

Carol V Robinson

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454
papers

35,250
citations

104
h-index

168
g-index

477
ext. papers

39,967
ext. citations

12.9
avg, IF

7.42
L-index

#	Paper	IF	Citations
454	Instability, unfolding and aggregation of human lysozyme variants underlying amyloid fibrillogenesis. <i>Nature</i> , 1997 , 385, 787-93	50.4	980
453	Ion mobility-mass spectrometry analysis of large protein complexes. <i>Nature Protocols</i> , 2008 , 3, 1139-52	18.8	843
452	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
451	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
450	Detection of transient protein folding populations by mass spectrometry. <i>Science</i> , 1993 , 262, 896-900	33.3	555
449	Determining the stoichiometry and interactions of macromolecular assemblies from mass spectrometry. <i>Nature Protocols</i> , 2007 , 2, 715-26	18.8	538
448	Targeting C-reactive protein for the treatment of cardiovascular disease. <i>Nature</i> , 2006 , 440, 1217-21	50.4	525
447	Membrane proteins bind lipids selectively to modulate their structure and function. <i>Nature</i> , 2014 , 510, 172-175	50.4	503
446	Evidence for macromolecular protein rings in the absence of bulk water. <i>Science</i> , 2005 , 310, 1658-61	33.3	502
445	A tandem mass spectrometer for improved transmission and analysis of large macromolecular assemblies. <i>Analytical Chemistry</i> , 2002 , 74, 1402-7	7.8	448
444	The molecular sociology of the cell. <i>Nature</i> , 2007 , 450, 973-82	50.4	424
443	Formation of insulin amyloid fibrils followed by FTIR simultaneously with CD and electron microscopy. <i>Protein Science</i> , 2000 , 9, 1960-7	6.3	408
442	Bayesian deconvolution of mass and ion mobility spectra: from binary interactions to polydisperse ensembles. <i>Analytical Chemistry</i> , 2015 , 87, 4370-6	7.8	373
441	Protein complexes in the gas phase: technology for structural genomics and proteomics. <i>Chemical Reviews</i> , 2007 , 107, 3544-67	68.1	342
440	The role of mass spectrometry in structure elucidation of dynamic protein complexes. <i>Annual Review of Biochemistry</i> , 2007 , 76, 167-93	29.1	320
439	Assembly reflects evolution of protein complexes. <i>Nature</i> , 2008 , 453, 1262-5	50.4	316
438	Molecular recycling within amyloid fibrils. <i>Nature</i> , 2005 , 436, 554-8	50.4	312

437	Micelles protect membrane complexes from solution to vacuum. <i>Science</i> , 2008 , 321, 243-6	33.3	291
436	Probing the Nature of Noncovalent Interactions by Mass Spectrometry. A Study of Protein- α A Ligand Binding and Assembly. <i>Journal of the American Chemical Society</i> , 1996 , 118, 8646-8653	16.4	285
435	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, 1026-33	7.8	283
434	The structure of the dynactin complex and its interaction with dynein. <i>Science</i> , 2015 , 347, 1441-1446	33.3	266
433	Mass spectrometry of intact membrane protein complexes. <i>Nature Protocols</i> , 2013 , 8, 639-51	18.8	263
432	An oligomeric signaling platform formed by the Toll-like receptor signal transducers MyD88 and IRAK-4. <i>Journal of Biological Chemistry</i> , 2009 , 284, 25404-11	5.4	251
431	Class I HDACs share a common mechanism of regulation by inositol phosphates. <i>Molecular Cell</i> , 2013 , 51, 57-67	17.6	247
430	Ion mobility mass spectrometry of peptide ions: effects of drift gas and calibration strategies. <i>Analytical Chemistry</i> , 2012 , 84, 7124-30	7.8	244
429	Crystal structures of truncated alphaA and alphaB crystallins reveal structural mechanisms of polydispersity important for eye lens function. <i>Protein Science</i> , 2010 , 19, 1031-43	6.3	244
428	Structures of SAS-6 suggest its organization in centrioles. <i>Science</i> , 2011 , 331, 1196-9	33.3	240
427	The role of interfacial lipids in stabilizing membrane protein oligomers. <i>Nature</i> , 2017 , 541, 421-424	50.4	238
426	Characterization of the oligomeric states of insulin in self-assembly and amyloid fibril formation by mass spectrometry. <i>Biophysical Journal</i> , 2000 , 79, 1053-65	2.9	228
425	Mass spectrometry of intact V-type ATPases reveals bound lipids and the effects of nucleotide binding. <i>Science</i> , 2011 , 334, 380-385	33.3	224
424	Structure of a designed protein cage that self-assembles into a highly porous cube. <i>Nature Chemistry</i> , 2014 , 6, 1065-71	17.6	223
423	A camelid antibody fragment inhibits the formation of amyloid fibrils by human lysozyme. <i>Nature</i> , 2003 , 424, 783-8	50.4	212
422	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, 18139-44	11.5	210
421	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, 1324-9	17.6	209
420	Polydispersity of a mammalian chaperone: mass spectrometry reveals the population of oligomers in alphaB-crystallin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003 , 100, 10611-6	11.5	206

419	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, 2007-12	11.5	205
418	DNA repair. PAXX, a paralog of XRCC4 and XLF, interacts with Ku to promote DNA double-strand break repair. <i>Science</i> , 2015 , 347, 185-188	33.3	202
417	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
416	Conformation of GroEL-bound alpha-lactalbumin probed by mass spectrometry. <i>Nature</i> , 1994 , 372, 646-651	51.4	202
415	Aspects of native proteins are retained in vacuum. <i>Current Opinion in Chemical Biology</i> , 2006 , 10, 402-8	9.7	199
414	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, 5185-90	11.5	195
413	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, 3429-38	16.4	193
412	Tandem mass spectrometry reveals the quaternary organization of macromolecular assemblies. <i>Chemistry and Biology</i> , 2006 , 13, 597-605		191
411	Mass spectrometry of macromolecular assemblies: preservation and dissociation. <i>Current Opinion in Structural Biology</i> , 2006 , 16, 245-51	8.1	190
410	Local cooperativity in the unfolding of an amyloidogenic variant of human lysozyme. <i>Nature Structural Biology</i> , 2002 , 9, 308-15		190
409	Electrospray Time-of-Flight Mass Spectrometry of the Intact MS2 Virus Capsid. <i>Journal of the American Chemical Society</i> , 2000 , 122, 3550-3551	16.4	187
408	Interaction of the molecular chaperone alphaB-crystallin with alpha-synuclein: effects on amyloid fibril formation and chaperone activity. <i>Journal of Molecular Biology</i> , 2004 , 340, 1167-83	6.5	179
407	Programmable polyproteins built using twin peptide superglues. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, 1202-7	11.5	175
406	Protein complexes of the Escherichia coli cell envelope. <i>Journal of Biological Chemistry</i> , 2005 , 280, 34409-19	5.19	171
405	Collision cross sections for structural proteomics. <i>Structure</i> , 2015 , 23, 791-9	5.2	169
404	Investigation of protein folding by mass spectrometry. <i>FASEB Journal</i> , 1996 , 10, 93-101	0.9	169
403	High-resolution mass spectrometry of small molecules bound to membrane proteins. <i>Nature Methods</i> , 2016 , 13, 333-6	21.6	164
402	Subunit architecture of multimeric complexes isolated directly from cells. <i>EMBO Reports</i> , 2006 , 7, 605-10	5.5	164

401	The co-chaperone p23 arrests the Hsp90 ATPase cycle to trap client proteins. <i>Journal of Molecular Biology</i> , 2006 , 356, 746-58	6.5	162
400	Subunit exchange of multimeric protein complexes. Real-time monitoring of subunit exchange between small heat shock proteins by using electrospray mass spectrometry. <i>Journal of Biological Chemistry</i> , 2002 , 277, 38921-9	5.4	161
399	Mechanistic studies of the folding of human lysozyme and the origin of amyloidogenic behavior in its disease-related variants. <i>Biochemistry</i> , 1999 , 38, 6419-27	3.2	160
398	Structural organization of the 19S proteasome lid: insights from MS of intact complexes. <i>PLoS Biology</i> , 2006 , 4, e267	9.7	159
397	Protein subunit interactions and structural integrity of amyloidogenic transthyretins: evidence from electrospray mass spectrometry. <i>Journal of Molecular Biology</i> , 1998 , 281, 553-64	6.5	159
396	The structured core domain of B-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	11.5	154
395	Protein complexes are under evolutionary selection to assemble via ordered pathways. <i>Cell</i> , 2013 , 153, 461-70	56.2	153
394	Recognition of a signal peptide by the signal recognition particle. <i>Nature</i> , 2010 , 465, 507-10	50.4	149
393	Mimicking phosphorylation of alphaB-crystallin affects its chaperone activity. <i>Biochemical Journal</i> , 2007 , 401, 129-41	3.8	147
392	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
391	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
390	Mass spectrometry of membrane transporters reveals subunit stoichiometry and interactions. <i>Nature Methods</i> , 2009 , 6, 585-7	21.6	146
389	Structure of the CRISPR interference complex CSM reveals key similarities with cascade. <i>Molecular Cell</i> , 2013 , 52, 124-34	17.6	145
388	Biomimetic spinning of artificial spider silk from a chimeric minispidroin. <i>Nature Chemical Biology</i> , 2017 , 13, 262-264	11.7	143
387	Principles of assembly reveal a periodic table of protein complexes. <i>Science</i> , 2015 , 350, aaa2245	33.3	142
386	PtdIns(4,5)P stabilizes active states of GPCRs and enhances selectivity of G-protein coupling. <i>Nature</i> , 2018 , 559, 423-427	50.4	141
385	Structural insights into the activity of enhancer-binding proteins. <i>Science</i> , 2005 , 307, 1972-5	33.3	141
384	Detection of the Intact GroEL Chaperonin Assembly by Mass Spectrometry. <i>Journal of the American Chemical Society</i> , 1999 , 121, 4718-4719	16.4	140

383	Do charge state signatures guarantee protein conformations?. <i>Journal of the American Society for Mass Spectrometry</i> , 2012 , 23, 1161-8	3.5	136
382	Thermal dissociation of multimeric protein complexes by using nanoelectrospray mass spectrometry. <i>Analytical Chemistry</i> , 2003 , 75, 2208-14	7.8	135
381	Mass spectrometry of protein complexes: from origins to applications. <i>Annual Review of Physical Chemistry</i> , 2015 , 66, 453-74	15.7	132
380	Structural basis for the subunit assembly of the anaphase-promoting complex. <i>Nature</i> , 2011 , 470, 227-32	50.4	132
379	A mass spectrometry-based hybrid method for structural modeling of protein complexes. <i>Nature Methods</i> , 2014 , 11, 403-406	21.6	131
378	Detergent-free mass spectrometry of membrane protein complexes. <i>Nature Methods</i> , 2013 , 10, 1206-8	21.6	131
377	Studies of the RNA degradosome-organizing domain of the Escherichia coli ribonuclease RNase E. <i>Journal of Molecular Biology</i> , 2004 , 340, 965-79	6.5	131
376	Advances in the mass spectrometry of membrane proteins: from individual proteins to intact complexes. <i>Annual Review of Biochemistry</i> , 2011 , 80, 247-71	29.1	129
375	Protein complexes gain momentum. <i>Current Opinion in Structural Biology</i> , 2002 , 12, 729-34	8.1	129
374	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, 9704-9	11.5	128
373	Phosphorylation of alphaB-crystallin alters chaperone function through loss of dimeric substructure. <i>Journal of Biological Chemistry</i> , 2004 , 279, 28675-80	5.4	128
372	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, 8192-7	11.5	127
371	Twenty years of gas phase structural biology. <i>Structure</i> , 2013 , 21, 1541-50	5.2	126
370	Structure of the TatC core of the twin-arginine protein transport system. <i>Nature</i> , 2012 , 492, 210-4	50.4	126
369	Alternate dissociation pathways identified in charge-reduced protein complex ions. <i>Analytical Chemistry</i> , 2010 , 82, 5363-72	7.8	126
368	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, 1181-93 ^{2,2}	3.2	124
367	Symmetrical modularity of the COP9 signalosome complex suggests its multifunctionality. <i>Structure</i> , 2009 , 17, 31-40	5.2	124
366	Gas-phase unfolding and disassembly reveals stability differences in ligand-bound multiprotein complexes. <i>Chemistry and Biology</i> , 2009 , 16, 382-90		124

365	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, 17146-51	11.5	120
364	Structural basis for nutrient acquisition by dominant members of the human gut microbiota. <i>Nature</i> , 2017 , 541, 407-411	50.4	119
363	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
362	Massign: an assignment strategy for maximizing information from the mass spectra of heterogeneous protein assemblies. <i>Analytical Chemistry</i> , 2012 , 84, 2939-48	7.8	115
361	The role of lipids in defining membrane protein interactions: insights from mass spectrometry. <i>Trends in Cell Biology</i> , 2013 , 23, 1-8	18.3	114
360	Comparative cross-linking and mass spectrometry of an intact F-type ATPase suggest a role for phosphorylation. <i>Nature Communications</i> , 2013 , 4, 1985	17.4	113
359	Oxygenase-catalyzed ribosome hydroxylation occurs in prokaryotes and humans. <i>Nature Chemical Biology</i> , 2012 , 8, 960-962	11.7	112
358	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
357	Quantifying the stabilizing effects of protein-ligand interactions in the gas phase. <i>Nature Communications</i> , 2015 , 6, 8551	17.4	111
356	The role of lipids in mechanosensation. <i>Nature Structural and Molecular Biology</i> , 2015 , 22, 991-8	17.6	111
355	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	11.5	111
354	The structural basis for CD36 binding by the malaria parasite. <i>Nature Communications</i> , 2016 , 7, 12837	17.4	106
353	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
352	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, 17705-10	11.5	105
351	Structural characterization of the human eukaryotic initiation factor 3 protein complex by mass spectrometry. <i>Molecular and Cellular Proteomics</i> , 2007 , 6, 1135-46	7.6	105
350	Atomic model for the membrane-embedded V motor of a eukaryotic V-ATPase. <i>Nature</i> , 2016 , 539, 118-122	32.4	104
349	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, 8606-15	3.4	104
348	Crystal structure of the open conformation of the mammalian chaperonin CCT in complex with tubulin. <i>Nature Structural and Molecular Biology</i> , 2011 , 18, 14-9	17.6	103

347	Structure of the core of the type III secretion system export apparatus. <i>Nature Structural and Molecular Biology</i> , 2018 , 25, 583-590	17.6	103
346	Structural modeling of heteromeric protein complexes from disassembly pathways and ion mobility-mass spectrometry. <i>Structure</i> , 2012 , 20, 1596-609	5.2	100
345	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, 7828-33	11.5	99
344	Screening transthyretin amyloid fibril inhibitors: characterization of novel multiprotein, multiligand complexes by mass spectrometry. <i>Structure</i> , 2002 , 10, 851-63	5.2	99
343	Protein assemblies ejected directly from native membranes yield complexes for mass spectrometry. <i>Science</i> , 2018 , 362, 829-834	33.3	99
342	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, 4577-81	16.4	97
341	Subunit architecture of multiprotein assemblies determined using restraints from gas-phase measurements. <i>Structure</i> , 2009 , 17, 1235-43	5.2	97
340	Intrinsically disordered protein threads through the bacterial outer-membrane porin OmpF. <i>Science</i> , 2013 , 340, 1570-4	33.3	96
339	B-crystallin polydispersity is a consequence of unbiased quaternary dynamics. <i>Journal of Molecular Biology</i> , 2011 , 413, 297-309	6.5	96
338	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, 14151-5	11.5	96
337	Reduced global cooperativity is a common feature underlying the amyloidogenicity of pathogenic lysozyme mutations. <i>Journal of Molecular Biology</i> , 2005 , 346, 773-88	6.5	95
336	Subunit exchange of polydisperse proteins: mass spectrometry reveals consequences of alphaA-crystallin truncation. <i>Journal of Biological Chemistry</i> , 2005 , 280, 14485-91	5.4	94
335	Optimal Synthetic Glycosylation of a Therapeutic Antibody. <i>Angewandte Chemie - International Edition</i> , 2016 , 55, 2361-7	16.4	92
334	A subset of annular lipids is linked to the flippase activity of an ABC transporter. <i>Nature Chemistry</i> , 2015 , 7, 255-62	17.6	91
333	Characterising electrosprayed biomolecules using tandem-MS: the noncovalent GroEL chaperonin assembly. <i>International Journal of Mass Spectrometry</i> , 2004 , 236, 25-32	1.9	90
332	Kinetic consequences of the removal of a disulfide bridge on the folding of hen lysozyme. <i>Biochemistry</i> , 1994 , 33, 13038-48	3.2	89
331	Hydrogen exchange properties of proteins in native and denatured states monitored by mass spectrometry and NMR. <i>Protein Science</i> , 1997 , 6, 1316-24	6.3	87
330	A comparative cross-linking strategy to probe conformational changes in protein complexes. <i>Nature Protocols</i> , 2014 , 9, 2224-36	18.8	86

329	Small heat shock protein activity is regulated by variable oligomeric substructure. <i>Journal of Biological Chemistry</i> , 2008 , 283, 28513-7	5.4	85
328	Hsp70 forms antiparallel dimers stabilized by post-translational modifications to position clients for transfer to Hsp90. <i>Cell Reports</i> , 2015 , 11, 759-69	10.6	83
327	Disassembly of intact multiprotein complexes in the gas phase. <i>Current Opinion in Structural Biology</i> , 1999 , 9, 135-41	8.1	83
326	Membrane Protein-Lipid Interactions Probed Using Mass Spectrometry. <i>Annual Review of Biochemistry</i> , 2019 , 88, 85-111	29.1	82
325	Dodecameric structure of the small heat shock protein Acr1 from <i>Mycobacterium tuberculosis</i> . <i>Journal of Biological Chemistry</i> , 2005 , 280, 33419-25	5.4	82
324	Architecture of eukaryotic mRNA 3'-end processing machinery. <i>Science</i> , 2017 , 358, 1056-1059	33.3	81
323	A novel mechano-enzymatic cleavage mechanism underlies transthyretin amyloidogenesis. <i>EMBO Molecular Medicine</i> , 2015 , 7, 1337-49	12	81
322	Heteronuclear NMR investigations of dynamic regions of intact <i>Escherichia coli</i> ribosomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004 , 101, 10949-54	11.5	80
321	A β 0 and A β 2 amyloid fibrils exhibit distinct molecular recycling properties. <i>Journal of the American Chemical Society</i> , 2011 , 133, 6505-8	16.4	79
320	Mass spectrometry guided structural biology. <i>Current Opinion in Structural Biology</i> , 2016 , 40, 136-144	8.1	79
319	Structure of a Blinkin-BUBR1 Complex Reveals an Interaction Crucial for Kinetochores-Mitotic Checkpoint Regulation via an Unanticipated Binding Site. <i>Structure</i> , 2011 , 19, 1895	5.2	78
318	Ion mobility-mass spectrometry of a rotary ATPase reveals ATP-induced reduction in conformational flexibility. <i>Nature Chemistry</i> , 2014 , 6, 208-215	17.6	77
317	Intrinsically disordered p53 and its complexes populate compact conformations in the gas phase. <i>Angewandte Chemie - International Edition</i> , 2013 , 52, 361-5	16.4	77
316	Tandem mass spectrometry of intact GroEL-substrate complexes reveals substrate-specific conformational changes in the trans ring. <i>Journal of the American Chemical Society</i> , 2006 , 128, 4694-702	16.4	77
315	An electron transfer path connects subunits of a mycobacterial respiratory supercomplex. <i>Science</i> , 2018 , 362,	33.3	76
314	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, 1145-54	5.4	75
313	The extracellular chaperone clusterin potently inhibits human lysozyme amyloid formation by interacting with prefibrillar species. <i>Journal of Molecular Biology</i> , 2007 , 369, 157-67	6.5	74
312	Acetylation of lysine 120 of p53 endows DNA-binding specificity at effective physiological salt concentration. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 8251-6	11.5	73

311	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, 1539-44	11.5	72
310	Structure of V-ATPase from the mammalian brain. <i>Science</i> , 2020 , 367, 1240-1246	33.3	71
309	The role of salt bridges, charge density, and subunit flexibility in determining disassembly routes of protein complexes. <i>Structure</i> , 2013 , 21, 1325-37	5.2	71
308	Ion mobility mass spectrometry of two tetrameric membrane protein complexes reveals compact structures and differences in stability and packing. <i>Journal of the American Chemical Society</i> , 2010 , 132, 15468-70	16.4	70
307	Polypyrimidine tract binding protein stabilizes the encephalomyocarditis virus IRES structure via binding multiple sites in a unique orientation. <i>Molecular Cell</i> , 2009 , 34, 556-68	17.6	70
306	Probing molecular interactions in intact antibody: antigen complexes, an electrospray time-of-flight mass spectrometry approach. <i>Biophysical Journal</i> , 2001 , 81, 3503-9	2.9	70
305	Probing the Lipid Annular Belt by Gas-Phase Dissociation of Membrane Proteins in Nanodiscs. <i>Angewandte Chemie - International Edition</i> , 2016 , 55, 550-4	16.4	68
304	Significant hydrogen exchange protection in GroEL-bound DHFR is maintained during iterative rounds of substrate cycling. <i>Protein Science</i> , 1996 , 5, 2506-13	6.3	66
303	Architecture and dynamics of an A-kinase anchoring protein 79 (AKAP79) signaling complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 6426-31	11.5	65
302	Quaternary structure and catalytic activity of the Escherichia coli ribonuclease E amino-terminal catalytic domain. <i>Biochemistry</i> , 2003 , 42, 13848-55	3.2	65
301	Real-time monitoring of protein complexes reveals their quaternary organization and dynamics. <i>Chemistry and Biology</i> , 2008 , 15, 246-53		64
300	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	11.5	62
299	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
298	The flight of macromolecular complexes in a mass spectrometer. <i>Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences</i> , 2005 , 363, 379-89; discussion 389-91	3	62
297	The catalytic activity of Ubp6 enhances maturation of the proteasomal regulatory particle. <i>Molecular Cell</i> , 2011 , 42, 637-49	17.6	60
296	When proteomics meets structural biology. <i>Trends in Biochemical Sciences</i> , 2010 , 35, 522-9	10.3	60
295	Drug binding revealed by tandem mass spectrometry of a protein-micelle complex. <i>Journal of the American Chemical Society</i> , 2004 , 126, 14362-3	16.4	60
294	Hsp70 oligomerization is mediated by an interaction between the interdomain linker and the substrate-binding domain. <i>PLoS ONE</i> , 2013 , 8, e67961	3.7	60

293	Non-homologous end-joining partners in a helical dance: structural studies of XLF-XRCC4 interactions. <i>Biochemical Society Transactions</i> , 2011 , 39, 1387-92, suppl 2 p following 1392	5.1	59
292	Tandem mass spectrometry defines the stoichiometry and quaternary structural arrangement of tryptophan molecules in the multiprotein complex TRAP. <i>Journal of the American Chemical Society</i> , 2004 , 126, 5950-1	16.4	59
291	Structure of a Blinkin-BUBR1 complex reveals an interaction crucial for kinetochore-mitotic checkpoint regulation via an unanticipated binding Site. <i>Structure</i> , 2011 , 19, 1691-700	5.2	58
290	Polypyrimidine tract-binding protein stimulates the poliovirus IRES by modulating eIF4G binding. <i>EMBO Journal</i> , 2010 , 29, 3710-22	13	58
289	Discrete, multi-component complexes with cucurbit[8]uril in the gas-phase. <i>Chemical Communications</i> , 2009 , 644-6	5.8	58
288	Engineering a camelid antibody fragment that binds to the active site of human lysozyme and inhibits its conversion into amyloid fibrils. <i>Biochemistry</i> , 2008 , 47, 11041-54	3.2	58
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