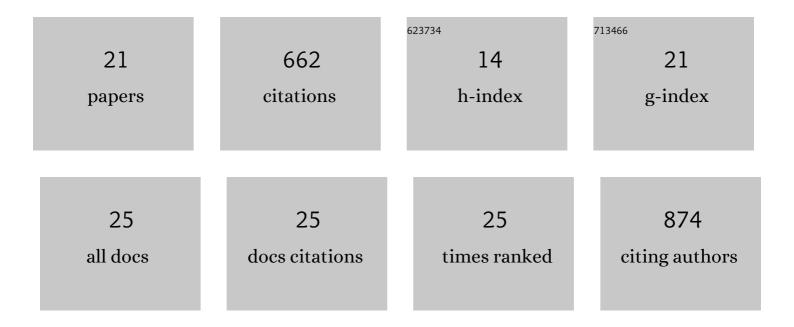
Andy M C Lau

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Direct protein-lipid interactions shape the conformational landscape of secondary transporters. Nature Communications, 2018, 9, 4151.	12.8	112
2	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
3	Deuteros 2.0: peptide-level significance testing of data from hydrogen deuterium exchange mass spectrometry. Bioinformatics, 2021, 37, 270-272.	4.1	63
4	Deuteros: software for rapid analysis and visualization of data from differential hydrogen deuterium exchange-mass spectrometry. Bioinformatics, 2019, 35, 3171-3173.	4.1	60
5	Surface Accessibility and Dynamics of Macromolecular Assemblies Probed by Covalent Labeling Mass Spectrometry and Integrative Modeling. Analytical Chemistry, 2017, 89, 1459-1468.	6.5	46
6	Structural basis of Cullin 2 RING E3 ligase regulation by the COP9 signalosome. Nature Communications, 2019, 10, 3814.	12.8	40
7	A Massâ€Spectrometryâ€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
8	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
9	Hydrogen-deuterium exchange mass spectrometry captures distinct dynamics upon substrate and inhibitor binding to a transporter. Nature Communications, 2020, 11, 6162.	12.8	35
10	Perturbed structural dynamics underlie inhibition and altered efflux of the multidrugÂresistance pump AcrB. Nature Communications, 2020, 11, 5565.	12.8	34
11	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
12	Mechanistic insight into the assembly of the HerA–NurA helicase–nuclease DNA end resection complex. Nucleic Acids Research, 2017, 45, 12025-12038.	14.5	23
13	Analysis of protein-DNA interactions in chromatin by UV induced cross-linking and mass spectrometry. Nature Communications, 2020, 11, 5250.	12.8	22
14	Zinc-induced oligomerization of zinc α2 glycoprotein reveals multiple fatty acid-binding sites. Biochemical Journal, 2016, 473, 43-54.	3.7	19
15	Structural predictions of the functions of membrane proteins from HDX-MS. Biochemical Society Transactions, 2020, 48, 971-979.	3.4	7
16	A Massâ€5pectrometryâ€Based Modelling Workflow for Accurate Prediction of IgG Antibody Conformations in the Gas Phase. Angewandte Chemie, 2018, 130, 17440-17445.	2.0	5
17	Integrative Mass Spectrometry–Based Approaches for Modeling Macromolecular Assemblies. Methods in Molecular Biology, 2021, 2247, 221-241.	0.9	5
18	Analyzing Protein Architectures and Protein-Ligand Complexes by Integrative Structural Mass Spectrometry. Journal of Visualized Experiments, 2018, , .	0.3	3

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#	Article	IF	CITATIONS
19	Identification of diverse lipidâ€binding modes in the groove of zinc α ₂ glycoprotein reveals its functional versatility. FEBS Journal, 2022, 289, 1876-1896.	4.7	3
20	Crystal structure of zinc-α2-glycoprotein in complex with a fatty acid reveals multiple different modes of protein-lipid binding. Biochemical Journal, 2019, 476, 2815-2834.	3.7	2
21	Moderated Test Statistics to Detect Differential Deuteration in Hydrogen/Deuterium Exchange Mass Spectrometry Experiments. Analytical Chemistry, 2021, , .	6.5	2