

Alison E Ashcroft

List of Publications by Year in descending order

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90
papers

4,552
citations

71061

41
h-index

106281

65
g-index

91
all docs

91
docs citations

91
times ranked

5086
citing authors

#	ARTICLE	IF	CITATIONS
1	Investigation of D76N β -Microglobulin Using Protein Footprinting and Structural Mass Spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2021, 32, 1583-1592.	1.2	3
2	Reference Protocol to Assess Analytical Performance of Higher Order Structural Analysis Measurements: Results from an Interlaboratory Comparison. <i>Analytical Chemistry</i> , 2021, 93, 9041-9048.	3.2	4
3	Validation of ion mobility spectrometry -- mass spectrometry as a screening tool to identify type II kinase inhibitors of FGFR1 kinase. <i>Rapid Communications in Mass Spectrometry</i> , 2021, , e9130.	0.7	4
4	Mass Spectrometry Characterization of Higher Order Structural Changes Associated with the Fc-glycan Structure of the NISTmAb Reference Material, RM 8761. <i>Journal of the American Society for Mass Spectrometry</i> , 2020, 31, 553-564.	1.2	16
5	Inter-domain dynamics in the chaperone SurA and multi-site binding to its outer membrane protein clients. <i>Nature Communications</i> , 2020, 11, 2155.	5.8	48
6	An in vivo platform to select and evolve aggregation-resistant proteins. <i>Nature Communications</i> , 2020, 11, 1816.	5.8	22
7	Long-Range Conformational Changes in Monoclonal Antibodies Revealed Using FPOP-LC-MS/MS. <i>Analytical Chemistry</i> , 2019, 91, 15163-15170.	3.2	18
8	Molecular insights into the surface-catalyzed secondary nucleation of amyloid- β (A β) Tj ETQqO 0 0 rgBT /Overlock 10 Tf	4.7	54
9	Mass spectrometry-based studies of virus assembly. <i>Current Opinion in Virology</i> , 2019, 36, 17-24.	2.6	16
10	Conformational flexibility within the nascent polypeptide-associated complex enables its interactions with structurally diverse client proteins. <i>Journal of Biological Chemistry</i> , 2018, 293, 8554-8568.	1.6	20
11	Identification of a novel site of interaction between ataxin-3 and the amyloid aggregation inhibitor polyglutamine binding peptide 1. <i>European Journal of Mass Spectrometry</i> , 2018, 24, 129-140.	0.5	4
12	Comparing Hydrogen Deuterium Exchange and Fast Photochemical Oxidation of Proteins: a Structural Characterisation of Wild-Type and β -Microglobulin. <i>Journal of the American Society for Mass Spectrometry</i> , 2018, 29, 2413-2426.	1.2	43
13	Hydrodynamics of the VanA-type VanS histidine kinase: an extended solution conformation and first evidence for interactions with vancomycin. <i>Scientific Reports</i> , 2017, 7, 46180.	1.6	22
14	Inducing protein aggregation by extensional flow. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 4673-4678.	3.3	77
15	Understanding co-polymerization in amyloid formation by direct observation of mixed oligomers. <i>Chemical Science</i> , 2017, 8, 5030-5040.	3.7	37
16	Investigating the Structural Compaction of Biomolecules Upon Transition to the Gas-Phase Using ESI-TWIMS-MS. <i>Journal of the American Society for Mass Spectrometry</i> , 2017, 28, 1855-1862.	1.2	42
17	Effects of Periplasmic Chaperones and Membrane Thickness on BamA-Catalyzed Outer-Membrane Protein Folding. <i>Journal of Molecular Biology</i> , 2017, 429, 3776-3792.	2.0	63
18	Topological Dissection of the Membrane Transport Protein Mhp1 Derived from Cysteine Accessibility and Mass Spectrometry. <i>Analytical Chemistry</i> , 2017, 89, 8844-8852.	3.2	28

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19	Small molecule probes of protein aggregation. <i>Current Opinion in Chemical Biology</i> , 2017, 39, 90-99.	2.8	77
20	FPOP-LC-MS/MS Suggests Differences in Interaction Sites of Amphipols and Detergents with Outer Membrane Proteins. <i>Journal of the American Society for Mass Spectrometry</i> , 2017, 28, 50-55.	1.2	33
21	Widespread, routine occurrence of pharmaceuticals in sewage effluent, combined sewer overflows and receiving waters. <i>Environmental Pollution</i> , 2017, 220, 1447-1455.	3.7	95
22	Engineering the surface properties of a human monoclonal antibody prevents self-association and rapid clearance in vivo. <i>Scientific Reports</i> , 2016, 6, 38644.	1.6	89
23	Skp is a multivalent chaperone of outer-membrane proteins. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 786-793.	3.6	82
24	Lateral opening in the intact β^2 -barrel assembly machinery captured by cryo-EM. <i>Nature Communications</i> , 2016, 7, 12865.	5.8	157
25	An in vivo platform for identifying inhibitors of protein aggregation. <i>Nature Chemical Biology</i> , 2016, 12, 94-101.	3.9	75
26	Characterization of Amyloid Oligomers by Electrospray Ionization-Ion Mobility Spectrometry-Mass Spectrometry (ESI-IMS-MS). <i>Methods in Molecular Biology</i> , 2016, 1345, 115-132.	0.4	10
27	ESI-IMS-MS: A method for rapid analysis of protein aggregation and its inhibition by small molecules. <i>Methods</i> , 2016, 95, 62-69.	1.9	50
28	A comparison of the folding characteristics of free and ribosome-attached polypeptide chains using limited proteolysis and mass spectrometry. <i>Protein Science</i> , 2015, 24, 1282-1291.	3.1	6
29	Systematic analysis of the use of amphipathic polymers for studies of outer membrane proteins using mass spectrometry. <i>International Journal of Mass Spectrometry</i> , 2015, 391, 54-61.	0.7	30
30	Changes in protein structure monitored by use of gas-phase hydrogen/deuterium exchange. <i>Proteomics</i> , 2015, 15, 2842-2850.	1.3	12
31	Amphipols Outperform Dodecylmaltoside Micelles in Stabilizing Membrane Protein Structure in the Gas Phase. <i>Analytical Chemistry</i> , 2015, 87, 1118-1126.	3.2	50
32	Insights into the consequences of co-polymerisation in the early stages of IAPP and A β peptide assembly from mass spectrometry. <i>Analyst</i> , 2015, 140, 6990-6999.	1.7	48
33	Assembly Pathway of Hepatitis B Core Virus-like Particles from Genetically Fused Dimers. <i>Journal of Biological Chemistry</i> , 2015, 290, 16238-16245.	1.6	24
34	Using hydroxyl radical footprinting to explore the free energy landscape of protein folding. <i>Methods</i> , 2015, 89, 38-44.	1.9	31
35	Mass spectrometric methods to analyze the structural organization of macromolecular complexes. <i>Methods</i> , 2015, 89, 13-21.	1.9	55
36	Examination of Ataxin-3 (atx-3) Aggregation by Structural Mass Spectrometry Techniques: A Rationale for Expedited Aggregation upon Polyglutamine (polyQ) Expansion*. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 1241-1253.	2.5	33

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37	Screening and classifying small-molecule inhibitors of amyloid formation using ion mobility spectrometry-mass spectrometry. <i>Nature Chemistry</i> , 2015, 7, 73-81.	6.6	255
38	Probing Bunyavirus N protein oligomerisation using mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2014, 28, 793-800.	0.7	6
39	A comparison of the electromechanical properties of structurally diverse proteins by molecular dynamics simulation. <i>Journal of Biomolecular Structure and Dynamics</i> , 2014, 32, 1734-1741.	2.0	0
40	Insights into the role of the beta-2 microglobulin D-strand in amyloid propensity revealed by mass spectrometry. <i>Molecular BioSystems</i> , 2014, 10, 412-420.	2.9	22
41	Ion Mobility Spectrometry-mass Spectrometry Defines the Oligomeric Intermediates in Amylin Amyloid Formation and the Mode of Action of Inhibitors. <i>Journal of the American Chemical Society</i> , 2014, 136, 660-670.	6.6	158
42	The Feeding Tube of Cyst Nematodes: Characterisation of Protein Exclusion. <i>PLoS ONE</i> , 2014, 9, e87289.	1.1	14
43	Monitoring oligomer formation from self-aggregating amylin peptides using ESI-HMS-MS. <i>International Journal for Ion Mobility Spectrometry</i> , 2013, 16, 29-39.	1.4	13
44	A tale of a tail: Structural insights into the conformational properties of the polyglutamine protein ataxin-3. <i>International Journal of Mass Spectrometry</i> , 2013, 345-347, 63-70.	0.7	15
45	Using Ion Mobility Spectrometry-mass Spectrometry to Decipher the Conformational and Assembly Characteristics of the Hepatitis B Capsid Protein. <i>Biophysical Journal</i> , 2013, 105, 1258-1267.	0.2	21
46	<i>De novo</i> sequencing of short interfering ribonucleic acids facilitated by use of tandem mass spectrometry with ion mobility spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2013, 27, 2247-2254.	0.7	6
47	Thermodynamic origins of protein folding, allostery, and capsid formation in the human hepatitis B virus core protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E2782-91.	3.3	64
48	The Role of Ion Mobility Spectrometry-mass Spectrometry in the Analysis of Protein Reference Standards. <i>Analytical Chemistry</i> , 2013, 85, 7205-7212.	3.2	21
49	Expanding the Repertoire of Amyloid Polymorphs by Co-polymerization of Related Protein Precursors. <i>Journal of Biological Chemistry</i> , 2013, 288, 7327-7337.	1.6	36
50	A snapshot of electrified nanodroplets undergoing Coulomb fission. <i>Applied Physics Letters</i> , 2012, 100, 074103.	1.5	4
51	Amphipathic Polymers Enable the Study of Functional Membrane Proteins in the Gas Phase. <i>Analytical Chemistry</i> , 2012, 84, 9841-9847.	3.2	61
52	The role of conformational flexibility in β 2-microglobulin amyloid fibril formation at neutral pH. <i>Rapid Communications in Mass Spectrometry</i> , 2012, 26, 1783-1792.	0.7	24
53	Protein Misfolding and Toxicity in Dialysis-Related Amyloidosis. , 2012, , 377-405.		2
54	Determination of testosterone and epitestosterone glucuronides in urine by ultra performance liquid chromatography-ion mobility-mass spectrometry. <i>Analyst</i> , The, 2011, 136, 3911.	1.7	37

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55	Structure and Dynamics of Oligomeric Intermediates in β 2-Microglobulin Self-Assembly. <i>Biophysical Journal</i> , 2011, 101, 1238-1247.	0.2	25
56	Ligand binding to distinct states diverts aggregation of an amyloid-forming protein. <i>Nature Chemical Biology</i> , 2011, 7, 730-739.	3.9	93
57	Unraveling Lactococcal Phage Baseplate Assembly by Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M111.009787.	2.5	24
58	Mass spectrometry and the amyloid problem—How far can we go in the gas phase?. <i>Journal of the American Society for Mass Spectrometry</i> , 2010, 21, 1087-1096.	1.2	61
59	Considerations in experimental and theoretical collision cross-section measurements of small molecules using travelling wave ion mobility spectrometry-mass spectrometry. <i>International Journal of Mass Spectrometry</i> , 2010, 298, 17-23.	0.7	72
60	Defining topological features of membrane proteins by nanoelectrospray ionisation mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2010, 24, 276-284.	0.7	12
61	Determining the topology of virus assembly intermediates using ion mobility spectrometry—mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2010, 24, 3033-3042.	0.7	81
62	Elongated oligomers in β 2-microglobulin amyloid assembly revealed by ion mobility spectrometry-mass spectrometry. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 6794-6798.	3.3	147
63	Viral Genomic Single-Stranded RNA Directs the Pathway Toward a T=3 Capsid. <i>Journal of Molecular Biology</i> , 2010, 395, 924-936.	2.0	60
64	The Impact of Viral RNA on Assembly Pathway Selection. <i>Journal of Molecular Biology</i> , 2010, 401, 298-308.	2.0	64
65	HDX-ESI-MS reveals enhanced conformational dynamics of the amyloidogenic protein β 2-microglobulin upon release from the MHC-1. <i>Journal of the American Society for Mass Spectrometry</i> , 2009, 20, 278-286.	1.2	37
66	Deciphering Drift Time Measurements from Travelling Wave Ion Mobility Spectrometry-Mass Spectrometry Studies. <i>European Journal of Mass Spectrometry</i> , 2009, 15, 113-130.	0.5	312
67	Critical concentrations of β -sheet peptide self-assembly quantified directly by nanoelectrospray ionization mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2008, 22, 1611-1614.	0.7	4
68	Insights into virus capsid assembly from non-covalent mass spectrometry. <i>Mass Spectrometry Reviews</i> , 2008, 27, 575-595.	2.8	47
69	RNA Packing Specificity and Folding during Assembly of the Bacteriophage MS2. <i>Computational and Mathematical Methods in Medicine</i> , 2008, 9, 339-349.	0.7	12
70	A Simple, RNA-Mediated Allosteric Switch Controls the Pathway to Formation of a T=3 Viral Capsid. <i>Journal of Molecular Biology</i> , 2007, 369, 541-552.	2.0	128
71	Real-Time Measurement of Myosin—Nucleotide Noncovalent Complexes by Electrospray Ionization Mass Spectrometry. <i>Biophysical Journal</i> , 2007, 93, 914-919.	0.2	6
72	Review. <i>Journal of the American Society for Mass Spectrometry</i> , 2007, 18, R3-R4.	1.2	2

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73	Monitoring copopulated conformational states during protein folding events using electrospray ionization-ion mobility spectrometry-mass spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2007, 18, 2180-2190.	1.2	122
74	Direct Observation of Oligomeric Species formed in the Early Stages of Amyloid Fibril Formation using Electrospray Ionisation Mass Spectrometry. <i>Journal of Molecular Biology</i> , 2006, 364, 9-19.	2.0	137
75	Donor-Strand Exchange in Chaperone-Assisted Pilus Assembly Proceeds through a Concerted β^2 Strand Displacement Mechanism. <i>Molecular Cell</i> , 2006, 22, 831-842.	4.5	159
76	Investigating the structural properties of amyloid-like fibrils formed in vitro from β^2 -microglobulin using limited proteolysis and electrospray ionisation mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2006, 20, 1628-1636.	0.7	58
77	Engineering Thermal Stability in RNA Phage Capsids via Disulphide Bonds. <i>Journal of Nanoscience and Nanotechnology</i> , 2005, 5, 2034-2041.	0.9	64
78	Recent developments in electrospray ionisation mass spectrometry: noncovalently bound protein complexes. <i>Natural Product Reports</i> , 2005, 22, 452.	5.2	57
79	Co-populated Conformational Ensembles of β^2 -Microglobulin Uncovered Quantitatively by Electrospray Ionization Mass Spectrometry. <i>Journal of Biological Chemistry</i> , 2004, 279, 27069-27077.	1.6	68
80	Separation of β^2 -microglobulin conformers by high-field asymmetric waveform ion mobility spectrometry (FAIMS) coupled to electrospray ionisation mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2004, 18, 2229-2234.	0.7	54
81	Protein and peptide identification: the role of mass spectrometry in proteomics. <i>Natural Product Reports</i> , 2003, 20, 202-215.	5.2	47
82	The Effect of Dimethylbiguanide on Thrombin Activity, FXIII Activation, Fibrin Polymerization, and Fibrin Clot Formation. <i>Diabetes</i> , 2002, 51, 189-197.	0.3	90
83	Structural Plasticity and Noncovalent Substrate Binding in the GroEL Apical Domain. <i>Journal of Biological Chemistry</i> , 2002, 277, 33115-33126.	1.6	31
84	Molecular dissection of membrane-transport proteins: mass spectrometry and sequence determination of the galactose-H ⁺ symport protein, GalP, of <i>Escherichia coli</i> and quantitative assay of the incorporation of [ring-2- ¹³ C]histidine and ¹⁵ NH ₃ . <i>Biochemical Journal</i> , 2002, 363, 243-252.	1.7	33
85	An Investigation into the Properties of a Chaperone Domain and Analysis of the Non-covalently Bound Complexes with Peptide Substrates using Mass Spectrometry. <i>Biochemical Society Transactions</i> , 2000, 28, A70-A70.	1.6	0
86	A study of human coagulation factor XIII A-subunit by electrospray ionisation mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2000, 14, 1607-1611.	0.7	15
87	RNA aptamers for the MS2 bacteriophage coat protein and the wild-type RNA operator have similar solution behaviour. <i>Nucleic Acids Research</i> , 2000, 28, 489-497.	6.5	32
88	GroEL accelerates the refolding of hen lysozyme without changing its folding mechanism. <i>Nature Structural Biology</i> , 1999, 6, 683-690.	9.7	59
89	A near-native state on the slow refolding pathway of hen lysozyme. <i>Protein Science</i> , 1999, 8, 35-44.	3.1	35
90	The dhna gene of <i>Escherichia coli</i> encodes a Class I fructose bisphosphate aldolase. <i>Biochemical Journal</i> , 1998, 331, 437-445.	1.7	65