

# Michael Landreh

## List of Publications by Year in descending order

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145  
papers

13,671  
citations

26567

56  
h-index

22764

112  
g-index

149  
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149  
docs citations

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times ranked

10439  
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	Membrane proteins bind lipids selectively to modulate their structure and function. <i>Nature</i> , 2014, 510, 172-175.	13.7	665
3	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
4	Determining the stoichiometry and interactions of macromolecular assemblies from mass spectrometry. <i>Nature Protocols</i> , 2007, 2, 715-726.	5.5	597
5	Evidence for Macromolecular Protein Rings in the Absence of Bulk Water. <i>Science</i> , 2005, 310, 1658-1661.	6.0	551
6	A Tandem Mass Spectrometer for Improved Transmission and Analysis of Large Macromolecular Assemblies. <i>Analytical Chemistry</i> , 2002, 74, 1402-1407.	3.2	481
7	Protein Complexes in the Gas Phase: A Technology for Structural Genomics and Proteomics. <i>Chemical Reviews</i> , 2007, 107, 3544-3567.	23.0	376
8	Mass spectrometry of intact membrane protein complexes. <i>Nature Protocols</i> , 2013, 8, 639-651.	5.5	354
9	The role of interfacial lipids in stabilizing membrane protein oligomers. <i>Nature</i> , 2017, 541, 421-424.	13.7	344
10	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
11	Micelles Protect Membrane Complexes from Solution to Vacuum. <i>Science</i> , 2008, 321, 243-246.	6.0	333
12	Probing the Nature of Noncovalent Interactions by Mass Spectrometry. A Study of Protein <sup>13</sup> C <sup>15</sup> N CoA Ligand Binding and Assembly. <i>Journal of the American Chemical Society</i> , 1996, 118, 8646-8653.	6.6	304
13	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
14	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
15	Polydispersity of a mammalian chaperone: Mass spectrometry reveals the population of oligomers in ÅB-crystallin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 10611-10616.	3.3	235
16	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
17	Collision Cross Sections for Structural Proteomics. <i>Structure</i> , 2015, 23, 791-799.	1.6	231
18	Biomimetic spinning of artificial spider silk from a chimeric minispidroin. <i>Nature Chemical Biology</i> , 2017, 13, 262-264.	3.9	231

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19	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
20	High-resolution mass spectrometry of small molecules bound to membrane proteins. <i>Nature Methods</i> , 2016, 13, 333-336.	9.0	205
21	Mass spectrometry of macromolecular assemblies: preservation and dissociation. <i>Current Opinion in Structural Biology</i> , 2006, 16, 245-251.	2.6	199
22	The role of lipids in mechanosensation. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 991-998.	3.6	160
23	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
24	Protein assemblies ejected directly from native membranes yield complexes for mass spectrometry. <i>Science</i> , 2018, 362, 829-834.	6.0	155
25	Carbonic Anhydrase Generates CO <sub>2</sub> and H <sup>+</sup> That Drive Spider Silk Formation Via Opposite Effects on the Terminal Domains. <i>PLoS Biology</i> , 2014, 12, e1001921.	2.6	154
26	Detergent-free mass spectrometry of membrane protein complexes. <i>Nature Methods</i> , 2013, 10, 1206-1208.	9.0	152
27	Do Charge State Signatures Guarantee Protein Conformations?. <i>Journal of the American Society for Mass Spectrometry</i> , 2012, 23, 1161-1168.	1.2	149
28	A mass spectrometry-based hybrid method for structural modeling of protein complexes. <i>Nature Methods</i> , 2014, 11, 403-406.	9.0	149
29	Alternate Dissociation Pathways Identified in Charge-Reduced Protein Complex Ions. <i>Analytical Chemistry</i> , 2010, 82, 5363-5372.	3.2	145
30	Twenty Years of Gas Phase Structural Biology. <i>Structure</i> , 2013, 21, 1541-1550.	1.6	143
31	Quantifying the stabilizing effects of protein-ligand interactions in the gas phase. <i>Nature Communications</i> , 2015, 6, 8551.	5.8	136
32	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
33	Sequential pH-driven dimerization and stabilization of the N-terminal domain enables rapid spider silk formation. <i>Nature Communications</i> , 2014, 5, 3254.	5.8	134
34	Optimal Synthetic Glycosylation of a Therapeutic Antibody. <i>Angewandte Chemie - International Edition</i> , 2016, 55, 2361-2367.	7.2	122
35	Membrane Protein-Lipid Interactions Probed Using Mass Spectrometry. <i>Annual Review of Biochemistry</i> , 2019, 88, 85-111.	5.0	121
36	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

#	ARTICLE	IF	CITATIONS
37	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
38	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
39	Combining native and <sup>15</sup> N mass spectrometry to identify endogenous ligands bound to membrane proteins. <i>Nature Methods</i> , 2020, 17, 505-508.	9.0	111
40	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, 2325-2329.	3.3	108
41	Efficient protein production inspired by how spiders make silk. <i>Nature Communications</i> , 2017, 8, 15504.	5.8	102
42	Small Heat Shock Protein Activity Is Regulated by Variable Oligomeric Substructure. <i>Journal of Biological Chemistry</i> , 2008, 283, 28513-28517.	1.6	99
43	Subunit Architecture of Multiprotein Assemblies Determined Using Restraints from Gas-Phase Measurements. <i>Structure</i> , 2009, 17, 1235-1243.	1.6	99
44	Mass spectrometry guided structural biology. <i>Current Opinion in Structural Biology</i> , 2016, 40, 136-144.	2.6	98
45	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
46	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
47	Intrinsically Disordered p53 and Its Complexes Populate Compact Conformations in the Gas Phase. <i>Angewandte Chemie - International Edition</i> , 2013, 52, 361-365.	7.2	85
48	A PBX1 transcriptional network controls dopaminergic neuron development and is impaired in Parkinson's disease. <i>EMBO Journal</i> , 2016, 35, 1963-1978.	3.5	85
49	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, 477-487.	2.0	73
50	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.	6.2	72
51	Modular detergents tailor the purification and structural analysis of membrane proteins including G-protein coupled receptors. <i>Nature Communications</i> , 2020, 11, 564.	5.8	72
52	Interfacing Membrane Mimetics with Mass Spectrometry. <i>Accounts of Chemical Research</i> , 2016, 49, 2459-2467.	7.6	70
53	Integrating mass spectrometry with MD simulations reveals the role of lipids in Na <sup>+</sup> /H <sup>+</sup> antiporters. <i>Nature Communications</i> , 2017, 8, 13993.	5.8	68
54	Charge Reduction Stabilizes Intact Membrane Protein Complexes for Mass Spectrometry. <i>Journal of the American Chemical Society</i> , 2014, 136, 17010-17012.	6.6	67

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55	Bri2 BRICHOS client specificity and chaperone activity are governed by assembly state. <i>Nature Communications</i> , 2017, 8, 2081.	5.8	67
56	Direct observation of the influence of cardiolipin and antibiotics on lipid II binding to MurJ. <i>Nature Chemistry</i> , 2018, 10, 363-371.	6.6	65
57	Different Modes of Lipid Binding to Membrane Proteins Probed by Mass Spectrometry. <i>Journal of the American Chemical Society</i> , 2015, 137, 5240-5247.	6.6	63
58	A pH-Dependent Dimer Lock in Spider Silk Protein. <i>Journal of Molecular Biology</i> , 2010, 404, 328-336.	2.0	62
59	An engineered thermal-shift screen reveals specific lipid preferences of eukaryotic and prokaryotic membrane proteins. <i>Nature Communications</i> , 2018, 9, 4253.	5.8	60
60	Mass Spectrometry Defines the C-Terminal Dimerization Domain and Enables Modeling of the Structure of Full-Length OmpA. <i>Structure</i> , 2014, 22, 781-790.	1.6	58
61	A sliding selectivity scale for lipid binding to membrane proteins. <i>Current Opinion in Structural Biology</i> , 2016, 39, 54-60.	2.6	54
62	Structures of CD6 and Its Ligand CD166 Give Insight into Their Interaction. <i>Structure</i> , 2015, 23, 1426-1436.	1.6	53
63	A combined computational and structural model of the full-length human prolactin receptor. <i>Nature Communications</i> , 2016, 7, 11578.	5.8	52
64	Ligand binding to a G protein-coupled receptor captured in a mass spectrometer. <i>Science Advances</i> , 2017, 3, e1701016.	4.7	52
65	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.	3.3	49
66	Probing N-glycoprotein microheterogeneity by lectin affinity purification-mass spectrometry analysis. <i>Chemical Science</i> , 2019, 10, 5146-5155.	3.7	49
67	High-yield Production of Amyloid- $\beta$ Peptide Enabled by a Customized Spider Silk Domain. <i>Scientific Reports</i> , 2020, 10, 235.	1.6	45
68	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.	2.9	43
69	Augmentation of Bri2 molecular chaperone activity against amyloid- $\beta$ reduces neurotoxicity in mouse hippocampus in vitro. <i>Communications Biology</i> , 2020, 3, 32.	2.0	42
70	Dynamics of an LPS translocon induced by substrate and an antimicrobial peptide. <i>Nature Chemical Biology</i> , 2021, 17, 187-195.	3.9	41
71	Capturing a rhodopsin receptor signalling cascade across a native membrane. <i>Nature</i> , 2022, 604, 384-390.	13.7	41
72	Phospholipid Complexation and Association with Apolipoprotein C-II: Insights from Mass Spectrometry. <i>Biophysical Journal</i> , 2003, 85, 3802-3812.	0.2	40

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73	Unraveling the Composition and Behavior of Heterogeneous Lipid Nanodiscs by Mass Spectrometry. <i>Analytical Chemistry</i> , 2016, 88, 6199-6204.	3.2	40
74	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.	3.3	39
75	Diversified Structural Basis of a Conserved Molecular Mechanism for pH-Dependent Dimerization in Spider Silk N-Terminal Domains. <i>ChemBioChem</i> , 2015, 16, 1720-1724.	1.3	38
76	Topological Models of Heteromeric Protein Assemblies from Mass Spectrometry: Application to the Yeast eIF3:eIF5 Complex. <i>Chemistry and Biology</i> , 2015, 22, 117-128.	6.2	38
77	The "sticky business"™ of cleaning gas-phase membrane proteins: a detergent oriented perspective. <i>Physical Chemistry Chemical Physics</i> , 2012, 14, 14439.	1.3	37
78	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.	6.6	35
79	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.	7.2	33
80	Specific Chaperones and Regulatory Domains in Control of Amyloid Formation. <i>Journal of Biological Chemistry</i> , 2015, 290, 26430-26436.	1.6	32
81	A new window into the molecular physiology of membrane proteins. <i>Journal of Physiology</i> , 2015, 593, 355-362.	1.3	32
82	Structure and elevator mechanism of the mammalian sodium/proton exchanger NHE9. <i>EMBO Journal</i> , 2020, 39, 4541-4559.	3.5	31
83	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.	3.2	30
84	The use of sonicated lipid vesicles for mass spectrometry of membrane protein complexes. <i>Nature Protocols</i> , 2020, 15, 1690-1706.	5.5	30
85	Mass Spectrometry—From Peripheral Proteins to Membrane Motors. <i>Journal of Molecular Biology</i> , 2012, 423, 1-13.	2.0	28
86	Structure, mechanism and lipid-mediated remodeling of the mammalian Na <sup>+</sup> /H <sup>+</sup> exchanger NHA2. <i>Nature Structural and Molecular Biology</i> , 2022, 29, 108-120.	3.6	27
87	Effects of Detergent Micelles on Lipid Binding to Proteins in Electrospray Ionization Mass Spectrometry. <i>Analytical Chemistry</i> , 2017, 89, 7425-7430.	3.2	26
88	Lipids Shape the Electron Acceptor-Binding Site of the Peripheral Membrane Protein Dihydroorotate Dehydrogenase. <i>Cell Chemical Biology</i> , 2018, 25, 309-317.e4.	2.5	25
89	The importance of the membrane for biophysical measurements. <i>Nature Chemical Biology</i> , 2020, 16, 1285-1292.	3.9	25
90	Order and disorder—An integrative structure of the full-length human growth hormone receptor. <i>Science Advances</i> , 2021, 7, .	4.7	25

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91	Proinsulin C-peptide interferes with insulin fibril formation. <i>Biochemical and Biophysical Research Communications</i> , 2012, 418, 489-493.	1.0	23
92	New developments in protein structure–function analysis by MS and use of hydrogen–deuterium exchange microfluidics. <i>FEBS Journal</i> , 2011, 278, 3815-3821.	2.2	22
93	Dodecyl Maltoside Protects Membrane Proteins In Vacuo. <i>Biophysical Journal</i> , 2013, 105, 648-656.	0.2	22
94	Mass spectrometry captures structural intermediates in protein fiber self-assembly. <i>Chemical Communications</i> , 2017, 53, 3319-3322.	2.2	22
95	Negative Ions Enhance Survival of Membrane Protein Complexes. <i>Journal of the American Society for Mass Spectrometry</i> , 2016, 27, 1099-1104.	1.2	21
96	Mass Spectrometry Reveals the Direct Action of a Chemical Chaperone. <i>Journal of Physical Chemistry Letters</i> , 2018, 9, 4082-4086.	2.1	21
97	A new azobenzene-based design strategy for detergents in membrane protein research. <i>Chemical Science</i> , 2020, 11, 3538-3546.	3.7	21
98	Probing membrane protein–lipid interactions. <i>Current Opinion in Structural Biology</i> , 2021, 69, 78-85.	2.6	21
99	Separate Molecular Determinants in Amyloidogenic and Antimicrobial Peptides. <i>Journal of Molecular Biology</i> , 2014, 426, 2159-2166.	2.0	20
100	Scratching the surface: native mass spectrometry of peripheral membrane protein complexes. <i>Biochemical Society Transactions</i> , 2020, 48, 547-558.	1.6	20
101	Peptidoglycan biosynthesis is driven by lipid transfer along enzyme-substrate affinity gradients. <i>Nature Communications</i> , 2022, 13, 2278.	5.8	20
102	Alcohol dehydrogenase, SDR and MDR structural stages, present update and altered era. <i>Chemico-Biological Interactions</i> , 2015, 234, 75-79.	1.7	19
103	Predicting the Shapes of Protein Complexes through Collision Cross Section Measurements and Database Searches. <i>Analytical Chemistry</i> , 2020, 92, 12297-12303.	3.2	19
104	Controlling release, unfolding and dissociation of membrane protein complexes in the gas phase through collisional cooling. <i>Chemical Communications</i> , 2015, 51, 15582-15584.	2.2	18
105	Studies on citrullinated LL-37: detection in human airways, antibacterial effects and biophysical properties. <i>Scientific Reports</i> , 2020, 10, 2376.	1.6	18
106	Smallest Secondary Nucleation Competent $\text{A}\beta^2$ Aggregates Probed by an ATP-Independent Molecular Chaperone Domain. <i>Biochemistry</i> , 2021, 60, 678-688.	1.2	17
107	Insulin solubility transitions by pH–dependent interactions with proinsulin C-peptide. <i>FEBS Journal</i> , 2012, 279, 4589-4597.	2.2	15
108	The structure, molecular interactions and bioactivities of proinsulin C-peptide correlate with a tripartite molecule. <i>Biomolecular Concepts</i> , 2014, 5, 109-118.	1.0	15

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109	Protective Effects of Dimethyl Sulfoxide on Labile Protein Interactions during Electrospray Ionization. <i>Analytical Chemistry</i> , 2014, 86, 4135-4139.	3.2	14
110	Gas-Phase Collisions with Trimethylamine- <i>N</i> -Oxide Enable Activation-Controlled Protein Ion Charge Reduction. <i>Journal of the American Society for Mass Spectrometry</i> , 2019, 30, 1385-1388.	1.2	14
111	High intracellular stability of the spider 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.	2.2	14
112	Control of amyloid assembly by autoregulation. <i>Biochemical Journal</i> , 2012, 447, 185-192.	1.7	13
113	Probing the limits of Q-tag bioconjugation of antibodies. <i>Chemical Communications</i> , 2019, 55, 11342-11345.	2.2	13
114	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.	3.1	13
115	Complementing machine learning-based structure predictions with native mass spectrometry. <i>Protein Science</i> , 2022, 31, .	3.1	13
116	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.	2.4	12
117	Dendritic Oligoglycerol Regioisomer Mixtures and Their Utility for Membrane Protein Research. <i>Chemistry - A European Journal</i> , 2021, 27, 2537-2542.	1.7	12
118	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.	2.6	12
119	Charge Engineering Reveals the Roles of Ionizable Side Chains in Electrospray Ionization Mass Spectrometry. <i>Jacs Au</i> , 2021, 1, 2385-2393.	3.6	12
120	Anionic Dendritic Polyglycerol for Protein Purification and Delipidation. <i>ACS Applied Polymer Materials</i> , 2021, 3, 5903-5911.	2.0	11
121	Understanding glycoprotein structural heterogeneity and interactions: Insights from native mass spectrometry. <i>Current Opinion in Structural Biology</i> , 2022, 74, 102351.	2.6	11
122	Imidazolium-based catenane host for bromide recognition in aqueous media. <i>Chemical Communications</i> , 2021, 57, 101-104.	2.2	10
123	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, 298, 101913.	1.6	10
124	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.	2.5	9
125	Non-ionic hybrid detergents for protein delipidation. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2022, 1864, 183958.	1.4	9
126	Insulin, islet amyloid polypeptide and C-peptide interactions evaluated by mass spectrometric analysis. <i>Rapid Communications in Mass Spectrometry</i> , 2014, 28, 178-184.	0.7	8



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127	Response to Comment on "Protein assemblies ejected directly from native membranes yield complexes for mass spectrometry". Science, 2019, 366, .	6.0	8
128	N-Thio- $\beta$ -lactams targeting L,D-transpeptidase-2, with activity against drug-resistant strains of Mycobacterium tuberculosis. Cell Chemical Biology, 2021, 28, 1321-1332.e5.	2.5	8
129	Ion mobility-mass spectrometry shows stepwise protein unfolding under alkaline conditions. Chemical Communications, 2021, 57, 1450-1453.	2.2	8
130	Ion Mobility in Structural Biology. Comprehensive Analytical Chemistry, 2019, 83, 161-195.	0.7	7
131	A subdivided molecular architecture with separate features and stepwise emergence among proinsulin C-peptides. Biochemical and Biophysical Research Communications, 2014, 450, 1433-1438.	1.0	6
132	Structural and biophysical insights into the mode of covalent binding of rationally designed potent BMX inhibitors. RSC Chemical Biology, 2020, 1, 251-262.	2.0	6
133	Connecting "multi-omics" approaches to endogenous protein complexes. Trends in Chemistry, 2021, 3, 445-455.	4.4	6
134	Structural Basis for Dityrosine-Mediated Inhibition of $\alpha$ -Synuclein Fibrillization. Journal of the American Chemical Society, 2022, 144, 11949-11954.	6.6	6
135	<sc>ATP</sc>-independent molecular chaperone activity generated under reducing conditions. Protein Science, 2022, 31, .	3.1	6
136	Biological activity versus physiological function of proinsulin C-peptide. Cellular and Molecular Life Sciences, 2021, 78, 1131-1138.	2.4	5
137	A "spindle and thread" mechanism unblocks p53 translation by modulating N-terminal disorder. Structure, 2022, 30, 733-742.e7.	1.6	5
138	C-peptide evolution: Generation from few structural restrictions of bioactivities not necessarily functional. FEBS Letters, 2015, 589, 415-418.	1.3	4
139	A Genetically Encoded Picolyl Azide for Improved Live Cell Copper Click Labeling. Frontiers in Chemistry, 2021, 9, 768535.	1.8	4
140	Electrospray ionization of native membrane proteins proceeds <i>via</i> a charge equilibration step. RSC Advances, 2022, 12, 9671-9680.	1.7	4
141	Treatment of Respiratory Distress Syndrome with Single Recombinant Polypeptides that Combine Features of SP-B and SP-C. ACS Chemical Biology, 2021, 16, 2864-2873.	1.6	4
142	Efficient delipidation of a recombinant lung surfactant lipopeptide analogue by liquid-gel chromatography. PLoS ONE, 2019, 14, e0226072.	1.1	2
143	A Mass Spectrometry-Based Approach to Distinguish Annular and Specific Lipid Binding to Membrane Proteins. Angewandte Chemie, 2020, 132, 3551-3556.	1.6	2
144	Peptide Interactions of Proinsulin C-Peptide. , 2012, , 7-16.		1

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145	The synthesis and characterization of Bri2 BRICHOS coated magnetic particles and their application to protein fishing: Identification of novel binding proteins. Journal of Pharmaceutical and Biomedical Analysis, 2021, 198, 113996.	1.4	1