

Carol V Robinson

List of Publications by Year in Descending Order

Source: <https://exaly.com/author-pdf/1355260/carol-v-robinson-publications-by-year.pdf>

Version: 2024-04-26

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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	Ion currents through Kir potassium channels are gated by anionic lipids.. <i>Nature Communications</i> , 2022 , 13, 490	17.4	3
453	Cryo-EM structure of human GPR158 receptor coupled to the RGS7-Gβ signaling complex. <i>Science</i> , 2022 , 375, 86-91	33.3	5
452	Electrospray ionization of native membrane proteins proceeds a charge equilibration step.. <i>RSC Advances</i> , 2022 , 12, 9671-9680	3.7	1
451	Structure, mechanism and lipid-mediated remodeling of the mammalian Na/H exchanger NHA2.. <i>Nature Structural and Molecular Biology</i> , 2022 , 29, 108-120	17.6	2
450	Capturing a rhodopsin receptor signalling cascade across a native membrane.. <i>Nature</i> , 2022 ,	50.4	4
449	Understanding glycoprotein structural heterogeneity and interactions: Insights from native mass spectrometry.. <i>Current Opinion in Structural Biology</i> , 2022 , 74, 102351	8.1	1
448	Studies on enmetazobactam clarify mechanisms of widely used β-lactamase inhibitors.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022 , 119, e2117310119	11.5	1
447	Peptidoglycan biosynthesis is driven by lipid transfer along enzyme-substrate affinity gradients.. <i>Nature Communications</i> , 2022 , 13, 2278	17.4	1
446	Non-ionic hybrid detergents for protein delipidation.. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2022 , 183958	3.8	1
445	Acyl carrier protein promotes MukBEF action in Escherichia coli chromosome organization-segregation. <i>Nature Communications</i> , 2021 , 12, 6721	17.4	3
444	Charge Engineering Reveals the Roles of Ionizable Side Chains in Electrospray Ionization Mass Spectrometry.. <i>Jacs Au</i> , 2021 , 1, 2385-2393		2
443	The structure of nontypeable Haemophilus influenzae SapA in a closed conformation reveals a constricted ligand-binding cavity and a novel RNA binding motif. <i>PLoS ONE</i> , 2021 , 16, e0256070	3.7	0
442	Detergent-free Lipodisc Nanoparticles Facilitate High-Resolution Mass Spectrometry of Folded Integral Membrane Proteins. <i>Nano Letters</i> , 2021 , 21, 2824-2831	11.5	10
441	Structural insights into the lipid and ligand regulation of serotonin receptors. <i>Nature</i> , 2021 , 592, 469-473	50.4	32
440	Heterogeneity of Glycan Processing on Trimeric SARS-CoV-2 Spike Protein Revealed by Charge Detection Mass Spectrometry. <i>Journal of the American Chemical Society</i> , 2021 , 143, 3959-3966	16.4	26
439	The Effects of Sodium Ions on Ligand Binding and Conformational States of G Protein-Coupled Receptors-Insights from Mass Spectrometry. <i>Journal of the American Chemical Society</i> , 2021 , 143, 4085-4089	16.4	16
438	The antibiotic darobactin mimics a β-strand to inhibit outer membrane insertase. <i>Nature</i> , 2021 , 593, 125-130	30.4	25

437	Phospho-regulation, nucleotide binding and ion access control in potassium-chloride cotransporters. <i>EMBO Journal</i> , 2021 , 40, e107294	13	5
436	NaViA: A Program for the Visual Analysis of Complex Mass Spectra. <i>Bioinformatics</i> , 2021 ,	7.2	3
435	Connecting Multi-omics Approaches to endogenous protein complexes. <i>Trends in Chemistry</i> , 2021 , 3, 445-455	14.8	3
434	Multiple Roles of SARS-CoV-2 N Protein Facilitated by Proteoform-Specific Interactions with RNA, Host Proteins, and Convalescent Antibodies. <i>Jacs Au</i> , 2021 , 1, 1147-1157		6
433	Native Mass Spectrometry Meets Glycomics: Resolving Structural Detail and Occupancy of Glycans on Intact Glycoproteins. <i>Analytical Chemistry</i> , 2021 , 93, 10435-10443	7.8	4
432	Architecture of cell-cell junctions in situ reveals a mechanism for bacterial biofilm inhibition. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	3
431	Toxin import through the antibiotic efflux channel TolC. <i>Nature Communications</i> , 2021 , 12, 4625	17.4	4
430	Dendritic Oligoglycerol Regioisomer Mixtures and Their Utility for Membrane Protein Research. <i>Chemistry - A European Journal</i> , 2021 , 27, 2537-2542	4.8	7
429	Dynamics of an LPS translocon induced by substrate and an antimicrobial peptide. <i>Nature Chemical Biology</i> , 2021 , 17, 187-195	11.7	18
428	Structures of the archaerhodopsin-3 transporter reveal that disordering of internal water networks underpins receptor sensitization. <i>Nature Communications</i> , 2021 , 12, 629	17.4	10
427	Insights into SusCD-mediated glycan import by a prominent gut symbiont. <i>Nature Communications</i> , 2021 , 12, 44	17.4	15
426	The molecular basis of regulation of bacterial capsule assembly by Wzc. <i>Nature Communications</i> , 2021 , 12, 4349	17.4	6
425	X-ray free-electron laser studies reveal correlated motion during isopenicillin synthase catalysis. <i>Science Advances</i> , 2021 , 7,	14.3	4
424	Probing membrane protein-lipid interactions. <i>Current Opinion in Structural Biology</i> , 2021 , 69, 78-85	8.1	3
423	Colicin-Mediated Transport of DNA through the Iron Transporter FepA. <i>MBio</i> , 2021 , 12, e0178721	7.8	1
422	Competitive binding of MatP and topoisomerase IV to the MukB hinge domain. <i>ELife</i> , 2021 , 10,	8.9	1
421	Mass spectrometry informs the structure and dynamics of membrane proteins involved in lipid and drug transport. <i>Current Opinion in Structural Biology</i> , 2021 , 70, 53-60	8.1	4
420	Structural Basis for Silicic Acid Uptake by Higher Plants. <i>Journal of Molecular Biology</i> , 2021 , 433, 167226	6.5	2

4 ¹⁹	A 'Build and Retrieve' methodology to simultaneously solve cryo-EM structures of membrane proteins. <i>Nature Methods</i> , 2021 , 18, 69-75	21.6	31
4 ¹⁸	Mass spectrometry enables the discovery of inhibitors of an LPS transport assembly disruption of protein-protein interactions. <i>Chemical Communications</i> , 2021 , 57, 10747-10750	5.8	1
4 ¹⁷	Cryo-EM structure of human GPR158 receptor coupled to the RGS7-Gβ signaling complex. <i>Science</i> , 2021 , eabl4732	33.3	0
4 ¹⁶	Low-energy electron holography imaging of conformational variability of single-antibody molecules from electrospray ion beam deposition.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	4
4 ¹⁵	Christopher Dobson, 1949-2019: Mentor, Friend, Scientist Extraordinaire. <i>Annual Review of Biochemistry</i> , 2020 , 89, 1-19	29.1	7
4 ¹⁴	Combining native and 'omics' mass spectrometry to identify endogenous ligands bound to membrane proteins. <i>Nature Methods</i> , 2020 , 17, 505-508	21.6	43
4 ¹³	Pyocin S5 Import into <i>Pseudomonas aeruginosa</i> Reveals a Generic Mode of Bacteriocin Transport. <i>MBio</i> , 2020 , 11,	7.8	18
4 ¹²	Engineered anti-inflammatory peptides inspired by mapping an evasin-chemokine interaction. <i>Journal of Biological Chemistry</i> , 2020 , 295, 10926-10939	5.4	5
4 ¹¹	Bifurcated binding of the OmpF receptor underpins import of the bacteriocin colicin N into. <i>Journal of Biological Chemistry</i> , 2020 , 295, 9147-9156	5.4	9
4 ¹⁰	A constricted opening in Kir channels does not impede potassium conduction. <i>Nature Communications</i> , 2020 , 11, 3024	17.4	5
4 ⁰⁹	Cryo-EM structures provide insight into how <i>E. coli</i> FF ATP synthase accommodates symmetry mismatch. <i>Nature Communications</i> , 2020 , 11, 2615	17.4	33
4 ⁰⁸	Structure of V-ATPase from the mammalian brain. <i>Science</i> , 2020 , 367, 1240-1246	33.3	71
4 ⁰⁷	The use of sonicated lipid vesicles for mass spectrometry of membrane protein complexes. <i>Nature Protocols</i> , 2020 , 15, 1690-1706	18.8	20
4 ⁰⁶	A new azobenzene-based design strategy for detergents in membrane protein research. <i>Chemical Science</i> , 2020 , 11, 3538-3546	9.4	10
4 ⁰⁵	Structure and function of LCI1: a plasma membrane CO channel in the <i>Chlamydomonas</i> CO concentrating mechanism. <i>Plant Journal</i> , 2020 , 102, 1107-1126	6.9	9
4 ⁰⁴	Correlating Glycoforms of DC-SIGN with Stability Using a Combination of Enzymatic Digestion and Ion Mobility Mass Spectrometry. <i>Angewandte Chemie - International Edition</i> , 2020 , 59, 15560-15564	16.4	10
4 ⁰³	Assembly and regulation of the chlorhexidine-specific efflux pump Acel. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 17011-17018	11.5	21
4 ⁰²	Structure and elevator mechanism of the mammalian sodium/proton exchanger NHE9. <i>EMBO Journal</i> , 2020 , 39, e105908	13	11

401	Modular detergents tailor the purification and structural analysis of membrane proteins including G-protein coupled receptors. <i>Nature Communications</i> , 2020 , 11, 564	17.4	36
400	In Situ Structure of an Intact Lipopolysaccharide-Bound Bacterial Surface Layer. <i>Cell</i> , 2020 , 180, 348-358.e15	16.5	37
399	A Mass-Spectrometry-Based Approach to Distinguish Annular and Specific Lipid Binding to Membrane Proteins. <i>Angewandte Chemie - International Edition</i> , 2020 , 59, 3523-3528	16.4	18
398	A bipartite structural organization defines the SERINC family of HIV-1 restriction factors. <i>Nature Structural and Molecular Biology</i> , 2020 , 27, 78-83	17.6	34
397	A Mass-Spectrometry-Based Approach to Distinguish Annular and Specific Lipid Binding to Membrane Proteins. <i>Angewandte Chemie</i> , 2020 , 132, 3551-3556	3.6	1
396	Structural Basis of Tail-Anchored Membrane Protein Biogenesis by the GET Insertase Complex. <i>Molecular Cell</i> , 2020 , 80, 72-86.e7	17.6	28
395	Structures of a Complete Human V-ATPase Reveal Mechanisms of Its Assembly. <i>Molecular Cell</i> , 2020 , 80, 501-511.e3	17.6	22
394	The importance of the membrane for biophysical measurements. <i>Nature Chemical Biology</i> , 2020 , 16, 1285-1292.10	11.2	10
393	Allosteric Inhibition of the SARS-CoV-2 Main Protease: Insights from Mass Spectrometry Based Assays**. <i>Angewandte Chemie</i> , 2020 , 132, 23750-23754	3.6	9
392	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	16.4	52
391	Correlating Glycoforms of DC-SIGN with Stability Using a Combination of Enzymatic Digestion and Ion Mobility Mass Spectrometry. <i>Angewandte Chemie</i> , 2020 , 132, 15690-15694	3.6	1
390	A five-level classification system for proteoform identifications. <i>Nature Methods</i> , 2019 , 16, 939-940	21.6	25
389	Probing the limits of Q-tag bioconjugation of antibodies. <i>Chemical Communications</i> , 2019 , 55, 11342-11348	11.5	9
388	Mass spectrometry: From plasma proteins to mitochondrial membranes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 2814-2820	11.5	29
387	Human Antibodies that Slow Erythrocyte Invasion Potentiate Malaria-Neutralizing Antibodies. <i>Cell</i> , 2019 , 178, 216-228.e21	56.2	55
386	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	11.5	53
385	Mass Spectrometry of Intact Protein Complexes 2019 , 145-173		6
384	Tools for Understanding Nanoscale Lipid Regulation of Ion Channels. <i>Trends in Biochemical Sciences</i> , 2019 , 44, 795-806	10.3	35

383	Probing -glycoprotein microheterogeneity by lectin affinity purification-mass spectrometry analysis. <i>Chemical Science</i> , 2019 , 10, 5146-5155	9.4	34
382	Membrane Protein-Lipid Interactions Probed Using Mass Spectrometry. <i>Annual Review of Biochemistry</i> , 2019 , 88, 85-111	29.1	82
381	Structural comparison of the vacuolar and Golgi V-ATPases from. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 7272-7277	11.5	36
380	Capturing Biology in Flight. <i>Journal of the American Society for Mass Spectrometry</i> , 2019 , 30, 4-6	3.5	
379	Structural determinants of lipid specificity within Ups/PRELI lipid transfer proteins. <i>Nature Communications</i> , 2019 , 10, 1130	17.4	18
378	The Different Effects of Substrates and Nucleotides on the Complex Formation of ABC Transporters. <i>Structure</i> , 2019 , 27, 651-659.e3	5.2	13
377	Dynamic architecture of the Escherichia coli structural maintenance of chromosomes (SMC) complex, MukBEF. <i>Nucleic Acids Research</i> , 2019 , 47, 9696-9707	20.1	16
376	Relating glycoprotein structural heterogeneity to function - insights from native mass spectrometry. <i>Current Opinion in Structural Biology</i> , 2019 , 58, 241-248	8.1	24
375	Response to Comment on "Protein assemblies ejected directly from native membranes yield complexes for mass spectrometry". <i>Science</i> , 2019 , 366,	33.3	5
374	Homage to Chris Dobson. <i>Frontiers in Molecular Biosciences</i> , 2019 , 6, 137	5.6	
373	Structure of the Fanconi anaemia monoubiquitin ligase complex. <i>Nature</i> , 2019 , 575, 234-237	50.4	46
372	State-dependent Lipid Interactions with the A2a Receptor Revealed by MD Simulations Using InVivo-Mimetic Membranes. <i>Structure</i> , 2019 , 27, 392-403.e3	5.2	42
371	Precursor-Receptor Interactions in the Twin Arginine Protein Transport Pathway Probed with a New Receptor Complex Preparation. <i>Biochemistry</i> , 2018 , 57, 1663-1671	3.2	1
370	Identifying key membrane protein lipid interactions using mass spectrometry. <i>Nature Protocols</i> , 2018 , 13, 1106-1120	18.8	55
369	Cotranslational protein assembly imposes evolutionary constraints on homomeric proteins. <i>Nature Structural and Molecular Biology</i> , 2018 , 25, 279-288	17.6	19
368	The structure of serum resistance-associated protein and its implications for human African trypanosomiasis. <i>Nature Microbiology</i> , 2018 , 3, 295-301	26.6	13
367	Direct observation of the influence of cardiolipin and antibiotics on lipid II binding to MurJ. <i>Nature Chemistry</i> , 2018 , 10, 363-371	17.6	44
366	Direct binding of CEP85 to STIL ensures robust PLK4 activation and efficient centriole assembly. <i>Nature Communications</i> , 2018 , 9, 1731	17.4	24

365	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
364	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
363	Lipid binding attenuates channel closure of the outer membrane protein OmpF. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, 6691-6696	11.5	21
362	Self-assembly of toroidal proteins explored using native mass spectrometry. <i>Chemical Science</i> , 2018 , 9, 6099-6106	9.4	21
361	Protein assemblies ejected directly from native membranes yield complexes for mass spectrometry. <i>Science</i> , 2018 , 362, 829-834	33.3	99
360	Structure of native lens connexin 46/50 intercellular channels by cryo-EM. <i>Nature</i> , 2018 , 564, 372-377	50.4	52
359	Elongation/Termination Factor Exchange Mediated by PP1 Phosphatase Orchestrates Transcription Termination. <i>Cell Reports</i> , 2018 , 25, 259-269.e5	10.6	32
358	An electron transfer path connects subunits of a mycobacterial respiratory supercomplex. <i>Science</i> , 2018 , 362,	33.3	76
357	Structural Basis for Natural Product Selection and Export by Bacterial ABC Transporters. <i>ACS Chemical Biology</i> , 2018 , 13, 1598-1609	4.9	21
356	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
355	Biomimetic spinning of artificial spider silk from a chimeric minispidroin. <i>Nature Chemical Biology</i> , 2017 , 13, 262-264	11.7	143
354	Mass spectrometry captures structural intermediates in protein fiber self-assembly. <i>Chemical Communications</i> , 2017 , 53, 3319-3322	5.8	12
353	The role of interfacial lipids in stabilizing membrane protein oligomers. <i>Nature</i> , 2017 , 541, 421-424	50.4	238
352	Structural basis for nutrient acquisition by dominant members of the human gut microbiota. <i>Nature</i> , 2017 , 541, 407-411	50.4	119
351	Integrating mass spectrometry with MD simulations reveals the role of lipids in Na/H antiporters. <i>Nature Communications</i> , 2017 , 8, 13993	17.4	50
350	From molecular chaperones to membrane motors: through the lens of a mass spectrometrist. <i>Biochemical Society Transactions</i> , 2017 , 45, 251-260	5.1	15
349	Acetylation and phosphorylation control both local and global stability of the chloroplast F ATP synthase. <i>Scientific Reports</i> , 2017 , 7, 44068	4.9	14
348	The Tetrameric Plant Lectin BanLec Neutralizes HIV through Bidentate Binding to Specific Viral Glycans. <i>Structure</i> , 2017 , 25, 773-782.e5	5.2	28

347	A specific nanobody prevents amyloidogenesis of D76N β microglobulin in vitro and modifies its tissue distribution in vivo. <i>Scientific Reports</i> , 2017 , 7, 46711	4.9	12
346	Key features of an Hsp70 chaperone allosteric landscape revealed by ion-mobility native mass spectrometry and double electron-electron resonance. <i>Journal of Biological Chemistry</i> , 2017 , 292, 8773-8785	5.4	33
345	Ligand binding to a G protein-coupled receptor captured in a mass spectrometer. <i>Science Advances</i> , 2017 , 3, e1701016	14.3	39
344	Effects of Detergent Micelles on Lipid Binding to Proteins in Electrospray Ionization Mass Spectrometry. <i>Analytical Chemistry</i> , 2017 , 89, 7425-7430	7.8	20
343	Efficient protein production inspired by how spiders make silk. <i>Nature Communications</i> , 2017 , 8, 15504	17.4	48
342	Architecture of eukaryotic mRNA 3'-end processing machinery. <i>Science</i> , 2017 , 358, 1056-1059	33.3	81
341	Carbene Footprinting Reveals Binding Interfaces of a Multimeric Membrane-Spanning Protein. <i>Angewandte Chemie</i> , 2017 , 129, 15069-15073	3.6	10
340	Carbene Footprinting Reveals Binding Interfaces of a Multimeric Membrane-Spanning Protein. <i>Angewandte Chemie - International Edition</i> , 2017 , 56, 14873-14877	16.4	25
339	Molecular basis for inner kinetochore configuration through RWD domain-peptide interactions. <i>EMBO Journal</i> , 2017 , 36, 3458-3482	13	22
338	A new class of hybrid secretion system is employed in <i>Pseudomonas</i> amyloid biogenesis. <i>Nature Communications</i> , 2017 , 8, 263	17.4	41
337	Native Desorption Electrospray Ionization Liberates Soluble and Membrane Protein Complexes from Surfaces. <i>Angewandte Chemie</i> , 2017 , 129, 14655-14660	3.6	8
336	Native Desorption Electrospray Ionization Liberates Soluble and Membrane Protein Complexes from Surfaces. <i>Angewandte Chemie - International Edition</i> , 2017 , 56, 14463-14468	16.4	30
335	Innenrücktitelbild: Native Desorption Electrospray Ionization Liberates Soluble and Membrane Protein Complexes from Surfaces (Angew. Chem. 46/2017). <i>Angewandte Chemie</i> , 2017 , 129, 14965-14968	3.6	
334	Architecture of TAF11/TAF13/TBP complex suggests novel regulation properties of general transcription factor TFIID. <i>ELife</i> , 2017 , 6,	8.9	19
333	Author response: Architecture of TAF11/TAF13/TBP complex suggests novel regulation properties of general transcription factor TFIID 2017 ,		2
332	Structural and Functional Basis for Lipid Synergy on the Activity of the Antibacterial Peptide ABC Transporter McjD. <i>Journal of Biological Chemistry</i> , 2016 , 291, 21656-21668	5.4	22
331	Mass spectrometry captures off-target drug binding and provides mechanistic insights into the human metalloprotease ZMPSTE24. <i>Nature Chemistry</i> , 2016 , 8, 1152-1158	17.6	49
330	The structural basis for CD36 binding by the malaria parasite. <i>Nature Communications</i> , 2016 , 7, 12837	17.4	106

329	Atomic model for the membrane-embedded V motor of a eukaryotic V-ATPase. <i>Nature</i> , 2016 , 539, 118-124	17.4	104
328	Interfacing Membrane Mimetics with Mass Spectrometry. <i>Accounts of Chemical Research</i> , 2016 , 49, 2459-2467	14.7	51
327	Crystal structure of an invertebrate cytolysin pore reveals unique properties and mechanism of assembly. <i>Nature Communications</i> , 2016 , 7, 11598	17.4	54
326	The interchange of immunophilins leads to parallel pathways and different intermediates in the assembly of Hsp90 glucocorticoid receptor complexes. <i>Cell Discovery</i> , 2016 , 2, 16002	22.3	29
325	Infrared Laser Activation of Soluble and Membrane Protein Assemblies in the Gas Phase. <i>Analytical Chemistry</i> , 2016 , 88, 7060-7	7.8	22
324	The human Na(+)/H(+) exchanger 1 is a membrane scaffold protein for extracellular signal-regulated kinase 2. <i>BMC Biology</i> , 2016 , 14, 31	7.3	35
323	Elucidation of Drug Metabolite Structural Isomers Using Molecular Modeling Coupled with Ion Mobility Mass Spectrometry. <i>Analytical Chemistry</i> , 2016 , 88, 2273-80	7.8	40
322	High-resolution mass spectrometry of small molecules bound to membrane proteins. <i>Nature Methods</i> , 2016 , 13, 333-6	21.6	164
321	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
320	Structure of BRCA1-BRCT/Abraxas Complex Reveals Phosphorylation-Dependent BRCT Dimerization at DNA Damage Sites. <i>Molecular Cell</i> , 2016 , 61, 434-448	17.6	48
319	Insights into Eukaryotic Translation Initiation from Mass Spectrometry of Macromolecular Protein Assemblies. <i>Journal of Molecular Biology</i> , 2016 , 428, 344-356	6.5	13
318	Structural and Functional Characterization of the Bacterial Type III Secretion Export Apparatus. <i>PLoS Pathogens</i> , 2016 , 12, e1006071	7.6	53
317	Optimal Synthetic Glycosylation of a Therapeutic Antibody. <i>Angewandte Chemie - International Edition</i> , 2016 , 55, 2361-7	16.4	92
316	Dimer interface of bovine cytochrome c oxidase is influenced by local posttranslational modifications and lipid binding. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, 8230-5	11.5	30
315	A combined computational and structural model of the full-length human prolactin receptor. <i>Nature Communications</i> , 2016 , 7, 11578	17.4	38
314	The anti-sigma factor RsrA responds to oxidative stress by reburying its hydrophobic core. <i>Nature Communications</i> , 2016 , 7, 12194	17.4	16
313	The Significance of the Location of Mutations for the Native-State Dynamics of Human Lysozyme. <i>Biophysical Journal</i> , 2016 , 111, 2358-2367	2.9	12
312	Three-Dimensional Architecture of the Human BRCA1-A Histone Deubiquitinase Core Complex. <i>Cell Reports</i> , 2016 , 17, 3099-3106	10.6	16

311	Structural evidence for Nap1-dependent H2A-H2B deposition and nucleosome assembly. <i>EMBO Journal</i> , 2016 , 35, 1465-82	13	42
310	Super-complexes of adhesion GPCRs and neural guidance receptors. <i>Nature Communications</i> , 2016 , 7, 11184	17.4	53
309	Probing the Lipid Annular Belt by Gas-Phase Dissociation of Membrane Proteins in Nanodiscs. <i>Angewandte Chemie</i> , 2016 , 128, 560-564	3.6	5
308	Unraveling the Composition and Behavior of Heterogeneous Lipid Nanodiscs by Mass Spectrometry. <i>Analytical Chemistry</i> , 2016 , 88, 6199-204	7.8	27
307	Characterisation of Shigella Spa33 and Thermotoga FliM/N reveals a new model for C-ring assembly in T3SS. <i>Molecular Microbiology</i> , 2016 , 99, 749-66	4.1	48
306	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
305	Negative Ions Enhance Survival of Membrane Protein Complexes. <i>Journal of the American Society for Mass Spectrometry</i> , 2016 , 27, 1099-104	3.5	15
304	Low Charge and Reduced Mobility of Membrane Protein Complexes Has Implications for Calibration of Collision Cross Section Measurements. <i>Analytical Chemistry</i> , 2016 , 88, 5879-5884	7.8	28
303	A sliding selectivity scale for lipid binding to membrane proteins. <i>Current Opinion in Structural Biology</i> , 2016 , 39, 54-60	8.1	41
302	Mass spectrometry guided structural biology. <i>Current Opinion in Structural Biology</i> , 2016 , 40, 136-144	8.1	79
301	Mass spectrometry of protein complexes: from origins to applications. <i>Annual Review of Physical Chemistry</i> , 2015 , 66, 453-74	15.7	132
300	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
299	Collision cross sections for structural proteomics. <i>Structure</i> , 2015 , 23, 791-9	5.2	169
298	Different modes of lipid binding to membrane proteins probed by mass spectrometry. <i>Journal of the American Chemical Society</i> , 2015 , 137, 5240-7	16.4	51
297	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
296	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
295	Bifunctional crosslinking ligands for transthyretin. <i>Open Biology</i> , 2015 , 5, 150105	7	2
294	Quantifying the stabilizing effects of protein-ligand interactions in the gas phase. <i>Nature Communications</i> , 2015 , 6, 8551	17.4	111

293	Controlling release, unfolding and dissociation of membrane protein complexes in the gas phase through collisional cooling. <i>Chemical Communications</i> , 2015 , 51, 15582-4	5.8	14
292	Generation of a synthetic GlcNAcylated nucleosome reveals regulation of stability by H2A-Thr101 GlcNAcylation. <i>Nature Communications</i> , 2015 , 6, 7978	17.4	40
291	Structure and function of the Escherichia coli Tol-Pal stator protein TolR. <i>Journal of Biological Chemistry</i> , 2015 , 290, 26675-87	5.4	16
290	Structures of CD6 and Its Ligand CD166 Give Insight into Their Interaction. <i>Structure</i> , 2015 , 23, 1426-1436	6.2	39
289	A new window into the molecular physiology of membrane proteins. <i>Journal of Physiology</i> , 2015 , 593, 355-62	3.9	29
288	In vivo formation of Plasmodium falciparum ribosomal stalk - a unique mode of assembly without stable heterodimeric intermediates. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2015 , 1850, 150-8	4	4
287	A novel mechano-enzymatic cleavage mechanism underlies transthyretin amyloidogenesis. <i>EMBO Molecular Medicine</i> , 2015 , 7, 1337-49	12	81
286	eIF2 interactions with initiator tRNA and eIF2B are regulated by post-translational modifications and conformational dynamics. <i>Cell Discovery</i> , 2015 , 1, 15020	22.3	18
285	Dual stoichiometry and subunit organization in the ClpP1/P2 protease from the cyanobacterium Synechococcus elongatus. <i>Journal of Structural Biology</i> , 2015 , 192, 519-527	3.4	3
284	The Role of the Detergent Micelle in Preserving the Structure of Membrane Proteins in the Gas Phase. <i>Angewandte Chemie</i> , 2015 , 127, 4660-4664	3.6	5
283	Maturation of 6S regulatory RNA to a highly elongated structure. <i>FEBS Journal</i> , 2015 , 282, 4548-64	5.7	3
282	The Effect of Detergent, Temperature, and Lipid on the Oligomeric State of MscL Constructs: Insights from Mass Spectrometry. <i>Chemistry and Biology</i> , 2015 , 22, 593-603		50
281	Principles of assembly reveal a periodic table of protein complexes. <i>Science</i> , 2015 , 350, aaa2245	33.3	142
280	The role of lipids in mechanosensation. <i>Nature Structural and Molecular Biology</i> , 2015 , 22, 991-8	17.6	111
279	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
278	Topological models of heteromeric protein assemblies from mass spectrometry: application to the yeast eIF3:eIF5 complex. <i>Chemistry and Biology</i> , 2015 , 22, 117-28		34
277	The structure of the dynactin complex and its interaction with dynein. <i>Science</i> , 2015 , 347, 1441-1446	33.3	266
276	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

275	Small molecule inhibitors of disulfide bond formation by the bacterial DsbA-DsbB dual enzyme system. <i>ACS Chemical Biology</i> , 2015 , 10, 957-64	4.9	20
274	Flexible stoichiometry and asymmetry of the PIDDosome core complex by heteronuclear NMR spectroscopy and mass spectrometry. <i>Journal of Molecular Biology</i> , 2015 , 427, 737-752	6.5	12
273	Cytoplasmic TAF2-TAF8-TAF10 complex provides evidence for nuclear holo-TFIID assembly from preformed submodules. <i>Nature Communications</i> , 2015 , 6, 6011	17.4	57
272	The joining of the Hsp90 and Hsp70 chaperone cycles yields transient interactions and stable intermediates: insights from mass spectrometry. <i>Oncotarget</i> , 2015 , 6, 18276-81	3.3	6
271	The <i>Caenorhabditis elegans</i> protein SAS-5 forms large oligomeric assemblies critical for centriole formation. <i>ELife</i> , 2015 , 4, e07410	8.9	30
270	A mass spectrometry-based hybrid method for structural modeling of protein complexes. <i>Nature Methods</i> , 2014 , 11, 403-406	21.6	131
269	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
268	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
267	Flexible membrane proteins: functional dynamics captured by mass spectrometry. <i>Current Opinion in Structural Biology</i> , 2014 , 28, 122-30	8.1	18
266	Catenane versus ring: do both assemblies of CS2 hydrolase exhibit the same stability and catalytic activity?. <i>Chemical Science</i> , 2014 , 5, 2879	9.4	5
265	A comparative cross-linking strategy to probe conformational changes in protein complexes. <i>Nature Protocols</i> , 2014 , 9, 2224-36	18.8	86
264	Structural basis for hijacking siderophore receptors by antimicrobial lasso peptides. <i>Nature Chemical Biology</i> , 2014 , 10, 340-2	11.7	52
263	SpyAvidin hubs enable precise and ultrastable orthogonal nanoassembly. <i>Journal of the American Chemical Society</i> , 2014 , 136, 12355-63	16.4	43
262	Structural basis for Pan3 binding to Pan2 and its function in mRNA recruitment and deadenylation. <i>EMBO Journal</i> , 2014 , 33, 1514-26	13	38
261	A hydrodynamic comparison of solution and gas phase proteins and their complexes. <i>Journal of Physical Chemistry B</i> , 2014 , 118, 8489-95	3.4	27
260	Mass-selective soft-landing of protein assemblies with controlled landing energies. <i>Analytical Chemistry</i> , 2014 , 86, 8321-8	7.8	42
259	Membrane proteins bind lipids selectively to modulate their structure and function. <i>Nature</i> , 2014 , 510, 172-175	50.4	503
258	Subunit dynamics and nucleotide-dependent asymmetry of an AAA(+) transcription complex. <i>Journal of Molecular Biology</i> , 2014 , 426, 71-83	6.5	11

257	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
256	Mass spectrometry defines the C-terminal dimerization domain and enables modeling of the structure of full-length OmpA. <i>Structure</i> , 2014 , 22, 781-90	5.2	46
255	Mass spectrometry quantifies protein interactions--from molecular chaperones to membrane porins. <i>Angewandte Chemie - International Edition</i> , 2014 , 53, 14002-15	16.4	45
254	The structures of cytosolic and plastid-located glutamine synthetases from <i>Medicago truncatula</i> reveal a common and dynamic architecture. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014 , 70, 981-93		18
253	Analysis of the subunit organization of the eIF2B complex reveals new insights into its structure and regulation. <i>FASEB Journal</i> , 2014 , 28, 2225-37	0.9	44
252	The p97-FAF1 protein complex reveals a common mode of p97 adaptor binding. <i>Journal of Biological Chemistry</i> , 2014 , 289, 12077-12084	5.4	21
251	Massenspektrometrie zur Quantifizierung von Wechselwirkungen zwischen Proteinen Von molekularen Chaperonen zu Membranporinen. <i>Angewandte Chemie</i> , 2014 , 126, 14224-14238	3.6	4
250	Dynamic protein ligand interactions--insights from MS. <i>FEBS Journal</i> , 2014 , 281, 1950-64	5.7	50
249	Charge reduction stabilizes intact membrane protein complexes for mass spectrometry. <i>Journal of the American Chemical Society</i> , 2014 , 136, 17010-2	16.4	56
248	eIF2B is a decameric guanine nucleotide exchange factor with a $\alpha\alpha$ tetrameric core. <i>Nature Communications</i> , 2014 , 5, 3902	17.4	52
247	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
246	Intrinsically Disordered p53 and Its Complexes Populate Compact Conformations in the Gas Phase. <i>Angewandte Chemie</i> , 2013 , 125, 379-383	3.6	4
245	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
244	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
243	Detergent-free mass spectrometry of membrane protein complexes. <i>Nature Methods</i> , 2013 , 10, 1206-8	21.6	131
242	Structure of Cu(I)-bound DJ-1 reveals a biscysteinate metal binding site at the homodimer interface: insights into mutational inactivation of DJ-1 in Parkinsonism. <i>Journal of the American Chemical Society</i> , 2013 , 135, 15974-7	16.4	14
241	Class I HDACs share a common mechanism of regulation by inositol phosphates. <i>Molecular Cell</i> , 2013 , 51, 57-67	17.6	247
240	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

239	Dodecyl maltoside protects membrane proteins in vacuo. <i>Biophysical Journal</i> , 2013 , 105, 648-56	2.9	19
238	Twenty years of gas phase structural biology. <i>Structure</i> , 2013 , 21, 1541-50	5.2	126
237	Structure of the CRISPR interference complex CSM reveals key similarities with cascade. <i>Molecular Cell</i> , 2013 , 52, 124-34	17.6	145
236	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, 4790-801	6.5	44
235	Protein complexes are under evolutionary selection to assemble via ordered pathways. <i>Cell</i> , 2013 , 153, 461-70	56.2	153
234	Mass spectrometry of intact membrane protein complexes. <i>Nature Protocols</i> , 2013 , 8, 639-51	18.8	263
233	Evidence that the catenane form of CS2 hydrolase is not an artefact. <i>Chemical Communications</i> , 2013 , 49, 7770-2	5.8	24
232	Detergent release prolongs the lifetime of native-like membrane protein conformations in the gas-phase. <i>Journal of the American Chemical Society</i> , 2013 , 135, 6078-83	16.4	48
231	A nanobody binding to non-amyloidogenic regions of the protein human lysozyme enhances partial unfolding but inhibits amyloid fibril formation. <i>Journal of Physical Chemistry B</i> , 2013 , 117, 13245-13258	3.4	33
230	Structural model of lymphocyte receptor NKR-P1C revealed by mass spectrometry and molecular modeling. <i>Analytical Chemistry</i> , 2013 , 85, 1597-604	7.8	16
229	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
228	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
227	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
226	Intrinsically disordered protein threads through the bacterial outer-membrane porin OmpF. <i>Science</i> , 2013 , 340, 1570-4	33.3	96
225	The N-terminal region of the human autophagy protein ATG16L1 contains a domain that folds into a helical structure consistent with formation of a coiled-coil. <i>PLoS ONE</i> , 2013 , 8, e76237	3.7	14
224	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
223	Crystal structure of the human short coiled coil protein and insights into SCOC-FEZ1 complex formation. <i>PLoS ONE</i> , 2013 , 8, e76355	3.7	6
222	Gas-phase protein assemblies: Unfolding landscapes and preserving native-like structures using noncovalent adducts. <i>Chemical Physics Letters</i> , 2012 , 524, 1-9	2.5	39

221	Linking structural change with functional regulation-insights from mass spectrometry. <i>Current Opinion in Structural Biology</i> , 2012 , 22, 44-51	8.1	18
220	Structural basis for DNA recognition and loading into a viral packaging motor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 811-6	11.5	47
219	Structure of the TatC core of the twin-arginine protein transport system. <i>Nature</i> , 2012 , 492, 210-4	50.4	126
218	The 'sticky business' of cleaning gas-phase membrane proteins: a detergent oriented perspective. <i>Physical Chemistry Chemical Physics</i> , 2012 , 14, 14439-49	3.6	32
217	Host-guest interactions in acid-porphyrin complexes. <i>Chemical Communications</i> , 2012 , 48, 9358-60	5.8	8
216	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
215	Formation and dissociation processes of gas-phase detergent micelles. <i>Langmuir</i> , 2012 , 28, 7160-7	4	30
214	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
213	The unusual mycobacterial chaperonins: evidence for in vivo oligomerization and specialization of function. <i>Molecular Microbiology</i> , 2012 , 85, 934-44	4.1	21
212	Structural modeling of heteromeric protein complexes from disassembly pathways and ion mobility-mass spectrometry. <i>Structure</i> , 2012 , 20, 1596-609	5.2	100
211	Mass spectrometry--from peripheral proteins to membrane motors. <i>Journal of Molecular Biology</i> , 2012 , 423, 1-13	6.5	23
210	Oxygenase-catalyzed ribosome hydroxylation occurs in prokaryotes and humans. <i>Nature Chemical Biology</i> , 2012 , 8, 960-962	11.7	112
209	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
208	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
207	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	93.2	124
206	Advancing cell biology through proteomics in space and time (PROSPECTS). <i>Molecular and Cellular Proteomics</i> , 2012 , 11, O112.017731	7.6	52
205	The interaction of the antitoxin DM43 with a snake venom metalloproteinase analyzed by mass spectrometry and surface plasmon resonance. <i>Journal of Mass Spectrometry</i> , 2012 , 47, 567-73	2.2	11
204	Mechanism and rates of exchange of L7/L12 between ribosomes and the effects of binding EF-G. <i>ACS Chemical Biology</i> , 2012 , 7, 1120-7	4.9	19

203	Do charge state signatures guarantee protein conformations?. <i>Journal of the American Society for Mass Spectrometry</i> , 2012 , 23, 1161-8	3.5	136
202	Finding the right balance: a personal journey from individual proteins to membrane-embedded motors: based on a lecture delivered at the 36th FEBS Congress in Torino, Italy, June 2011. <i>FEBS Journal</i> , 2012 , 279, 663-77	5.7	2
201	Joining forces: integrating proteomics and cross-linking with the mass spectrometry of intact complexes. <i>Molecular and Cellular Proteomics</i> , 2012 , 11, R111.014027	7.6	57
200	Structure and location of the regulatory β subunits in the β phosphorylase kinase complex. <i>Journal of Biological Chemistry</i> , 2012 , 287, 36651-61	5.4	13
199	Mass spectrometry reveals differences in stability and subunit interactions between activated and nonactivated conformers of the β phosphorylase kinase complex. <i>Molecular and Cellular Proteomics</i> , 2012 , 11, 1768-76	7.6	11
198	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
197	The catalytic activity of Ubp6 enhances maturation of the proteasomal regulatory particle. <i>Molecular Cell</i> , 2011 , 42, 637-49	17.6	60
196	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, 358-68	6.5	54
195	β -crystallin polydispersity is a consequence of unbiased quaternary dynamics. <i>Journal of Molecular Biology</i> , 2011 , 413, 297-309	6.5	96
194	Characterisation of serpin polymers in vitro and in vivo. <i>Methods</i> , 2011 , 53, 255-66	4.6	28
193	A Quantitative Perspective on Hydrophobic Interactions in the Gas-Phase. <i>Current Proteomics</i> , 2011 , 8, 47-58	0.7	12
192	Assembly states of the nucleosome assembly protein 1 (NAP-1) revealed by sedimentation velocity and non-denaturing MS. <i>Biochemical Journal</i> , 2011 , 436, 101-12	3.8	17
191	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
190	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
189	Multimeric assembly and biochemical characterization of the Trax-translin endonuclease complex. <i>Nature Structural and Molecular Biology</i> , 2011 , 18, 658-64	17.6	56
188	Structural basis for the subunit assembly of the anaphase-promoting complex. <i>Nature</i> , 2011 , 470, 227-32	50.4	132
187	John Fenn (1917-2010). <i>Nature</i> , 2011 , 469, 300	50.4	2
186	Mass spectrometry reveals stable modules in holo and apo RNA polymerases I and III. <i>Structure</i> , 2011 , 19, 90-100	5.2	44

185	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
184	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, 1895	5.2	78
183	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
182	Women in science: In pursuit of female chemists. <i>Nature</i> , 2011 , 476, 273-5	50.4	12
181	Protein-nucleic acid complexes and the role of mass spectrometry in their structure determination. <i>Critical Reviews in Biochemistry and Molecular Biology</i> , 2011 , 46, 152-64	8.7	12
180	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
179	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
178	Evidence for the assembly of a bacterial tripartite multidrug pump with a stoichiometry of 3:6:3. <i>Journal of Biological Chemistry</i> , 2011 , 286, 26900-12	5.4	41
177	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
176	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
175	Heterogeneity and dynamics in the assembly of the heat shock protein 90 chaperone complexes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 17939-44	11.5	55
174	Opening of the outer membrane protein channel in tripartite efflux pumps is induced by interaction with the membrane fusion partner. <i>Journal of Biological Chemistry</i> , 2011 , 286, 5484-93	5.4	28
173	Structures of SAS-6 suggest its organization in centrioles. <i>Science</i> , 2011 , 331, 1196-9	33.3	240
172	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
171	Polypyrimidine tract-binding protein stimulates the poliovirus IRES by modulating eIF4G binding. <i>EMBO Journal</i> , 2010 , 29, 3710-22	13	58
170	Recognition of a signal peptide by the signal recognition particle. <i>Nature</i> , 2010 , 465, 507-10	50.4	149
169	Trapping of palindromic ligands within native transthyretin prevents amyloid formation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 20483-8	11.5	50
168	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

167	Mass spectrometry defines the stoichiometry of ribosomal stalk complexes across the phylogenetic tree. <i>Molecular and Cellular Proteomics</i> , 2010 , 9, 1774-83	7.6	27
166	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
165	A non-natural variant of human lysozyme (I59T) mimics the in vitro behaviour of the I56T variant that is responsible for a form of familial amyloidosis. <i>Protein Engineering, Design and Selection</i> , 2010 , 23, 499-506	1.9	17
164	The regulatory protein RraA modulates RNA-binding and helicase activities of the E. coli RNA degradosome. <i>Rna</i> , 2010 , 16, 553-62	5.8	54
163	Alternate dissociation pathways identified in charge-reduced protein complex ions. <i>Analytical Chemistry</i> , 2010 , 82, 5363-72	7.8	126
162	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
161	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
160	Potassium is critical for the Ni(II)-responsive DNA-binding activity of Escherichia coli NikR. <i>Journal of the American Chemical Society</i> , 2010 , 132, 1506-7	16.4	12
159	Separating and visualising protein assemblies by means of preparative mass spectrometry and microscopy. <i>Journal of Structural Biology</i> , 2010 , 172, 161-8	3.4	54
158	Retinol and retinol-binding protein stabilize transthyretin via formation of retinol transport complex. <i>ACS Chemical Biology</i> , 2010 , 5, 1137-46	4.9	35
157	Structure and intermolecular dynamics of aggregates populated during amyloid fibril formation studied by hydrogen/deuterium exchange. <i>Accounts of Chemical Research</i> , 2010 , 43, 1072-9	24.3	53
156	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
155	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
154	Biophysical properties of the eukaryotic ribosomal stalk. <i>Biochemistry</i> , 2010 , 49, 924-33	3.2	26
153	A single subunit directs the assembly of the Escherichia coli DNA sliding clamp loader. <i>Structure</i> , 2010 , 18, 285-92	5.2	17
152	Solution NMR investigation of the CD95/FADD homotypic death domain complex suggests lack of engagement of the CD95 C terminus. <i>Structure</i> , 2010 , 18, 1378-90	5.2	46
151	When proteomics meets structural biology. <i>Trends in Biochemical Sciences</i> , 2010 , 35, 522-9	10.3	60
150	Residual counter ions can stabilise a large protein complex in the gas phase. <i>International Journal of Mass Spectrometry</i> , 2010 , 298, 91-98	1.9	57

149	The quaternary organization and dynamics of the molecular chaperone HSP26 are thermally regulated. <i>Chemistry and Biology</i> , 2010 , 17, 1008-17		41
148	Molecular recognition between Escherichia coli enolase and ribonuclease E. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2010 , 66, 1036-40		19
147	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
146	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
145	Isoforms of U1-70k control subunit dynamics in the human spliceosomal U1 snRNP. <i>PLoS ONE</i> , 2009 , 4, e7202	3.7	39
144	Structure and function of a novel type of ATP-dependent Clp protease. <i>Journal of Biological Chemistry</i> , 2009 , 284, 13519-13532	5.4	53
143	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
142	Molecular dissection of Alzheimer's disease neuropathology by depletion of serum amyloid P component. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 7619-23	11.5	55
141	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
140	The structure of CrgA from Neisseria meningitidis reveals a new octameric assembly state for LysR transcriptional regulators. <i>Nucleic Acids Research</i> , 2009 , 37, 4545-58	20.1	51
139	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
138	Defining the structural basis of human plasminogen binding by streptococcal surface enolase. <i>Journal of Biological Chemistry</i> , 2009 , 284, 17129-17137	5.4	52
137	Ultraslow oligomerization equilibria of p53 and its implications. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 14327-32	11.5	44
136	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
135	Symmetrical modularity of the COP9 signalosome complex suggests its multifunctionality. <i>Structure</i> , 2009 , 17, 31-40	5.2	124
134	The crystal structure of the N-terminal region of BUB1 provides insight into the mechanism of BUB1 recruitment to kinetochores. <i>Structure</i> , 2009 , 17, 105-16	5.2	36
133	Subunit architecture of multiprotein assemblies determined using restraints from gas-phase measurements. <i>Structure</i> , 2009 , 17, 1235-43	5.2	97
132	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

131	Methodology for measuring conformation of solvent-disrupted protein subunits using T-WAVE ion mobility MS: an investigation into eukaryotic initiation factors. <i>Journal of the American Society for Mass Spectrometry</i> , 2009 , 20, 1699-706	3.5	50
130	AU-rich RNA-binding induces changes in the quaternary structure of AUH. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009 , 75, 360-72	4.2	8
129	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
128	Mass spectrometry of membrane transporters reveals subunit stoichiometry and interactions. <i>Nature Methods</i> , 2009 , 6, 585-7	21.6	146
127	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	1.9	25
126	Gas-phase unfolding and disassembly reveals stability differences in ligand-bound multiprotein complexes. <i>Chemistry and Biology</i> , 2009 , 16, 382-90		124
125	Quadrupole-time-of-flight mass spectrometer modified for higher-energy dissociation reduces protein assemblies to peptide fragments. <i>Analytical Chemistry</i> , 2009 , 81, 1270-4	7.8	46
124	How to switch off a histidine kinase: crystal structure of <i>Geobacillus stearothermophilus</i> KinB with the inhibitor Sda. <i>Journal of Molecular Biology</i> , 2009 , 386, 163-77	6.5	53
123	The small heat-shock proteins HSPB2 and HSPB3 form well-defined heterooligomers in a unique 3 to 1 subunit ratio. <i>Journal of Molecular Biology</i> , 2009 , 393, 1022-32	6.5	40
122	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
121	Effects of antibody affinity and antigen valence on molecular forms of immune complexes. <i>Molecular Immunology</i> , 2009 , 47, 357-64	4.3	33
120	Two-phase dynamic combinatorial discovery of a spermine transporter. <i>Chemical Communications</i> , 2009 , 3708-10	5.8	42
119	Mass spectrometry characterization of multiprotein complexes. <i>Cold Spring Harbor Protocols</i> , 2009 , pdb.prot5180	1.2	5
118	Discrete, multi-component complexes with cucurbit[8]uril in the gas-phase. <i>Chemical Communications</i> , 2009 , 644-6	5.8	58
117	A multidrug ABC transporter with a taste for salt. <i>PLoS ONE</i> , 2009 , 4, e6137	3.7	30
116	Assembly reflects evolution of protein complexes. <i>Nature</i> , 2008 , 453, 1262-5	50.4	316
115	Ion mobility-mass spectrometry analysis of large protein complexes. <i>Nature Protocols</i> , 2008 , 3, 1139-52	18.8	843
114	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

113	Micelles protect membrane complexes from solution to vacuum. <i>Science</i> , 2008 , 321, 243-6	33.3	291
112	Mutating the tight-dimer interface of dihydrodipicolinate synthase disrupts the enzyme quaternary structure: toward a monomeric enzyme. <i>Biochemistry</i> , 2008 , 47, 12108-17	3.2	14
111	Acetylation of L12 increases interactions in the Escherichia coli ribosomal stalk complex. <i>Journal of Molecular Biology</i> , 2008 , 380, 404-14	6.5	50
110	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
109	Small heat shock protein activity is regulated by variable oligomeric substructure. <i>Journal of Biological Chemistry</i> , 2008 , 283, 28513-7	5.4	85
108	Allosteric activation of the ATPase activity of the Escherichia coli RhlB RNA helicase. <i>Journal of Biological Chemistry</i> , 2008 , 283, 5567-76	5.4	26
107	Stoichiometry and localization of the stator subunits E and G in Thermus thermophilus H ⁺ -ATPase/synthase. <i>Journal of Biological Chemistry</i> , 2008 , 283, 2595-603	5.4	51
106	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
105	Structural properties of the human acidic ribosomal P proteins forming the P1-P2 heterocomplex. <i>Journal of Biochemistry</i> , 2008 , 143, 169-77	3.1	23
104	The emerging role of MS in structure elucidation of protein-nucleic acid complexes. <i>Biochemical Society Transactions</i> , 2008 , 36, 723-31	5.1	17
103	Real-time monitoring of protein complexes reveals their quaternary organization and dynamics. <i>Chemistry and Biology</i> , 2008 , 15, 246-53		64
102	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
101	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
100	Determining the stoichiometry and interactions of macromolecular assemblies from mass spectrometry. <i>Nature Protocols</i> , 2007 , 2, 715-26	18.8	538
99	The molecular sociology of the cell. <i>Nature</i> , 2007 , 450, 973-82	50.4	424
98	Evidence for micellar structure in the gas phase. <i>Journal of the American Chemical Society</i> , 2007 , 129, 8740-6	16.4	50
97	Chemical cross-linking of the chloroplast localized small heat-shock protein, Hsp21, and the model substrate citrate synthase. <i>Protein Science</i> , 2007 , 16, 1464-78	6.3	43
96	Three binding sites for stalk protein dimers are generally present in ribosomes from archaeal organism. <i>Journal of Biological Chemistry</i> , 2007 , 282, 32827-33	5.4	29

95	Mass spectrometry reveals the missing links in the assembly pathway of the bacterial 20 S proteasome. <i>Journal of Biological Chemistry</i> , 2007 , 282, 18448-18457	5.4	44
94	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
93	Elevated copy number of L-A virus in yeast mutant strains defective in ribosomal stalk. <i>Biochemical and Biophysical Research Communications</i> , 2007 , 355, 575-80	3.4	11
92	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
91	Mimicking phosphorylation of alphaB-crystallin affects its chaperone activity. <i>Biochemical Journal</i> , 2007 , 401, 129-41	3.8	147
90	Protein complexes in the gas phase: technology for structural genomics and proteomics. <i>Chemical Reviews</i> , 2007 , 107, 3544-67	68.1	342
89	Mass spectrometry of macromolecular assemblies: preservation and dissociation. <i>Current Opinion in Structural Biology</i> , 2006 , 16, 245-51	8.1	190
88	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
87	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
86	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
85	Characterization of Functional Protein Complexes 2006 , 157-169		
84	Structural organization of the 19S proteasome lid: insights from MS of intact complexes. <i>PLoS Biology</i> , 2006 , 4, e267	9.7	159
83	Multimers of the fibroblast growth factor (FGF)-FGF receptor-saccharide complex are formed on long oligomers of heparin. <i>Biochemical Journal</i> , 2006 , 393, 741-8	3.8	44
82	Impact of the native-state stability of human lysozyme variants on protein secretion by <i>Pichia pastoris</i> . <i>FEBS Journal</i> , 2006 , 273, 711-20	5.7	43
81	Regional and segmental flexibility of antibodies in interaction with antigens of different size. <i>FEBS Journal</i> , 2006 , 273, 1476-87	5.7	42
80	Targeting C-reactive protein for the treatment of cardiovascular disease. <i>Nature</i> , 2006 , 440, 1217-21	50.4	525
79	Subunit architecture of multimeric complexes isolated directly from cells. <i>EMBO Reports</i> , 2006 , 7, 605-10	6.5	164
78	Aspects of native proteins are retained in vacuum. <i>Current Opinion in Chemical Biology</i> , 2006 , 10, 402-8	9.7	199

77	Tandem mass spectrometry reveals the quaternary organization of macromolecular assemblies. <i>Chemistry and Biology</i> , 2006 , 13, 597-605		191
76	Evidence for macromolecular protein rings in the absence of bulk water. <i>Science</i> , 2005 , 310, 1658-61	33.3	502
75	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
74	Rationalising lysozyme amyloidosis: insights from the structure and solution dynamics of T70N lysozyme. <i>Journal of Molecular Biology</i> , 2005 , 352, 823-36	6.5	39
73	Mass spectrometry of intact ribosomes. <i>FEBS Letters</i> , 2005 , 579, 943-7	3.8	42
72	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
71	Molecular recycling within amyloid fibrils. <i>Nature</i> , 2005 , 436, 554-8	50.4	312
70	Me, my cell, and I: the role of the collision cell in the tandem mass spectrometry of macromolecules. <i>BioTechniques</i> , 2005 , 39, 447, 449, 451 passim	2.5	4
69	Structural insights into the activity of enhancer-binding proteins. <i>Science</i> , 2005 , 307, 1972-5	33.3	141
68	The polypyrimidine tract binding protein is a monomer. <i>Rna</i> , 2005 , 11, 1803-8	5.8	27
67	L55P transthyretin accelerates subunit exchange and leads to rapid formation of hybrid tetramers. <i>Journal of Biological Chemistry</i> , 2005 , 280, 41667-74	5.4	54
66	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
65	Protein complexes of the Escherichia coli cell envelope. <i>Journal of Biological Chemistry</i> , 2005 , 280, 34409-19	5.19	171
64	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
63	Dodecameric structure of the small heat shock protein Acr1 from Mycobacterium tuberculosis. <i>Journal of Biological Chemistry</i> , 2005 , 280, 33419-25	5.4	82
62	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, 10949-54	11.5	80
61	Mass spectrometry of ribosomes from Saccharomyces cerevisiae: implications for assembly of the stalk complex. <i>Journal of Biological Chemistry</i> , 2004 , 279, 42750-7	5.4	37
60	Tsp36, a tapeworm small heat-shock protein with a duplicated alpha-crystallin domain, forms dimers and tetramers with good chaperone-like activity. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004 , 57, 109-17	4.2	11

59	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
58	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
57	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
56	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
55	The structure and biochemical properties of the human spliceosomal protein U1C. <i>Journal of Molecular Biology</i> , 2004 , 341, 185-98	6.5	44
54	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
53	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
52	Dissociation of intact Escherichia coli ribosomes in a mass spectrometer. Evidence for conformational change in a ribosome elongation factor G complex. <i>Journal of Biological Chemistry</i> , 2003 , 278, 1259-67	5.4	39
51	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
50	Gas-phase dissociation pathways of a tetrameric protein complex. <i>International Journal of Mass Spectrometry</i> , 2003 , 230, 193-200	1.9	53
49	A camelid antibody fragment inhibits the formation of amyloid fibrils by human lysozyme. <i>Nature</i> , 2003 , 424, 783-8	50.4	212
48	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
47	Thermal dissociation of multimeric protein complexes by using nanoelectrospray mass spectrometry. <i>Analytical Chemistry</i> , 2003 , 75, 2208-14	7.8	135
46	Use of a microchip device coupled with mass spectrometry for ligand screening of a multi-protein target. <i>Analytical Chemistry</i> , 2003 , 75, 4937-41	7.8	45
45	Phospholipid complexation and association with apolipoprotein C-II: insights from mass spectrometry. <i>Biophysical Journal</i> , 2003 , 85, 3802-12	2.9	36
44	Protein complexes gain momentum. <i>Current Opinion in Structural Biology</i> , 2002 , 12, 729-34	8.1	129
43	Protein complexes take flight. <i>Nature Structural Biology</i> , 2002 , 9, 505-6		17
42	Local cooperativity in the unfolding of an amyloidogenic variant of human lysozyme. <i>Nature Structural Biology</i> , 2002 , 9, 308-15		190

41	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
40	A single-domain antibody fragment that stabilises the native state of two amyloidogenic lysozyme variants and hence prevents aggregation. <i>Biochemical Society Transactions</i> , 2002 , 30, A68-A68	5.1	
39	A single-domain antibody fragment that stabilises the native state of two amyloidogenic lysozyme variants and hence prevents aggregation. <i>Biochemical Society Transactions</i> , 2002 , 30, A93-A93	5.1	
38	A tandem mass spectrometer for improved transmission and analysis of large macromolecular assemblies. <i>Analytical Chemistry</i> , 2002 , 74, 1402-7	7.8	448
37	Screening transthyretin amyloid fibril inhibitors: characterization of novel multiprotein, multiligand complexes by mass spectrometry. <i>Structure</i> , 2002 , 10, 851-63	5.2	99
36	Macromolecular organization of the <i>Yersinia pestis</i> capsular F1 antigen: insights from time-of-flight mass spectrometry. <i>Protein Science</i> , 2001 , 10, 2408-13	6.3	19
35	Reconstitution of the spliceosomal U1 snRNP from all recombinant subunits and its characterisation by ionspray Q-tof mass-spectrometry. <i>Nucleic Acids Symposium Series</i> , 2001 , 275-6		4
34	Dynamic protein complexes: insights from mass spectrometry. <i>Journal of Biological Chemistry</i> , 2001 , 276, 46685-8	5.4	52
33	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
32	Competitive binding to the oligopeptide binding protein, OppA: in-trap cleanup in an Fourier transform ion cyclotron resonance mass spectrometer. <i>Journal of the American Society for Mass Spectrometry</i> , 2000 , 11, 1023-6	3.5	11
31	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
30	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
29	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
28	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
27	Solvent effects on the conformation of the transmembrane peptide gramicidin A: insights from electrospray ionization mass spectrometry. <i>Biophysical Journal</i> , 2000 , 78, 1010-7	2.9	26
26	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
25	A near-native state on the slow refolding pathway of hen lysozyme. <i>Protein Science</i> , 1999 , 8, 35-44	6.3	32
24	GroEL accelerates the refolding of hen lysozyme without changing its folding mechanism. <i>Nature Structural Biology</i> , 1999 , 6, 683-90		54

23	Probing the nature of interactions in SH2 binding interfaces--evidence from electrospray ionization mass spectrometry. <i>Protein Science</i> , 1999 , 8, 1962-70	6.3	32
22	Selective association of protein molecules followed by mass spectrometry. <i>Protein Science</i> , 1999 , 8, 1368-70	6.3	23
21	Disassembly of intact multiprotein complexes in the gas phase. <i>Current Opinion in Structural Biology</i> , 1999 , 9, 135-41	8.1	83
20	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
19	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
18	Dissection of multi-protein complexes using mass spectrometry: Subunit interactions in transthyretin and retinol-binding protein complexes 1998 , 33, 3-11		47
17	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
16	Dissection of multi-protein complexes using mass spectrometry: Subunit interactions in transthyretin and retinol-binding protein complexes. <i>Proteins: Structure, Function and Bioinformatics</i> , 1998 , 33, 3-11	4.2	8
15	Dissection of multi-protein complexes using mass spectrometry: subunit interactions in transthyretin and retinol-binding protein complexes. <i>Proteins: Structure, Function and Bioinformatics</i> , 1998 , Suppl 2, 3-11	4.2	23
14	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
13	Instability, unfolding and aggregation of human lysozyme variants underlying amyloid fibrillogenesis. <i>Nature</i> , 1997 , 385, 787-93	50.4	980
12	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	16.4	285
11	Investigation of protein folding by mass spectrometry. <i>FASEB Journal</i> , 1996 , 10, 93-101	0.9	169
10	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
9	Weighing the evidence for structure: electrospray ionization mass spectrometry of proteins. <i>Structure</i> , 1995 , 3, 861-5	5.2	16
8	Conformation of GroEL-bound alpha-lactalbumin probed by mass spectrometry. <i>Nature</i> , 1994 , 372, 646-51	50.4	202
7	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
6	Detection of transient protein folding populations by mass spectrometry. <i>Science</i> , 1993 , 262, 896-900	33.3	555

- 5 Mass-selective and ice-free cryo-EM protein sample preparation via native electrospray ion-beam deposition 2
- 4 Anionic Dendritic Polyglycerol for Protein Purification and Delipidation. *ACS Applied Polymer Materials*, 4:3 2
- 3 Spontaneous oligomerization of BAK/BAX is suppressed by hetero-dimerization with MCL-1 1
- 2 Competitive binding of MatP and topoisomerase IV to the MukB dimerization hinge 1
- 1 Acyl Carrier Protein is essential for MukBEF action in Escherichia coli chromosome organization-segregation 1