

Prasenjit Bhaumik

List of Publications by Year in descending order

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Version: 2024-02-01

28
papers

514
citations

759055

12
h-index

677027

22
g-index

31
all docs

31
docs citations

31
times ranked

716
citing authors

#	ARTICLE	IF	CITATIONS
1	Molecular insights into the inhibition of glutamate dehydrogenase by the dicarboxylic acid metabolites. <i>Proteins: Structure, Function and Bioinformatics</i> , 2022, 90, 810-823.	1.5	4
2	Structures of plasmepsin X from <i>Plasmodium falciparum</i> reveal a novel inactivation mechanism of the zymogen and molecular basis for binding of inhibitors in mature enzyme. <i>Protein Science</i> , 2022, 31, 882-899.	3.1	10
3	Activation mechanism of plasmepsins, pepsin-like aspartic proteases from Plasmodium, follows a unique trans-activation pathway. <i>FEBS Journal</i> , 2021, 288, 678-698.	2.2	3
4	Advancements in macromolecular crystallography: from past to present. <i>Emerging Topics in Life Sciences</i> , 2021, 5, 127-149.	1.1	17
5	Structural insights into loss of function of a pore forming toxin and its role in pneumococcal adaptation to an intracellular lifestyle. <i>PLoS Pathogens</i> , 2020, 16, e1009016.	2.1	13
6	Title is missing!. , 2020, 16, e1009016.		0
7	Title is missing!. , 2020, 16, e1009016.		0
8	Title is missing!. , 2020, 16, e1009016.		0
9	Title is missing!. , 2020, 16, e1009016.		0
10	Title is missing!. , 2020, 16, e1009016.		0
11	Cytotoxicity of apo bovine α -lactalbumin complexed with La ³⁺ on cancer cells supported by its high resolution crystal structure. <i>Scientific Reports</i> , 2019, 9, 1780.	1.6	15
12	Bacteriophage N4 large terminase: expression, purification and X-ray crystallographic analysis. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2018, 74, 198-204.	0.4	5
13	Structural basis for the catalytic mechanism and α -ketoglutarate cooperativity of glutamate dehydrogenase. <i>Journal of Biological Chemistry</i> , 2018, 293, 6241-6258.	1.6	36
14	Structural modulation of a periplasmic sugar-binding protein probes into its evolutionary ancestry. <i>Journal of Structural Biology</i> , 2018, 204, 498-506.	1.3	0
15	Deciphering the mechanism of potent peptidomimetic inhibitors targeting plasmepsins – biochemical and structural insights. <i>FEBS Journal</i> , 2018, 285, 3077-3096.	2.2	11
16	Curcumin Inhibits Tau Aggregation and Disintegrates Preformed Tau Filaments in vitro. <i>Journal of Alzheimer's Disease</i> , 2017, 60, 999-1014.	1.2	115
17	Understanding the structural basis of substrate recognition by Plasmodium falciparum plasmepsin V to aid in the design of potent inhibitors. <i>Scientific Reports</i> , 2016, 6, 31420.	1.6	28
18	High Resolution Structures of Periplasmic Glucose-binding Protein of Pseudomonas putida CSV86 Reveal Structural Basis of Its Substrate Specificity. <i>Journal of Biological Chemistry</i> , 2016, 291, 7844-7857.	1.6	19

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19	The prosegment catalyzes native folding of Plasmodium falciparum plasmepsin II. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2016, 1864, 1356-1362.	1.1	3
20	Cloning, Purification, Crystallization and Preliminary X-Ray Diffraction Studies of Periplasmic Glucose Binding Protein of <i>Pseudomonas putida</i> CSV86. <i>Advances in Bioscience and Biotechnology (Print)</i> , 2015, 06, 164-171.	0.3	2
21	The zymogen of plasmepsin V from Plasmodium falciparum is enzymatically active. <i>Molecular and Biochemical Parasitology</i> , 2014, 197, 56-63.	0.5	20
22	Purification, crystallization and preliminary X-ray diffraction analysis of NADP-dependent glutamate dehydrogenase from <i>Aspergillus niger</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 1508-1512.	0.4	1
23	Periplasmic glucose-binding protein from <i>Pseudomonas putida</i> CSV86: identification of the glucose-binding pocket by homology-guided site-specific mutagenesis. <i>FEBS Journal</i> , 2014, 281, 365-375.	2.2	9
24	Elucidating the Role of Disulfide Bond on Amyloid Formation and Fibril Reversibility of Somatostatin-14. <i>Journal of Biological Chemistry</i> , 2014, 289, 16884-16903.	1.6	65
25	Structural studies of vacuolar plasmepsins. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2012, 1824, 207-223.	1.1	39
26	Structural Insights into the Activation and Inhibition of Histo-Aspartic Protease from <i>Plasmodium falciparum</i> . <i>Biochemistry</i> , 2011, 50, 8862-8879.	1.2	15
27	Crystal structures of the free and inhibited forms of plasmepsin I (PMI) from Plasmodium falciparum. <i>Journal of Structural Biology</i> , 2011, 175, 73-84.	1.3	35
28	Crystal Structures of the Histo-Aspartic Protease (HAP) from Plasmodium falciparum. <i>Journal of Molecular Biology</i> , 2009, 388, 520-540.	2.0	49