

Andy M C Lau

List of Publications by Year in descending order

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Version: 2024-02-01

21
papers

662
citations

623574

14
h-index

713332

21
g-index

25
all docs

25
docs citations

25
times ranked

874
citing authors

#	ARTICLE	IF	CITATIONS
1	Direct protein-lipid interactions shape the conformational landscape of secondary transporters. <i>Nature Communications</i> , 2018, 9, 4151.	5.8	112
2	Structural Lipids Enable the Formation of Functional Oligomers of the Eukaryotic Purine Symporter UapA. <i>Cell Chemical Biology</i> , 2018, 25, 840-848.e4.	2.5	64
3	Deuterios 2.0: peptide-level significance testing of data from hydrogen deuterium exchange mass spectrometry. <i>Bioinformatics</i> , 2021, 37, 270-272.	1.8	63
4	Deuterios: software for rapid analysis and visualization of data from differential hydrogen deuterium exchange-mass spectrometry. <i>Bioinformatics</i> , 2019, 35, 3171-3173.	1.8	60
5	Surface Accessibility and Dynamics of Macromolecular Assemblies Probed by Covalent Labeling Mass Spectrometry and Integrative Modeling. <i>Analytical Chemistry</i> , 2017, 89, 1459-1468.	3.2	46
6	Structural basis of Cullin 2 RING E3 ligase regulation by the COP9 signalosome. <i>Nature Communications</i> , 2019, 10, 3814.	5.8	40
7	A Mass Spectrometry-Based Modelling Workflow for Accurate Prediction of IgG Antibody Conformations in the Gas Phase. <i>Angewandte Chemie - International Edition</i> , 2018, 57, 17194-17199.	7.2	39
8	Integrating hydrogen-deuterium exchange mass spectrometry with molecular dynamics simulations to probe lipid-modulated conformational changes in membrane proteins. <i>Nature Protocols</i> , 2019, 14, 3183-3204.	5.5	39
9	Hydrogen-deuterium exchange mass spectrometry captures distinct dynamics upon substrate and inhibitor binding to a transporter. <i>Nature Communications</i> , 2020, 11, 6162.	5.8	35
10	Perturbed structural dynamics underlie inhibition and altered efflux of the multidrug resistance pump AcrB. <i>Nature Communications</i> , 2020, 11, 5565.	5.8	34
11	Ultrafast end-to-end protein structure prediction enables high-throughput exploration of uncharacterized proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	26
12	Mechanistic insight into the assembly of the HerA-NurA helicase-nuclease DNA end resection complex. <i>Nucleic Acids Research</i> , 2017, 45, 12025-12038.	6.5	23
13	Analysis of protein-DNA interactions in chromatin by UV induced cross-linking and mass spectrometry. <i>Nature Communications</i> , 2020, 11, 5250.	5.8	22
14	Zinc-induced oligomerization of zinc β glycoprotein reveals multiple fatty acid-binding sites. <i>Biochemical Journal</i> , 2016, 473, 43-54.	1.7	19
15	Structural predictions of the functions of membrane proteins from HDX-MS. <i>Biochemical Society Transactions</i> , 2020, 48, 971-979.	1.6	7
16	A Mass Spectrometry-Based Modelling Workflow for Accurate Prediction of IgG Antibody Conformations in the Gas Phase. <i>Angewandte Chemie</i> , 2018, 130, 17440-17445.	1.6	5
17	Integrative Mass Spectrometry-Based Approaches for Modeling Macromolecular Assemblies. <i>Methods in Molecular Biology</i> , 2021, 2247, 221-241.	0.4	5
18	Analyzing Protein Architectures and Protein-Ligand Complexes by Integrative Structural Mass Spectrometry. <i>Journal of Visualized Experiments</i> , 2018, , .	0.2	3

#	ARTICLE	IF	CITATIONS
19	Identification of diverse lipid-binding modes in the groove of zinc β 2-glycoprotein reveals its functional versatility. FEBS Journal, 2022, 289, 1876-1896.	2.2	3
20	Crystal structure of zinc- β 2-glycoprotein in complex with a fatty acid reveals multiple different modes of protein-lipid binding. Biochemical Journal, 2019, 476, 2815-2834.	1.7	2
21	Moderated Test Statistics to Detect Differential Deuteration in Hydrogen/Deuterium Exchange Mass Spectrometry Experiments. Analytical Chemistry, 2021, , .	3.2	2