

Kunchithapadam Swaminathan

List of Publications by Year in descending order

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Version: 2024-02-01

57
papers

2,449
citations

236925

25
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206112

48
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57
all docs

57
docs citations

57
times ranked

4476
citing authors

#	ARTICLE	IF	CITATIONS
1	Structural basis of typhoid: <i>Salmonella typhi</i> type IVb pilin (PilS) and cystic fibrosis transmembrane conductance regulator interaction. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 77, 253-261.	2.6	284
2	A C9ORF72/SMCR8-containing complex regulates ULK1 and plays a dual role in autophagy. <i>Science Advances</i> , 2016, 2, e1601167.	10.3	210
3	A Crystal Structure of the Dengue Virus NS5 Protein Reveals a Novel Inter-domain Interface Essential for Protein Flexibility and Virus Replication. <i>PLoS Pathogens</i> , 2015, 11, e1004682.	4.7	180
4	Enzymatic catalysis of anti-Baldwin ring closure in polyether biosynthesis. <i>Nature</i> , 2012, 483, 355-358.	27.8	117
5	Structural analysis uncovers a role for redox in regulating FKBP13, an immunophilin of the chloroplast thylakoid lumen. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 13945-13950.	7.1	97
6	Molecular basis for specific viral RNA recognition and 2'-O-ribose methylation by the dengue virus nonstructural protein 5 (NS5). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 14834-14839.	7.1	89
7	Crystal structure of a PUT3-DNA complex reveals a novel mechanism for DMA recognition by a protein containing a Zn2Cys6 binuclear cluster. <i>Nature Structural Biology</i> , 1997, 4, 751-759.	9.7	87
8	Crystal structure of the CDK4/6 inhibitory protein p18INK4c provides insights into ankyrin-like repeat structure/function and tumor-derived p16INK4 mutations. <i>Nature Structural Biology</i> , 1998, 5, 74-81.	9.7	80
9	Crystal Structure of the Polyextremophilic α -Amylase AmyB from <i>Halothermothrix orenii</i> : Details of a Productive Enzyme-Substrate Complex and an N Domain with a Role in Binding Raw Starch. <i>Journal of Molecular Biology</i> , 2008, 378, 852-870.	4.2	80
10	A HEX-1 crystal lattice required for Woronin body function in <i>Neurospora crassa</i> . <i>Nature Structural and Molecular Biology</i> , 2003, 10, 264-270.	8.2	77
11	A Dimerized Coiled-Coil Domain and an Adjoining Part of Geminin Interact with Two Sites on Cdt1 for Replication Inhibition. <i>Molecular Cell</i> , 2004, 15, 245-258.	9.7	73
12	Structural Basis for Hormone Recognition by the Human CRFR2 \pm G Protein-coupled Receptor. <i>Journal of Biological Chemistry</i> , 2010, 285, 40351-40361.	3.4	73
13	Crystal Structure of Full-length <i>Mycobacterium tuberculosis</i> H37Rv Glycogen Branching Enzyme. <i>Journal of Biological Chemistry</i> , 2010, 285, 20897-20903.	3.4	67
14	Crystal structure of AmyA lacks acidic surface and provide insights into protein stability at poly-extreme condition. <i>FEBS Letters</i> , 2006, 580, 2646-2652.	2.8	64
15	Structural and Functional Studies of trans-Encoded HLA-DQ2.3 (DQA1*03:01/DQB1*02:01) Protein Molecule. <i>Journal of Biological Chemistry</i> , 2012, 287, 13611-13619.	3.4	63
16	Crystal Structure of the PAC1R Extracellular Domain Unifies a Consensus Fold for Hormone Recognition by Class B G-Protein Coupled Receptors. <i>PLoS ONE</i> , 2011, 6, e19682.	2.5	58
17	Isomaltulose Synthase (Pall) of <i>Klebsiella</i> sp. LX3. <i>Journal of Biological Chemistry</i> , 2003, 278, 35428-35434.	3.4	56
18	Engineering of serine protease for improved thermostability and catalytic activity using rational design. <i>International Journal of Biological Macromolecules</i> , 2019, 126, 229-237.	7.5	47

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19	Crystal Structure of <i>Arabidopsis</i> Cyclophilin38 Reveals a Previously Uncharacterized Immunophilin Fold and a Possible Autoinhibitory Mechanism. <i>Plant Cell</i> , 2012, 24, 2666-2674.	6.6	42
20	Flexibility of NS5 Methyltransferase-Polymerase Linker Region Is Essential for Dengue Virus Replication. <i>Journal of Virology</i> , 2015, 89, 10717-10721.	3.4	41
21	Crystal Structure of Thrombin in Complex with S-Variagin: Insights of a Novel Mechanism of Inhibition and Design of Tunable Thrombin Inhibitors. <i>PLoS ONE</i> , 2011, 6, e26367.	2.5	40
22	Structural determinants of heparin-transforming growth factor- β 1 interactions and their effects on signaling. <i>Glycobiology</i> , 2015, 25, 1491-1504.	2.5	38
23	Plant immunophilins: a review of their structure-function relationship. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2015, 1850, 2145-2158.	2.4	38
24	Crystal structure of uncleaved L-aspartate-decarboxylase from <i>Mycobacterium tuberculosis</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 65, 796-802.	2.6	34
25	Affinity Selection of FGF2-Binding Heparan Sulfates for Ex Vivo Expansion of Human Mesenchymal Stem Cells. <i>Journal of Cellular Physiology</i> , 2017, 232, 566-575.	4.1	27
26	H ₂ O ₂ Inhibits ABA-Signaling Protein Phosphatase HAB1. <i>PLoS ONE</i> , 2014, 9, e113643.	2.5	25
27	A motif rich in charged residues determines product specificity in isomaltulose synthase. <i>FEBS Letters</i> , 2003, 534, 151-155.	2.8	23
28	Structure of a Diguanylate Cyclase from <i>Thermotoga maritima</i> : Insights into Activation, Feedback Inhibition and Thermostability. <i>PLoS ONE</i> , 2014, 9, e110912.	2.5	22
29	Identification and molecular characterization of human antibody fragments specific for dengue NS5 protein. <i>Virus Research</i> , 2014, 179, 225-230.	2.2	21
30	Structural comparison of oxidized and reduced FKBP13 from <i>Arabidopsis thaliana</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 65, 789-795.	2.6	20
31	A feedforward relationship between active Rac1 and phosphorylated Bcl-2 is critical for sustaining Bcl-2 phosphorylation and promoting cancer progression. <i>Cancer Letters</i> , 2019, 457, 151-167.	7.2	20
32	Lack of TNF expression protects anaplastic lymphoma kinase-positive T-cell lymphoma (ALK+ TCL) cells from apoptosis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 15843-15848.	7.1	19
33	Discovery of <i>Mycobacterium tuberculosis</i> α -1,4-Glucan Branching Enzyme (GlgB) Inhibitors by Structure- and Ligand-based Virtual Screening. <i>Journal of Biological Chemistry</i> , 2015, 290, 76-89.	3.4	18
34	Investigating the Molecular Basis of Siah1 and Siah2 E3 Ubiquitin Ligase Substrate Specificity. <i>PLoS ONE</i> , 2014, 9, e106547.	2.5	17
35	A Heparan Sulfate Device for the Regeneration of Osteochondral Defects. <i>Tissue Engineering - Part A</i> , 2019, 25, 352-363.	3.1	15
36	Chemoinformatic Identification of Novel Inhibitors against <i>Mycobacterium tuberculosis</i> L-aspartate α -decarboxylase. <i>PLoS ONE</i> , 2012, 7, e33521.	2.5	15

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37	Structure and function comparison of Micropechis ikaheka snake venom phospholipase A2 isoenzymes. FEBS Journal, 2005, 272, 1211-1220.	4.7	14
38	Interaction of Mycobacterium tuberculosis RshA and SigH Is Mediated by Salt Bridges. PLoS ONE, 2012, 7, e43676.	2.5	14
39	Avathrin: a novel thrombin inhibitor derived from a multicopy precursor in the salivary glands of the ixodid tick, <i>Amblyomma variegatum</i> . FASEB Journal, 2017, 31, 2981-2995.	0.5	14
40	Structural and pharmacological comparison of daboiatoxin from <i>Daboia russelli siamensis</i> with viperotoxin F and vipoxin from other vipers. Acta Crystallographica Section D: Biological Crystallography, 2007, 63, 722-729.	2.5	13
41	Yersinia effector protein (YopO)-mediated phosphorylation of host gelsolin causes calcium-independent activation leading to disruption of actin dynamics. Journal of Biological Chemistry, 2017, 292, 8092-8100.	3.4	13
42	Hibiscus Chlorotic Ringspot Virus Coat Protein Is Essential for Cell-to-Cell and Long-Distance Movement but Not for Viral RNA Replication. PLoS ONE, 2014, 9, e113347.	2.5	11
43	Validation of Drug-Like Inhibitors against Mycobacterium Tuberculosis L-Aspartate β -Decarboxylase Using Nuclear Magnetic Resonance (^1H NMR). PLoS ONE, 2012, 7, e45947.	2.5	10
44	Mechanisms of Yersinia YopO kinase substrate specificity. Scientific Reports, 2017, 7, 39998.	3.3	10
45	Proteobacterial Origin of Protein Arginine Methylation and Regulation of Complex I Assembly by MidA. Cell Reports, 2018, 24, 1996-2004.	6.4	10
46	Crystallization of an α -amylase, AmyA, from the thermophilic halophile <i>Halothermothrix orenii</i> . Acta Crystallographica Section D: Biological Crystallography, 2002, 58, 2125-2126.	2.5	9
47	Crystallization of a novel α -amylase, AmyB, from the thermophilic halophile <i>Halothermothrix orenii</i> . Acta Crystallographica Section D: Biological Crystallography, 2003, 59, 2257-2258.	2.5	8
48	Structure of Hibiscus Latent Singapore Virus by Fiber Diffraction: A Nonconserved His122 Contributes to Coat Protein Stability. Journal of Molecular Biology, 2011, 406, 516-526.	4.2	8
49	Crystal structure of mouse RhoA:GTP γ S complex in a centered lattice. Journal of Structural and Functional Genomics, 2012, 13, 241-245.	1.2	7
50	Functional characterization of selective exosite-binding inhibitors of matrix metalloproteinase-13 (MMP-13) – experimental validation in human breast and colon cancer. Bioscience, Biotechnology and Biochemistry, 2016, 80, 2122-2131.	1.3	7
51	Modifying the Substrate Specificity of <i>Carcinoscorpius rotundicauda</i> Serine Protease Inhibitor Domain 1 to Target Thrombin. PLoS ONE, 2010, 5, e15258.	2.5	6
52	Expression, crystallization and preliminary X-ray analysis of isomaltulose synthase (Pall) from <i>Klebsiella</i> sp. LX3. Acta Crystallographica Section D: Biological Crystallography, 2003, 59, 150-151.	2.5	4
53	Tilapia and human CLIC2 structures are highly conserved. Biochemical and Biophysical Research Communications, 2018, 495, 1752-1757.	2.1	4
54	Structural and functional analyses of the PPlase domain of <i>Arabidopsis thaliana</i> CYP71 reveal its catalytic activity toward histone H3. FEBS Letters, 2021, 595, 145-154.	2.8	4

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55	α-Glucan Pathway as a Novel Mtb Drug Target: Structural Insights and Cues for Polypharmacological Targeting of GlgB and GlgE. <i>Current Medicinal Chemistry</i> , 2014, 21, 4074-4084.	2.4	3
56	Molecular modeling and interaction between Arabidopsis sulfite oxidase and the GW motif of Turnip crinkle virus coat protein. <i>Virology</i> , 2020, 551, 64-74.	2.4	2
57	Frequency distribution of the reduced unit cells of centred lattices from the Protein Data Bank. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 2012, 68, 295-297.	0.3	1