

Brandon Ruotolo

List of Publications by Year in descending order

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138
papers

10,893
citations

31949

53
h-index

31818

101
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148
all docs

148
docs citations

148
times ranked

6926
citing authors

#	ARTICLE	IF	CITATIONS
1	Ion mobility mass spectrometry analysis of large protein complexes. <i>Nature Protocols</i> , 2008, 3, 1139-1152.	5.5	973
2	Amyloid- β^2 protein oligomerization and the importance of tetramers and dodecamers in the aetiology of Alzheimer's disease. <i>Nature Chemistry</i> , 2009, 1, 326-331.	6.6	835
3	Collision Cross Sections of Proteins and Their Complexes: A Calibration Framework and Database for Gas-Phase Structural Biology. <i>Analytical Chemistry</i> , 2010, 82, 9557-9565.	3.2	694
4	Evidence for Macromolecular Protein Rings in the Absence of Bulk Water. <i>Science</i> , 2005, 310, 1658-1661.	6.0	551
5	Protein Complexes in the Gas Phase: Technology for Structural Genomics and Proteomics. <i>Chemical Reviews</i> , 2007, 107, 3544-3567.	23.0	376
6	Ion mobility mass spectrometry: a new paradigm for proteomics. <i>International Journal of Mass Spectrometry</i> , 2005, 240, 301-315.	0.7	282
7	Mass spectrometry: come of age for structural and dynamical biology. <i>Current Opinion in Structural Biology</i> , 2011, 21, 641-649.	2.6	240
8	Insights into antiamyloidogenic properties of the green tea extract (EGCG)-epigallocatechin-3-gallate toward metal-associated amyloid- β^2 species. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 3743-3748.	3.3	221
9	Aspects of native proteins are retained in vacuum. <i>Current Opinion in Chemical Biology</i> , 2006, 10, 402-408.	2.8	217
10	Ion Mobility Mass Spectrometry Reveals Long-Lived, Unfolded Intermediates in the Dissociation of Protein Complexes. <i>Angewandte Chemie - International Edition</i> , 2007, 46, 8001-8004.	7.2	213
11	Tandem Mass Spectrometry Reveals the Quaternary Organization of Macromolecular Assemblies. <i>Chemistry and Biology</i> , 2006, 13, 597-605.	6.2	206
12	Mass Measurements of Increased Accuracy Resolve Heterogeneous Populations of Intact Ribosomes. <i>Journal of the American Chemical Society</i> , 2006, 128, 11433-11442.	6.6	166
13	Coupling Microdroplet Microreactors with Mass Spectrometry: Reading the Contents of Single Droplets Online. <i>Angewandte Chemie - International Edition</i> , 2009, 48, 3665-3668.	7.2	162
14	Coupling High-Pressure MALDI with Ion Mobility/Orthogonal Time-of-Flight Mass Spectrometry. <i>Analytical Chemistry</i> , 2000, 72, 3965-3971.	3.2	152
15	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.	2.8	151
16	Ion mobility mass spectrometry for structural proteomics. <i>Expert Review of Proteomics</i> , 2012, 9, 47-58.	1.3	150
17	Alternate Dissociation Pathways Identified in Charge-Reduced Protein Complex Ions. <i>Analytical Chemistry</i> , 2010, 82, 5363-5372.	3.2	145
18	Structural basis for the inhibition of activin signalling by follistatin. <i>EMBO Journal</i> , 2006, 25, 1035-1045.	3.5	141

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19	Gas-Phase Unfolding and Disassembly Reveals Stability Differences in Ligand-Bound Multiprotein Complexes. <i>Chemistry and Biology</i> , 2009, 16, 382-390.	6.2	141
20	Characterizing the resolution and accuracy of a second-generation traveling-wave ion mobility separator for biomolecular ions. <i>Analyst, The</i> , 2011, 136, 3534.	1.7	130
21	Collision Induced Unfolding of Intact Antibodies: Rapid Characterization of Disulfide Bonding Patterns, Glycosylation, and Structures. <i>Analytical Chemistry</i> , 2015, 87, 11509-11515.	3.2	129
22	Subunit Architecture of Intact Protein Complexes from Mass Spectrometry and Homology Modeling. <i>Accounts of Chemical Research</i> , 2008, 41, 617-627.	7.6	123
23	Integrating Ion Mobility Mass Spectrometry with Molecular Modelling to Determine the Architecture of Multiprotein Complexes. <i>PLoS ONE</i> , 2010, 5, e12080.	1.1	119
24	Tandem Differential Mobility Analysis-Mass Spectrometry Reveals Partial Gas-Phase Collapse of the GroEL Complex. <i>Journal of Physical Chemistry B</i> , 2011, 115, 3614-3621.	1.2	116
25	A Two-Site Mechanism for the Inhibition of IAPP Amyloidogenesis by Zinc. <i>Journal of Molecular Biology</i> , 2011, 410, 294-306.	2.0	111
26	Collisional and Coulombic Unfolding of Gas-Phase Proteins: High Correlation to Their Domain Structures in Solution. <i>Angewandte Chemie - International Edition</i> , 2014, 53, 9209-9212.	7.2	110
27	CIUSuite: A Quantitative Analysis Package for Collision Induced Unfolding Measurements of Gas-Phase Protein Ions. <i>Analytical Chemistry</i> , 2015, 87, 11516-11522.	3.2	101
28	Subunit Architecture of Multiprotein Assemblies Determined Using Restraints from Gas-Phase Measurements. <i>Structure</i> , 2009, 17, 1235-1243.	1.6	99
29	Resolution of Oligomeric Species during the Aggregation of \hat{A}^2 Using ^{19}F NMR. <i>Biochemistry</i> , 2013, 52, 1903-1912.	1.2	97
30	An electrostatic focusing ion guide for ion mobility-mass spectrometry. <i>International Journal of Mass Spectrometry</i> , 2004, 239, 43-49.	0.7	92
31	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, 8681-8686.	3.3	91
32	Bound Anions Differentially Stabilize Multiprotein Complexes in the Absence of Bulk Solvent. <i>Journal of the American Chemical Society</i> , 2011, 133, 11358-11367.	6.6	89
33	Distinguishing between Phosphorylated and Nonphosphorylated Peptides with Ion Mobility ⁺ Mass Spectrometry. <i>Journal of Proteome Research</i> , 2002, 1, 303-306.	1.8	86
34	CIUSuite 2: Next-Generation Software for the Analysis of Gas-Phase Protein Unfolding Data. <i>Analytical Chemistry</i> , 2019, 91, 3147-3155.	3.2	86
35	Surface-Induced Dissociation on a MALDI-Ion Mobility-Orthogonal Time-of-Flight Mass Spectrometer: \hat{A} Sequencing Peptides from an In-Solution Protein Digest. <i>Analytical Chemistry</i> , 2001, 73, 2233-2238.	3.2	83
36	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, 361-367.	0.7	83

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37	Peak capacity of ion mobility mass spectrometry: Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences, 2002, 782, 385-392.	1.2	82
38	Integrating mass spectrometry of intact protein complexes into structural proteomics. Proteomics, 2012, 12, 1547-1564.	1.3	82
39	Structure-mechanism-based engineering of chemical regulators targeting distinct pathological factors in Alzheimer's disease. Nature Communications, 2016, 7, 13115.	5.8	80
40	Analysis of Phosphorylated Peptides by Ion Mobility-Mass Spectrometry. Analytical Chemistry, 2004, 76, 6727-6733.	3.2	72
41	Oligonucleotide analysis with MALDI ion-mobility TOFMS. Analytical and Bioanalytical Chemistry, 2002, 373, 612-617.	1.9	70
42	Ion mobility-mass spectrometry of intact protein-ligand complexes for pharmaceutical drug discovery and development. Current Opinion in Chemical Biology, 2013, 17, 809-817.	2.8	68
43	Ion Mobility-Mass Spectrometry Reveals the Influence of Subunit Packing and Charge on the Dissociation of Multiprotein Complexes. Analytical Chemistry, 2010, 82, 9702-9710.	3.2	66
44	Variable-Velocity Traveling-Wave Ion Mobility Separation Enhancing Peak Capacity for Data-Independent Acquisition Proteomics. Analytical Chemistry, 2017, 89, 5669-5672.	3.2	66
45	Activation State-Selective Kinase Inhibitor Assay Based on Ion Mobility-Mass Spectrometry. Analytical Chemistry, 2013, 85, 6995-7002.	3.2	65
46	A Redox-Active, Compact Molecule for Cross-Linking Amyloidogenic Peptides into Nontoxic, Off-Pathway Aggregates: In Vitro and In Vivo Efficacy and Molecular Mechanisms. Journal of the American Chemical Society, 2015, 137, 14785-14797.	6.6	65
47	Separating and visualising protein assemblies by means of preparative mass spectrometry and microscopy. Journal of Structural Biology, 2010, 172, 161-168.	1.3	64
48	A Multidimensional Analytical Comparison of Remicade and the Biosimilar Remsima. Analytical Chemistry, 2017, 89, 4838-4846.	3.2	64
49	Residual counter ions can stabilise a large protein complex in the gas phase. International Journal of Mass Spectrometry, 2010, 298, 91-98.	0.7	63
50	A study of peptide-peptide interactions using MALDI ion mobility o-TOF and ESI mass spectrometry. Journal of the American Society for Mass Spectrometry, 2002, 13, 166-169.	1.2	61
51	Observation of Conserved Solution-Phase Secondary Structure in Gas-Phase Tryptic Peptides. Journal of the American Chemical Society, 2002, 124, 4214-4215.	6.6	60
52	A rationally designed small molecule for identifying an in vivo link between metal-amyloid- β complexes and the pathogenesis of Alzheimer's disease. Chemical Science, 2015, 6, 1879-1886.	3.7	60
53	Ion mobility-mass spectrometry applied to cyclic peptide analysis: Conformational preferences of gramicidin S and linear analogs in the gas phase. Journal of the American Society for Mass Spectrometry, 2004, 15, 870-878.	1.2	59
54	Methodology for measuring conformation of solvent-disrupted protein subunits using T-WAVE ion mobility MS: An investigation into eukaryotic initiation factors. Journal of the American Society for Mass Spectrometry, 2009, 20, 1699-1706.	1.2	54

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55	The structure of gas-phase bradykinin fragment 1â€“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.	1.2	53
56	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, 4790-4801.	2.0	51
57	Quadrupole-Time-of-Flight Mass Spectrometer Modified for Higher-Energy Dissociation Reduces Protein Assemblies to Peptide Fragments. <i>Analytical Chemistry</i> , 2009, 81, 1270-1274.	3.2	50
58	Bound Cations Significantly Stabilize the Structure of Multiprotein Complexes in the Gas Phase. <i>Angewandte Chemie - International Edition</i> , 2012, 51, 5692-5695.	7.2	50
59	Sizing Up Proteinâ€“Ligand Complexes: The Rise of Structural Mass Spectrometry Approaches in the Pharmaceutical Sciences. <i>Annual Review of Analytical Chemistry</i> , 2017, 10, 25-44.	2.8	50
60	Gas-phase protein assemblies: Unfolding landscapes and preserving native-like structures using noncovalent adducts. <i>Chemical Physics Letters</i> , 2012, 524, 1-9.	1.2	48
61	A fundamental introduction to ion mobility mass spectrometry applied to the analysis of biomolecules. <i>Journal of Biomolecular Techniques</i> , 2002, 13, 56-61.	0.8	48
62	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.	6.6	46
63	An Improved Calibration Approach for Traveling Wave Ion Mobility Spectrometry: Robust, High-Precision Collision Cross Sections. <i>Analytical Chemistry</i> , 2021, 93, 3542-3550.	3.2	44
64	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.	0.7	43
65	Symmetryâ€“Directed Selfâ€“Assembly of a Tetrahedral Protein Cage Mediated by de Novoâ€“Designed Coiled Coils. <i>ChemBioChem</i> , 2017, 18, 1888-1892.	1.3	42
66	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.	1.2	39
67	Collisional unfolding of multiprotein complexes reveals cooperative stabilization upon ligand binding. <i>Protein Science</i> , 2015, 24, 1272-1281.	3.1	39
68	Enhanced Collision Induced Unfolding and Electron Capture Dissociation of Native-like Protein Ions. <i>Analytical Chemistry</i> , 2020, 92, 15489-15496.	3.2	38
69	Resolution equations for high-field ion mobility. <i>Journal of the American Society for Mass Spectrometry</i> , 2004, 15, 1320-1324.	1.2	37
70	Reactivity of Diphenylpropynone Derivatives Toward Metal-Associated Amyloid-Î² Species. <i>Inorganic Chemistry</i> , 2012, 51, 12959-12967.	1.9	36
71	Biosimilarity under stress: A forced degradation study of RemicadeÂ® and Remsimaâ„¢. <i>MABs</i> , 2017, 9, 1197-1209.	2.6	36
72	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.	0.7	35

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73	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, 158-165.	1.2	35
74	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.	1.2	34
75	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, 33453-33460.	1.6	34
76	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.	1.2	33
77	A Modified Drift Tube Ion Mobility-Mass Spectrometer for Charge-Multiplexed Collision-Induced Unfolding. <i>Analytical Chemistry</i> , 2019, 91, 8137-8146.	3.2	31
78	Mass Spectrometry Methods for Measuring Protein Stability. <i>Chemical Reviews</i> , 2022, 122, 7690-7719.	23.0	31
79	Exploring the reactivity of flavonoid compounds with metal-associated amyloid- β^2 species. <i>Dalton Transactions</i> , 2012, 41, 6558.	1.6	30
80	Amyloid- β^2 neuropeptide interactions assessed by ion mobility-mass spectrometry. <i>Physical Chemistry Chemical Physics</i> , 2013, 15, 8952.	1.3	30
81	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.	6.6	30
82	Collision induced unfolding detects subtle differences in intact antibody glycoforms and associated fragments. <i>International Journal of Mass Spectrometry</i> , 2018, 425, 1-9.	0.7	30
83	The growing role of structural mass spectrometry in the discovery and development of therapeutic antibodies. <i>Analyst</i> , 2018, 143, 2459-2468.	1.7	29
84	Collision Induced Unfolding Classifies Ligands Bound to the Integral Membrane Translocator Protein. <i>Analytical Chemistry</i> , 2019, 91, 15469-15476.	3.2	29
85	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.	6.6	29
86	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.	0.7	28
87	Effects of hydroxyl group variations on a flavonoid backbone toward modulation of metal-free and metal-induced amyloid- β^2 aggregation. <i>Inorganic Chemistry Frontiers</i> , 2016, 3, 381-392.	3.0	28
88	Quantitative collision-induced unfolding differentiates model antibody drug conjugates. <i>Protein Science</i> , 2019, 28, 598-608.	3.1	26
89	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.	1.7	25
90	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.	1.6	25

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91	SERF engages in a fuzzy complex that accelerates primary nucleation of amyloid proteins. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 23040-23049.	3.3	25
92	Native Mass Spectrometry, Ion Mobility, Electron-Capture Dissociation, and Modeling Provide Structural Information for Gas-Phase Apolipoprotein E Oligomers. Journal of the American Society for Mass Spectrometry, 2019, 30, 876-885.	1.2	25
93	Evaluation of de novo-designed coiled coils as off-the-shelf components for protein assembly. Molecular Systems Design and Engineering, 2017, 2, 140-148.	1.7	22
94	Multifaceted assessment of rituximab biosimilarity: The impact of glycan microheterogeneity on Fc function. European Journal of Pharmaceutics and Biopharmaceutics, 2020, 146, 111-124.	2.0	21
95	A Single Subunit Directs the Assembly of the Escherichia coli DNA Sliding Clamp Loader. Structure, 2010, 18, 285-292.	1.6	20
96	Mechanism of the small ATP-independent chaperone Spy is substrate specific. Nature Communications, 2021, 12, 851.	5.8	20
97	Ion Mobility-Mass Spectrometry Differentiates Protein Quaternary Structures Formed in Solution and in Electrospray Droplets. Analytical Chemistry, 2015, 87, 6808-6813.	3.2	19
98	Importance of the Dimethylamino Functionality on a Multifunctional Framework for Regulating Metals, Amyloid- β , and Oxidative Stress in Alzheimer's Disease. Inorganic Chemistry, 2016, 55, 5000-5013.	1.9	19
99	Ion Mobility-Mass Spectrometry Reveals Highly-Compact Intermediates in the Collision Induced Dissociation of Charge-Reduced Protein Complexes. Journal of the American Society for Mass Spectrometry, 2016, 27, 41-49.	1.2	19
100	Fixed-Charge Trimethyl Pyridinium Modification for Enabling Enhanced Top-Down Mass Spectrometry Sequencing of Intact Protein Complexes. Analytical Chemistry, 2018, 90, 2756-2764.	3.2	19
101	Assessment of biosimilarity under native and heat-stressed conditions: rituximab, bevacizumab, and trastuzumab originators and biosimilars. Analytical and Bioanalytical Chemistry, 2020, 412, 763-775.	1.9	19
102	Hofmeister Salts Recover a Misfolded Multiprotein Complex for Subsequent Structural Measurements in the Gas Phase. Angewandte Chemie - International Edition, 2013, 52, 8329-8332.	7.2	18
103	Collision induced unfolding and dissociation differentiates ATP-competitive from allosteric protein tyrosine kinase inhibitors. International Journal of Mass Spectrometry, 2018, 427, 151-156.	0.7	18
104	Ion mobility mass spectrometry reveals the role of peripheral myelin protein dimers in peripheral neuropathy. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	18
105	Pervasive Charge Solvation Permeates Native-like Protein Ions and Dramatically Influences Top-down Sequencing Data. Journal of the American Chemical Society, 2020, 142, 6750-6760.	6.6	15
106	Traveling-wave ion mobility-mass spectrometry reveals additional mechanistic details in the stabilization of protein complex ions through tuned salt additives. International Journal for Ion Mobility Spectrometry, 2013, 16, 41-50.	1.4	14
107	Dramatically stabilizing multiprotein complex structure in the absence of bulk water using tuned Hofmeister salts. Faraday Discussions, 2013, 160, 371-388.	1.6	14
108	Ion Mobility-Mass Spectrometry Analysis of Cross-Linked Intact Multiprotein Complexes: Enhanced Gas-Phase Stabilities and Altered Dissociation Pathways. Analytical Chemistry, 2016, 88, 5290-5298.	3.2	14

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109	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, 1328-1337.	1.2	13
110	Ion mobility-mass spectrometry of charge-reduced protein complexes reveals general trends in the collisional ejection of compact subunits. <i>Analyst</i> , The, 2015, 140, 7020-7029.	1.7	13
111	Minor Structural Variations of Small Molecules Tune Regulatory Activities toward Pathological Factors in Alzheimer's Disease. <i>ChemMedChem</i> , 2017, 12, 1828-1838.	1.6	13
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.	1.2	13
113	Infliximab Biosimilars in the Age of Personalized Medicine. <i>Trends in Biotechnology</i> , 2018, 36, 987-992.	4.9	12
114	Mechanistic insights into accelerated $\hat{1}\pm$ -synuclein aggregation mediated by human microbiome-associated functional amyloids. <i>Journal of Biological Chemistry</i> , 2022, 298, 102088.	1.6	12
115	An Algorithm for Building Multi-State Classifiers Based on Collision-Induced Unfolding Data. <i>Analytical Chemistry</i> , 2019, 91, 10407-10412.	3.2	11
116	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.	1.3	10
117	IMTBX and Grppr: Software for Top-Down Proteomics Utilizing Ion Mobility-Mass Spectrometry. <i>Analytical Chemistry</i> , 2018, 90, 2369-2375.	3.2	10
118	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.	1.2	10
119	Collision-Induced Unfolding Reveals Stability Differences in Infliximab Therapeutics under Native and Heat Stress Conditions. <i>Analytical Chemistry</i> , 2021, 93, 16166-16174.	3.2	10
120	Ion Mobility- $\hat{1}\pm$ Mass Spectrometry Reveals the Structures and Stabilities of Biotherapeutic Antibody Aggregates. <i>Analytical Chemistry</i> , 2022, 94, 6745-6753.	3.2	10
121	Characterization of a [4Fe-4S]-dependent LarE sulfur insertase that facilitates nickel-pincer nucleotide cofactor biosynthesis in <i>Thermotoga maritima</i> . <i>Journal of Biological Chemistry</i> , 2022, 298, 102131.	1.6	10
122	Ion Mobility-Mass Spectrometry Reveals a Dipeptide That Acts as a Molecular Chaperone for Amyloid $\hat{1}^2$. <i>ACS Chemical Biology</i> , 2017, 12, 1113-1120.	1.6	9
123	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, 11360-11368.	3.2	8
124	Collision Cross Sections for Native Proteomics: Challenges and Opportunities. <i>Journal of Proteome Research</i> , 2022, 21, 2-8.	1.8	8
125	Comparing Selected-Ion Collision Induced Unfolding with All Ion Unfolding Methods for Comprehensive Protein Conformational Characterization. <i>Journal of the American Society for Mass Spectrometry</i> , 2022, 33, 944-951.	1.2	8
126	Hydrogen/deuterium exchange-mass spectrometry analysis of high concentration biotherapeutics: application to phase-separated antibody formulations. <i>MAbs</i> , 2019, 11, 779-788.	2.6	7

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127	Complex Formed between Intramembrane Metalloprotease SpoIVFB and Its Substrate, Pro- β K. <i>Journal of Biological Chemistry</i> , 2016, 291, 10347-10362.	1.6	6
128	Kinetic Analysis of Transient Intermediates in the Mechanism of Prenyl-Flavin-Dependent Ferulic Acid Decarboxylase. <i>Biochemistry</i> , 2021, 60, 125-134.	1.2	6
129	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.	1.2	5
130	Biochemical characterization of the interaction between KRAS and Argonaute 2. <i>Biochemistry and Biophysics Reports</i> , 2022, 29, 101191.	0.7	5
131	Ion Mobility Mass Spectrometry. <i>Analyst</i> , The, 2015, 140, 6772-6774.	1.7	4
132	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.	1.2	4
133	Oligomerization, trans-reduction, and instability of mutant NOTCH3 in inherited vascular dementia. <i>Communications Biology</i> , 2022, 5, 331.	2.0	4
134	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.	2.6	3
135	Verteporfin is a substrate-selective β -secretase inhibitor that binds the amyloid precursor protein transmembrane domain. <i>Journal of Biological Chemistry</i> , 2022, 298, 101792.	1.6	3
136	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.	0.7	2
137	Bicarbonate buffers can promote crosslinking and alternative gas-phase dissociation pathways for multiprotein complexes. <i>International Journal of Mass Spectrometry</i> , 2021, 469, 116687.	0.7	1
138	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, 870-878.	1.2	0