Andras Boeszoermenyi

List of Publications by Year
in descending order

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24	1,411	430874	610901
papers	citations	18 h-index	24 g-index

25	25	25	2566
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	An open-source drug discovery platform enables ultra-large virtual screens. Nature, 2020, 580, 663-668.	27.8	345
2	The Kinetochore-Bound Ska1 Complex Tracks Depolymerizing Microtubules and Binds to Curved Protofilaments. Developmental Cell, 2012, 23, 968-980.	7.0	194
3	Inhibiting fungal multidrug resistance by disrupting an activatorâ€“Mediator interaction. Nature, 2016, 530, 485-489.	27.8	120
4	Aromatic 19F-13C TROSY: a background-free approach to probe biomolecular structure, function, and dynamics. Nature Methods, 2019, 16, 333-340.	19.0	82
5	The Minimal Domain of Adipose Triglyceride Lipase (ATGL) Ranges until Leucine 254 and Can Be Activated and Inhibited by CGI-58 and G0S2, Respectively. PLoS ONE, 2011, 6, e26349.	2.5	76
6	CGI-58/ABHD5 is phosphorylated on Ser239 by protein kinase A: control of subcellular localization. Journal of Lipid Research, 2015, 56, 109-121.	4.2	60
7	The T Cell Antigen Receptor Î± Transmembrane Domain Coordinates Triggering through Regulation of Bilayer Immersion and CD3 Subunit Associations. Immunity, 2018, 49, 829-841.e6.	14.3	58
8	Structure of a herpesvirus nuclear egress complex subunit reveals an interaction groove that is essential for viral replication. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 9010-9015.	7.1	52
9	Fatty Acid-binding Proteins Interact with Comparative Gene Identification-58 Linking Lipolysis with Lipid Ligand Shuttling. Journal of Biological Chemistry, 2015, 290, 18438-18453.	3.4	49
10	Structure of a CGI-58 Motif Provides the Molecular Basis of Lipid Droplet Anchoring. Journal of Biological Chemistry, 2015, 290, 26361-26372.	3.4	43
11	The structural determinants of PH domain-mediated regulation of Akt revealed by segmental labeling. ELife, 2020, 9, .	6.0	41
12	The structure of monoacylglycerol lipase from Bacillus sp. H257 reveals unexpected conservation of the cap architecture between bacterial and human enzymes. Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids, 2012, 1821, 1012-1021.	2.4	40
13	¹⁵ N detection harnesses the slow relaxation property of nitrogen: Delivering enhanced resolution for intrinsically disordered proteins. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E1710-E1719.	7.1	40
14	A Peptide Derived from G0/G1 Switch Gene 2 Acts as Noncompetitive Inhibitor of Adipose Triglyceride Lipase. Journal of Biological Chemistry, 2014, 289, 32559-32570.	3.4	39
15	Recent insights into the structure and function of comparative gene identification-58. Current Opinion in Lipidology, 2011, 22, 149-158.	2.7	36
16	The precious fluorine on the ring: fluorine NMR for biological systems. Journal of Biomolecular NMR, 2020, 74, 365-379.	2.8	31
17	Increased resolution of aromatic cross peaks using alternate 13C labeling and TROSY. Journal of Biomolecular NMR, 2015, 62, 291-301.	2.8	26
18	Optimal control theory enables homonuclear decoupling without Blochâ€“Siegert shifts in NMR spectroscopy. Nature Communications, 2018, 9, 3014.	12.8	26

#	Article	IF	Citations
19	Structural basis for LeishIF4E-1 modulation by an interacting protein in the human parasite Leishmania major. Nucleic Acids Research, 2018, 46, 3791-3801.	14.5	19
20	The Genetic Codeâ€"More Than Just a Table. Cell Biochemistry and Biophysics, 2009, 55, 107-116.	1.8	14
21	Mixed pyruvate labeling enables backbone resonance assignment of large proteins using a single experiment. Nature Communications, 2018, 9, 356.	12.8	13
22	Resonance assignments of the microtubule-binding domain of the C. elegans spindle and kinetochore-associated protein 1. Biomolecular NMR Assignments, 2014, 8, 275-278.	0.8	5
23	1H, 13C, and 15N backbone chemical shift assignments of 4E-BP144â€"87 and 4E-BP144â€"87 bound to eIF4E. Biomolecular NMR Assignments, 2017, 11, 187-191.	0.8	1
24	The fission yeast FLCN/FNIP complex augments TORC1 repression or activation in response to amino acid (AA) availability. IScience, 2021, 24, 103338.	4.1	1