

# Leland Mayne

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/942272/publications.pdf>

Version: 2024-02-01

27  
papers

3,975  
citations

430874

18  
h-index

580821

25  
g-index

27  
all docs

27  
docs citations

27  
times ranked

4491  
citing authors

#	ARTICLE	IF	CITATIONS
1	Characterization of Small-Molecule-Induced Changes in Parkinson's-Related Trafficking via the Nedd4 Ubiquitin Signaling Cascade. <i>Cell Chemical Biology</i> , 2021, 28, 14-25.e9.	5.2	15
2	A conserved strategy for structure change and energy transduction in Hsp104 and other AAA+ protein motors. <i>Journal of Biological Chemistry</i> , 2021, 297, 101066.	3.4	2
3	Structural and mechanistic insights into Hsp104 function revealed by synchrotron X-ray footprinting. <i>Journal of Biological Chemistry</i> , 2020, 295, 1517-1538.	3.4	16
4	Structural and kinetic basis for the regulation and potentiation of Hsp104 function. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 9384-9392.	7.1	16
5	Recommendations for performing, interpreting and reporting hydrogen deuterium exchange mass spectrometry (HDX-MS) experiments. <i>Nature Methods</i> , 2019, 16, 595-602.	19.0	452
6	ExMS2: An Integrated Solution for Hydrogen-Deuterium Exchange Mass Spectrometry Data Analysis. <i>Analytical Chemistry</i> , 2019, 91, 7474-7481.	6.5	39
7	Hydrogen exchange reveals Hsp104 architecture, structural dynamics, and energetics in physiological solution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 7333-7342.	7.1	22
8	Folding of maltose binding protein outside of and in GroEL. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 519-524.	7.1	25
9	Reference Parameters for Protein Hydrogen Exchange Rates. <i>Journal of the American Society for Mass Spectrometry</i> , 2018, 29, 1936-1939.	2.8	61
10	Helical structure, stability, and dynamics in human apolipoprotein E3 and E4 by hydrogen exchange and mass spectrometry. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 968-973.	7.1	38
11	Enhanced Local Disorder in a Clinically Elusive von Willebrand Factor Provokes High-Affinity Platelet Clumping. <i>Journal of Molecular Biology</i> , 2017, 429, 2161-2177.	4.2	36
12	Reply to Eaton and Wolynes: How do proteins fold?. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E9761-E9762.	7.1	13
13	The case for defined protein folding pathways. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 8253-8258.	7.1	119
14	Protein Folding—How and Why: By Hydrogen Exchange, Fragment Separation, and Mass Spectrometry. <i>Annual Review of Biophysics</i> , 2016, 45, 135-152.	10.0	86
15	Cytochrome <i>c</i> folds through foldon-dependent native-like intermediates in an ordered pathway. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 3809-3814.	7.1	72
16	Hydrogen Exchange Mass Spectrometry. <i>Methods in Enzymology</i> , 2016, 566, 335-356.	1.0	40
17	High-resolution epitope mapping by HX MS reveals the pathogenic mechanism and a possible therapy for autoimmune TTP syndrome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 9620-9625.	7.1	46
18	The nature of protein folding pathways. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 15873-15880.	7.1	284

#	ARTICLE	IF	CITATIONS
19	Comparison of apoA-I helical structure and stability in discoidal and spherical HDL particles by HX and mass spectrometry. <i>Journal of Lipid Research</i> , 2013, 54, 1589-1597.	4.2	30
20	Protein hydrogen exchange at residue resolution by proteolytic fragmentation mass spectrometry analysis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 16438-16443.	7.1	131
21	Deuterium-Hydrogen Exchange Coupled With Mass Spectrometry Revealed A Novel Autoantibody Binding Epitope and Substrate Recognition Site In ADAMTS13 Protease,. <i>Blood</i> , 2013, 122, 455-455.	1.4	0
22	Many Overlapping Peptides for Protein Hydrogen Exchange Experiments by the Fragment Separation-Mass Spectrometry Method. <i>Journal of the American Society for Mass Spectrometry</i> , 2011, 22, 1898-905.	2.8	112
23	Structure and properties of $\hat{A}$ -synuclein and other amyloids determined at the amino acid level. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 15477-15482.	7.1	203
24	Distortion of the Active Site of Chymotrypsin Complexed with a Serpinâ€. <i>Biochemistry</i> , 1996, 35, 7586-7590.	2.5	94
25	Molecular collapse: The rate-limiting step in two-state cytochrome c folding. , 1996, 24, 413-426.		213
26	Molecular collapse: The rateâ€limiting step in twoâ€state cytochrome c folding. <i>Proteins: Structure, Function and Bioinformatics</i> , 1996, 24, 413-426.	2.6	5
27	Primary structure effects on peptide group hydrogen exchange. <i>Proteins: Structure, Function and Bioinformatics</i> , 1993, 17, 75-86.	2.6	1,805