

Antonio N Calabrese

List of Publications by Citations

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

45
papers

892
citations

17
h-index

29
g-index

56
ext. papers

1,156
ext. citations

6.9
avg, IF

4.47
L-index

#	Paper	IF	Citations
45	Lateral opening in the intact β barrel assembly machinery captured by cryo-EM. <i>Nature Communications</i> , 2016 , 7, 12865	17.4	117
44	Gallic acid interacts with β synuclein to prevent the structural collapse necessary for its aggregation. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014 , 1844, 1481-5	4	71
43	Skp is a multivalent chaperone of outer-membrane proteins. <i>Nature Structural and Molecular Biology</i> , 2016 , 23, 786-793	17.6	62
42	Mass spectrometry-enabled structural biology of membrane proteins. <i>Methods</i> , 2018 , 147, 187-205	4.6	55
41	Effects of Periplasmic Chaperones and Membrane Thickness on BamA-Catalyzed Outer-Membrane Protein Folding. <i>Journal of Molecular Biology</i> , 2017 , 429, 3776-3792	6.5	49
40	Amphipols outperform dodecylmaltoside micelles in stabilizing membrane protein structure in the gas phase. <i>Analytical Chemistry</i> , 2015 , 87, 1118-26	7.8	40
39	Synthesis, characterization and applications of a perdeuterated amphipol. <i>Journal of Membrane Biology</i> , 2014 , 247, 909-24	2.3	36
38	Rapid Mapping of Protein Interactions Using Tag-Transfer Photocrosslinkers. <i>Angewandte Chemie - International Edition</i> , 2018 , 57, 16688-16692	16.4	36
37	Investigating the Structural Compaction of Biomolecules Upon Transition to the Gas-Phase Using ESI-TWIMS-MS. <i>Journal of the American Society for Mass Spectrometry</i> , 2017 , 28, 1855-1862	3.5	35
36	Inter-domain dynamics in the chaperone SurA and multi-site binding to its outer membrane protein clients. <i>Nature Communications</i> , 2020 , 11, 2155	17.4	28
35	Using hydroxyl radical footprinting to explore the free energy landscape of protein folding. <i>Methods</i> , 2015 , 89, 38-44	4.6	27
34	Structural mapping of oligomeric intermediates in an amyloid assembly pathway. <i>ELife</i> , 2019 , 8,	8.9	27
33	FPOP-LC-MS/MS Suggests Differences in Interaction Sites of Amphipols and Detergents with Outer Membrane Proteins. <i>Journal of the American Society for Mass Spectrometry</i> , 2017 , 28, 50-55	3.5	24
32	Systematic analysis of the use of amphipathic polymers for studies of outer membrane proteins using mass spectrometry. <i>International Journal of Mass Spectrometry</i> , 2015 , 391, 54-61	1.9	23
31	The Amyloid Fibril-Forming Properties of the Amphibian Antimicrobial Peptide Uperin 3.5. <i>ChemBioChem</i> , 2016 , 17, 239-46	3.8	21
30	Structural insight into the formation of lipoprotein- β barrel complexes. <i>Nature Chemical Biology</i> , 2020 , 16, 1019-1025	11.7	20
29	Stability of local secondary structure determines selectivity of viral RNA chaperones. <i>Nucleic Acids Research</i> , 2018 , 46, 7924-7937	20.1	19

28	Amyloid aggregation and membrane activity of the antimicrobial peptide uperin 3.5. <i>Peptide Science</i> , 2018 , 110, e24052	3	17
27	Dual Role of Ribosome-Binding Domain of NAC as a Potent Suppressor of Protein Aggregation and Aging-Related Proteinopathies. <i>Molecular Cell</i> , 2019 , 74, 729-741.e7	17.6	16
26	PyXlinkViewer: A flexible tool for visualization of protein chemical crosslinking data within the PyMOL molecular graphics system. <i>Protein Science</i> , 2020 , 29, 1851-1857	6.3	16
25	Chemical Cross-linking and Mass Spectrometry for the Structural Analysis of Protein Assemblies. <i>Australian Journal of Chemistry</i> , 2013 , 66, 749	1.2	15
24	A negative ion mass spectrometry approach to identify cross-linked peptides utilizing characteristic disulfide fragmentations. <i>Journal of the American Society for Mass Spectrometry</i> , 2012 , 23, 1364-75	3.5	15
23	Distortion of the bilayer and dynamics of the BAM complex in lipid nanodiscs. <i>Communications Biology</i> , 2020 , 3, 766	6.7	13
22	Topological Dissection of the Membrane Transport Protein Mhp1 Derived from Cysteine Accessibility and Mass Spectrometry. <i>Analytical Chemistry</i> , 2017 , 89, 8844-8852	7.8	13
21	The Role of SurA PPlase Domains in Preventing Aggregation of the Outer-Membrane Proteins tOmpA and OmpT. <i>Journal of Molecular Biology</i> , 2019 , 431, 1267-1283	6.5	11
20	Structural Proteomics Methods to Interrogate the Conformations and Dynamics of Intrinsically Disordered Proteins. <i>Frontiers in Chemistry</i> , 2021 , 9, 603639	5	8
19	Backbone fragmentations of [M-H] ⁻ anions from peptides. Reinvestigation of the mechanism of the beta prime cleavage. <i>Rapid Communications in Mass Spectrometry</i> , 2012 , 26, 1832-40	2.2	7
18	Histidine-containing host-defence skin peptides of anurans bind Cu ²⁺ . An electrospray ionisation mass spectrometry and computational modelling study. <i>Rapid Communications in Mass Spectrometry</i> , 2011 , 25, 1209-21	2.2	7
17	Negative ion fragmentations of disulfide-containing cross-linking reagents are competitive with aspartic acid side-chain-induced cleavages. <i>Rapid Communications in Mass Spectrometry</i> , 2013 , 27, 238-48	2.2	6
16	Structural analysis of calmodulin binding by nNOS inhibitory amphibian peptides. <i>Biochemistry</i> , 2015 , 54, 567-76	3.2	6
15	Characterisation of Calmodulin Structural Transitions by Ion Mobility Mass Spectrometry. <i>Australian Journal of Chemistry</i> , 2012 , 65, 504	1.2	6
14	Rapid Mapping of Protein Interactions Using Tag-Transfer Photocrosslinkers. <i>Angewandte Chemie</i> , 2018 , 130, 16930-16934	3.6	6
13	Chemical Synthesis of a Fluorescent IGF-II Analogue. <i>International Journal of Peptide Research and Therapeutics</i> , 2013 , 19, 61-69	2.1	5
12	Structural basis of rotavirus RNA chaperone displacement and RNA annealing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	5
11	Fusidic acid resistance through changes in the dynamics of the drug target. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 25523-25531	11.5	5

10	Structural insight into the formation of lipoprotein-β-barrel complexes by the β-barrel assembly machinery		4
9	The role of membrane destabilisation and protein dynamics in BAM catalysed OMP folding. <i>Nature Communications</i> , 2021 , 12, 4174	17.4	4
8	Interrogating Membrane Protein Structure and Lipid Interactions by Native Mass Spectrometry. <i>Methods in Molecular Biology</i> , 2020 , 2168, 233-261	1.4	4
7	The membrane-active amphibian peptide caerin 1.8 inhibits fibril formation of amyloid β-42. <i>Peptides</i> , 2015 , 73, 1-6	3.8	3
6	Pocket delipidation induced by membrane tension or modification leads to a structurally analogous mechanosensitive channel state.. <i>Structure</i> , 2021 ,	5.2	3
5	Structural and activity changes in three bioactive anuran peptides when Asp is replaced by isoAsp. <i>Peptides</i> , 2012 , 38, 427-36	3.8	2
4	Stability of local secondary structure determines selectivity of viral RNA chaperones		2
3	Dynamic interplay between the periplasmic chaperone SurA and the BAM complex in outer membrane protein folding. <i>Communications Biology</i> , 2022 , 5,	6.7	2
2	PyXlinkViewer: a flexible tool for visualisation of protein chemical crosslinking data within the PyMOL molecular graphics system		1
1	Membrane Transport Proteins: The Amino Acid-Polyamine-Organocation (APC) Superfamily 2019 , 1-8		