

# Andy M C Lau

## List of Publications by Year in descending order

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Version: 2024-02-01

21  
papers

662  
citations

623734

14  
h-index

713466

21  
g-index

25  
all docs

25  
docs citations

25  
times ranked

874  
citing authors

#	ARTICLE	IF	CITATIONS
1	Identification of diverse lipid-binding modes in the groove of zinc $\beta$ 2 glycoprotein reveals its functional versatility. FEBS Journal, 2022, 289, 1876-1896.	4.7	3
2	Ultrafast end-to-end protein structure prediction enables high-throughput exploration of uncharacterized proteins. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	26
3	Deuterios 2.0: peptide-level significance testing of data from hydrogen deuterium exchange mass spectrometry. Bioinformatics, 2021, 37, 270-272.	4.1	63
4	Integrative Mass Spectrometry-Based Approaches for Modeling Macromolecular Assemblies. Methods in Molecular Biology, 2021, 2247, 221-241.	0.9	5
5	Moderated Test Statistics to Detect Differential Deuteration in Hydrogen/Deuterium Exchange Mass Spectrometry Experiments. Analytical Chemistry, 2021, , .	6.5	2
6	Analysis of protein-DNA interactions in chromatin by UV induced cross-linking and mass spectrometry. Nature Communications, 2020, 11, 5250.	12.8	22
7	Hydrogen-deuterium exchange mass spectrometry captures distinct dynamics upon substrate and inhibitor binding to a transporter. Nature Communications, 2020, 11, 6162.	12.8	35
8	Perturbed structural dynamics underlie inhibition and altered efflux of the multidrug-resistance pump AcrB. Nature Communications, 2020, 11, 5565.	12.8	34
9	Structural predictions of the functions of membrane proteins from HDX-MS. Biochemical Society Transactions, 2020, 48, 971-979.	3.4	7
10	Structural basis of Cullin 2 RING E3 ligase regulation by the COP9 signalosome. Nature Communications, 2019, 10, 3814.	12.8	40
11	Integrating hydrogen-deuterium exchange mass spectrometry with molecular dynamics simulations to probe lipid-modulated conformational changes in membrane proteins. Nature Protocols, 2019, 14, 3183-3204.	12.0	39
12	Deuterios: software for rapid analysis and visualization of data from differential hydrogen deuterium exchange-mass spectrometry. Bioinformatics, 2019, 35, 3171-3173.	4.1	60
13	Crystal structure of zinc- $\beta$ 2-glycoprotein in complex with a fatty acid reveals multiple different modes of protein-lipid binding. Biochemical Journal, 2019, 476, 2815-2834.	3.7	2
14	A Mass Spectrometry-Based Modelling Workflow for Accurate Prediction of IgG Antibody Conformations in the Gas Phase. Angewandte Chemie, 2018, 130, 17440-17445.	2.0	5
15	A Mass Spectrometry-Based Modelling Workflow for Accurate Prediction of IgG Antibody Conformations in the Gas Phase. Angewandte Chemie - International Edition, 2018, 57, 17194-17199.	13.8	39
16	Direct protein-lipid interactions shape the conformational landscape of secondary transporters. Nature Communications, 2018, 9, 4151.	12.8	112
17	Analyzing Protein Architectures and Protein-Ligand Complexes by Integrative Structural Mass Spectrometry. Journal of Visualized Experiments, 2018, , .	0.3	3
18	Structural Lipids Enable the Formation of Functional Oligomers of the Eukaryotic Purine Symporter UapA. Cell Chemical Biology, 2018, 25, 840-848.e4.	5.2	64

#	ARTICLE	IF	CITATIONS
19	Surface Accessibility and Dynamics of Macromolecular Assemblies Probed by Covalent Labeling Mass Spectrometry and Integrative Modeling. <i>Analytical Chemistry</i> , 2017, 89, 1459-1468.	6.5	46
20	Mechanistic insight into the assembly of the HerAâ€œNurA helicaseâ€œnuclease DNA end resection complex. <i>Nucleic Acids Research</i> , 2017, 45, 12025-12038.	14.5	23
21	Zinc-induced oligomerization of zinc $\beta$ 2 glycoprotein reveals multiple fatty acid-binding sites. <i>Biochemical Journal</i> , 2016, 473, 43-54.	3.7	19