

# Amit Kumar Das

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/11453164/publications.pdf>

Version: 2024-02-01

41  
papers

547  
citations

623734

14  
h-index

677142

22  
g-index

43  
all docs

43  
docs citations

43  
times ranked

897  
citing authors

#	ARTICLE	IF	CITATIONS
1	Crystal Structure of Low-Molecular-Weight Protein Tyrosine Phosphatase from <i>Mycobacterium tuberculosis</i> at 1.9-Å Resolution. <i>Journal of Bacteriology</i> , 2005, 187, 2175-2181.	2.2	68
2	Crystal Structure of Glyceraldehyde-3-Phosphate Dehydrogenase 1 from Methicillin-Resistant <i>Staphylococcus aureus</i> MRSA252 Provides Novel Insights into Substrate Binding and Catalytic Mechanism. <i>Journal of Molecular Biology</i> , 2010, 401, 949-968.	4.2	42
3	Crystal structure of hexanoyl-CoA bound to $\beta^2$ -ketoacyl reductase FabG4 of <i>Mycobacterium tuberculosis</i> . <i>Biochemical Journal</i> , 2013, 450, 127-139.	3.7	34
4	Benzene fused monocyclic enediynyl amides: synthesis, reactivity and DNA-Cleavage activity in comparison to the corresponding sulfonamides. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2002, 12, 873-877.	2.2	31
5	NMR ( $^1\text{H}$ and $^{13}\text{C}$ ) based signatures of abnormal choline metabolism in oral squamous cell carcinoma with no prominent Warburg effect. <i>Biochemical and Biophysical Research Communications</i> , 2015, 459, 574-578.	2.1	30
6	Crystal structure and fluorescence studies reveal the role of helical dimeric interface of staphylococcal fabg1 in positive cooperativity for NADPH. <i>Proteins: Structure, Function and Bioinformatics</i> , 2012, 80, 1250-1257.	2.6	29
7	Interaction analysis of TcrX/Y two component system from <i>Mycobacterium tuberculosis</i> . <i>Biochimie</i> , 2010, 92, 263-272.	2.6	27
8	Macroscopic amyloid fiber formation by staphylococcal biofilm associated SuhB protein. <i>Biophysical Chemistry</i> , 2016, 217, 32-41.	2.8	23
9	Inverted repeats in the promoter as an autoregulatory sequence for TcrX in <i>Mycobacterium tuberculosis</i> . <i>Biochemical and Biophysical Research Communications</i> , 2011, 415, 17-23.	2.1	20
10	Structural elucidation of the binding site and mode of inhibition of $\text{Li}^{2+}$ and $\text{Mg}^{2+}$ in inositol monophosphatase. <i>FEBS Journal</i> , 2014, 281, 5309-5324.	4.7	20
11	Functional insights from the molecular modelling of a novel two-component system. <i>Biochemical and Biophysical Research Communications</i> , 2006, 344, 1327-1333.	2.1	17
12	Probing the nucleotide binding and phosphorylation by the histidine kinase of a novel three-protein two-component system from <i>Mycobacterium tuberculosis</i> . <i>FEBS Letters</i> , 2007, 581, 1903-1909.	2.8	16
13	Protection of human $\beta$ -crystallin from UV-induced damage by epigallocatechin gallate: spectroscopic and docking studies. <i>Molecular BioSystems</i> , 2016, 12, 2901-2909.	2.9	16
14	Analyzing the catalytic mechanism of MPtpA: A low molecular weight protein tyrosine phosphatase from <i>Mycobacterium tuberculosis</i> through site-directed mutagenesis. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 71, 706-714.	2.6	15
15	Crystal structure of FabG4 from <i>Mycobacterium tuberculosis</i> reveals the importance of C-terminal residues in ketoreductase activity. <i>Journal of Structural Biology</i> , 2011, 174, 147-155.	2.8	15
16	Crystal structure of dehydratase component HadAB complex of mycobacterial FAS-II pathway. <i>Biochemical and Biophysical Research Communications</i> , 2015, 458, 369-374.	2.1	15
17	Intra- and intermolecular domain interactions among novel two-component system proteins coded by Rv0600c, Rv0601c and Rv0602c of <i>Mycobacterium tuberculosis</i> . <i>Microbiology (United Kingdom)</i> , 2009, 155, 772-779.	1.8	13
18	Crystal structure of a fungal protease inhibitor from <i>Antheraea mylitta</i> . <i>Journal of Structural Biology</i> , 2009, 166, 79-87.	2.8	12

#	ARTICLE	IF	CITATIONS
19	Probing the inhibitory potency of epigallocatechin gallate against human $\beta$ -crystallin aggregation: Spectroscopic, microscopic and simulation studies. <i>Spectrochimica Acta - Part A: Molecular and Biomolecular Spectroscopy</i> , 2018, 192, 318-327.	3.9	10
20	Crystal structures of triosephosphate isomerase from methicillin resistant <i>Staphylococcus aureus</i> MRSA252 provide structural insights into novel modes of ligand binding and unique conformations of catalytic loop. <i>Biochimie</i> , 2012, 94, 2532-2544.	2.6	9
21	Temperature and urea induced conformational changes of the histidine kinases from <i>Mycobacterium tuberculosis</i> . <i>International Journal of Biological Macromolecules</i> , 2007, 41, 154-161.	7.5	8
22	Complete catalytic cycle of cofactor-independent phosphoglycerate mutase involves a spring-loaded mechanism. <i>FEBS Journal</i> , 2015, 282, 1097-1110.	4.7	8
23	Structure-based Epitope Mapping of <i>Mycobacterium tuberculosis</i> Secretary Antigen MTC28. <i>Journal of Biological Chemistry</i> , 2016, 291, 13943-13954.	3.4	8
24	NanoLC MALDI MS/MS based quantitative metabolomics reveals the alteration of membrane biogenesis in oral cancer. <i>RSC Advances</i> , 2016, 6, 62420-62433.	3.6	8
25	The $\beta$ 1 region is crucial for biofilm enhancement activity of MTC28 in <i>Mycobacterium smegmatis</i> . <i>FEBS Letters</i> , 2017, 591, 3333-3347.	2.8	7
26	Expression, purification, crystallization and preliminary X-ray diffraction studies of phosphoglycerate kinase from methicillin-resistant <i>Staphylococcus aureus</i> MRSA252. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 668-671.	0.7	6
27	Analyzing the catalytic mechanism of protein tyrosine phosphatase PtpB from <i>Staphylococcus aureus</i> through site-directed mutagenesis. <i>International Journal of Biological Macromolecules</i> , 2009, 45, 463-469.	7.5	5
28	Functional insights from molecular modeling, docking, and dynamics study of a cypoviral RNA dependent RNA polymerase. <i>Journal of Molecular Graphics and Modelling</i> , 2015, 61, 160-174.	2.4	5
29	Crystallization and preliminary X-ray diffraction analysis of a protease inhibitor from the haemolymph of the Indian tasar silkworm <i>Antheraea mylitta</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 669-671.	0.7	4
30	Expression, purification, crystallization and preliminary X-ray diffraction studies of glyceraldehyde-3-phosphate dehydrogenase 1 from methicillin-resistant <i>Staphylococcus aureus</i> (MRSA252). <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2008, 64, 929-932.	0.7	4
31	Crystallization and preliminary X-ray diffraction analysis of the high molecular weight ketoacyl reductase FabG4 complexed with NADH. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 786-789.	0.7	4
32	Structural elucidation of the NADP(H) phosphatase activity of staphylococcal dual-specific IMPase/NADP(H) phosphatase. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016, 72, 281-290.	2.3	3
33	Cloning, overexpression, purification, crystallization and preliminary X-ray diffraction analysis of Rv0241c (HtdX) from <i>Mycobacterium tuberculosis</i> H37Rv. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2013, 69, 1110-1113.	0.7	3
34	Expression, purification, crystallization and preliminary X-ray diffraction studies of phosphoglycerate mutase from <i>Staphylococcus aureus</i> NCTC8325. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 53-56.	0.8	3
35	Purification, crystallization and preliminary X-ray analysis of apo glyceraldehyde-3-phosphate dehydrogenase 1 (GAP1) from methicillin-resistant <i>Staphylococcus aureus</i> (MRSA252). <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 506-508.	0.7	2
36	Cloning, overexpression, purification, crystallization and preliminary X-ray diffraction analysis of an inositol monophosphatase family protein (SAS2203) from <i>Staphylococcus aureus</i> MSSA476. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 471-474.	0.7	2

#	ARTICLE	IF	CITATIONS
37	Kinetic Analysis, Expression Pattern, and Production of a Recombinant Fungal Protease Inhibitor of Tasar Silkworm <i>Antheraea mylitta</i> . <i>Applied Biochemistry and Biotechnology</i> , 2012, 168, 1076-1085.	2.9	2
38	Domain swapping between FabGs deciphers the structural determinant for in-solution oligomerization and substrate binding. <i>Biophysical Chemistry</i> , 2018, 237, 9-21.	2.8	2
39	Design and synthesis of azobenzene template based sulfonamide for capture of HCAII: dependence of efficiency on Eâ€Z geometry. <i>Tetrahedron Letters</i> , 2014, 55, 2625-2628.	1.4	1
40	Molecular insights into RNA-binding properties of <i>Escherichia coli</i> â€expressed RNA-dependent RNA polymerase of <i>Antheraea mylitta</i> cytoplasmic polyhedrosis virus. <i>Archives of Virology</i> , 2017, 162, 2727-2736.	2.1	0
41	Reconstitution of the RNA-dependent RNA polymerase activity of <i>Antheraea mylitta</i> cyovirus in vitro using separately expressed different functional domains of the enzyme. <i>Journal of General Virology</i> , 2016, 97, 1709-1719.	2.9	0