

# Alison E Ashcroft

## List of Publications by Year in descending order

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90  
papers

4,552  
citations

71102

41  
h-index

106344

65  
g-index

91  
all docs

91  
docs citations

91  
times ranked

5086  
citing authors

#	ARTICLE	IF	CITATIONS
1	Investigation of D76N $\beta$ -Microglobulin Using Protein Footprinting and Structural Mass Spectrometry. Journal of the American Society for Mass Spectrometry, 2021, 32, 1583-1592.	2.8	3
2	Reference Protocol to Assess Analytical Performance of Higher Order Structural Analysis Measurements: Results from an Interlaboratory Comparison. Analytical Chemistry, 2021, 93, 9041-9048.	6.5	4
3	Validation of ion mobility spectrometry $\times$ mass spectrometry as a screening tool to identify type II kinase inhibitors of FGFR1 kinase. Rapid Communications in Mass Spectrometry, 2021, , e9130.	1.5	4
4	Mass Spectrometry Characterization of Higher Order Structural Changes Associated with the Fc-glycan Structure of the NISTmAb Reference Material, RM 8761. Journal of the American Society for Mass Spectrometry, 2020, 31, 553-564.	2.8	16
5	Inter-domain dynamics in the chaperone SurA and multi-site binding to its outer membrane protein clients. Nature Communications, 2020, 11, 2155.	12.8	48
6	An in vivo platform to select and evolve aggregation-resistant proteins. Nature Communications, 2020, 11, 1816.	12.8	22
7	Long-Range Conformational Changes in Monoclonal Antibodies Revealed Using FPOP-LC-MS/MS. Analytical Chemistry, 2019, 91, 15163-15170.	6.5	18
8	Molecular insights into the surface-catalyzed secondary nucleation of amyloid- $\beta$ (A $\beta$ ) Tj ETQq0 0 0 r gBT /Overlock 10 Tf	10.3	54
9	Mass spectrometry-based studies of virus assembly. Current Opinion in Virology, 2019, 36, 17-24.	5.4	16
10	Conformational flexibility within the nascent polypeptide-associated complex enables its interactions with structurally diverse client proteins. Journal of Biological Chemistry, 2018, 293, 8554-8568.	3.4	20
11	Identification of a novel site of interaction between ataxin-3 and the amyloid aggregation inhibitor polyglutamine binding peptide 1. European Journal of Mass Spectrometry, 2018, 24, 129-140.	1.0	4
12	Comparing Hydrogen Deuterium Exchange and Fast Photochemical Oxidation of Proteins: a Structural Characterisation of Wild-Type and $\beta$ -N6 $\beta$ -Microglobulin. Journal of the American Society for Mass Spectrometry, 2018, 29, 2413-2426.	2.8	43
13	Hydrodynamics of the VanA-type VanS histidine kinase: an extended solution conformation and first evidence for interactions with vancomycin. Scientific Reports, 2017, 7, 46180.	3.3	22
14	Inducing protein aggregation by extensional flow. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 4673-4678.	7.1	77
15	Understanding co-polymerization in amyloid formation by direct observation of mixed oligomers. Chemical Science, 2017, 8, 5030-5040.	7.4	37
16	Investigating the Structural Compaction of Biomolecules Upon Transition to the Gas-Phase Using ESI-TWIMS-MS. Journal of the American Society for Mass Spectrometry, 2017, 28, 1855-1862.	2.8	42
17	Effects of Periplasmic Chaperones and Membrane Thickness on BamA-Catalyzed Outer-Membrane Protein Folding. Journal of Molecular Biology, 2017, 429, 3776-3792.	4.2	63
18	Topological Dissection of the Membrane Transport Protein Mhp1 Derived from Cysteine Accessibility and Mass Spectrometry. Analytical Chemistry, 2017, 89, 8844-8852.	6.5	28

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19	Small molecule probes of protein aggregation. <i>Current Opinion in Chemical Biology</i> , 2017, 39, 90-99.	6.1	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.	2.8	33
21	Widespread, routine occurrence of pharmaceuticals in sewage effluent, combined sewer overflows and receiving waters. <i>Environmental Pollution</i> , 2017, 220, 1447-1455.	7.5	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.	3.3	89
23	Skp is a multivalent chaperone of outer-membrane proteins. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 786-793.	8.2	82
24	Lateral opening in the intact $\beta^2$ -barrel assembly machinery captured by cryo-EM. <i>Nature Communications</i> , 2016, 7, 12865.	12.8	157
25	An in vivo platform for identifying inhibitors of protein aggregation. <i>Nature Chemical Biology</i> , 2016, 12, 94-101.	8.0	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.	0.9	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.	3.8	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.	7.6	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.	1.5	30
30	Changes in protein structure monitored by use of gas-phase hydrogen/deuterium exchange. <i>Proteomics</i> , 2015, 15, 2842-2850.	2.2	12
31	Amphipols Outperform Dodecylmaltoside Micelles in Stabilizing Membrane Protein Structure in the Gas Phase. <i>Analytical Chemistry</i> , 2015, 87, 1118-1126.	6.5	50
32	Insights into the consequences of co-polymerisation in the early stages of IAPP and $\text{A}\beta$ peptide assembly from mass spectrometry. <i>Analyst</i> , 2015, 140, 6990-6999.	3.5	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.	3.4	24
34	Using hydroxyl radical footprinting to explore the free energy landscape of protein folding. <i>Methods</i> , 2015, 89, 38-44.	3.8	31
35	Mass spectrometric methods to analyze the structural organization of macromolecular complexes. <i>Methods</i> , 2015, 89, 13-21.	3.8	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.	3.8	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.	13.6	255
38	Probing Bunyavirus N protein oligomerisation using mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2014, 28, 793-800.	1.5	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.	3.5	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.	13.7	158
42	The Feeding Tube of Cyst Nematodes: Characterisation of Protein Exclusion. <i>PLoS ONE</i> , 2014, 9, e87289.	2.5	14
43	Monitoring oligomer formation from self-aggregating amylin peptides using ESI-IMS-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.	1.5	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.	0.5	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.	1.5	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.	7.1	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.	6.5	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.	3.4	36
50	A snapshot of electrified nanodroplets undergoing Coulomb fission. <i>Applied Physics Letters</i> , 2012, 100, 074103.	3.3	4
51	Amphipathic Polymers Enable the Study of Functional Membrane Proteins in the Gas Phase. <i>Analytical Chemistry</i> , 2012, 84, 9841-9847.	6.5	61
52	The role of conformational flexibility in $\beta_2$ -microglobulin amyloid fibril formation at neutral pH. <i>Rapid Communications in Mass Spectrometry</i> , 2012, 26, 1783-1792.	1.5	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.	3.5	37

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55	Structure and Dynamics of Oligomeric Intermediates in $\beta$ 2-Microglobulin Self-Assembly. Biophysical Journal, 2011, 101, 1238-1247.	0.5	25
56	Ligand binding to distinct states diverts aggregation of an amyloid-forming protein. Nature Chemical Biology, 2011, 7, 730-739.	8.0	93
57	Unraveling Lactococcal Phage Baseplate Assembly by Mass Spectrometry. Molecular and Cellular Proteomics, 2011, 10, M111.009787.	3.8	24
58	Mass spectrometry and the amyloid problem—How far can we go in the gas phase?. Journal of the American Society for Mass Spectrometry, 2010, 21, 1087-1096.	2.8	61
59	Considerations in experimental and theoretical collision cross-section measurements of small molecules using travelling wave ion mobility spectrometry-mass spectrometry. International Journal of Mass Spectrometry, 2010, 298, 17-23.	1.5	72
60	Defining topological features of membrane proteins by nanoelectrospray ionisation mass spectrometry. Rapid Communications in Mass Spectrometry, 2010, 24, 276-284.	1.5	12
61	Determining the topology of virus assembly intermediates using ion mobility spectrometry—mass spectrometry. Rapid Communications in Mass Spectrometry, 2010, 24, 3033-3042.	1.5	81
62	Elongated oligomers in $\beta$ 2-microglobulin amyloid assembly revealed by ion mobility spectrometry-mass spectrometry. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 6794-6798.	7.1	147
63	Viral Genomic Single-Stranded RNA Directs the Pathway Toward a T=3 Capsid. Journal of Molecular Biology, 2010, 395, 924-936.	4.2	60
64	The Impact of Viral RNA on Assembly Pathway Selection. Journal of Molecular Biology, 2010, 401, 298-308.	4.2	64
65	HDX-ESI-MS reveals enhanced conformational dynamics of the amyloidogenic protein $\beta$ 2-microglobulin upon release from the MHC-1. Journal of the American Society for Mass Spectrometry, 2009, 20, 278-286.	2.8	37
66	Deciphering Drift Time Measurements from Travelling Wave Ion Mobility Spectrometry-Mass Spectrometry Studies. European Journal of Mass Spectrometry, 2009, 15, 113-130.	1.0	312
67	Critical concentrations of $\beta$ -sheet peptide self-assembly quantified directly by nanoelectrospray ionization mass spectrometry. Rapid Communications in Mass Spectrometry, 2008, 22, 1611-1614.	1.5	4
68	Insights into virus capsid assembly from non-covalent mass spectrometry. Mass Spectrometry Reviews, 2008, 27, 575-595.	5.4	47
69	RNA Packing Specificity and Folding during Assembly of the Bacteriophage MS2. Computational and Mathematical Methods in Medicine, 2008, 9, 339-349.	1.3	12
70	A Simple, RNA-Mediated Allosteric Switch Controls the Pathway to Formation of a T=3 Viral Capsid. Journal of Molecular Biology, 2007, 369, 541-552.	4.2	128
71	Real-Time Measurement of Myosin—Nucleotide Noncovalent Complexes by Electrospray Ionization Mass Spectrometry. Biophysical Journal, 2007, 93, 914-919.	0.5	6
72	Review. Journal of the American Society for Mass Spectrometry, 2007, 18, R3-R4.	2.8	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.	2.8	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.	4.2	137
75	Donor-Strand Exchange in Chaperone-Assisted Pilus Assembly Proceeds through a Concerted $\beta^2$ Strand Displacement Mechanism. <i>Molecular Cell</i> , 2006, 22, 831-842.	9.7	159
76	Investigating the structural properties of amyloid-like fibrils formed in vitro from $\beta^2$ -microglobulin using limited proteolysis and electrospray ionisation mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2006, 20, 1628-1636.	1.5	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.	10.3	57
79	Co-populated Conformational Ensembles of $\beta^2$ -Microglobulin Uncovered Quantitatively by Electrospray Ionization Mass Spectrometry. <i>Journal of Biological Chemistry</i> , 2004, 279, 27069-27077.	3.4	68
80	Separation of $\beta^2$ -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.	1.5	54
81	Protein and peptide identification: the role of mass spectrometry in proteomics. <i>Natural Product Reports</i> , 2003, 20, 202-215.	10.3	47
82	The Effect of Dimethylbiguanide on Thrombin Activity, FXIII Activation, Fibrin Polymerization, and Fibrin Clot Formation. <i>Diabetes</i> , 2002, 51, 189-197.	0.6	90
83	Structural Plasticity and Noncovalent Substrate Binding in the GroEL Apical Domain. <i>Journal of Biological Chemistry</i> , 2002, 277, 33115-33126.	3.4	31
84	Molecular dissection of membrane-transport proteins: mass spectrometry and sequence determination of the galactose $\epsilon$ -H <sup>+</sup> symport protein, GalP, of <i>Escherichia coli</i> and quantitative assay of the incorporation of [ring-2- <sup>13</sup> C]histidine and <sup>15</sup> NH <sub>3</sub> . <i>Biochemical Journal</i> , 2002, 363, 243-252.	3.7	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.	3.4	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.	1.5	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.	14.5	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.	7.6	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.	3.7	65