

# Carol V Robinson

## List of Publications by Year in descending order

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Version: 2024-02-01

454  
papers

43,203  
citations

1094

112  
h-index

3638

180  
g-index

477  
all docs

477  
docs citations

477  
times ranked

33447  
citing authors

| #  | ARTICLE   | IF   | CITATIONS |
|----|---|------|-----------|
| 1  | Instability, unfolding and aggregation of human lysozyme variants underlying amyloid fibrillogenesis. <i>Nature</i> , 1997, 385, 787-793.   | 13.7 | 1,061     |
| 2  | Ion mobility mass spectrometry analysis of large protein complexes. <i>Nature Protocols</i> , 2008, 3, 1139-1152.   | 5.5  | 973       |
| 3  | Amyloid- $\beta$ protein oligomerization and the importance of tetramers and dodecamers in the aetiology of Alzheimer's disease. <i>Nature Chemistry</i> , 2009, 1, 326-331.        | 6.6  | 835       |
| 4  | Collision Cross Sections of Proteins and Their Complexes: A Calibration Framework and Database for Gas-Phase Structural Biology. <i>Analytical Chemistry</i> , 2010, 82, 9557-9565. | 3.2  | 694       |
| 5  | Membrane proteins bind lipids selectively to modulate their structure and function. <i>Nature</i> , 2014, 510, 172-175.   | 13.7 | 665       |
| 6  | Bayesian Deconvolution of Mass and Ion Mobility Spectra: From Binary Interactions to Polydisperse Ensembles. <i>Analytical Chemistry</i> , 2015, 87, 4370-4376.                     | 3.2  | 663       |
| 7  | Targeting C-reactive protein for the treatment of cardiovascular disease. <i>Nature</i> , 2006, 440, 1217-1221.   | 13.7 | 621       |
| 8  | Determining the stoichiometry and interactions of macromolecular assemblies from mass spectrometry. <i>Nature Protocols</i> , 2007, 2, 715-726.                                     | 5.5  | 597       |
| 9  | Detection of transient protein folding populations by mass spectrometry. <i>Science</i> , 1993, 262, 896-900.   | 6.0  | 590       |
| 10 | Evidence for Macromolecular Protein Rings in the Absence of Bulk Water. <i>Science</i> , 2005, 310, 1658-1661.  | 6.0  | 551       |
| 11 | The molecular sociology of the cell. <i>Nature</i> , 2007, 450, 973-982.  | 13.7 | 497       |
| 12 | A Tandem Mass Spectrometer for Improved Transmission and Analysis of Large Macromolecular Assemblies. <i>Analytical Chemistry</i> , 2002, 74, 1402-1407.                            | 3.2  | 481       |
| 13 | Formation of insulin amyloid fibrils followed by FTIR simultaneously with CD and electron microscopy. <i>Protein Science</i> , 2000, 9, 1960-1967.                                  | 3.1  | 453       |
| 14 | The structure of the dynactin complex and its interaction with dynein. <i>Science</i> , 2015, 347, 1441-1446.   | 6.0  | 389       |
| 15 | Assembly reflects evolution of protein complexes. <i>Nature</i> , 2008, 453, 1262-1265.   | 13.7 | 383       |
| 16 | Protein Complexes in the Gas Phase: Technology for Structural Genomics and Proteomics. <i>Chemical Reviews</i> , 2007, 107, 3544-3567.  | 23.0 | 376       |
| 17 | Mass spectrometry of intact membrane protein complexes. <i>Nature Protocols</i> , 2013, 8, 639-651.   | 5.5  | 354       |
| 18 | The role of interfacial lipids in stabilizing membrane protein oligomers. <i>Nature</i> , 2017, 541, 421-424.   | 13.7 | 344       |

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|----|--|------|-----------|
| 19 | Molecular recycling within amyloid fibrils. <i>Nature</i> , 2005, 436, 554-558.  | 13.7 | 342       |
| 20 | Structural Characterization of Drug-like Compounds by Ion Mobility Mass Spectrometry: Comparison of Theoretical and Experimentally Derived Nitrogen Collision Cross Sections. <i>Analytical Chemistry</i> , 2012, 84, 1026-1033.         | 3.2  | 340       |
| 21 | The Role of Mass Spectrometry in Structure Elucidation of Dynamic Protein Complexes. <i>Annual Review of Biochemistry</i> , 2007, 76, 167-193.   | 5.0  | 337       |
| 22 | Micelles Protect Membrane Complexes from Solution to Vacuum. <i>Science</i> , 2008, 321, 243-246.  | 6.0  | 333       |
| 23 | An Oligomeric Signaling Platform Formed by the Toll-like Receptor Signal Transducers MyD88 and IRAK-4. <i>Journal of Biological Chemistry</i> , 2009, 284, 25404-25411.  | 1.6  | 323       |
| 24 | Class I HDACs Share a Common Mechanism of Regulation by Inositol Phosphates. <i>Molecular Cell</i> , 2013, 51, 57-67.  | 4.5  | 314       |
| 25 | Probing the Nature of Noncovalent Interactions by Mass Spectrometry. A Study of Protein <sup>+</sup> CoA Ligand Binding and Assembly. <i>Journal of the American Chemical Society</i> , 1996, 118, 8646-8653.                            | 6.6  | 304       |
| 26 | Structures of SAS-6 Suggest Its Organization in Centrioles. <i>Science</i> , 2011, 331, 1196-1199.   | 6.0  | 284       |
| 27 | Ion Mobility Mass Spectrometry of Peptide Ions: Effects of Drift Gas and Calibration Strategies. <i>Analytical Chemistry</i> , 2012, 84, 7124-7130.  | 3.2  | 281       |
| 28 | Structure of a designed protein cage that self-assembles into a highly porous cube. <i>Nature Chemistry</i> , 2014, 6, 1065-1071.  | 6.6  | 267       |
| 29 | Crystal structures of truncated alphaA and alphaB crystallins reveal structural mechanisms of polydispersity important for eye lens function. <i>Protein Science</i> , 2010, 19, 1031-1043.  | 3.1  | 264       |
| 30 | Programmable polyproteins built using twin peptide superglues. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 1202-1207.  | 3.3  | 262       |
| 31 | Characterization of the Oligomeric States of Insulin in Self-Assembly and Amyloid Fibril Formation by Mass Spectrometry. <i>Biophysical Journal</i> , 2000, 79, 1053-1065.   | 0.2  | 258       |
| 32 | PAXX, a paralog of XRCC4 and XLF, interacts with Ku to promote DNA double-strand break repair. <i>Science</i> , 2015, 347, 185-188.  | 6.0  | 252       |
| 33 | Mass Spectrometry of Intact V-Type ATPases Reveals Bound Lipids and the Effects of Nucleotide Binding. <i>Science</i> , 2011, 334, 380-385.  | 6.0  | 251       |
| 34 | The Fas <sup>+</sup> FADD death domain complex structure reveals the basis of DISC assembly and disease mutations. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 1324-1329.   | 3.6  | 236       |
| 35 | PtdIns(4,5)P <sub>2</sub> stabilizes active states of GPCRs and enhances selectivity of G-protein coupling. <i>Nature</i> , 2018, 559, 423-427.  | 13.7 | 236       |
| 36 | Polydispersity of a mammalian chaperone: Mass spectrometry reveals the population of oligomers in $\gamma$ -crystallin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 10611-10616. | 3.3  | 235       |

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|----|---|------|-----------|
| 37 | Mass spectrometry reveals modularity and a complete subunit interaction map of the eukaryotic translation factor eIF3. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 18139-18144. | 3.3  | 233       |
| 38 | Quaternary dynamics and plasticity underlie small heat shock protein chaperone function. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 2007-2012.                                 | 3.3  | 231       |
| 39 | Collision Cross Sections for Structural Proteomics. <i>Structure</i> , 2015, 23, 791-799.   | 1.6  | 231       |
| 40 | Biomimetic spinning of artificial spider silk from a chimeric minispidroin. <i>Nature Chemical Biology</i> , 2017, 13, 262-264.   | 3.9  | 231       |
| 41 | A camelid antibody fragment inhibits the formation of amyloid fibrils by human lysozyme. <i>Nature</i> , 2003, 424, 783-788.  | 13.7 | 227       |
| 42 | Charge-State Dependent Compaction and Dissociation of Protein Complexes: Insights from Ion Mobility and Molecular Dynamics. <i>Journal of the American Chemical Society</i> , 2012, 134, 3429-3438.                                     | 6.6  | 223       |
| 43 | Conformation of GroEL-bound $\alpha$ -lactalbumin probed by mass spectrometry. <i>Nature</i> , 1994, 372, 646-651.  | 13.7 | 221       |
| 44 | Aspects of native proteins are retained in vacuum. <i>Current Opinion in Chemical Biology</i> , 2006, 10, 402-408.  | 2.8  | 217       |
| 45 | Protein Complexes Are under Evolutionary Selection to Assemble via Ordered Pathways. <i>Cell</i> , 2013, 153, 461-470.  | 13.5 | 215       |
| 46 | Ion Mobility–Mass Spectrometry Reveals Long-Lived, Unfolded Intermediates in the Dissociation of Protein Complexes. <i>Angewandte Chemie - International Edition</i> , 2007, 46, 8001-8004.   | 7.2  | 213       |
| 47 | Detection and selective dissociation of intact ribosomes in a mass spectrometer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2000, 97, 5185-5190.  | 3.3  | 209       |
| 48 | Local cooperativity in the unfolding of an amyloidogenic variant of human lysozyme. <i>Nature Structural Biology</i> , 2002, 9, 308-315.  | 9.7  | 208       |
| 49 | Tandem Mass Spectrometry Reveals the Quaternary Organization of Macromolecular Assemblies. <i>Chemistry and Biology</i> , 2006, 13, 597-605.  | 6.2  | 206       |
| 50 | High-resolution mass spectrometry of small molecules bound to membrane proteins. <i>Nature Methods</i> , 2016, 13, 333-336.   | 9.0  | 205       |
| 51 | Electrospray Time-of-Flight Mass Spectrometry of the Intact MS2 Virus Capsid. <i>Journal of the American Chemical Society</i> , 2000, 122, 3550-3551.   | 6.6  | 199       |
| 52 | Mass spectrometry of macromolecular assemblies: preservation and dissociation. <i>Current Opinion in Structural Biology</i> , 2006, 16, 245-251.  | 2.6  | 199       |
| 53 | Interaction of the Molecular Chaperone $\beta$ -Crystallin with $\alpha$ -Synuclein: Effects on Amyloid Fibril Formation and Chaperone Activity. <i>Journal of Molecular Biology</i> , 2004, 340, 1167-1183.                            | 2.0  | 198       |
| 54 | Principles of assembly reveal a periodic table of protein complexes. <i>Science</i> , 2015, 350, aaa2245.   | 6.0  | 198       |

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|----|---|------|-----------|
| 55 | Structural basis for nutrient acquisition by dominant members of the human gut microbiota. <i>Nature</i> , 2017, 541, 407-411.  | 13.7 | 188       |
| 56 | Protein Complexes of the Escherichia coli Cell Envelope*. <i>Journal of Biological Chemistry</i> , 2005, 280, 34409-34419.  | 1.6  | 183       |
| 57 | Structure of the CRISPR Interference Complex CSM Reveals Key Similarities with Cascade. <i>Molecular Cell</i> , 2013, 52, 124-134.  | 4.5  | 181       |
| 58 | The structured core domain of I $\beta$ -crystallin can prevent amyloid fibrillation and associated toxicity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E1562-70. | 3.3  | 181       |
| 59 | Subunit Exchange of Multimeric Protein Complexes. <i>Journal of Biological Chemistry</i> , 2002, 277, 38921-38929.  | 1.6  | 180       |
| 60 | The Co-chaperone p23 Arrests the Hsp90 ATPase Cycle to Trap Client Proteins. <i>Journal of Molecular Biology</i> , 2006, 356, 746-758.  | 2.0  | 179       |
| 61 | Structural Organization of the 19S Proteasome Lid: Insights from MS of Intact Complexes. <i>PLoS Biology</i> , 2006, 4, e267.   | 2.6  | 176       |
| 62 | Investigation of protein folding by mass spectrometry. <i>FASEB Journal</i> , 1996, 10, 93-101.   | 0.2  | 175       |
| 63 | Recognition of a signal peptide by the signal recognition particle. <i>Nature</i> , 2010, 465, 507-510.   | 13.7 | 172       |
| 64 | Mass Spectrometry of Protein Complexes: From Origins to Applications. <i>Annual Review of Physical Chemistry</i> , 2015, 66, 453-474.   | 4.8  | 169       |
| 65 | Subunit architecture of multimeric complexes isolated directly from cells. <i>EMBO Reports</i> , 2006, 7, 605-610.  | 2.0  | 168       |
| 66 | Protein subunit interactions and structural integrity of amyloidogenic transthyretins: evidence from electrospray mass spectrometry. <i>Journal of Molecular Biology</i> , 1998, 281, 553-564.                              | 2.0  | 167       |
| 67 | Mass Measurements of Increased Accuracy Resolve Heterogeneous Populations of Intact Ribosomes. <i>Journal of the American Chemical Society</i> , 2006, 128, 11433-11442.  | 6.6  | 166       |
| 68 | Mechanistic Studies of the Folding of Human Lysozyme and the Origin of Amyloidogenic Behavior in Its Disease-Related Variants. <i>Biochemistry</i> , 1999, 38, 6419-6427.   | 1.2  | 165       |
| 69 | Mass spectrometry of membrane transporters reveals subunit stoichiometry and interactions. <i>Nature Methods</i> , 2009, 6, 585-587.  | 9.0  | 164       |
| 70 | Structure of the TatC core of the twin-arginine protein transport system. <i>Nature</i> , 2012, 492, 210-214.   | 13.7 | 164       |
| 71 | Coupling Microdroplet Microreactors with Mass Spectrometry: Reading the Contents of Single Droplets Online. <i>Angewandte Chemie - International Edition</i> , 2009, 48, 3665-3668.   | 7.2  | 162       |
| 72 | Detection of the Intact GroEL Chaperonin Assembly by Mass Spectrometry. <i>Journal of the American Chemical Society</i> , 1999, 121, 4718-4719.   | 6.6  | 161       |

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|----|---|------|-----------|
| 73 | Thermal Dissociation of Multimeric Protein Complexes by Using Nanoelectrospray Mass Spectrometry. <i>Analytical Chemistry</i> , 2003, 75, 2208-2214.  | 3.2  | 161       |
| 74 | The role of lipids in mechanosensation. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 991-998.   | 3.6  | 160       |
| 75 | The structural basis for CD36 binding by the malaria parasite. <i>Nature Communications</i> , 2016, 7, 12837.   | 5.8  | 160       |
| 76 | Mimicking phosphorylation of $\alpha$ -crystallin affects its chaperone activity. <i>Biochemical Journal</i> , 2007, 401, 129-141.  | 1.7  | 159       |
| 77 | Mass spectrometry reveals synergistic effects of nucleotides, lipids, and drugs binding to a multidrug resistance efflux pump. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 9704-9709. | 3.3  | 156       |
| 78 | Protein assemblies ejected directly from native membranes yield complexes for mass spectrometry. <i>Science</i> , 2018, 362, 829-834.   | 6.0  | 155       |
| 79 | Studies of the RNA Degradosome-organizing Domain of the Escherichia coli Ribonuclease RNase E. <i>Journal of Molecular Biology</i> , 2004, 340, 965-979.  | 2.0  | 153       |
| 80 | Structural Insights into the Activity of Enhancer-Binding Proteins. <i>Science</i> , 2005, 307, 1972-1975.  | 6.0  | 153       |
| 81 | Structure of the core of the type III secretion system export apparatus. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 583-590.  | 3.6  | 153       |
| 82 | Structure of V-ATPase from the mammalian brain. <i>Science</i> , 2020, 367, 1240-1246.  | 6.0  | 153       |
| 83 | Detergent-free mass spectrometry of membrane protein complexes. <i>Nature Methods</i> , 2013, 10, 1206-1208.  | 9.0  | 152       |
| 84 | Structural basis for the subunit assembly of the anaphase-promoting complex. <i>Nature</i> , 2011, 470, 227-232.  | 13.7 | 150       |
| 85 | Do Charge State Signatures Guarantee Protein Conformations?. <i>Journal of the American Society for Mass Spectrometry</i> , 2012, 23, 1161-1168.  | 1.2  | 149       |
| 86 | A mass spectrometry-based hybrid method for structural modeling of protein complexes. <i>Nature Methods</i> , 2014, 11, 403-406.  | 9.0  | 149       |
| 87 | Alternate Dissociation Pathways Identified in Charge-Reduced Protein Complex Ions. <i>Analytical Chemistry</i> , 2010, 82, 5363-5372.   | 3.2  | 145       |
| 88 | Phosphorylation of $\alpha$ -Crystallin Alters Chaperone Function through Loss of Dimeric Substructure. <i>Journal of Biological Chemistry</i> , 2004, 279, 28675-28680.  | 1.6  | 144       |
| 89 | Twenty Years of Gas Phase Structural Biology. <i>Structure</i> , 2013, 21, 1541-1550.   | 1.6  | 143       |
| 90 | Gas-Phase Unfolding and Disassembly Reveals Stability Differences in Ligand-Bound Multiprotein Complexes. <i>Chemistry and Biology</i> , 2009, 16, 382-390.   | 6.2  | 141       |

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|-----|--|------|-----------|
| 91  | Advances in the Mass Spectrometry of Membrane Proteins: From Individual Proteins to Intact Complexes. <i>Annual Review of Biochemistry</i> , 2011, 80, 247-271.  | 5.0  | 141       |
| 92  | Atomic model for the membrane-embedded VO motor of a eukaryotic V-ATPase. <i>Nature</i> , 2016, 539, 118-122.  | 13.7 | 141       |
| 93  | Mass Sign: An Assignment Strategy for Maximizing Information from the Mass Spectra of Heterogeneous Protein Assemblies. <i>Analytical Chemistry</i> , 2012, 84, 2939-2948.   | 3.2  | 140       |
| 94  | Protein complexes gain momentum. <i>Current Opinion in Structural Biology</i> , 2002, 12, 729-734.   | 2.6  | 138       |
| 95  | Traveling-wave ion mobility mass spectrometry of protein complexes: accurate calibrated collision cross-sections of human insulin oligomers. <i>Rapid Communications in Mass Spectrometry</i> , 2012, 26, 1181-1193.                                   | 0.7  | 138       |
| 96  | Structural insights into the lipid and ligand regulation of serotonin receptors. <i>Nature</i> , 2021, 592, 469-473.   | 13.7 | 138       |
| 97  | Quantifying the stabilizing effects of protein-ligand interactions in the gas phase. <i>Nature Communications</i> , 2015, 6, 8551.   | 5.8  | 136       |
| 98  | Defining the mechanism of polymerization in the serpinopathies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 17146-17151.   | 3.3  | 135       |
| 99  | Oxygenase-catalyzed ribosome hydroxylation occurs in prokaryotes and humans. <i>Nature Chemical Biology</i> , 2012, 8, 960-962.  | 3.9  | 135       |
| 100 | Heptameric (L12)6/L10 rather than canonical pentameric complexes are found by tandem MS of intact ribosomes from thermophilic bacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 8192-8197. | 3.3  | 134       |
| 101 | The role of lipids in defining membrane protein interactions: insights from mass spectrometry. <i>Trends in Cell Biology</i> , 2013, 23, 1-8.  | 3.6  | 134       |
| 102 | Structural evolution of p53, p63, and p73: Implication for heterotetramer formation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 17705-17710.  | 3.3  | 133       |
| 103 | Symmetrical Modularity of the COP9 Signalosome Complex Suggests its Multifunctionality. <i>Structure</i> , 2009, 17, 31-40.  | 1.6  | 133       |
| 104 | Crystal structure of the open conformation of the mammalian chaperonin CCT in complex with tubulin. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 14-19.  | 3.6  | 128       |
| 105 | Steroid-based facial amphiphiles for stabilization and crystallization of membrane proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E1203-11.   | 3.3  | 127       |
| 106 | Architecture of eukaryotic mRNA 3'-end processing machinery. <i>Science</i> , 2017, 358, 1056-1059.  | 6.0  | 124       |
| 107 | Subunit Architecture of Intact Protein Complexes from Mass Spectrometry and Homology Modeling. <i>Accounts of Chemical Research</i> , 2008, 41, 617-627.   | 7.6  | 123       |
| 108 | $\beta$ -Crystallin Polydispersity Is a Consequence of Unbiased Quaternary Dynamics. <i>Journal of Molecular Biology</i> , 2011, 413, 297-309.   | 2.0  | 122       |

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|-----|---|------|-----------|
| 109 | Comparative cross-linking and mass spectrometry of an intact F-type ATPase suggest a role for phosphorylation. <i>Nature Communications</i> , 2013, 4, 1985.  | 5.8  | 122       |
| 110 | Optimal Synthetic Glycosylation of a Therapeutic Antibody. <i>Angewandte Chemie - International Edition</i> , 2016, 55, 2361-2367.  | 7.2  | 122       |
| 111 | Membrane Protein-Lipid Interactions Probed Using Mass Spectrometry. <i>Annual Review of Biochemistry</i> , 2019, 88, 85-111.  | 5.0  | 121       |
| 112 | Integrating Ion Mobility Mass Spectrometry with Molecular Modelling to Determine the Architecture of Multiprotein Complexes. <i>PLoS ONE</i> , 2010, 5, e12080.   | 1.1  | 119       |
| 113 | Correlating Solution Binding and ESI-MS Stabilities by Incorporating Solvation Effects in a Confined Cucurbit[8]uril System. <i>Journal of Physical Chemistry B</i> , 2010, 114, 8606-8615.   | 1.2  | 118       |
| 114 | The Role of the Detergent Micelle in Preserving the Structure of Membrane Proteins in the Gas Phase. <i>Angewandte Chemie - International Edition</i> , 2015, 54, 4577-4581.  | 7.2  | 117       |
| 115 | An electron transfer path connects subunits of a mycobacterial respiratory supercomplex. <i>Science</i> , 2018, 362, .  | 6.0  | 117       |
| 116 | Structural Characterization of the Human Eukaryotic Initiation Factor 3 Protein Complex by Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2007, 6, 1135-1146.  | 2.5  | 116       |
| 117 | Tandem Differential Mobility Analysis-Mass Spectrometry Reveals Partial Gas-Phase Collapse of the GroEL Complex. <i>Journal of Physical Chemistry B</i> , 2011, 115, 3614-3621.   | 1.2  | 116       |
| 118 | A subset of annular lipids is linked to the flippase activity of an ABC transporter. <i>Nature Chemistry</i> , 2015, 7, 255-262.  | 6.6  | 112       |
| 119 | The antibiotic darobactin mimics a $\beta^2$ -strand to inhibit outer membrane insertase. <i>Nature</i> , 2021, 593, 125-129.   | 13.7 | 112       |
| 120 | Combining native and $\tilde{\text{omics}}^{\text{TM}}$ mass spectrometry to identify endogenous ligands bound to membrane proteins. <i>Nature Methods</i> , 2020, 17, 505-508.   | 9.0  | 111       |
| 121 | Structural Modeling of Heteromeric Protein Complexes from Disassembly Pathways and Ion Mobility-Mass Spectrometry. <i>Structure</i> , 2012, 20, 1596-1609.  | 1.6  | 110       |
| 122 | Subunit Exchange of Polydisperse Proteins. <i>Journal of Biological Chemistry</i> , 2005, 280, 14485-14491.   | 1.6  | 109       |
| 123 | Experimental characterization of disordered and ordered aggregates populated during the process of amyloid fibril formation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 7828-7833. | 3.3  | 109       |
| 124 | Intrinsically Disordered Protein Threads Through the Bacterial Outer-Membrane Porin OmpF. <i>Science</i> , 2013, 340, 1570-1574.  | 6.0  | 109       |
| 125 | A novel mechano-enzymatic cleavage mechanism underlies transthyretin amyloidogenesis. <i>EMBO Molecular Medicine</i> , 2015, 7, 1337-1349.  | 3.3  | 109       |
| 126 | Structure of native lens connexin 46/50 intercellular channels by cryo-EM. <i>Nature</i> , 2018, 564, 372-377.  | 13.7 | 107       |

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|-----|--|------|-----------|
| 127 | Human Antibodies that Slow Erythrocyte Invasion Potentiate Malaria-Neutralizing Antibodies. <i>Cell</i> , 2019, 178, 216-228.e21.  | 13.5 | 107       |
| 128 | Screening Transthyretin Amyloid Fibril Inhibitors. <i>Structure</i> , 2002, 10, 851-863.   | 1.6  | 106       |
| 129 | Observation of the noncovalent assembly and disassembly pathways of the chaperone complex MtGimC by mass spectrometry. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2000, 97, 14151-14155. | 3.3  | 102       |
| 130 | Characterising electrosprayed biomolecules using tandem-MS—the noncovalent GroEL chaperonin assembly. <i>International Journal of Mass Spectrometry</i> , 2004, 236, 25-32.  | 0.7  | 102       |
| 131 | Efficient protein production inspired by how spiders make silk. <i>Nature Communications</i> , 2017, 8, 15504.   | 5.8  | 102       |
| 132 | Reduced Global Cooperativity is a Common Feature Underlying the Amyloidogenicity of Pathogenic Lysozyme Mutations. <i>Journal of Molecular Biology</i> , 2005, 346, 773-788.   | 2.0  | 100       |
| 133 | Small Heat Shock Protein Activity Is Regulated by Variable Oligomeric Substructure. <i>Journal of Biological Chemistry</i> , 2008, 283, 28513-28517.   | 1.6  | 99        |
| 134 | Subunit Architecture of Multiprotein Assemblies Determined Using Restraints from Gas-Phase Measurements. <i>Structure</i> , 2009, 17, 1235-1243.   | 1.6  | 99        |
| 135 | Mass spectrometry guided structural biology. <i>Current Opinion in Structural Biology</i> , 2016, 40, 136-144.   | 2.6  | 98        |
| 136 | Kinetic Consequences of the Removal of a Disulfide Bridge on the Folding of Hen Lysozyme. <i>Biochemistry</i> , 1994, 33, 13038-13048.   | 1.2  | 97        |
| 137 | Probing the Lipid Annular Belt by Gas-Phase Dissociation of Membrane Proteins in Nanodiscs. <i>Angewandte Chemie - International Edition</i> , 2016, 55, 550-554.  | 7.2  | 95        |
| 138 | N-glycan microheterogeneity regulates interactions of plasma proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 8763-8768.  | 3.3  | 94        |
| 139 | MmpL3 is a lipid transporter that binds trehalose monomycolate and phosphatidylethanolamine. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 11241-11246.                          | 3.3  | 94        |
| 140 | A $\beta$ 240 and A $\beta$ 242 Amyloid Fibrils Exhibit Distinct Molecular Recycling Properties. <i>Journal of the American Chemical Society</i> , 2011, 133, 6505-6508.   | 6.6  | 93        |
| 141 | A comparative cross-linking strategy to probe conformational changes in protein complexes. <i>Nature Protocols</i> , 2014, 9, 2224-2236.   | 5.5  | 93        |
| 142 | Hsp70 Forms Antiparallel Dimers Stabilized by Post-translational Modifications to Position Clients for Transfer to Hsp90. <i>Cell Reports</i> , 2015, 11, 759-769.   | 2.9  | 93        |
| 143 | Allosteric Inhibition of the SARS-CoV-2 Main Protease: Insights from Mass Spectrometry Based Assays**. <i>Angewandte Chemie - International Edition</i> , 2020, 59, 23544-23548.   | 7.2  | 92        |
| 144 | Dodecameric Structure of the Small Heat Shock Protein Acr1 from <i>Mycobacterium tuberculosis</i> . <i>Journal of Biological Chemistry</i> , 2005, 280, 33419-33425.   | 1.6  | 91        |

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