

# Carol V Robinson

## List of Publications by Year in descending order

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454  
papers

43,203  
citations

1099

112  
h-index

3650

180  
g-index

477  
all docs

477  
docs citations

477  
times ranked

33447  
citing authors

#	ARTICLE	IF	CITATIONS
1	Instability, unfolding and aggregation of human lysozyme variants underlying amyloid fibrillogenesis. <i>Nature</i> , 1997, 385, 787-793.	27.8	1,061
2	Ion mobility mass spectrometry analysis of large protein complexes. <i>Nature Protocols</i> , 2008, 3, 1139-1152.	12.0	973
3	Amyloid- $\beta$ protein oligomerization and the importance of tetramers and dodecamers in the aetiology of Alzheimer's disease. <i>Nature Chemistry</i> , 2009, 1, 326-331.	13.6	835
4	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.	6.5	694
5	Membrane proteins bind lipids selectively to modulate their structure and function. <i>Nature</i> , 2014, 510, 172-175.	27.8	665
6	Bayesian Deconvolution of Mass and Ion Mobility Spectra: From Binary Interactions to Polydisperse Ensembles. <i>Analytical Chemistry</i> , 2015, 87, 4370-4376.	6.5	663
7	Targeting C-reactive protein for the treatment of cardiovascular disease. <i>Nature</i> , 2006, 440, 1217-1221.	27.8	621
8	Determining the stoichiometry and interactions of macromolecular assemblies from mass spectrometry. <i>Nature Protocols</i> , 2007, 2, 715-726.	12.0	597
9	Detection of transient protein folding populations by mass spectrometry. <i>Science</i> , 1993, 262, 896-900.	12.6	590
10	Evidence for Macromolecular Protein Rings in the Absence of Bulk Water. <i>Science</i> , 2005, 310, 1658-1661.	12.6	551
11	The molecular sociology of the cell. <i>Nature</i> , 2007, 450, 973-982.	27.8	497
12	A Tandem Mass Spectrometer for Improved Transmission and Analysis of Large Macromolecular Assemblies. <i>Analytical Chemistry</i> , 2002, 74, 1402-1407.	6.5	481
13	Formation of insulin amyloid fibrils followed by FTIR simultaneously with CD and electron microscopy. <i>Protein Science</i> , 2000, 9, 1960-1967.	7.6	453
14	The structure of the dynactin complex and its interaction with dynein. <i>Science</i> , 2015, 347, 1441-1446.	12.6	389
15	Assembly reflects evolution of protein complexes. <i>Nature</i> , 2008, 453, 1262-1265.	27.8	383
16	Protein Complexes in the Gas Phase: Technology for Structural Genomics and Proteomics. <i>Chemical Reviews</i> , 2007, 107, 3544-3567.	47.7	376
17	Mass spectrometry of intact membrane protein complexes. <i>Nature Protocols</i> , 2013, 8, 639-651.	12.0	354
18	The role of interfacial lipids in stabilizing membrane protein oligomers. <i>Nature</i> , 2017, 541, 421-424.	27.8	344

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19	Molecular recycling within amyloid fibrils. <i>Nature</i> , 2005, 436, 554-558.	27.8	342
20	Structural Characterization of Drug-like Compounds by Ion Mobility Mass Spectrometry: Comparison of Theoretical and Experimentally Derived Nitrogen Collision Cross Sections. <i>Analytical Chemistry</i> , 2012, 84, 1026-1033.	6.5	340
21	The Role of Mass Spectrometry in Structure Elucidation of Dynamic Protein Complexes. <i>Annual Review of Biochemistry</i> , 2007, 76, 167-193.	11.1	337
22	Micelles Protect Membrane Complexes from Solution to Vacuum. <i>Science</i> , 2008, 321, 243-246.	12.6	333
23	An Oligomeric Signaling Platform Formed by the Toll-like Receptor Signal Transducers MyD88 and IRAK-4. <i>Journal of Biological Chemistry</i> , 2009, 284, 25404-25411.	3.4	323
24	Class I HDACs Share a Common Mechanism of Regulation by Inositol Phosphates. <i>Molecular Cell</i> , 2013, 51, 57-67.	9.7	314
25	Probing the Nature of Noncovalent Interactions by Mass Spectrometry. A Study of Protein-CoA Ligand Binding and Assembly. <i>Journal of the American Chemical Society</i> , 1996, 118, 8646-8653.	13.7	304
26	Structures of SAS-6 Suggest Its Organization in Centrioles. <i>Science</i> , 2011, 331, 1196-1199.	12.6	284
27	Ion Mobility Mass Spectrometry of Peptide Ions: Effects of Drift Gas and Calibration Strategies. <i>Analytical Chemistry</i> , 2012, 84, 7124-7130.	6.5	281
28	Structure of a designed protein cage that self-assembles into a highly porous cube. <i>Nature Chemistry</i> , 2014, 6, 1065-1071.	13.6	267
29	Crystal structures of truncated alphaA and alphaB crystallins reveal structural mechanisms of polydispersity important for eye lens function. <i>Protein Science</i> , 2010, 19, 1031-1043.	7.6	264
30	Programmable polyproteins built using twin peptide superglues. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 1202-1207.	7.1	262
31	Characterization of the Oligomeric States of Insulin in Self-Assembly and Amyloid Fibril Formation by Mass Spectrometry. <i>Biophysical Journal</i> , 2000, 79, 1053-1065.	0.5	258
32	PAXX, a paralog of XRCC4 and XLF, interacts with Ku to promote DNA double-strand break repair. <i>Science</i> , 2015, 347, 185-188.	12.6	252
33	Mass Spectrometry of Intact V-Type ATPases Reveals Bound Lipids and the Effects of Nucleotide Binding. <i>Science</i> , 2011, 334, 380-385.	12.6	251
34	The Fas-FADD death domain complex structure reveals the basis of DISC assembly and disease mutations. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 1324-1329.	8.2	236
35	PtdIns(4,5)P <sub>2</sub> stabilizes active states of GPCRs and enhances selectivity of G-protein coupling. <i>Nature</i> , 2018, 559, 423-427.	27.8	236
36	Polydispersity of a mammalian chaperone: Mass spectrometry reveals the population of oligomers in ÅB-crystallin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 10611-10616.	7.1	235

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37	Mass spectrometry reveals modularity and a complete subunit interaction map of the eukaryotic translation factor eIF3. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 18139-18144.	7.1	233
38	Quaternary dynamics and plasticity underlie small heat shock protein chaperone function. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 2007-2012.	7.1	231
39	Collision Cross Sections for Structural Proteomics. <i>Structure</i> , 2015, 23, 791-799.	3.3	231
40	Biomimetic spinning of artificial spider silk from a chimeric minispidroin. <i>Nature Chemical Biology</i> , 2017, 13, 262-264.	8.0	231
41	A camelid antibody fragment inhibits the formation of amyloid fibrils by human lysozyme. <i>Nature</i> , 2003, 424, 783-788.	27.8	227
42	Charge-State Dependent Compaction and Dissociation of Protein Complexes: Insights from Ion Mobility and Molecular Dynamics. <i>Journal of the American Chemical Society</i> , 2012, 134, 3429-3438.	13.7	223
43	Conformation of GroEL-bound $\alpha$ -lactalbumin probed by mass spectrometry. <i>Nature</i> , 1994, 372, 646-651.	27.8	221
44	Aspects of native proteins are retained in vacuum. <i>Current Opinion in Chemical Biology</i> , 2006, 10, 402-408.	6.1	217
45	Protein Complexes Are under Evolutionary Selection to Assemble via Ordered Pathways. <i>Cell</i> , 2013, 153, 461-470.	28.9	215
46	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.	13.8	213
47	Detection and selective dissociation of intact ribosomes in a mass spectrometer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2000, 97, 5185-5190.	7.1	209
48	Local cooperativity in the unfolding of an amyloidogenic variant of human lysozyme. <i>Nature Structural Biology</i> , 2002, 9, 308-315.	9.7	208
49	Tandem Mass Spectrometry Reveals the Quaternary Organization of Macromolecular Assemblies. <i>Chemistry and Biology</i> , 2006, 13, 597-605.	6.0	206
50	High-resolution mass spectrometry of small molecules bound to membrane proteins. <i>Nature Methods</i> , 2016, 13, 333-336.	19.0	205
51	Electrospray Time-of-Flight Mass Spectrometry of the Intact MS2 Virus Capsid. <i>Journal of the American Chemical Society</i> , 2000, 122, 3550-3551.	13.7	199
52	Mass spectrometry of macromolecular assemblies: preservation and dissociation. <i>Current Opinion in Structural Biology</i> , 2006, 16, 245-251.	5.7	199
53	Interaction of the Molecular Chaperone $\beta$ -Crystallin with $\alpha$ -Synuclein: Effects on Amyloid Fibril Formation and Chaperone Activity. <i>Journal of Molecular Biology</i> , 2004, 340, 1167-1183.	4.2	198
54	Principles of assembly reveal a periodic table of protein complexes. <i>Science</i> , 2015, 350, aaa2245.	12.6	198

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55	Structural basis for nutrient acquisition by dominant members of the human gut microbiota. <i>Nature</i> , 2017, 541, 407-411.	27.8	188
56	Protein Complexes of the Escherichia coli Cell Envelope*. <i>Journal of Biological Chemistry</i> , 2005, 280, 34409-34419.	3.4	183
57	Structure of the CRISPR Interference Complex CSM Reveals Key Similarities with Cascade. <i>Molecular Cell</i> , 2013, 52, 124-134.	9.7	181
58	The structured core domain of I $\beta$ -crystallin can prevent amyloid fibrillation and associated toxicity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E1562-70.	7.1	181
59	Subunit Exchange of Multimeric Protein Complexes. <i>Journal of Biological Chemistry</i> , 2002, 277, 38921-38929.	3.4	180
60	The Co-chaperone p23 Arrests the Hsp90 ATPase Cycle to Trap Client Proteins. <i>Journal of Molecular Biology</i> , 2006, 356, 746-758.	4.2	179
61	Structural Organization of the 19S Proteasome Lid: Insights from MS of Intact Complexes. <i>PLoS Biology</i> , 2006, 4, e267.	5.6	176
62	Investigation of protein folding by mass spectrometry. <i>FASEB Journal</i> , 1996, 10, 93-101.	0.5	175
63	Recognition of a signal peptide by the signal recognition particle. <i>Nature</i> , 2010, 465, 507-510.	27.8	172
64	Mass Spectrometry of Protein Complexes: From Origins to Applications. <i>Annual Review of Physical Chemistry</i> , 2015, 66, 453-474.	10.8	169
65	Subunit architecture of multimeric complexes isolated directly from cells. <i>EMBO Reports</i> , 2006, 7, 605-610.	4.5	168
66	Protein subunit interactions and structural integrity of amyloidogenic transthyretins: evidence from electrospray mass spectrometry. <i>Journal of Molecular Biology</i> , 1998, 281, 553-564.	4.2	167
67	Mass Measurements of Increased Accuracy Resolve Heterogeneous Populations of Intact Ribosomes. <i>Journal of the American Chemical Society</i> , 2006, 128, 11433-11442.	13.7	166
68	Mechanistic Studies of the Folding of Human Lysozyme and the Origin of Amyloidogenic Behavior in Its Disease-Related Variants. <i>Biochemistry</i> , 1999, 38, 6419-6427.	2.5	165
69	Mass spectrometry of membrane transporters reveals subunit stoichiometry and interactions. <i>Nature Methods</i> , 2009, 6, 585-587.	19.0	164
70	Structure of the TatC core of the twin-arginine protein transport system. <i>Nature</i> , 2012, 492, 210-214.	27.8	164
71	Coupling Microdroplet Microreactors with Mass Spectrometry: Reading the Contents of Single Droplets Online. <i>Angewandte Chemie - International Edition</i> , 2009, 48, 3665-3668.	13.8	162
72	Detection of the Intact GroEL Chaperonin Assembly by Mass Spectrometry. <i>Journal of the American Chemical Society</i> , 1999, 121, 4718-4719.	13.7	161

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73	Thermal Dissociation of Multimeric Protein Complexes by Using Nanoelectrospray Mass Spectrometry. <i>Analytical Chemistry</i> , 2003, 75, 2208-2214.	6.5	161
74	The role of lipids in mechanosensation. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 991-998.	8.2	160
75	The structural basis for CD36 binding by the malaria parasite. <i>Nature Communications</i> , 2016, 7, 12837.	12.8	160
76	Mimicking phosphorylation of $\alpha$ -crystallin affects its chaperone activity. <i>Biochemical Journal</i> , 2007, 401, 129-141.	3.7	159
77	Mass spectrometry reveals synergistic effects of nucleotides, lipids, and drugs binding to a multidrug resistance efflux pump. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 9704-9709.	7.1	156
78	Protein assemblies ejected directly from native membranes yield complexes for mass spectrometry. <i>Science</i> , 2018, 362, 829-834.	12.6	155
79	Studies of the RNA Degradosome-organizing Domain of the Escherichia coli Ribonuclease RNase E. <i>Journal of Molecular Biology</i> , 2004, 340, 965-979.	4.2	153
80	Structural Insights into the Activity of Enhancer-Binding Proteins. <i>Science</i> , 2005, 307, 1972-1975.	12.6	153
81	Structure of the core of the type III secretion system export apparatus. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 583-590.	8.2	153
82	Structure of V-ATPase from the mammalian brain. <i>Science</i> , 2020, 367, 1240-1246.	12.6	153
83	Detergent-free mass spectrometry of membrane protein complexes. <i>Nature Methods</i> , 2013, 10, 1206-1208.	19.0	152
84	Structural basis for the subunit assembly of the anaphase-promoting complex. <i>Nature</i> , 2011, 470, 227-232.	27.8	150
85	Do Charge State Signatures Guarantee Protein Conformations?. <i>Journal of the American Society for Mass Spectrometry</i> , 2012, 23, 1161-1168.	2.8	149
86	A mass spectrometry-based hybrid method for structural modeling of protein complexes. <i>Nature Methods</i> , 2014, 11, 403-406.	19.0	149
87	Alternate Dissociation Pathways Identified in Charge-Reduced Protein Complex Ions. <i>Analytical Chemistry</i> , 2010, 82, 5363-5372.	6.5	145
88	Phosphorylation of $\alpha$ -Crystallin Alters Chaperone Function through Loss of Dimeric Substructure. <i>Journal of Biological Chemistry</i> , 2004, 279, 28675-28680.	3.4	144
89	Twenty Years of Gas Phase Structural Biology. <i>Structure</i> , 2013, 21, 1541-1550.	3.3	143
90	Gas-Phase Unfolding and Disassembly Reveals Stability Differences in Ligand-Bound Multiprotein Complexes. <i>Chemistry and Biology</i> , 2009, 16, 382-390.	6.0	141

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91	Advances in the Mass Spectrometry of Membrane Proteins: From Individual Proteins to Intact Complexes. <i>Annual Review of Biochemistry</i> , 2011, 80, 247-271.	11.1	141
92	Atomic model for the membrane-embedded VO motor of a eukaryotic V-ATPase. <i>Nature</i> , 2016, 539, 118-122.	27.8	141
93	Mass Sign: An Assignment Strategy for Maximizing Information from the Mass Spectra of Heterogeneous Protein Assemblies. <i>Analytical Chemistry</i> , 2012, 84, 2939-2948.	6.5	140
94	Protein complexes gain momentum. <i>Current Opinion in Structural Biology</i> , 2002, 12, 729-734.	5.7	138
95	Traveling-wave ion mobility mass spectrometry of protein complexes: accurate calibrated collision cross-sections of human insulin oligomers. <i>Rapid Communications in Mass Spectrometry</i> , 2012, 26, 1181-1193.	1.5	138
96	Structural insights into the lipid and ligand regulation of serotonin receptors. <i>Nature</i> , 2021, 592, 469-473.	27.8	138
97	Quantifying the stabilizing effects of protein-ligand interactions in the gas phase. <i>Nature Communications</i> , 2015, 6, 8551.	12.8	136
98	Defining the mechanism of polymerization in the serpinopathies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 17146-17151.	7.1	135
99	Oxygenase-catalyzed ribosome hydroxylation occurs in prokaryotes and humans. <i>Nature Chemical Biology</i> , 2012, 8, 960-962.	8.0	135
100	Heptameric (L12)6/L10 rather than canonical pentameric complexes are found by tandem MS of intact ribosomes from thermophilic bacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 8192-8197.	7.1	134
101	The role of lipids in defining membrane protein interactions: insights from mass spectrometry. <i>Trends in Cell Biology</i> , 2013, 23, 1-8.	7.9	134
102	Structural evolution of p53, p63, and p73: Implication for heterotetramer formation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 17705-17710.	7.1	133
103	Symmetrical Modularity of the COP9 Signalosome Complex Suggests its Multifunctionality. <i>Structure</i> , 2009, 17, 31-40.	3.3	133
104	Crystal structure of the open conformation of the mammalian chaperonin CCT in complex with tubulin. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 14-19.	8.2	128
105	Steroid-based facial amphiphiles for stabilization and crystallization of membrane proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E1203-11.	7.1	127
106	Architecture of eukaryotic mRNA 3'-end processing machinery. <i>Science</i> , 2017, 358, 1056-1059.	12.6	124
107	Subunit Architecture of Intact Protein Complexes from Mass Spectrometry and Homology Modeling. <i>Accounts of Chemical Research</i> , 2008, 41, 617-627.	15.6	123
108	$\beta$ -Crystallin Polydispersity Is a Consequence of Unbiased Quaternary Dynamics. <i>Journal of Molecular Biology</i> , 2011, 413, 297-309.	4.2	122

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109	Comparative cross-linking and mass spectrometry of an intact F-type ATPase suggest a role for phosphorylation. <i>Nature Communications</i> , 2013, 4, 1985.	12.8	122
110	Optimal Synthetic Glycosylation of a Therapeutic Antibody. <i>Angewandte Chemie - International Edition</i> , 2016, 55, 2361-2367.	13.8	122
111	Membrane Protein-Lipid Interactions Probed Using Mass Spectrometry. <i>Annual Review of Biochemistry</i> , 2019, 88, 85-111.	11.1	121
112	Integrating Ion Mobility Mass Spectrometry with Molecular Modelling to Determine the Architecture of Multiprotein Complexes. <i>PLoS ONE</i> , 2010, 5, e12080.	2.5	119
113	Correlating Solution Binding and ESI-MS Stabilities by Incorporating Solvation Effects in a Confined Cucurbit[8]uril System. <i>Journal of Physical Chemistry B</i> , 2010, 114, 8606-8615.	2.6	118
114	The Role of the Detergent Micelle in Preserving the Structure of Membrane Proteins in the Gas Phase. <i>Angewandte Chemie - International Edition</i> , 2015, 54, 4577-4581.	13.8	117
115	An electron transfer path connects subunits of a mycobacterial respiratory supercomplex. <i>Science</i> , 2018, 362, .	12.6	117
116	Structural Characterization of the Human Eukaryotic Initiation Factor 3 Protein Complex by Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2007, 6, 1135-1146.	3.8	116
117	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.	2.6	116
118	A subset of annular lipids is linked to the flippase activity of an ABC transporter. <i>Nature Chemistry</i> , 2015, 7, 255-262.	13.6	112
119	The antibiotic darobactin mimics a $\beta^2$ -strand to inhibit outer membrane insertase. <i>Nature</i> , 2021, 593, 125-129.	27.8	112
120	Combining native and $\tilde{\text{omics}}^{\text{TM}}$ mass spectrometry to identify endogenous ligands bound to membrane proteins. <i>Nature Methods</i> , 2020, 17, 505-508.	19.0	111
121	Structural Modeling of Heteromeric Protein Complexes from Disassembly Pathways and Ion Mobility-Mass Spectrometry. <i>Structure</i> , 2012, 20, 1596-1609.	3.3	110
122	Subunit Exchange of Polydisperse Proteins. <i>Journal of Biological Chemistry</i> , 2005, 280, 14485-14491.	3.4	109
123	Experimental characterization of disordered and ordered aggregates populated during the process of amyloid fibril formation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 7828-7833.	7.1	109
124	Intrinsically Disordered Protein Threads Through the Bacterial Outer-Membrane Porin OmpF. <i>Science</i> , 2013, 340, 1570-1574.	12.6	109
125	A novel mechano-enzymatic cleavage mechanism underlies transthyretin amyloidogenesis. <i>EMBO Molecular Medicine</i> , 2015, 7, 1337-1349.	6.9	109
126	Structure of native lens connexin 46/50 intercellular channels by cryo-EM. <i>Nature</i> , 2018, 564, 372-377.	27.8	107



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127	Human Antibodies that Slow Erythrocyte Invasion Potentiate Malaria-Neutralizing Antibodies. <i>Cell</i> , 2019, 178, 216-228.e21.	28.9	107
128	Screening Transthyretin Amyloid Fibril Inhibitors. <i>Structure</i> , 2002, 10, 851-863.	3.3	106
129	Observation of the noncovalent assembly and disassembly pathways of the chaperone complex MtGimC by mass spectrometry. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2000, 97, 14151-14155.	7.1	102
130	Characterising electrosprayed biomolecules using tandem-MS—the noncovalent GroEL chaperonin assembly. <i>International Journal of Mass Spectrometry</i> , 2004, 236, 25-32.	1.5	102
131	Efficient protein production inspired by how spiders make silk. <i>Nature Communications</i> , 2017, 8, 15504.	12.8	102
132	Reduced Global Cooperativity is a Common Feature Underlying the Amyloidogenicity of Pathogenic Lysozyme Mutations. <i>Journal of Molecular Biology</i> , 2005, 346, 773-788.	4.2	100
133	Small Heat Shock Protein Activity Is Regulated by Variable Oligomeric Substructure. <i>Journal of Biological Chemistry</i> , 2008, 283, 28513-28517.	3.4	99
134	Subunit Architecture of Multiprotein Assemblies Determined Using Restraints from Gas-Phase Measurements. <i>Structure</i> , 2009, 17, 1235-1243.	3.3	99
135	Mass spectrometry guided structural biology. <i>Current Opinion in Structural Biology</i> , 2016, 40, 136-144.	5.7	98
136	Kinetic Consequences of the Removal of a Disulfide Bridge on the Folding of Hen Lysozyme. <i>Biochemistry</i> , 1994, 33, 13038-13048.	2.5	97
137	Probing the Lipid Annular Belt by Gas-Phase Dissociation of Membrane Proteins in Nanodiscs. <i>Angewandte Chemie - International Edition</i> , 2016, 55, 550-554.	13.8	95
138	N-glycan microheterogeneity regulates interactions of plasma proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 8763-8768.	7.1	94
139	MmpL3 is a lipid transporter that binds trehalose monomycolate and phosphatidylethanolamine. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 11241-11246.	7.1	94
140	A $\beta$ 240 and A $\beta$ 242 Amyloid Fibrils Exhibit Distinct Molecular Recycling Properties. <i>Journal of the American Chemical Society</i> , 2011, 133, 6505-6508.	13.7	93
141	A comparative cross-linking strategy to probe conformational changes in protein complexes. <i>Nature Protocols</i> , 2014, 9, 2224-2236.	12.0	93
142	Hsp70 Forms Antiparallel Dimers Stabilized by Post-translational Modifications to Position Clients for Transfer to Hsp90. <i>Cell Reports</i> , 2015, 11, 759-769.	6.4	93
143	Allosteric Inhibition of the SARS-CoV-2 Main Protease: Insights from Mass Spectrometry Based Assays**. <i>Angewandte Chemie - International Edition</i> , 2020, 59, 23544-23548.	13.8	92
144	Dodecameric Structure of the Small Heat Shock Protein Acr1 from <i>Mycobacterium tuberculosis</i> . <i>Journal of Biological Chemistry</i> , 2005, 280, 33419-33425.	3.4	91

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145	Proteolytic cleavage of Ser52Pro variant transthyretin triggers its amyloid fibrillogenesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 1539-1544.	7.1	91
146	Hydrogen exchange properties of proteins in native and denatured states monitored by mass spectrometry and NMR. <i>Protein Science</i> , 1997, 6, 1316-1324.	7.6	90
147	Disassembly of intact multiprotein complexes in the gas phase. <i>Current Opinion in Structural Biology</i> , 1999, 9, 135-141.	5.7	89
148	MacB ABC Transporter Is a Dimer Whose ATPase Activity and Macrolide-binding Capacity Are Regulated by the Membrane Fusion Protein MacA. <i>Journal of Biological Chemistry</i> , 2009, 284, 1145-1154.	3.4	88
149	Structures of a Complete Human V-ATPase Reveal Mechanisms of Its Assembly. <i>Molecular Cell</i> , 2020, 80, 501-511.e3.	9.7	88
150	Heteronuclear NMR investigations of dynamic regions of intact Escherichia coli ribosomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 10949-10954.	7.1	87
151	Tandem Mass Spectrometry of Intact GroEL-Substrate Complexes Reveals Substrate-Specific Conformational Changes in the transRing. <i>Journal of the American Chemical Society</i> , 2006, 128, 4694-4702.	13.7	87
152	Intrinsically Disordered p53 and Its Complexes Populate Compact Conformations in the Gas Phase. <i>Angewandte Chemie - International Edition</i> , 2013, 52, 361-365.	13.8	85
153	Ion mobility-mass spectrometry of a rotary ATPase reveals ATP-induced reduction in conformational flexibility. <i>Nature Chemistry</i> , 2014, 6, 208-215.	13.6	85
154	Identifying key membrane protein lipid interactions using mass spectrometry. <i>Nature Protocols</i> , 2018, 13, 1106-1120.	12.0	85
155	Cryo-EM structures provide insight into how E. coli F1Fo ATP synthase accommodates symmetry mismatch. <i>Nature Communications</i> , 2020, 11, 2615.	12.8	85
156	The Extracellular Chaperone Clusterin Potently Inhibits Human Lysozyme Amyloid Formation by Interacting with Prefibrillar Species. <i>Journal of Molecular Biology</i> , 2007, 369, 157-167.	4.2	84
157	Super-complexes of adhesion GPCRs and neural guidance receptors. <i>Nature Communications</i> , 2016, 7, 11184.	12.8	84
158	The Role of Salt Bridges, Charge Density, and Subunit Flexibility in Determining Disassembly Routes of Protein Complexes. <i>Structure</i> , 2013, 21, 1325-1337.	3.3	82
159	Polypyrimidine Tract Binding Protein Stabilizes the Encephalomyocarditis Virus IRES Structure via Binding Multiple Sites in a Unique Orientation. <i>Molecular Cell</i> , 2009, 34, 556-568.	9.7	81
160	Interaction of the p53 DNA-Binding Domain with Its N-Terminal Extension Modulates the Stability of the p53 Tetramer. <i>Journal of Molecular Biology</i> , 2011, 409, 358-368.	4.2	81
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