

Alok K Mitra

List of Publications by Year in descending order

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73
papers

3,018
citations

201575

27
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161767

54
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74
all docs

74
docs citations

74
times ranked

3677
citing authors

#	ARTICLE	IF	CITATIONS
1	Clusterin is involved in mediating the metabolic function of adipose SIRT1. <i>IScience</i> , 2022, 25, 103709.	1.9	3
2	Investigating the Process of Sheath Maturation in Antifeeding Prophage: a Phage Tail-Like Protein Translocation Structure. <i>Journal of Bacteriology</i> , 2021, 203, e0010421.	1.0	3
3	Atomic structures of an entire contractile injection system in both the extended and contracted states. <i>Nature Microbiology</i> , 2019, 4, 1885-1894.	5.9	45
4	Engineering peroxiredoxin 3 to facilitate control over self-assembly. <i>Biochemical and Biophysical Research Communications</i> , 2019, 512, 263-268.	1.0	3
5	Visualization of biological macromolecules at near-atomic resolution: cryo-electron microscopy comes of age. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2019, 75, 3-11.	0.4	22
6	Aquaporins: Novel Targets for Age-Related Ocular Disorders. <i>Journal of Ocular Pharmacology and Therapeutics</i> , 2018, 34, 177-187.	0.6	10
7	The phase problem for two-dimensional crystals. II. Simulations. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2018, 74, 537-544.	0.0	0
8	Supramolecular Threading of Peptide Hydrogel Fibrils. <i>ACS Biomaterials Science and Engineering</i> , 2018, 4, 2733-2738.	2.6	12
9	Structural Model of the Tubular Assembly of the Rous Sarcoma Virus Capsid Protein. <i>Journal of the American Chemical Society</i> , 2017, 139, 2006-2013.	6.6	10
10	TORC1 organized in inhibited domains (TOROIDS) regulate TORC1 activity. <i>Nature</i> , 2017, 550, 265-269.	13.7	100
11	Synthetic peptides designed to modulate adiponectin assembly improve obesity-related metabolic disorders. <i>British Journal of Pharmacology</i> , 2017, 174, 4478-4492.	2.7	15
12	Stoichiometry and mechanistic implications of the MacAB-TolC tripartite efflux pump. <i>Biochemical and Biophysical Research Communications</i> , 2017, 494, 668-673.	1.0	10
13	In vitro assembly of the Rous Sarcoma Virus capsid protein into hexamer tubes at physiological temperature. <i>Scientific Reports</i> , 2017, 7, 2913.	1.6	7
14	Multifunctional thermoresponsive designer peptide hydrogels. <i>Acta Biomaterialia</i> , 2017, 47, 40-49.	4.1	13
15	Understanding the metal mediated assembly and hydrogel formation of a β -hairpin peptide. <i>Biomaterials Science</i> , 2017, 5, 1993-1997.	2.6	10
16	Rapid Identification of Novel Inhibitors of the Human Aquaporin-1 Water Channel. <i>Chemical Biology and Drug Design</i> , 2016, 87, 794-805.	1.5	21
17	Structures of Human Peroxiredoxin 3 Suggest Self-Chaperoning Assembly that Maintains Catalytic State. <i>Structure</i> , 2016, 24, 1120-1129.	1.6	39
18	Volta phase plate cryo-EM of the small protein complex Prx3. <i>Nature Communications</i> , 2016, 7, 10534.	5.8	64

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19	A peptide hydrogel derived from a fragment of human cardiac troponin C. <i>Chemical Communications</i> , 2016, 52, 4056-4059.	2.2	14
20	<sc>A</sc>fp14 is involved in regulating the length of Anti-feeding prophage (<sc>A</sc>fp). <i>Molecular Microbiology</i> , 2015, 96, 815-826.	1.2	13
21	Cryo-Electron Microscopy Structure of Human Peroxiredoxin-3 Filament Reveals the Assembly of a Putative Chaperone. <i>Structure</i> , 2015, 23, 912-920.	1.6	30
22	Regulation and Quality Control of Adiponectin Assembly by Endoplasmic Reticulum Chaperone ERp44. <i>Journal of Biological Chemistry</i> , 2015, 290, 18111-18123.	1.6	33
23	Overexpression, purification and biophysical characterisation of E. coli MerT. <i>Protein Expression and Purification</i> , 2015, 108, 85-89.	0.6	1
24	A novel packing arrangement of AcrB in the lipid bilayer membrane. <i>FEBS Letters</i> , 2014, 588, 4776-4783.	1.3	0
25	An investigation of the role of the adiponectin variable domain on the stability of the collagen-like domain. <i>Biopolymers</i> , 2014, 102, 313-321.	1.2	4
26	Peroxiredoxin is a Versatile Self-Assembling Tecton for Protein Nanotechnology. <i>Biomacromolecules</i> , 2014, 15, 1871-1881.	2.6	43
27	Purification and TEM of Afp and Its Variants. <i>Bio-protocol</i> , 2014, 4, .	0.2	3
28	Role of antifeeding prophage (<sc>Afp</sc>) protein <sc>Afp</sc>16 in terminating the length of the <sc>Afp</sc> tailocin and stabilizing its sheath. <i>Molecular Microbiology</i> , 2013, 89, 702-714.	1.2	30
29	Three-dimensional Structure of the Toxin-delivery Particle Antifeeding Prophage of <i>Serratia entomophila</i> . <i>Journal of Biological Chemistry</i> , 2013, 288, 25276-25284.	1.6	57
30	A Structural Model for the Generation of Continuous Curvature on the Surface of a Retroviral Capsid. <i>Journal of Molecular Biology</i> , 2012, 417, 212-223.	2.0	32
31	The Structure of the Oligomerization Domain of Lsr2 from <i>Mycobacterium tuberculosis</i> Reveals a Mechanism for Chromosome Organization and Protection. <i>PLoS ONE</i> , 2012, 7, e38542.	1.1	37
32	A highly conserved tryptophan in the N-terminal variable domain regulates disulfide bond formation and oligomeric assembly of adiponectin. <i>FEBS Journal</i> , 2012, 279, 2495-2507.	2.2	10
33	A PCR-directed cell-free approach to optimize protein expression using diverse fusion tags. <i>Protein Expression and Purification</i> , 2011, 80, 117-124.	0.6	12
34	Membrane Remodeling by the Double-Barrel Scaffolding Protein of Poxvirus. <i>PLoS Pathogens</i> , 2011, 7, e1002239.	2.1	44
35	Proton-driven Assembly of the Rous Sarcoma Virus Capsid Protein Results in the Formation of Icosahedral Particles. <i>Journal of Biological Chemistry</i> , 2010, 285, 15056-15064.	1.6	24
36	Structural Study of the <i>Serratia entomophila</i> Antifeeding Prophage: Three-Dimensional Structure of the Helical Sheath. <i>Journal of Bacteriology</i> , 2010, 192, 4522-4525.	1.0	8

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37	Anthrax toxin-neutralizing antibody reconfigures the protective antigen heptamer into a supercomplex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 14070-14074.	3.3	16
38	Oligomeric Structure of Colicin Ia Channel in Lipid Bilayer Membranes. <i>Journal of Biological Chemistry</i> , 2009, 284, 16126-16134.	1.6	15
39	The multifunctional histone-like protein Lsr2 protects mycobacteria against reactive oxygen intermediates. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 4414-4418.	3.3	109
40	Proton-Linked Dimerization of a Retroviral Capsid Protein Initiates Capsid Assembly. <i>Structure</i> , 2009, 17, 737-748.	1.6	33
41	Structural Polymorphism of Oligomeric Adiponectin Visualized by Electron Microscopy. <i>Journal of Molecular Biology</i> , 2008, 381, 419-430.	2.0	31
42	The Architecture of a Water-Selective Pore in the Lipid Bilayer Visualized by Electron Crystallography in Vitreous Ice. <i>Novartis Foundation Symposium</i> , 2008, , 33-50.	1.2	4
43	The Structure of a Putative Scaffolding Protein of Immature Poxvirus Particles as Determined by Electron Microscopy Suggests Similarity with Capsid Proteins of Large Icosahedral DNA Viruses. <i>Journal of Virology</i> , 2007, 81, 11075-11083.	1.5	19
44	Dissecting the 3-D structure of vimentin intermediate filaments by cryo-electron tomography. <i>Journal of Structural Biology</i> , 2007, 158, 378-385.	1.3	80
45	Structural Determinants of Rotavirus Subgroup Specificity Mapped by Cryo-electron Microscopy. <i>Journal of Molecular Biology</i> , 2006, 356, 209-221.	2.0	14
46	Model of the toxic complex of anthrax: Responsive conformational changes in both the lethal factor and the protective antigen heptamer. <i>Protein Science</i> , 2006, 15, 2190-2200.	3.1	22
47	Large-Scale Structural Changes Accompany Binding of Lethal Factor to Anthrax Protective Antigen. <i>Structure</i> , 2004, 12, 2059-2066.	1.6	25
48	Supine Orientation of a Murine MHC Class I Molecule on the Membrane Bilayer. <i>Current Biology</i> , 2004, 14, 718-724.	1.8	29
49	The architecture of a water-selective pore in the lipid bilayer visualized by electron crystallography in vitreous ice. <i>Novartis Foundation Symposium</i> , 2002, 245, 33-46; discussion 46-50; 165-8.	1.2	0
50	Chapter 5 Genetic and biophysical approaches to study water channel biology. <i>Current Topics in Membranes</i> , 2001, 51, 185-233.	0.5	1
51	Three-dimensional organization of the aquaporin water channel: What can structure tell us about function?. <i>Vitamins and Hormones</i> , 2001, 62, 133-166.	0.7	2
52	Visualization of a water-selective pore by electron crystallography in vitreous ice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001, 98, 1398-1403.	3.3	79
53	3D reconstruction from electron micrographs of tilted 2D crystal: structure of a human water channel. , 2000, 4123, 224.		0
54	Structure and function of aquaporin water channels. <i>American Journal of Physiology - Renal Physiology</i> , 2000, 278, F13-F28.	1.3	558

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55	Three-dimensional fold of the human AQP1 water channel determined at 4 Å... resolution by electron crystallography of two-dimensional crystals embedded in ice 1 Edited by W. Baumeister. Journal of Molecular Biology, 2000, 301, 369-387.	2.0	72
56	Polymorphism in the Packing of Aquaporin-1 Tetramers in 2-D Crystals. Journal of Structural Biology, 2000, 130, 45-53.	1.3	18
57	Three-Dimensional Fold of Human AQP1 Water Channel Determined by Electron Cryo-Crystallography of 2-Dimensional Crystals Embedded in Ice. , 2000, , 35-39.		0
58	Expression, Purification, and Structural Characterization of the Bacteriorhodopsinâ€™Aspartyl Transcarbamylase Fusion Protein. Protein Expression and Purification, 1999, 17, 324-338.	0.6	12
59	[7] Three-dimensional structure of membrane proteins determined by two-dimensional crystallization, electron cryomicroscopy, and image analysis. Methods in Enzymology, 1999, 294, 135-180.	0.4	40
60	Three-dimensional organization of a human water channel. Nature, 1997, 387, 627-630.	13.7	288
61	Structure and function of kidney water channels. Kidney International, 1995, 48, 1069-1081.	2.6	38
62	Two-dimensional crystallization of Escherichia coli-expressed bacteriorhodopsin and its D96N variant: high resolution structural studies in projection. Biophysical Journal, 1993, 65, 1295-1306.	0.2	18
63	Electron crystallographic studies on E.coli- expressed variants of bacteriorhodopsin. Proceedings Annual Meeting Electron Microscopy Society of America, 1992, 50, 436-437.	0.0	0
64	Wild-type and mutant bacterioopsins D85N, D96N, and R82Q: high-level expression in Escherichia coli. Biochemistry, 1991, 30, 3082-3088.	1.2	32
65	Wild-type and mutant bacteriorhodopsins D85N, D96N, and R82Q: purification to homogeneity, pH dependence of pumping and electron diffraction. Biochemistry, 1991, 30, 3088-3098.	1.2	37
66	Membrane Structures in Normal and Essential Fatty Acid-Deficient Stratum Corneum: Characterization by Ruthenium Tetroxide Staining and X-Ray Diffraction. Journal of Investigative Dermatology, 1991, 96, 215-223.	0.3	284
67	High sensitivity electron diffraction analysis. A study of divalent cation binding to purple membrane. Biophysical Journal, 1990, 57, 301-311.	0.2	30
68	Three-dimensional structure of the nicotinic acetylcholine receptor and location of the major associated 43-kD cytoskeletal protein, determined at 22 Å by low dose electron microscopy and x-ray diffraction to 12.5 Å [published erratum appears in J Cell Biol 1989 Oct;109(4 Pt 1):1185]. Journal of Cell Biology, 1989, 109, 755-774.	2.3	115
69	Conformational flexibilities in malformin A. Biopolymers, 1984, 23, 2513-2524.	1.2	9
70	BACKBONE TORSIONAL POTENTIAL FUNCTIONS FOR ROTATIONS ABOUT Nâ€™C _{â€™} AND C _{â€™} â€™BONDS IN DIPEPTIDE MODEL SYSTEMS IN RELATION TO NUCLEAR MAGNETIC RESONANCE AND INFRA RED SPECTRAL DATA*. International Journal of Peptide and Protein Research, 1978, 11, 166-178.	0.1	4
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73	Engineering a stable complex of ERp44 with a designed peptide ligand for analyzing the mode of interaction of ERp44 with its clients. Peptide Science, 0, , e24230.	1.0	0