation methods. <i>Proteomics</i> , 2014 , 14, 1271-82	4.8	17
207	Subcellular metal imaging identifies dynamic sites of Cu accumulation in <i>Chlamydomonas</i> . <i>Nature Chemical Biology</i> , 2014 , 10, 1034-42	11.7	106
206	Native top-down electrospray ionization-mass spectrometry of 158 kDa protein complex by high-resolution Fourier transform ion cyclotron resonance mass spectrometry. <i>Analytical Chemistry</i> , 2014 , 86, 317-20	7.8	90
205	What protein charging (and supercharging) reveal about the mechanism of electrospray ionization. <i>Journal of the American Society for Mass Spectrometry</i> , 2014 , 25, 1675-93	3.5	100
204	Bioengineered vaults: self-assembling protein shell-lipophilic core nanoparticles for drug delivery. <i>ACS Nano</i> , 2014 , 8, 7723-32	16.7	49
203	Revealing ligand binding sites and quantifying subunit variants of noncovalent protein complexes in a single native top-down FTICR MS experiment. <i>Journal of the American Society for Mass Spectrometry</i> , 2014 , 25, 2060-8	3.5	57
202	Addressing the needs of traumatic brain injury with clinical proteomics. <i>Clinical Proteomics</i> , 2014 , 11, 11	5	12
201	Radical-directed dissociation of peptides and proteins by infrared multiphoton dissociation and sustained off-resonance irradiation collision-induced dissociation with Fourier transform ion cyclotron resonance mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2014 , 28, 2729-34	2.2	5
200	Focus on advancing high performance mass spectrometry, honoring dr. Richard d. Smith, recipient of the 2013 award for a distinguished contribution in mass spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2014 , 25, 1997-9	3.5	
199	A new type of protein lysine methyltransferase trimethylates Lys-79 of elongation factor 1A. <i>Biochemical and Biophysical Research Communications</i> , 2014 , 455, 382-9	3.4	14
198	A conserved START domain coenzyme Q-binding polypeptide is required for efficient Q biosynthesis, respiratory electron transport, and antioxidant function in <i>Saccharomyces cerevisiae</i> . <i>Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids</i> , 2013 , 1831, 776-791	5	26
197	Protein complexes: breaking up is hard to do well. <i>Structure</i> , 2013 , 21, 1265-6	5.2	1
196	Thermal-stable proteins of fruit of long-living Sacred Lotus Gaertn var. China Antique. <i>Tropical Plant Biology</i> , 2013 , 6, 69	1.6	15
195	Ion Sources Used for Secondary Ion Mass Spectrometry 2013 , 57-75		2
194	An Introduction to Cluster Secondary Ion Mass Spectrometry (Cluster SIMS) 2013 , 1-11		3
193	Surface Analysis of Organic Materials with Polyatomic Primary Ion Sources 2013 , 77-116		

192	Cluster SIMS of Organic Materials: Theoretical Insights 2013 , 13-55		1
191	Molecular Depth Profiling with Cluster Ion Beams 2013 , 117-205		5
190	Future Challenges and Prospects of Cluster SIMS 2013 , 313-327		
189	Cluster TOF-SIMS Imaging and the Characterization of Biological Materials 2013 , 269-312		10
188	Cluster Secondary Ion Mass Spectrometry (SIMS) For Semiconductor and Metals Depth Profiling 2013 , 247-268		
187	Three-Dimensional Imaging with Cluster Ion Beams 2013 , 207-246		4
186	Investigation of stable and transient protein-protein interactions: Past, present, and future. <i>Proteomics</i> , 2013 , 13, 538-57	4.8	105
185	A heparin-mimicking polymer conjugate stabilizes basic fibroblast growth factor. <i>Nature Chemistry</i> , 2013 , 5, 221-7	17.6	163
184	Measuring protein-ligand interactions using liquid sample desorption electrospray ionization mass spectrometry. <i>Analytical Chemistry</i> , 2013 , 85, 11966-72	7.8	27
183	The proteome of copper, iron, zinc, and manganese micronutrient deficiency in <i>Chlamydomonas reinhardtii</i> . <i>Molecular and Cellular Proteomics</i> , 2013 , 12, 65-86	7.6	65
182	<i>Staphylococcus aureus</i> uses a novel multidomain receptor to break apart human hemoglobin and steal its heme. <i>Journal of Biological Chemistry</i> , 2013 , 288, 1065-78	5.4	44
181	Zinc deficiency impacts CO ₂ assimilation and disrupts copper homeostasis in <i>Chlamydomonas reinhardtii</i> . <i>Journal of Biological Chemistry</i> , 2013 , 288, 10672-83	5.4	59
180	Integrating Native Mass Spectrometry and Top-Down MS for Defining Protein Interactions Important in Biology and Medicine. <i>Mass Spectrometry</i> , 2013 , 2, S0013	1.7	11
179	Signal and Charge Enhancement for Protein Analysis by Liquid Chromatography-Mass Spectrometry with Desorption Electrospray Ionization. <i>International Journal of Mass Spectrometry</i> , 2012 , 325-327, 161-186	1.8	27
178	Network organization of the huntingtin proteomic interactome in mammalian brain. <i>Neuron</i> , 2012 , 75, 41-57	13.9	204
177	EGFR and HER2 receptor kinase signaling mediate epithelial cell invasion by <i>Candida albicans</i> during oropharyngeal infection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 14194-9	11.5	110
176	The Role of Mass Spectrometry for Peptide, Protein, and Proteome Characterization 2012 , 683-721		1
175	Click chemistry facilitates formation of reporter ions and simplified synthesis of amine-reactive multiplexed isobaric tags for protein quantification. <i>Journal of the American Chemical Society</i> , 2012 , 134, 2672-80	16.4	28

174	Designer reagents for mass spectrometry-based proteomics: clickable cross-linkers for elucidation of protein structures and interactions. <i>Analytical Chemistry</i> , 2012 , 84, 2662-9	7.8	39
173	A novel "molecular tweezer" inhibitor of β -synuclein neurotoxicity in vitro and in vivo. <i>Neurotherapeutics</i> , 2012 , 9, 464-76	6.4	123
172	Fe sparing and Fe recycling contribute to increased superoxide dismutase capacity in iron-starved <i>Chlamydomonas reinhardtii</i> . <i>Plant Cell</i> , 2012 , 24, 2649-65	11.6	59
171	Systems and trans-system level analysis identifies conserved iron deficiency responses in the plant lineage. <i>Plant Cell</i> , 2012 , 24, 3921-48	11.6	104
170	Cardiolipin defines the interactome of the major ADP/ATP carrier protein of the mitochondrial inner membrane. <i>Journal of Cell Biology</i> , 2012 , 197, 1029-1029	7.3	78
169	Lysine-specific molecular tweezers are broad-spectrum inhibitors of assembly and toxicity of amyloid proteins. <i>Journal of the American Chemical Society</i> , 2011 , 133, 16958-69	16.4	219
168	Characterization of morphine-glucose-6-phosphate dehydrogenase conjugates by mass spectrometry. <i>Bioconjugate Chemistry</i> , 2011 , 22, 1595-604	6.3	5
167	The <i>Trichomonas vaginalis</i> hydrogenosome proteome is highly reduced relative to mitochondria, yet complex compared with mitosomes. <i>International Journal for Parasitology</i> , 2011 , 41, 1421-34	4.3	82
166	Concomitant inhibition of HSP90, its mitochondrial localized homologue TRAP1 and HSP27 by green tea in pancreatic cancer HPAF-II cells. <i>Proteomics</i> , 2011 , 11, 4638-47	4.8	22
165	Direct ionization of large proteins and protein complexes by desorption electrospray ionization-mass spectrometry. <i>Analytical Chemistry</i> , 2011 , 83, 6468-73	7.8	85
164	Top-Down Mass Spectrometry of Supercharged Native Protein-Ligand Complexes. <i>International Journal of Mass Spectrometry</i> , 2011 , 300, 118-122	1.9	102
163	Systems biology approach in <i>Chlamydomonas</i> reveals connections between copper nutrition and multiple metabolic steps. <i>Plant Cell</i> , 2011 , 23, 1273-92	11.6	170
162	Sample Preparation of Primary Astrocyte Cellular and Released Proteins for 2-D Gel Electrophoresis and Protein Identification by Mass Spectrometry 2011 , 829-849		4
161	Antifibrinolytic Efficacy of Truncated L17R Mutant of Kunitz Domain 1 (KD1) of Tissue Factor Pathway Inhibitor-2 (TFPI-2): Comparison with Lysine Analogues. <i>Blood</i> , 2011 , 118, 855-855	2.2	
160	Identification of tetranectin as a potential biomarker for metastatic oral cancer. <i>International Journal of Molecular Sciences</i> , 2010 , 11, 3106-21	6.3	46
159	Negative feedback in noncanonical NF-kappaB signaling modulates NIK stability through IKKalpha-mediated phosphorylation. <i>Science Signaling</i> , 2010 , 3, ra41	8.8	85
158	Incubated protein reduction and digestion on an electrowetting-on-dielectric digital microfluidic chip for MALDI-MS. <i>Analytical Chemistry</i> , 2010 , 82, 9932-7	7.8	90
157	Mapping of drebrin binding site on F-actin. <i>Journal of Molecular Biology</i> , 2010 , 398, 542-54	6.5	41

156	Integration of protein processing steps on a droplet microfluidics platform for MALDI-MS analysis. <i>Analytical Chemistry</i> , 2010 , 82, 2095-101	7.8	61
155	Ion mobility-mass spectrometry of phosphorylase B ions generated with supercharging reagents but in charge-reducing buffer. <i>Physical Chemistry Chemical Physics</i> , 2010 , 12, 13476-83	3.6	52
154	Electrospray-assisted laser desorption ionization mass spectrometry (ELDI-MS) with an infrared laser for characterizing peptides and proteins. <i>Analyst, The</i> , 2010 , 135, 767-72	5	41
153	Radical directed dissociation for facile identification of iodotyrosine residues using electrospray ionization mass spectrometry. <i>Analytical Chemistry</i> , 2010 , 82, 3826-33	7.8	33
152	Biomarkers to predict antidepressant response. <i>Current Psychiatry Reports</i> , 2010 , 12, 553-62	9.1	111
151	New reagents for increasing ESI multiple charging of proteins and protein complexes. <i>Journal of the American Society for Mass Spectrometry</i> , 2010 , 21, 127-31	3.5	143
150	Elucidating the site of protein-ATP binding by top-down mass spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2010 , 21, 899-907	3.5	62
149	Confident assignment of intact mass tags to human salivary cystatins using top-down Fourier-transform ion cyclotron resonance mass spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2010 , 21, 908-17	3.5	36
148	Micro-heterogeneity of human saliva Peptide P-C characterized by high-resolution top-down Fourier-transform mass spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2010 , 21, 868-77	3.5	18
147	Structure of the dimerization domain of DiGeorge critical region 8. <i>Protein Science</i> , 2010 , 19, 1354-65	6.3	45
146	Adjuvant effects of ambient particulate matter monitored by proteomics of bronchoalveolar lavage fluid. <i>Proteomics</i> , 2010 , 10, 520-31	4.8	24
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