

Biswaranjan Mohanty

List of Publications by Year in descending order

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52
papers

1,100
citations

471509

17
h-index

434195

31
g-index

55
all docs

55
docs citations

55
times ranked

1791
citing authors

#	ARTICLE	IF	CITATIONS
1	Selective Binding of Small Molecules to <i>Vibrio cholerae</i> DsbA Offers a Starting Point for the Design of Novel Antibacterials. ChemMedChem, 2022, 17, .	3.2	3
2	Identification and characterization of two drug-like fragments that bind to the same cryptic binding pocket of <i>Burkholderia pseudomallei</i> DsbA. Acta Crystallographica Section D: Structural Biology, 2022, 78, 75-90.	2.3	2
3	Methyl probes in proteins for determining ligand binding mode in weak protein-ligand complexes. Scientific Reports, 2022, 12, .	3.3	3
4	Side-Chain Interactions in α -Peptide Nanotubes: Studies by Crystallography, NMR Spectroscopy and Molecular Dynamics. Chemistry - A European Journal, 2021, 27, 14489-14500.	3.3	5
5	Binding of a pyrimidine RNA base-mimic to SARS-CoV-2 nonstructural protein 9. Journal of Biological Chemistry, 2021, 297, 101018.	3.4	10
6	NMR fragment screening reveals a novel small molecule binding site near the catalytic surface of the disulfide-dithiol oxidoreductase enzyme DsbA from <i>Burkholderia pseudomallei</i> . Journal of Biomolecular NMR, 2020, 74, 595-611.	2.8	7
7	Rapid Elaboration of Fragments into Leads by X-ray Crystallographic Screening of Parallel Chemical Libraries (REFIL-X). Journal of Medicinal Chemistry, 2020, 63, 6863-6875.	6.4	16
8	A ligand-induced structural change in fatty acid-binding protein 1 is associated with potentiation of peroxisome proliferator-activated receptor β agonists. Journal of Biological Chemistry, 2019, 294, 3720-3734.	3.4	17
9	The uncharacterized bacterial protein YejG has the same architecture as domain III of elongation factor G. Proteins: Structure, Function and Bioinformatics, 2019, 87, 699-705.	2.6	0
10	Classification of the human phox homology (PX) domains based on their phosphoinositide binding specificities. Nature Communications, 2019, 10, 1528.	12.8	101
11	Controlled Construction of Cyclic α -Peptide Nanorods. Angewandte Chemie - International Edition, 2019, 58, 596-601.	13.8	8
12	Controlled Construction of Cyclic α -Peptide Nanorods. Angewandte Chemie, 2019, 131, 606-611.	2.0	2
13	Structural and biochemical insights into the disulfide reductase mechanism of DsbD, an essential enzyme for neisserial pathogens. Journal of Biological Chemistry, 2018, 293, 16559-16571.	3.4	10
14	Applications of NMR Spectroscopy in FBDD. , 2018, , 2211-2231.		2
15	^1H , ^13C and ^15N assignments of the two periplasmic domains of <i>Neisseria meningitidis</i> DsbD. Biomolecular NMR Assignments, 2017, 11, 181-186.	0.8	1
16	The first total synthesis and solution structure of a polypeptin, PE2, a cyclic lipopeptide with broad spectrum antibiotic activity. Organic and Biomolecular Chemistry, 2017, 15, 7173-7180.	2.8	5
17	Fragment library screening identifies hits that bind to the non-catalytic surface of <i>Pseudomonas aeruginosa</i> DsbA1. PLoS ONE, 2017, 12, e0173436.	2.5	17
18	Applications of NMR Spectroscopy in FBDD. , 2017, , 1-22.		0

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19	<scp>NMR</scp> reveals structural rearrangements associated to substrate insertion in nucleotide-adding enzymes. <i>Protein Science</i> , 2016, 25, 917-925.	7.6	1
20	<scp>NMR</scp> in structural genomics to increase structural coverage of the protein universe. <i>FEBS Journal</i> , 2016, 283, 3870-3881.	4.7	5
21	The Chromatin Remodelling Protein CHD1 Contains a Previously Unrecognised C-Terminal Helical Domain. <i>Journal of Molecular Biology</i> , 2016, 428, 4298-4314.	4.2	14
22	Structure-Activity Studies of ¹² I-Hairpin Peptide Inhibitors of the Plasmodium falciparum AMA1- ¹ RON2 Interaction. <i>Journal of Molecular Biology</i> , 2016, 428, 3986-3998.	4.2	22
23	Determination of ligand binding modes in weak protein-ligand complexes using sparse NMR data. <i>Journal of Biomolecular NMR</i> , 2016, 66, 195-208.	2.8	19
24	¹ H, ¹³ C and ¹⁵ N resonance assignments of a C-terminal domain of human CHD1. <i>Biomolecular NMR Assignments</i> , 2016, 10, 31-34.	0.8	1
25	Structure of amylase-binding protein A of <i>Streptococcus gordonii</i> : A potential receptor for human salivary α -amylase enzyme. <i>Protein Science</i> , 2015, 24, 1013-1018.	7.6	8
26	Application of Fragment-Based Screening to the Design of Inhibitors of <i>Escherichia coli</i> DsbA. <i>Angewandte Chemie - International Edition</i> , 2015, 54, 2179-2184.	13.8	46
27	Small Molecule Inhibitors of Disulfide Bond Formation by the Bacterial DsbA-DsbB Dual Enzyme System. <i>ACS Chemical Biology</i> , 2015, 10, 957-964.	3.4	27
28	Promiscuous 2-Aminothiazoles (PrATs): A Frequent Hitting Scaffold. <i>Journal of Medicinal Chemistry</i> , 2015, 58, 1205-1214.	6.4	75
29	Structure and Functional Characterization of the Conserved JAK Interaction Region in the Intrinsically Disordered N-Terminus of SOCS5. <i>Biochemistry</i> , 2015, 54, 4672-4682.	2.5	14
30	NMR structure determination of the protein NP_344798.1 as the first representative of Pfam PF06042. <i>Journal of Biomolecular NMR</i> , 2015, 61, 83-87.	2.8	4
31	Assignments of human integrin β 11 domain in the apo and Mg ²⁺ bound states. <i>Biomolecular NMR Assignments</i> , 2014, 8, 117-121.	0.8	4
32	Kv1.3 channel-blocking immunomodulatory peptides from parasitic worms: implications for autoimmune diseases. <i>FASEB Journal</i> , 2014, 28, 3952-3964.	0.5	76
33	Characterization of Two Distinct Modes of Drug Binding to Human Intestinal Fatty Acid Binding Protein. <i>ACS Chemical Biology</i> , 2014, 9, 2526-2534.	3.4	24
34	NMR Structures of β -Proteobacterial ATPase-Regulating β -Subunits. <i>Journal of Molecular Biology</i> , 2014, 426, 2547-2553.	4.2	18
35	Molecular Insights into the Interaction between Plasmodium falciparum Apical Membrane Antigen 1 and an Invasion-Inhibitory Peptide. <i>PLoS ONE</i> , 2014, 9, e109674.	2.5	10
36	Structural representative of the protein family PF14466 has a new fold and establishes links with the C2 and PLAT domains from the widely distant Pfams PF00168 and PF01477. <i>Protein Science</i> , 2013, 22, 1000-1007.	7.6	5

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37	NMR profiles of protein solutions. <i>Biopolymers</i> , 2013, 99, 825-831.	2.4	17
38	The Structure of Integrin $\alpha 1$ Domain in Complex with a Collagen-mimetic Peptide. <i>Journal of Biological Chemistry</i> , 2013, 288, 36796-36809.	3.4	22
39	The Relaxin Receptor (RXFP1) Utilizes Hydrophobic Moieties on a Signaling Surface of Its N-terminal Low Density Lipoprotein Class A Module to Mediate Receptor Activation. <i>Journal of Biological Chemistry</i> , 2013, 288, 28138-28151.	3.4	25
40	Comparative Sequence, Structure and Redox Analyses of <i>Klebsiella pneumoniae</i> DsbA Show That Anti-Virulence Target DsbA Enzymes Fall into Distinct Classes. <i>PLoS ONE</i> , 2013, 8, e80210.	2.5	24
41	The J-UNIO protocol for automated protein structure determination by NMR in solution. <i>Journal of Biomolecular NMR</i> , 2012, 53, 341-354.	2.8	57
42	NMR structure of the protein NP_247299.1: comparison with the crystal structure. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1367-1380.	0.7	13
43	Comparison of NMR and crystal structures for the proteins TM1112 and TM1367. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1381-1392.	0.7	14
44	Comparison of NMR and crystal structures highlights conformational isomerism in protein active sites. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1393-1405.	0.7	18
45	Physical and anti-microbial characteristics of carbon nanoparticles prepared from lamp soot. <i>Nanotechnology</i> , 2007, 18, 445102.	2.6	33
46	Effect of gelatin molecular charge heterogeneity on formation of intermolecular complexes and coacervation transition. <i>Journal of Polymer Science, Part B: Polymer Physics</i> , 2007, 45, 1511-1520.	2.1	17
47	Internal pressure fluctuations in coacervates and syneresis. <i>Europhysics Letters</i> , 2006, 76, 965-971.	2.0	7
48	Length scale hierarchy in sol, gel, and coacervate phases of gelatin. <i>Journal of Polymer Science, Part B: Polymer Physics</i> , 2006, 44, 1653-1667.	2.1	29
49	Flory Temperature and Upper Critical Solution Temperature of Gelatin Solutions. <i>Biomacromolecules</i> , 2005, 6, 1623-1627.	5.4	43
50	Microscopic structure of gelatin coacervates. <i>International Journal of Biological Macromolecules</i> , 2005, 36, 39-46.	7.5	62
51	Anomalous self-assembly of gelatin in ethanol-water marginal solvent. <i>Physical Review E</i> , 2004, 69, 021902.	2.1	29
52	Systematic of Alcohol-Induced Simple Coacervation in Aqueous Gelatin Solutions. <i>Biomacromolecules</i> , 2003, 4, 1080-1086.	5.4	105