Bhushan Nagar

List of Publications by Year
in descending order

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33	4,507	430754	434063
papers	citations	18	31
		h-index	g-index

35	35	35	5174
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Targeting <scp>DEAD</scp>â€box <scp>RNA</scp> helicases: The emergence of molecular staples. Wiley Interdisciplinary Reviews RNA, 2023, 14, e1738.	3.2	8
2	Structure of the murine lysosomal multienzyme complex core. Science Advances, 2021, 7, .	4.7	7
3	Functional mimicry revealed by the crystal structure of an eIF4A:RNA complex bound to the interfacial inhibitor, desmethyl pateamine A. Cell Chemical Biology, 2021, 28, 825-834.e6.	2.5	25
4	The mTORC1/S6K/PDCD4/eIF4A Axis Determines Outcome of Mitotic Arrest. Cell Reports, 2020, 33, 108230.	2.9	17
5	Crystal structure of the nucleotideâ€metabolizing enzyme NTPDase4. Protein Science, 2020, 29, 2054-2061.	3.1	7
6	Crystal Structure of the Mannose-6-Phosphate Uncovering Enzyme. Structure, 2020, 28, 426-436.e3.	1.6	6
7	Molecular models should not be published without the corresponding atomic coordinates. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 11099-11100.	3.3	4
8	Identification of Allosteric Inhibitors against Active Caspase-6. Scientific Reports, 2019, 9, 5504.	1.6	15
9	The structure of mammalian Î²â€mannosidase provides insight into Î²â€mannosidosis and nystagmus. FEBS Journal, 2019, 286, 1319-1331.	2.2	14
10	Molecular Mechanism of Inhibition of Acid Ceramidase by Carmofur. Journal of Medicinal Chemistry, 2019, 62, 987-992.	2.9	46
11	Crystal structure of the mammalian lipopolysaccharide detoxifier. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E896-E905.	3.3	24
12	Structural basis for the activation of acid ceramidase. Nature Communications, 2018, 9, 1621.	5.8	72
13	Double-Stranded Biotinylated Donor Enhances Homology-Directed Repair in Combination with Cas9 Monoavidin in Mammalian Cells. CRISPR Journal, 2018, 1, 414-430.	1.4	12
14	Molecular mechanism of activation of the immunoregulatory amidase NAAA. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E10032-E10040.	3.3	36
15	Structural Analysis of the Bacterial Effector AvrA Identifies a Critical Helix Involved in Substrate Recognition. Biochemistry, 2018, 57, 4985-4996.	1.2	12
16	Crystal structure of saposin D in an open conformation. Journal of Structural Biology, 2018, 204, 145-150.	1.3	10
17	Structural basis for nucleotide recognition by the ectoenzyme <scp>CD</scp>203c. FEBS Journal, 2018, 285, 2481-2494.	2.2	30
18	Structure of human IFIT1 with capped RNA reveals adaptable mRNA binding and mechanisms for sensing N1 and N2 ribose 2â€²-O methylations. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E2106-E2115.	3.3	86

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19	Structural and Functional Characterization of Plant ARGONAUTE MID Domains. Methods in Molecular Biology, 2017, 1640, 227-239.	0.4	0
20	Crystal structure of the human alkaline sphingomyelinase provides insights into substrate recognition. Journal of Biological Chemistry, 2017, 292, 7087-7094.	1.6	30
21	A key tyrosine substitution restricts nucleotide hydrolysis by the ectoenzyme <scp>NPP</scp>5. FEBS Journal, 2017, 284, 3718-3726.	2.2	25
22	Crystal structure of mammalian acid sphingomyelinase. Nature Communications, 2016, 7, 12196.	5.8	76
23	Crystal Structure of the Acid Sphingomyelinase-like Phosphodiesterase SMPDL3B Provides Insights into Determinants of Substrate Specificity. Journal of Biological Chemistry, 2016, 291, 24054-24064.	1.6	20
24	Structural Basis for Nucleotide Hydrolysis by the Acid Sphingomyelinase-like Phosphodiesterase SMPDL3A. Journal of Biological Chemistry, 2016, 291, 6376-6385.	1.6	13
25	DAP5 associates with eIF2Î² and eIF4AI to promote Internal Ribosome Entry Site driven translation. Nucleic Acids Research, 2015, 43, 3764-3775.	6.5	81
26	Structural basis for viral 5â€²-PPP-RNA recognition by human IFIT proteins. Nature, 2013, 494, 60-64.	13.7	193
27	Structural biology in the battle against BCR-Abl. Expert Opinion on Therapeutic Patents, 2008, 18, 975-988.	2.4	0
28	c-Abl Tyrosine Kinase and Inhibition by the Cancer Drug Imatinib (Gleevec/STI-571). Journal of Nutrition, 2007, 137, 1518S-1523S.	1.3	44
29	Organization of the SH3-SH2 Unit in Active and Inactive Forms of the c-Abl Tyrosine Kinase. Molecular Cell, 2006, 21, 787-798.	4.5	192
30	A Myristoyl/Phosphotyrosine Switch Regulates c-Abl. Cell, 2003, 112, 845-857.	13.5	404
31	Structural Basis for the Autoinhibition of c-Abl Tyrosine Kinase. Cell, 2003, 112, 859-871.	13.5	762
32	Multiple BCR-ABL kinase domain mutations confer polyclonal resistance to the tyrosine kinase inhibitor imatinib (STI571) in chronic phase and blast crisis chronic myeloid leukemia. Cancer Cell, 2002, 2, 117-125.	7.7	1,548
33	Crystal structures of the kinase domain of c-Abl in complex with the small molecule inhibitors PD173955 and imatinib (STI-571). Cancer Research, 2002, 62, 4236-43.	0.4	684