

Bhushan Nagar

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2331780/publications.pdf>

Version: 2024-02-01

33
papers

4,507
citations

430874

18
h-index

434195

31
g-index

35
all docs

35
docs citations

35
times ranked

5174
citing authors

#	ARTICLE	IF	CITATIONS
1	Targeting DEAD-box RNA helicases: The emergence of molecular staples. Wiley Interdisciplinary Reviews RNA, 2023, 14, e1738.	6.4	8
2	Structure of the murine lysosomal multienzyme complex core. Science Advances, 2021, 7, .	10.3	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.	5.2	25
4	The mTORC1/S6K/PDCD4/eIF4A Axis Determines Outcome of Mitotic Arrest. Cell Reports, 2020, 33, 108230.	6.4	17
5	Crystal structure of the nucleotide-metabolizing enzyme NTPDase4. Protein Science, 2020, 29, 2054-2061.	7.6	7
6	Crystal Structure of the Mannose-6-Phosphate Uncovering Enzyme. Structure, 2020, 28, 426-436.e3.	3.3	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7	Molecular models should not be published without the corresponding atomic coordinates.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.	7.1	4
8	Identification of Allosteric Inhibitors against Active Caspase-6. Scientific Reports, 2019, 9, 5504.	3.3	15
9	The structure of mammalian β -mannosidase provides insight into β -mannosidosis and nystagmus. FEBS Journal, 2019, 286, 1319-1331.	4.7	14
10	Molecular Mechanism of Inhibition of Acid Ceramidase by Carmofur. Journal of Medicinal Chemistry, 2019, 62, 987-992.	6.4	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.	7.1	24
12	Structural basis for the activation of acid ceramidase. Nature Communications, 2018, 9, 1621.	12.8	72
13	Double-Stranded Biotinylated Donor Enhances Homology-Directed Repair in Combination with Cas9 Monoavidin in Mammalian Cells. CRISPR Journal, 2018, 1, 414-430.	2.9	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.	7.1	36
15	Structural Analysis of the Bacterial Effector AvrA Identifies a Critical Helix Involved in Substrate Recognition. Biochemistry, 2018, 57, 4985-4996.	2.5	12
16	Crystal structure of saposin D in an open conformation. Journal of Structural Biology, 2018, 204, 145-150.	2.8	10
17	Structural basis for nucleotide recognition by the ectoenzyme CD203c. FEBS Journal, 2018, 285, 2481-2494.	4.7	30
18	Structure of human IFIT1 with capped RNA reveals adaptable mRNA binding and mechanisms for sensing N1 and N2 ribose 2'-O methylations. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E2106-E2115.	7.1	86

#	ARTICLE	IF	CITATIONS
19	Structural and Functional Characterization of Plant ARGONAUTE MID Domains. <i>Methods in Molecular Biology</i> , 2017, 1640, 227-239.	0.9	0
20	Crystal structure of the human alkaline sphingomyelinase provides insights into substrate recognition. <i>Journal of Biological Chemistry</i> , 2017, 292, 7087-7094.	3.4	30
21	A key tyrosine substitution restricts nucleotide hydrolysis by the ectoenzyme <i><sc>NPP</sc></i> 5. <i>FEBS Journal</i> , 2017, 284, 3718-3726.	4.7	25
22	Crystal structure of mammalian acid sphingomyelinase. <i>Nature Communications</i> , 2016, 7, 12196.	12.8	76
23	Crystal Structure of the Acid Sphingomyelinase-like Phosphodiesterase SMPDL3B Provides Insights into Determinants of Substrate Specificity. <i>Journal of Biological Chemistry</i> , 2016, 291, 24054-24064.	3.4	20
24	Structural Basis for Nucleotide Hydrolysis by the Acid Sphingomyelinase-like Phosphodiesterase SMPDL3A. <i>Journal of Biological Chemistry</i> , 2016, 291, 6376-6385.	3.4	13
25	DAP5 associates with eIF2 ¹ and eIF4A1 to promote Internal Ribosome Entry Site driven translation. <i>Nucleic Acids Research</i> , 2015, 43, 3764-3775.	14.5	81
26	Structural basis for viral 5â€²-PPP-RNA recognition by human IFIT proteins. <i>Nature</i> , 2013, 494, 60-64.	27.8	193
27	Structural biology in the battle against BCR-Abl. <i>Expert Opinion on Therapeutic Patents</i> , 2008, 18, 975-988.	5.0	0
28	c-Abl Tyrosine Kinase and Inhibition by the Cancer Drug Imatinib (Gleevec/STI-571). <i>Journal of Nutrition</i> , 2007, 137, 1518S-1523S.	2.9	44
29	Organization of the SH3-SH2 Unit in Active and Inactive Forms of the c-Abl Tyrosine Kinase. <i>Molecular Cell</i> , 2006, 21, 787-798.	9.7	192
30	A Myristoyl/Phosphotyrosine Switch Regulates c-Abl. <i>Cell</i> , 2003, 112, 845-857.	28.9	404
31	Structural Basis for the Autoinhibition of c-Abl Tyrosine Kinase. <i>Cell</i> , 2003, 112, 859-871.	28.9	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. <i>Cancer Cell</i> , 2002, 2, 117-125.	16.8	1,548
33	Crystal structures of the kinase domain of c-Abl in complex with the small molecule inhibitors PD173955 and imatinib (STI-571). <i>Cancer Research</i> , 2002, 62, 4236-43.	0.9	684