

Michael P Latham

List of Publications by Year in Descending Order

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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.

29
papers

610
citations

14
h-index

24
g-index

36
ext. papers

708
ext. citations

6.5
avg, IF

4.15
L-index

#	Paper	IF	Citations
29	LRET-derived HADDOCK structural models describe the conformational heterogeneity required for DNA cleavage by the Mre11-Rad50 DNA damage repair complex.. <i>ELife</i> , 2022 , 11,	8.9	1
28	Biochemical and structural characterization of analogs of MRE11 breast cancer-associated mutant F237C. <i>Scientific Reports</i> , 2021 , 11, 7089	4.9	1
27	The dynamic nature of the Mre11-Rad50 DNA break repair complex. <i>Progress in Biophysics and Molecular Biology</i> , 2021 , 163, 14-22	4.7	0
26	Maturation of the functional mouse CRES amyloid from globular form. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 16363-16372	11.5	3
25	Mutation of Conserved Mre11 Residues Alter Protein Dynamics to Separate Nuclease Functions. <i>Journal of Molecular Biology</i> , 2020 , 432, 3289-3308	6.5	5
24	Adjacent mutations in the archaeal Rad50 ABC ATPase D-loop disrupt allosteric regulation of ATP hydrolysis through different mechanisms. <i>Nucleic Acids Research</i> , 2020 , 48, 2457-2472	20.1	7
23	A Survey of Reported Disease-Related Mutations in the MRE11-RAD50-NBS1 Complex. <i>Cells</i> , 2020 , 9,	7.9	9
22	A missense mutation in the CSTF2 gene that impairs the function of the RNA recognition motif and causes defects in 3' end processing is associated with intellectual disability in humans. <i>Nucleic Acids Research</i> , 2020 , 48, 9804-9821	20.1	2
21	A DNA aptamer reveals an allosteric site for inhibition in metallo- β -lactamases. <i>PLoS ONE</i> , 2019 , 14, e0214440	3.7	15
20	The Functional Mammalian CRES (Cystatin-Related Epididymal Spermatogenic) Amyloid is Antiparallel β -Sheet Rich and Forms a Metastable Oligomer During Assembly. <i>Scientific Reports</i> , 2019 , 9, 9210	4.9	5
19	Increasing the buffering capacity of minimal media leads to higher protein yield. <i>Journal of Biomolecular NMR</i> , 2019 , 73, 11-17	3	20
18	Methyl-Based NMR Spectroscopy Methods for Uncovering Structural Dynamics in Large Proteins and Protein Complexes. <i>Biochemistry</i> , 2019 , 58, 144-155	3.2	21
17	A dynamic allosteric pathway underlies Rad50 ABC ATPase function in DNA repair. <i>Scientific Reports</i> , 2018 , 8, 1639	4.9	14
16	The structural basis of CstF-77 modulation of cleavage and polyadenylation through stimulation of CstF-64 activity. <i>Nucleic Acids Research</i> , 2018 , 46, 12022-12039	20.1	11
15	Structure-Based Assignment of Ile, Leu, and Val Methyl Groups in the Active and Inactive Forms of the Mitogen-Activated Protein Kinase Extracellular Signal-Regulated Kinase 2. <i>Biochemistry</i> , 2015 , 54, 4307-19	3.2	18
14	ClpB N-terminal domain plays a regulatory role in protein disaggregation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, E6872-81	11.5	57
13	Understanding the mechanism of proteasome 20S core particle gating. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 5532-7	11.5	41

12	A similar in vitro and in cell lysate folding intermediate for the FF domain. <i>Journal of Molecular Biology</i> , 2014 , 426, 3214-3220	6.5	12
11	Viscosity-dependent kinetics of protein conformational exchange: microviscosity effects and the need for a small viscogen. <i>Journal of Physical Chemistry B</i> , 2014 , 118, 4546-51	3.4	20
10	Phosphorylation releases constraints to domain motion in ERK2. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 2506-11	11.5	48
9	Probing non-specific interactions of Ca ²⁺ -calmodulin in E. coli lysate. <i>Journal of Biomolecular NMR</i> , 2013 , 55, 239-47	3	21
8	Is buffer a good proxy for a crowded cell-like environment? A comparative NMR study of calmodulin side-chain dynamics in buffer and E. coli lysate. <i>PLoS ONE</i> , 2012 , 7, e48226	3.7	34
7	NMR chemical exchange as a probe for ligand-binding kinetics in a theophylline-binding RNA aptamer. <i>Journal of the American Chemical Society</i> , 2009 , 131, 5052-3	16.4	64
6	Measurement of imino 1H-1H residual dipolar couplings in RNA. <i>Journal of Biomolecular NMR</i> , 2009 , 43, 121-9	3	5
5	Comparison of alignment tensors generated for native tRNA(Val) using magnetic fields and liquid crystalline media. <i>Journal of Biomolecular NMR</i> , 2008 , 40, 83-94	3	25
4	High-resolution pyrimidine- and ribose-specific 4D HCCH-COSY spectra of RNA using the filter diagonalization method. <i>Journal of Biomolecular NMR</i> , 2008 , 41, 209-19	3	3
3	Magnetic field induced residual dipolar couplings of imino groups in nucleic acids from measurements at a single magnetic field. <i>Journal of Biomolecular NMR</i> , 2007 , 39, 91-6	3	17
2	NMR methods for studying the structure and dynamics of RNA. <i>ChemBioChem</i> , 2005 , 6, 1492-505	3.8	125
1	Sequence-specific 1H, 13C and 15N resonance assignments of the N-terminal, 135-residue domain of KaiA, a clock protein from <i>Synechococcus elongatus</i> . <i>Journal of Biomolecular NMR</i> , 2001 , 21, 179-80	3	5