

Brandon Ruotolo

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.

134
papers

9,319
citations

51
h-index

95
g-index

148
ext. papers

10,190
ext. citations

7.9
avg, IF

6.23
L-index

#	Paper	IF	Citations
134	Biochemical characterization of the interaction between KRAS and Argonaute 2.. <i>Biochemistry and Biophysics Reports</i> , 2022 , 29, 101191	2.2	1
133	Verteoporfin is a Substrate-Selective β Secretase Inhibitor that Binds the Amyloid Precursor Protein Transmembrane Domain.. <i>Journal of Biological Chemistry</i> , 2022 , 101792	5.4	1
132	Oligomerization, trans-reduction, and instability of mutant NOTCH3 in inherited vascular dementia.. <i>Communications Biology</i> , 2022 , 5, 331	6.7	2
131	Mechanistic insights into accelerated β synuclein aggregation mediated by human microbiome-associated functional amyloids. <i>Journal of Biological Chemistry</i> , 2022 , 102088	5.4	0
130	Collision-Induced Unfolding Reveals Stability Differences in Infliximab Therapeutics under Native and Heat Stress Conditions. <i>Analytical Chemistry</i> , 2021 , 93, 16166-16174	7.8	2
129	Ion mobility-mass spectrometry reveals the role of peripheral myelin protein dimers in peripheral neuropathy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	3
128	Kinetic Analysis of Transient Intermediates in the Mechanism of Prenyl-Flavin-Dependent Ferulic Acid Decarboxylase. <i>Biochemistry</i> , 2021 , 60, 125-134	3.2	2
127	Mechanism of the small ATP-independent chaperone Spy is substrate specific. <i>Nature Communications</i> , 2021 , 12, 851	17.4	5
126	An Improved Calibration Approach for Traveling Wave Ion Mobility Spectrometry: Robust, High-Precision Collision Cross Sections. <i>Analytical Chemistry</i> , 2021 , 93, 3542-3550	7.8	11
125	Bicarbonate buffers can promote crosslinking and alternative gas-phase dissociation pathways for multiprotein complexes. <i>International Journal of Mass Spectrometry</i> , 2021 , 469, 116687	1.9	
124	Bicelles Rich in both Sphingolipids and Cholesterol and Their Use in Studies of Membrane Proteins. <i>Journal of the American Chemical Society</i> , 2020 , 142, 12715-12729	16.4	10
123	Pervasive Charge Solvation Permeates Native-like Protein Ions and Dramatically Influences Top-down Sequencing Data. <i>Journal of the American Chemical Society</i> , 2020 , 142, 6750-6760	16.4	9
122	A Novel Ion Pseudo-trapping Phenomenon within Traveling Wave Ion Guides. <i>Journal of the American Society for Mass Spectrometry</i> , 2020 , 31, 880-887	3.5	4
121	Assessment of biosimilarity under native and heat-stressed conditions: rituximab, bevacizumab, and trastuzumab originators and biosimilars. <i>Analytical and Bioanalytical Chemistry</i> , 2020 , 412, 763-775	4.4	5
120	Multifaceted assessment of rituximab biosimilarity: The impact of glycan microheterogeneity on Fc function. <i>European Journal of Pharmaceutics and Biopharmaceutics</i> , 2020 , 146, 111-124	5.7	8
119	Collision-Induced Unfolding Differentiates Functional Variants of the KCNQ1 Voltage Sensor Domain. <i>Journal of the American Society for Mass Spectrometry</i> , 2020 , 31, 2348-2355	3.5	4
118	Enhanced Collision Induced Unfolding and Electron Capture Dissociation of Native-like Protein Ions. <i>Analytical Chemistry</i> , 2020 , 92, 15489-15496	7.8	18

117	CIUSuite 2: Next-Generation Software for the Analysis of Gas-Phase Protein Unfolding Data. <i>Analytical Chemistry</i> , 2019 , 91, 3147-3155	7.8	53
116	A Modified Drift Tube Ion Mobility-Mass Spectrometer for Charge-Multiplexed Collision-Induced Unfolding. <i>Analytical Chemistry</i> , 2019 , 91, 8137-8146	7.8	17
115	Hydrogen/deuterium exchange-mass spectrometry analysis of high concentration biotherapeutics: application to phase-separated antibody formulations. <i>MAbs</i> , 2019 , 11, 779-788	6.6	4
114	Native Mass Spectrometry, Ion Mobility, Electron-Capture Dissociation, and Modeling Provide Structural Information for Gas-Phase Apolipoprotein E Oligomers. <i>Journal of the American Society for Mass Spectrometry</i> , 2019 , 30, 876-885	3.5	17
113	A Semi-Empirical Framework for Interpreting Traveling Wave Ion Mobility Arrival Time Distributions. <i>Journal of the American Society for Mass Spectrometry</i> , 2019 , 30, 956-966	3.5	3
112	Collision-Induced Unfolding Reveals Unique Fingerprints for Remote Protein Interaction Sites in the KIX Regulation Domain. <i>Journal of the American Society for Mass Spectrometry</i> , 2019 , 30, 94-102	3.5	11
111	An Algorithm for Building Multi-State Classifiers Based on Collision-Induced Unfolding Data. <i>Analytical Chemistry</i> , 2019 , 91, 10407-10412	7.8	9
110	SERF engages in a fuzzy complex that accelerates primary nucleation of amyloid proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 23040-23049	11.5	8
109	Collision Induced Unfolding Classifies Ligands Bound to the Integral Membrane Translocator Protein. <i>Analytical Chemistry</i> , 2019 , 91, 15469-15476	7.8	15
108	Quantitative collision-induced unfolding differentiates model antibody-drug conjugates. <i>Protein Science</i> , 2019 , 28, 598-608	6.3	17
107	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
106	Collision induced unfolding detects subtle differences in intact antibody glycoforms and associated fragments. <i>International Journal of Mass Spectrometry</i> , 2018 , 425, 1-9	1.9	20
105	Collision induced unfolding of isolated proteins in the gas phase: past, present, and future. <i>Current Opinion in Chemical Biology</i> , 2018 , 42, 93-100	9.7	101
104	IMTBX and Grppr: Software for Top-Down Proteomics Utilizing Ion Mobility-Mass Spectrometry. <i>Analytical Chemistry</i> , 2018 , 90, 2369-2375	7.8	5
103	Collision induced unfolding and dissociation differentiates ATP-competitive from allosteric protein tyrosine kinase inhibitors. <i>International Journal of Mass Spectrometry</i> , 2018 , 427, 151-156	1.9	13
102	A Structural Model of the Urease Activation Complex Derived from Ion Mobility-Mass Spectrometry and Integrative Modeling. <i>Structure</i> , 2018 , 26, 599-606.e3	5.2	18
101	The growing role of structural mass spectrometry in the discovery and development of therapeutic antibodies. <i>Analyst, The</i> , 2018 , 143, 2459-2468	5	21
100	Infliximab Biosimilars in the Age of Personalized Medicine. <i>Trends in Biotechnology</i> , 2018 , 36, 987-992	15.1	7

99	Ion Mobility-Mass Spectrometry Reveals Evidence of Specific Complex Formation between Human Histone Deacetylase 8 and Poly-r(C)-binding Protein 1. <i>International Journal of Mass Spectrometry</i> , 2017 , 420, 9-15	1.9	2
98	Ion Mobility-Mass Spectrometry Reveals a Dipeptide That Acts as a Molecular Chaperone for Amyloid β . <i>ACS Chemical Biology</i> , 2017 , 12, 1113-1120	4.9	6
97	Evaluation of de novo-designed coiled coils as off-the-shelf components for protein assembly. <i>Molecular Systems Design and Engineering</i> , 2017 , 2, 140-148	4.6	16
96	Variable-Velocity Traveling-Wave Ion Mobility Separation Enhancing Peak Capacity for Data-Independent Acquisition Proteomics. <i>Analytical Chemistry</i> , 2017 , 89, 5669-5672	7.8	45
95	A Multidimensional Analytical Comparison of Remicade and the Biosimilar Remsima. <i>Analytical Chemistry</i> , 2017 , 89, 4838-4846	7.8	51
94	Sizing Up Protein-Ligand Complexes: The Rise of Structural Mass Spectrometry Approaches in the Pharmaceutical Sciences. <i>Annual Review of Analytical Chemistry</i> , 2017 , 10, 25-44	12.5	41
93	Structural and Mechanistic Insights into Development of Chemical Tools to Control Individual and Inter-Related Pathological Features in Alzheimer's Disease. <i>Chemistry - A European Journal</i> , 2017 , 23, 2706-2715	4.8	23
92	Affinity-Based Selectivity Profiling of an In-Class Selective Competitive Inhibitor of Acyl Protein Thioesterase 2. <i>ACS Medicinal Chemistry Letters</i> , 2017 , 8, 215-220	4.3	7
91	Chemical Probes and Engineered Constructs Reveal a Detailed Unfolding Mechanism for a Solvent-Free Multidomain Protein. <i>Journal of the American Chemical Society</i> , 2017 , 139, 534-540	16.4	33
90	Evidence for a 1,3-Dipolar Cyclo-addition Mechanism in the Decarboxylation of Phenylacrylic Acids Catalyzed by Ferulic Acid Decarboxylase. <i>Journal of the American Chemical Society</i> , 2017 , 139, 10972-10975	16.4	28
89	Coming to Grips with Ambiguity: Ion Mobility-Mass Spectrometry for Protein Quaternary Structure Assignment. <i>Journal of the American Society for Mass Spectrometry</i> , 2017 , 28, 1991-2000	3.5	27
88	Symmetry-Directed Self-Assembly of a Tetrahedral Protein Cage Mediated by de Novo-Designed Coiled Coils. <i>ChemBioChem</i> , 2017 , 18, 1888-1892	3.8	35
87	Biosimilarity under stress: A forced degradation study of Remicade β and Remsima β MAbs, 2017 , 9, 1197-1209	6.6	26
86	Minor Structural Variations of Small Molecules Tune Regulatory Activities toward Pathological Factors in Alzheimer's Disease. <i>ChemMedChem</i> , 2017 , 12, 1828-1838	3.7	10
85	Flexible, symmetry-directed approach to assembling protein cages. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, 8681-6	11.5	77
84	Structure-mechanism-based engineering of chemical regulators targeting distinct pathological factors in Alzheimer's disease. <i>Nature Communications</i> , 2016 , 7, 13115	17.4	66
83	Ion Mobility-Mass Spectrometry Reveals Highly-Compact Intermediates in the Collision Induced Dissociation of Charge-Reduced Protein Complexes. <i>Journal of the American Society for Mass Spectrometry</i> , 2016 , 27, 41-9	3.5	16
82	Effects of hydroxyl group variations on a flavonoid backbone toward modulation of metal-free and metal-induced amyloid- β aggregation. <i>Inorganic Chemistry Frontiers</i> , 2016 , 3, 381-392	6.8	21

81	Ion Mobility-Mass Spectrometry Analysis of Cross-Linked Intact Multiprotein Complexes: Enhanced Gas-Phase Stabilities and Altered Dissociation Pathways. <i>Analytical Chemistry</i> , 2016 , 88, 5290-8	7.8	13
80	Complex Formed between Intramembrane Metalloprotease SpoIVFB and Its Substrate, Pro- σ^70 . <i>Journal of Biological Chemistry</i> , 2016 , 291, 10347-62	5.4	5
79	Importance of the Dimethylamino Functionality on a Multifunctional Framework for Regulating Metals, Amyloid- β and Oxidative Stress in Alzheimer's Disease. <i>Inorganic Chemistry</i> , 2016 , 55, 5000-13	5.1	17
78	Ion Mobility-Mass Spectrometry Differentiates Protein Quaternary Structures Formed in Solution and in Electrospray Droplets. <i>Analytical Chemistry</i> , 2015 , 87, 6808-13	7.8	15
77	A rationally designed small molecule for identifying an link between metal-amyloid- β complexes and the pathogenesis of Alzheimer's disease. <i>Chemical Science</i> , 2015 , 6, 1879-1886	9.4	52
76	CIUSuite: A Quantitative Analysis Package for Collision Induced Unfolding Measurements of Gas-Phase Protein Ions. <i>Analytical Chemistry</i> , 2015 , 87, 11516-22	7.8	80
75	A Redox-Active, Compact Molecule for Cross-Linking Amyloidogenic Peptides into Nontoxic, Off-Pathway Aggregates: In Vitro and In Vivo Efficacy and Molecular Mechanisms. <i>Journal of the American Chemical Society</i> , 2015 , 137, 14785-97	16.4	52
74	Collisional unfolding of multiprotein complexes reveals cooperative stabilization upon ligand binding. <i>Protein Science</i> , 2015 , 24, 1272-81	6.3	35
73	Collision Induced Unfolding of Intact Antibodies: Rapid Characterization of Disulfide Bonding Patterns, Glycosylation, and Structures. <i>Analytical Chemistry</i> , 2015 , 87, 11509-15	7.8	99
72	Ion mobility-mass spectrometry of charge-reduced protein complexes reveals general trends in the collisional ejection of compact subunits. <i>Analyst</i> , 2015 , 140, 7020-9	5	12
71	Collisional and Coulombic unfolding of gas-phase proteins: high correlation to their domain structures in solution. <i>Angewandte Chemie - International Edition</i> , 2014 , 53, 9209-12	16.4	86
70	Collisional and Coulombic Unfolding of Gas-Phase Proteins: High Correlation to Their Domain Structures in Solution. <i>Angewandte Chemie</i> , 2014 , 126, 9363-9366	3.6	16
69	Analysis of a soluble (UreD:UreF:UreG) ₂ accessory protein complex and its interactions with <i>Klebsiella aerogenes</i> urease by mass spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2013 , 24, 1328-37	3.5	12
68	Activation state-selective kinase inhibitor assay based on ion mobility-mass spectrometry. <i>Analytical Chemistry</i> , 2013 , 85, 6995-7002	7.8	56
67	Traveling-wave Ion Mobility-Mass Spectrometry Reveals Additional Mechanistic Details in the Stabilization of Protein Complex Ions through Tuned Salt Additives. <i>International Journal for Ion Mobility Spectrometry</i> , 2013 , 16, 41-50	1.5	13
66	Dramatically stabilizing multiprotein complex structure in the absence of bulk water using tuned Hofmeister salts. <i>Faraday Discussions</i> , 2013 , 160, 371-88; discussion 389-403	3.6	11
65	Amyloid- β -neuropeptide interactions assessed by ion mobility-mass spectrometry. <i>Physical Chemistry Chemical Physics</i> , 2013 , 15, 8952-61	3.6	24
64	Ion mobility-mass spectrometry of intact protein-ligand complexes for pharmaceutical drug discovery and development. <i>Current Opinion in Chemical Biology</i> , 2013 , 17, 809-17	9.7	64

63	Resolution of oligomeric species during the aggregation of A β -40 using (19)F NMR. <i>Biochemistry</i> , 2013 , 52, 1903-12	3.2	85
62	Insights into antiamyloidogenic properties of the green tea extract (-)-epigallocatechin-3-gallate toward metal-associated amyloid- β species. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 3743-8	11.5	186
61	Integrative modelling coupled with ion mobility mass spectrometry reveals structural features of the clamp loader in complex with single-stranded DNA binding protein. <i>Journal of Molecular Biology</i> , 2013 , 425, 4790-801	6.5	44
60	Robotically assisted titration coupled to ion mobility-mass spectrometry reveals the interface structures and analysis parameters critical for multiprotein topology mapping. <i>Analytical Chemistry</i> , 2013 , 85, 11360-8	7.8	7
59	Hofmeister Salts Recover a Misfolded Multiprotein Complex for Subsequent Structural Measurements in the Gas Phase. <i>Angewandte Chemie</i> , 2013 , 125, 8487-8490	3.6	2
58	Hofmeister salts recover a misfolded multiprotein complex for subsequent structural measurements in the gas phase. <i>Angewandte Chemie - International Edition</i> , 2013 , 52, 8329-32	16.4	17
57	Gas-phase protein assemblies: Unfolding landscapes and preserving native-like structures using noncovalent adducts. <i>Chemical Physics Letters</i> , 2012 , 524, 1-9	2.5	39
56	Exploring the reactivity of flavonoid compounds with metal-associated amyloid- β species. <i>Dalton Transactions</i> , 2012 , 41, 6558-66	4.3	30
55	Reactivity of diphenylpropynone derivatives toward metal-associated amyloid- β species. <i>Inorganic Chemistry</i> , 2012 , 51, 12959-67	5.1	32
54	Integrating mass spectrometry of intact protein complexes into structural proteomics. <i>Proteomics</i> , 2012 , 12, 1547-64	4.8	75
53	Bound Cations Significantly Stabilize the Structure of Multiprotein Complexes in the Gas Phase. <i>Angewandte Chemie</i> , 2012 , 124, 5790-5793	3.6	8
52	Bound cations significantly stabilize the structure of multiprotein complexes in the gas phase. <i>Angewandte Chemie - International Edition</i> , 2012 , 51, 5692-5	16.4	46
51	Ion mobility-mass spectrometry for structural proteomics. <i>Expert Review of Proteomics</i> , 2012 , 9, 47-58	4.2	130
50	Characterizing the resolution and accuracy of a second-generation traveling-wave ion mobility separator for biomolecular ions. <i>Analyst, The</i> , 2011 , 136, 3534-41	5	121
49	A two-site mechanism for the inhibition of IAPP amyloidogenesis by zinc. <i>Journal of Molecular Biology</i> , 2011 , 410, 294-306	6.5	94
48	Mass spectrometry: come of age for structural and dynamical biology. <i>Current Opinion in Structural Biology</i> , 2011 , 21, 641-9	8.1	214
47	Ion mobility-mass spectrometry reveals conformational changes in charge reduced multiprotein complexes. <i>Journal of the American Society for Mass Spectrometry</i> , 2011 , 22, 1690-8	3.5	36
46	Tandem differential mobility analysis-mass spectrometry reveals partial gas-phase collapse of the GroEL complex. <i>Journal of Physical Chemistry B</i> , 2011 , 115, 3614-21	3.4	105

45	Bound anions differentially stabilize multiprotein complexes in the absence of bulk solvent. <i>Journal of the American Chemical Society</i> , 2011 , 133, 11358-67	16.4	82
44	Alternate dissociation pathways identified in charge-reduced protein complex ions. <i>Analytical Chemistry</i> , 2010 , 82, 5363-72	7.8	126
43	Collision cross sections of proteins and their complexes: a calibration framework and database for gas-phase structural biology. <i>Analytical Chemistry</i> , 2010 , 82, 9557-65	7.8	600
42	Separating and visualising protein assemblies by means of preparative mass spectrometry and microscopy. <i>Journal of Structural Biology</i> , 2010 , 172, 161-8	3.4	54
41	Ion mobility-mass spectrometry reveals the influence of subunit packing and charge on the dissociation of multiprotein complexes. <i>Analytical Chemistry</i> , 2010 , 82, 9702-10	7.8	62
40	A single subunit directs the assembly of the Escherichia coli DNA sliding clamp loader. <i>Structure</i> , 2010 , 18, 285-92	5.2	17
39	Residual counter ions can stabilise a large protein complex in the gas phase. <i>International Journal of Mass Spectrometry</i> , 2010 , 298, 91-98	1.9	57
38	Integrating ion mobility mass spectrometry with molecular modelling to determine the architecture of multiprotein complexes. <i>PLoS ONE</i> , 2010 , 5, e12080	3.7	112
37	Subunit architecture of multiprotein assemblies determined using restraints from gas-phase measurements. <i>Structure</i> , 2009 , 17, 1235-43	5.2	97
36	Coupling microdroplet microreactors with mass spectrometry: reading the contents of single droplets online. <i>Angewandte Chemie - International Edition</i> , 2009 , 48, 3665-8	16.4	146
35	Methodology for measuring conformation of solvent-disrupted protein subunits using T-WAVE ion mobility MS: an investigation into eukaryotic initiation factors. <i>Journal of the American Society for Mass Spectrometry</i> , 2009 , 20, 1699-706	3.5	50
34	Amyloid- β protein oligomerization and the importance of tetramers and dodecamers in the aetiology of Alzheimer's disease. <i>Nature Chemistry</i> , 2009 , 1, 326-31	17.6	737
33	A Monte Carlo approach for assessing the specificity of protein oligomers observed in nano-electrospray mass spectra. <i>International Journal of Mass Spectrometry</i> , 2009 , 283, 169-177	1.9	25
32	Gas-phase unfolding and disassembly reveals stability differences in ligand-bound multiprotein complexes. <i>Chemistry and Biology</i> , 2009 , 16, 382-90		124
31	Quadrupole-time-of-flight mass spectrometer modified for higher-energy dissociation reduces protein assemblies to peptide fragments. <i>Analytical Chemistry</i> , 2009 , 81, 1270-4	7.8	46
30	Ion mobility-mass spectrometry analysis of large protein complexes. <i>Nature Protocols</i> , 2008 , 3, 1139-52	18.8	843
29	Subunit architecture of intact protein complexes from mass spectrometry and homology modeling. <i>Accounts of Chemical Research</i> , 2008 , 41, 617-27	24.3	117
28	Ion mobility-mass spectrometry reveals long-lived, unfolded intermediates in the dissociation of protein complexes. <i>Angewandte Chemie - International Edition</i> , 2007 , 46, 8001-4	16.4	202

27	Protein complexes in the gas phase: technology for structural genomics and proteomics. <i>Chemical Reviews</i> , 2007 , 107, 3544-67	68.1	342
26	Mass measurements of increased accuracy resolve heterogeneous populations of intact ribosomes. <i>Journal of the American Chemical Society</i> , 2006 , 128, 11433-42	16.4	147
25	Structural basis for the inhibition of activin signalling by follistatin. <i>EMBO Journal</i> , 2006 , 25, 1035-45	13	126
24	Aspects of native proteins are retained in vacuum. <i>Current Opinion in Chemical Biology</i> , 2006 , 10, 402-8	9.7	199
23	Tandem mass spectrometry reveals the quaternary organization of macromolecular assemblies. <i>Chemistry and Biology</i> , 2006 , 13, 597-605		191
22	Evidence for macromolecular protein rings in the absence of bulk water. <i>Science</i> , 2005 , 310, 1658-61	33.3	502
21	The influence and utility of varying field strength for the separation of tryptic peptides by ion mobility-mass spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2005 , 16, 158-65	3.5	33
20	The structure of gas-phase bradykinin fragment 1-5 (RPPGF) ions: an ion mobility spectrometry and H/D exchange ion-molecule reaction chemistry study. <i>Journal of the American Society for Mass Spectrometry</i> , 2005 , 16, 893-905	3.5	50
19	Ion mobility-mass spectrometry: a new paradigm for proteomics. <i>International Journal of Mass Spectrometry</i> , 2005 , 240, 301-315	1.9	262
18	Characterization of symmetric complexes of nerve growth factor and the ectodomain of the pan-neurotrophin receptor, p75NTR. <i>Journal of Biological Chemistry</i> , 2005 , 280, 33453-60	5.4	31
17	Peak capacity of ion mobility mass spectrometry: the utility of varying drift gas polarizability for the separation of tryptic peptides. <i>Journal of Mass Spectrometry</i> , 2004 , 39, 361-7	2.2	78
16	An electrostatic focusing ion guide for ion mobility-mass spectrometry. <i>International Journal of Mass Spectrometry</i> , 2004 , 239, 43-49	1.9	88
15	Ion mobility-mass spectrometry applied to cyclic peptide analysis: conformational preferences of gramicidin S and linear analogs in the gas phase. <i>Journal of the American Society for Mass Spectrometry</i> , 2004 , 15, 870-8	3.5	58
14	Resolution equations for high-field ion mobility. <i>Journal of the American Society for Mass Spectrometry</i> , 2004 , 15, 1320-4	3.5	34
13	Analysis of phosphorylated peptides by ion mobility-mass spectrometry. <i>Analytical Chemistry</i> , 2004 , 76, 6727-33	7.8	67
12	Gas-Phase Conformations of Proteolytically Derived Protein Fragments: Influence of Solvent on Peptide Conformation. <i>Journal of Physical Chemistry B</i> , 2004 , 108, 15321-15331	3.4	30
11	Oligonucleotide analysis with MALDI-ion-mobility-TOFMS. <i>Analytical and Bioanalytical Chemistry</i> , 2002 , 373, 612-7	4.4	63
10	Analysis of protein mixtures by matrix-assisted laser desorption ionization-ion mobility-orthogonal-time-of-flight mass spectrometry. <i>International Journal of Mass Spectrometry</i> , 2002 , 219, 253-267	1.9	37

9	A study of peptide-peptide interactions using MALDI ion mobility o-TOF and ESI mass spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2002 , 13, 166-9	3.5	55
8	Peak capacity of ion mobility mass spectrometry: separation of peptides in helium buffer gas. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2002 , 782, 385-92	3.2	74
7	Distinguishing between phosphorylated and nonphosphorylated peptides with ion mobility-mass spectrometry. <i>Journal of Proteome Research</i> , 2002 , 1, 303-6	5.6	74
6	Observation of conserved solution-phase secondary structure in gas-phase tryptic peptides. <i>Journal of the American Chemical Society</i> , 2002 , 124, 4214-5	16.4	57
5	A fundamental introduction to ion mobility mass spectrometry applied to the analysis of biomolecules. <i>Journal of Biomolecular Techniques</i> , 2002 , 13, 56-61	1.1	46
4	Optimization of a matrix-assisted laser desorption ionization-ion mobility-surface-induced dissociation-orthogonal-time-of-flight mass spectrometer: simultaneous acquisition of multiple correlated MS 1 and MS 2 spectra. <i>International Journal of Mass Spectrometry</i> , 2001 , 212, 519-533	1.9	33
3	Surface-induced dissociation on a MALDI-ion mobility-orthogonal time-of-flight mass spectrometer: sequencing peptides from an "in-solution" protein digest. <i>Analytical Chemistry</i> , 2001 , 73, 2233-8	7.8	78
2	Development of a sequential injection system in the capillary format for determinations of the IpaC protein. <i>Analytica Chimica Acta</i> , 2000 , 409, 3-8	6.6	1
1	Coupling high-pressure MALDI with ion mobility/orthogonal time-of-flight mass spectrometry. <i>Analytical Chemistry</i> , 2000 , 72, 3965-71	7.8	144