

Michael Landreh

List of Publications by Citations

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141
papers

10,547
citations

50
h-index

102
g-index

149
ext. papers

12,356
ext. citations

11.7
avg, IF

6.5
L-index

| # | Paper | IF | Citations |
|-----|--|------|-----------|
| 141 | 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 |
| 140 | Determining the stoichiometry and interactions of macromolecular assemblies from mass spectrometry. <i>Nature Protocols</i> , 2007 , 2, 715-26 | 18.8 | 538 |
| 139 | Membrane proteins bind lipids selectively to modulate their structure and function. <i>Nature</i> , 2014 , 510, 172-175 | 50.4 | 503 |
| 138 | Evidence for macromolecular protein rings in the absence of bulk water. <i>Science</i> , 2005 , 310, 1658-61 | 33.3 | 502 |
| 137 | A tandem mass spectrometer for improved transmission and analysis of large macromolecular assemblies. <i>Analytical Chemistry</i> , 2002 , 74, 1402-7 | 7.8 | 448 |
| 136 | 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 |
| 135 | Protein complexes in the gas phase: technology for structural genomics and proteomics. <i>Chemical Reviews</i> , 2007 , 107, 3544-67 | 68.1 | 342 |
| 134 | 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 |
| 133 | Micelles protect membrane complexes from solution to vacuum. <i>Science</i> , 2008 , 321, 243-6 | 33.3 | 291 |
| 132 | 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 |
| 131 | Mass spectrometry of intact membrane protein complexes. <i>Nature Protocols</i> , 2013 , 8, 639-51 | 18.8 | 263 |
| 130 | The role of interfacial lipids in stabilizing membrane protein oligomers. <i>Nature</i> , 2017 , 541, 421-424 | 50.4 | 238 |
| 129 | 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 |
| 128 | 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 |
| 127 | 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 |
| 126 | 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 |
| 125 | Mass spectrometry of macromolecular assemblies: preservation and dissociation. <i>Current Opinion in Structural Biology</i> , 2006 , 16, 245-51 | 8.1 | 190 |

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| 124 | Collision cross sections for structural proteomics. <i>Structure</i> , 2015 , 23, 791-9 | 5.2 | 169 |
| 123 | High-resolution mass spectrometry of small molecules bound to membrane proteins. <i>Nature Methods</i> , 2016 , 13, 333-6 | 21.6 | 164 |
| 122 | Biomimetic spinning of artificial spider silk from a chimeric minispidroin. <i>Nature Chemical Biology</i> , 2017 , 13, 262-264 | 11.7 | 143 |
| 121 | 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 |
| 120 | Do charge state signatures guarantee protein conformations?. <i>Journal of the American Society for Mass Spectrometry</i> , 2012 , 23, 1161-8 | 3.5 | 136 |
| 119 | A mass spectrometry-based hybrid method for structural modeling of protein complexes. <i>Nature Methods</i> , 2014 , 11, 403-406 | 21.6 | 131 |
| 118 | Detergent-free mass spectrometry of membrane protein complexes. <i>Nature Methods</i> , 2013 , 10, 1206-8 | 21.6 | 131 |
| 117 | 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 |
| 116 | Twenty years of gas phase structural biology. <i>Structure</i> , 2013 , 21, 1541-50 | 5.2 | 126 |
| 115 | Alternate dissociation pathways identified in charge-reduced protein complex ions. <i>Analytical Chemistry</i> , 2010 , 82, 5363-72 | 7.8 | 126 |
| 114 | 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 |
| 113 | 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 |
| 112 | Quantifying the stabilizing effects of protein-ligand interactions in the gas phase. <i>Nature Communications</i> , 2015 , 6, 8551 | 17.4 | 111 |
| 111 | The role of lipids in mechanosensation. <i>Nature Structural and Molecular Biology</i> , 2015 , 22, 991-8 | 17.6 | 111 |
| 110 | Carbonic anhydrase generates CO ₂ and H ⁺ that drive spider silk formation via opposite effects on the terminal domains. <i>PLoS Biology</i> , 2014 , 12, e1001921 | 9.7 | 109 |
| 109 | Protein assemblies ejected directly from native membranes yield complexes for mass spectrometry. <i>Science</i> , 2018 , 362, 829-834 | 33.3 | 99 |
| 108 | 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 |
| 107 | Subunit architecture of multiprotein assemblies determined using restraints from gas-phase measurements. <i>Structure</i> , 2009 , 17, 1235-43 | 5.2 | 97 |

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|-----|---|------|----|
| 106 | Sequential pH-driven dimerization and stabilization of the N-terminal domain enables rapid spider silk formation. <i>Nature Communications</i> , 2014 , 5, 3254 | 17.4 | 96 |
| 105 | Optimal Synthetic Glycosylation of a Therapeutic Antibody. <i>Angewandte Chemie - International Edition</i> , 2016 , 55, 2361-7 | 16.4 | 92 |
| 104 | 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 |
| 103 | High-resolution structure of a BRICHOS domain and its implications for anti-amyloid chaperone activity on lung surfactant protein C. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 2325-9 | 11.5 | 87 |
| 102 | Small heat shock protein activity is regulated by variable oligomeric substructure. <i>Journal of Biological Chemistry</i> , 2008 , 283, 28513-7 | 5.4 | 85 |
| 101 | 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 |
| 100 | Membrane Protein-Lipid Interactions Probed Using Mass Spectrometry. <i>Annual Review of Biochemistry</i> , 2019 , 88, 85-111 | 29.1 | 82 |
| 99 | Mass spectrometry guided structural biology. <i>Current Opinion in Structural Biology</i> , 2016 , 40, 136-144 | 8.1 | 79 |
| 98 | 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 |
| 97 | 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 |
| 96 | pH-dependent dimerization of spider silk N-terminal domain requires relocation of a wedged tryptophan side chain. <i>Journal of Molecular Biology</i> , 2012 , 422, 477-87 | 6.5 | 61 |
| 95 | 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 |
| 94 | A PBX1 transcriptional network controls dopaminergic neuron development and is impaired in Parkinson's disease. <i>EMBO Journal</i> , 2016 , 35, 1963-78 | 13 | 52 |
| 93 | 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 |
| 92 | Interfacing Membrane Mimetics with Mass Spectrometry. <i>Accounts of Chemical Research</i> , 2016 , 49, 2459-2467 | 24.9 | 51 |
| 91 | 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 |
| 90 | 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 |
| 89 | Efficient protein production inspired by how spiders make silk. <i>Nature Communications</i> , 2017 , 8, 15504 | 17.4 | 48 |

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| 88 | A pH-dependent dimer lock in spider silk protein. <i>Journal of Molecular Biology</i> , 2010 , 404, 328-36 | 6.5 | 47 |
| 87 | 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 |
| 86 | 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 |
| 85 | 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 |
| 84 | A sliding selectivity scale for lipid binding to membrane proteins. <i>Current Opinion in Structural Biology</i> , 2016 , 39, 54-60 | 8.1 | 41 |
| 83 | Ligand binding to a G protein-coupled receptor captured in a mass spectrometer. <i>Science Advances</i> , 2017 , 3, e1701016 | 14.3 | 39 |
| 82 | Structures of CD6 and Its Ligand CD166 Give Insight into Their Interaction. <i>Structure</i> , 2015 , 23, 1426-1436 | 6.2 | 39 |
| 81 | A combined computational and structural model of the full-length human prolactin receptor. <i>Nature Communications</i> , 2016 , 7, 11578 | 17.4 | 38 |
| 80 | Phospholipid complexation and association with apolipoprotein C-II: insights from mass spectrometry. <i>Biophysical Journal</i> , 2003 , 85, 3802-12 | 2.9 | 36 |
| 79 | 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 |
| 78 | Bri2 BRICHOS client specificity and chaperone activity are governed by assembly state. <i>Nature Communications</i> , 2017 , 8, 2081 | 17.4 | 35 |
| 77 | An engineered thermal-shift screen reveals specific lipid preferences of eukaryotic and prokaryotic membrane proteins. <i>Nature Communications</i> , 2018 , 9, 4253 | 17.4 | 35 |
| 76 | Probing -glycoprotein microheterogeneity by lectin affinity purification-mass spectrometry analysis. <i>Chemical Science</i> , 2019 , 10, 5146-5155 | 9.4 | 34 |
| 75 | 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 |
| 74 | 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 |
| 73 | 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 |
| 72 | A new window into the molecular physiology of membrane proteins. <i>Journal of Physiology</i> , 2015 , 593, 355-62 | 3.9 | 29 |
| 71 | Diversified Structural Basis of a Conserved Molecular Mechanism for pH-Dependent Dimerization in Spider Silk N-Terminal Domains. <i>ChemBioChem</i> , 2015 , 16, 1720-4 | 3.8 | 29 |

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| 70 | 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 |
| 69 | Specific chaperones and regulatory domains in control of amyloid formation. <i>Journal of Biological Chemistry</i> , 2015 , 290, 26430-6 | 5.4 | 27 |
| 68 | Unraveling the Composition and Behavior of Heterogeneous Lipid Nanodiscs by Mass Spectrometry. <i>Analytical Chemistry</i> , 2016 , 88, 6199-204 | 7.8 | 27 |
| 67 | Mass spectrometry--from peripheral proteins to membrane motors. <i>Journal of Molecular Biology</i> , 2012 , 423, 1-13 | 6.5 | 23 |
| 66 | 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 |
| 65 | New developments in protein structure-function analysis by MS and use of hydrogen-deuterium exchange microfluidics. <i>FEBS Journal</i> , 2011 , 278, 3815-21 | 5.7 | 21 |
| 64 | 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 |
| 63 | The use of sonicated lipid vesicles for mass spectrometry of membrane protein complexes. <i>Nature Protocols</i> , 2020 , 15, 1690-1706 | 18.8 | 20 |
| 62 | Proinsulin C-peptide interferes with insulin fibril formation. <i>Biochemical and Biophysical Research Communications</i> , 2012 , 418, 489-93 | 3.4 | 20 |
| 61 | Site-Specific Incorporation of Two ncAAs for Two-Color Bioorthogonal Labeling and Crosslinking of Proteins on Live Mammalian Cells. <i>Cell Reports</i> , 2020 , 31, 107811 | 10.6 | 19 |
| 60 | Dodecyl maltoside protects membrane proteins in vacuo. <i>Biophysical Journal</i> , 2013 , 105, 648-56 | 2.9 | 19 |
| 59 | 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 |
| 58 | Dynamics of an LPS translocon induced by substrate and an antimicrobial peptide. <i>Nature Chemical Biology</i> , 2021 , 17, 187-195 | 11.7 | 18 |
| 57 | Alcohol dehydrogenase, SDR and MDR structural stages, present update and altered era. <i>Chemico-Biological Interactions</i> , 2015 , 234, 75-9 | 5 | 16 |
| 56 | High-yield Production of Amyloid- β Peptide Enabled by a Customized Spider Silk Domain. <i>Scientific Reports</i> , 2020 , 10, 235 | 4.9 | 16 |
| 55 | Mass Spectrometry Reveals the Direct Action of a Chemical Chaperone. <i>Journal of Physical Chemistry Letters</i> , 2018 , 9, 4082-4086 | 6.4 | 16 |
| 54 | Separate molecular determinants in amyloidogenic and antimicrobial peptides. <i>Journal of Molecular Biology</i> , 2014 , 426, 2159-66 | 6.5 | 16 |
| 53 | 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 |

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|----|---|------|----|
| 52 | 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 |
| 51 | 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 |
| 50 | Lipids Shape the Electron Acceptor-Binding Site of the Peripheral Membrane Protein Dihydroorotate Dehydrogenase. <i>Cell Chemical Biology</i> , 2018 , 25, 309-317.e4 | 8.2 | 13 |
| 49 | Control of amyloid assembly by autoregulation. <i>Biochemical Journal</i> , 2012 , 447, 185-92 | 3.8 | 13 |
| 48 | Mass spectrometry captures structural intermediates in protein fiber self-assembly. <i>Chemical Communications</i> , 2017 , 53, 3319-3322 | 5.8 | 12 |
| 47 | Studies on citrullinated LL-37: detection in human airways, antibacterial effects and biophysical properties. <i>Scientific Reports</i> , 2020 , 10, 2376 | 4.9 | 12 |
| 46 | Augmentation of Bri2 molecular chaperone activity against amyloid- β reduces neurotoxicity in mouse hippocampus in vitro. <i>Communications Biology</i> , 2020 , 3, 32 | 6.7 | 11 |
| 45 | Insulin solubility transitions by pH-dependent interactions with proinsulin C-peptide. <i>FEBS Journal</i> , 2012 , 279, 4589-97 | 5.7 | 11 |
| 44 | Structure and elevator mechanism of the mammalian sodium/proton exchanger NHE9. <i>EMBO Journal</i> , 2020 , 39, e105908 | 13 | 11 |
| 43 | A new azobenzene-based design strategy for detergents in membrane protein research. <i>Chemical Science</i> , 2020 , 11, 3538-3546 | 9.4 | 10 |
| 42 | Gas-Phase Collisions with Trimethylamine-N-Oxide Enable Activation-Controlled Protein Ion Charge Reduction. <i>Journal of the American Society for Mass Spectrometry</i> , 2019 , 30, 1385-1388 | 3.5 | 10 |
| 41 | Protective effects of dimethyl sulfoxide on labile protein interactions during electrospray ionization. <i>Analytical Chemistry</i> , 2014 , 86, 4135-9 | 7.8 | 10 |
| 40 | Scratching the surface: native mass spectrometry of peripheral membrane protein complexes. <i>Biochemical Society Transactions</i> , 2020 , 48, 547-558 | 5.1 | 10 |
| 39 | The importance of the membrane for biophysical measurements. <i>Nature Chemical Biology</i> , 2020 , 16, 1285-1292 | 11.0 | 10 |
| 38 | Probing the limits of Q-tag bioconjugation of antibodies. <i>Chemical Communications</i> , 2019 , 55, 11342-11348 | 4.8 | 9 |
| 37 | A membrane cell for on-line hydrogen/deuterium exchange to study protein folding and protein-protein interactions by mass spectrometry. <i>Molecular and Cellular Proteomics</i> , 2011 , 10, M110.006510 | 7.6 | 9 |
| 36 | A strategy for the identification of protein architectures directly from ion mobility mass spectrometry data reveals stabilizing subunit interactions in light harvesting complexes. <i>Protein Science</i> , 2019 , 28, 1024-1030 | 6.3 | 8 |
| 35 | The structure, molecular interactions and bioactivities of proinsulin C-peptide correlate with a tripartite molecule. <i>Biomolecular Concepts</i> , 2014 , 5, 109-18 | 3.7 | 8 |

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|----|--|------|---|
| 34 | Dendritic Oligoglycerol Regioisomer Mixtures and Their Utility for Membrane Protein Research. <i>Chemistry - A European Journal</i> , 2021 , 27, 2537-2542 | 4.8 | 7 |
| 33 | Insulin, islet amyloid polypeptide and C-peptide interactions evaluated by mass spectrometric analysis. <i>Rapid Communications in Mass Spectrometry</i> , 2014 , 28, 178-84 | 2.2 | 6 |
| 32 | Spatial variation and structural characteristics of phycobiliproteins from the red algae <i>Furcellaria lumbricalis</i> and <i>Coccotylus truncatus</i> . <i>Algal Research</i> , 2020 , 52, 102058 | 5 | 6 |
| 31 | Order and disorder-An integrative structure of the full-length human growth hormone receptor. <i>Science Advances</i> , 2021 , 7, | 14.3 | 6 |
| 30 | Ion Mobility in Structural Biology. <i>Comprehensive Analytical Chemistry</i> , 2019 , 83, 161-195 | 1.9 | 6 |
| 29 | Response to Comment on "Protein assemblies ejected directly from native membranes yield complexes for mass spectrometry". <i>Science</i> , 2019 , 366, | 33.3 | 5 |
| 28 | A subdivided molecular architecture with separate features and stepwise emergence among proinsulin C-peptides. <i>Biochemical and Biophysical Research Communications</i> , 2014 , 450, 1433-8 | 3.4 | 5 |
| 27 | Predicting the Shapes of Protein Complexes through Collision Cross Section Measurements and Database Searches. <i>Analytical Chemistry</i> , 2020 , 92, 12297-12303 | 7.8 | 5 |
| 26 | Imidazolium-based catenane host for bromide recognition in aqueous media. <i>Chemical Communications</i> , 2021 , 57, 101-104 | 5.8 | 5 |
| 25 | High intracellular stability of the spidroin N-terminal domain in spite of abundant amyloidogenic segments revealed by in-cell hydrogen/deuterium exchange mass spectrometry. <i>FEBS Journal</i> , 2020 , 287, 2823-2833 | 5.7 | 4 |
| 24 | 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 |
| 23 | Capturing a rhodopsin receptor signalling cascade across a native membrane.. <i>Nature</i> , 2022 , | 50.4 | 4 |
| 22 | Connecting Multi-omics Approaches to endogenous protein complexes. <i>Trends in Chemistry</i> , 2021 , 3, 445-455 | 14.8 | 3 |
| 21 | Smallest Secondary Nucleation Competent A β Aggregates Probed by an ATP-Independent Molecular Chaperone Domain. <i>Biochemistry</i> , 2021 , 60, 678-688 | 3.2 | 3 |
| 20 | Probing membrane protein-lipid interactions. <i>Current Opinion in Structural Biology</i> , 2021 , 69, 78-85 | 8.1 | 3 |
| 19 | C-peptide evolution: generation from few structural restrictions of bioactivities not necessarily functional. <i>FEBS Letters</i> , 2015 , 589, 415-8 | 3.8 | 2 |
| 18 | Charge Engineering Reveals the Roles of Ionizable Side Chains in Electrospray Ionization Mass Spectrometry.. <i>Jacs Au</i> , 2021 , 1, 2385-2393 | | 2 |
| 17 | Mass-selective and ice-free cryo-EM protein sample preparation via native electrospray ion-beam deposition | | 2 |

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|----|---|------|---|
| 16 | Anionic Dendritic Polyglycerol for Protein Purification and Delipidation. <i>ACS Applied Polymer Materials</i> , | 4.3 | 2 |
| 15 | Structural and biophysical insights into the mode of covalent binding of rationally designed potent BMX inhibitors. <i>RSC Chemical Biology</i> , 2020 , 1, 251-262 | 3 | 2 |
| 14 | 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 |
| 13 | 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 |
| 12 | N-Thio- β -lactams targeting L,D-transpeptidase-2, with activity against drug-resistant strains of Mycobacterium tuberculosis. <i>Cell Chemical Biology</i> , 2021 , 28, 1321-1332.e5 | 8.2 | 1 |
| 11 | Ion mobility-mass spectrometry shows stepwise protein unfolding under alkaline conditions. <i>Chemical Communications</i> , 2021 , 57, 1450-1453 | 5.8 | 1 |
| 10 | Electrospray ionization of native membrane proteins proceeds a charge equilibration step.. <i>RSC Advances</i> , 2022 , 12, 9671-9680 | 3.7 | 1 |
| 9 | A "spindle and thread" mechanism unblocks p53 translation by modulating N-terminal disorder.. <i>Structure</i> , 2022 , | 5.2 | 1 |
| 8 | The dimerization mechanism of the N-terminal domain of spider silk proteins is conserved despite extensive sequence divergence.. <i>Journal of Biological Chemistry</i> , 2022 , 101913 | 5.4 | 1 |
| 7 | Understanding glycoprotein structural heterogeneity and interactions: Insights from native mass spectrometry.. <i>Current Opinion in Structural Biology</i> , 2022 , 74, 102351 | 8.1 | 1 |
| 6 | Peptidoglycan biosynthesis is driven by lipid transfer along enzyme-substrate affinity gradients.. <i>Nature Communications</i> , 2022 , 13, 2278 | 17.4 | 1 |
| 5 | Non-ionic hybrid detergents for protein delipidation.. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2022 , 183958 | 3.8 | 1 |
| 4 | Peptide Interactions of Proinsulin C-Peptide 2012 , 7-16 | | 0 |
| 3 | A Genetically Encoded Picolyl Azide for Improved Live Cell Copper Click Labeling. <i>Frontiers in Chemistry</i> , 2021 , 9, 768535 | 5 | 0 |
| 2 | The synthesis and characterization of Bri2 BRICHOS coated magnetic particles and their application to protein fishing: Identification of novel binding proteins. <i>Journal of Pharmaceutical and Biomedical Analysis</i> , 2021 , 198, 113996 | 3.5 | 0 |
| 1 | Efficient delipidation of a recombinant lung surfactant lipopeptide analogue by liquid-gel chromatography. <i>PLoS ONE</i> , 2019 , 14, e0226072 | 3.7 | 0 |