

Ravindra D Makde

List of Publications by Year in descending order

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42
papers

892
citations

759055

12
h-index

477173

29
g-index

44
all docs

44
docs citations

44
times ranked

1370
citing authors

#	ARTICLE	IF	CITATIONS
1	Structure of RCC1 chromatin factor bound to the nucleosome core particle. <i>Nature</i> , 2010, 467, 562-566.	13.7	328
2	A Membrane Protein, EzrA, Regulates Assembly Dynamics of FtsZ by Interacting with the C-Terminal Tail of FtsZ. <i>Biochemistry</i> , 2007, 46, 11013-11022.	1.2	85
3	SepF Increases the Assembly and Bundling of FtsZ Polymers and Stabilizes FtsZ Protofilaments by Binding along Its Length. <i>Journal of Biological Chemistry</i> , 2008, 283, 31116-31124.	1.6	79
4	Protein crystallography beamline (PX-BL21) at Indus-2 synchrotron. <i>Journal of Synchrotron Radiation</i> , 2016, 23, 629-634.	1.0	53
5	RCC1 Uses a Conformationally Diverse Loop Region to Interact with the Nucleosome: A Model for the RCC1-Nucleosome Complex. <i>Journal of Molecular Biology</i> , 2010, 398, 518-529.	2.0	44
6	Structure and Mutational Analysis of the PhoN Protein of <i>Salmonella typhimurium</i> Provide Insight into Mechanistic Details. <i>Biochemistry</i> , 2007, 46, 2079-2090.	1.2	28
7	Structure of the human aminopeptidase XPNPEP3 and comparison of its in vitro activity with Icp55 orthologs: Insights into diverse cellular processes. <i>Journal of Biological Chemistry</i> , 2017, 292, 10035-10047.	1.6	23
8	Curcumin analogs exhibit anti-cancer activity by selectively targeting G-quadruplex forming c-myc promoter sequence. <i>Biochimie</i> , 2021, 180, 205-221.	1.3	21
9	Co-expressed recombinant human Translin-Trax complex binds DNA. <i>FEBS Letters</i> , 2005, 579, 3141-3146.	1.3	18
10	Carboxypeptidase in prolyl oligopeptidase family: Unique enzyme activation and substrate-screening mechanisms. <i>Journal of Biological Chemistry</i> , 2019, 294, 89-100.	1.6	16
11	Protein engineering of class-A non-specific acid phosphatase (PhoN) of <i>Salmonella typhimurium</i> : Modulation of the pH-activity profile. <i>New Biotechnology</i> , 2006, 23, 247-251.	2.7	14
12	Mixed-Stack Charge Transfer Crystals of Pillar[5]quinone and Tetrathiafulvalene Exhibiting Ferroelectric Features. <i>Chemistry - A European Journal</i> , 2017, 23, 12630-12635.	1.7	14
13	Characterization of the cry1Ac17 Gene from an Indigenous Strain of <i>Bacillus thuringiensis</i> subsp. <i>kenyae</i> . <i>Current Microbiology</i> , 2008, 57, 570-574.	1.0	13
14	Crystal structures of <i>Drosophila</i> mutant translin and characterization of translin variants reveal the structural plasticity of translin proteins. <i>FEBS Journal</i> , 2008, 275, 4235-4249.	2.2	12
15	Crystallization and preliminary X-ray diffraction analysis of Xaa-Pro dipeptidase from <i>Xanthomonas campestris</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 1268-1271.	0.4	10
16	Crystal structure and biochemical investigations reveal novel mode of substrate selectivity and illuminate substrate inhibition and allostericity in a subfamily of Xaa-Pro dipeptidases. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2017, 1865, 153-164.	1.1	10
17	Expression, purification and characterization of the Cry2Aa14 toxin from <i>Bacillus thuringiensis</i> subsp. <i>kenyae</i> . <i>Toxicon</i> , 2009, 54, 519-524.	0.8	9
18	Strategies for crystallizing a chromatin protein in complex with the nucleosome core particle. <i>Analytical Biochemistry</i> , 2013, 442, 138-145.	1.1	8

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19	Crystal structure and dynamics of Spt16N-domain of FACT complex from <i>Cicer arietinum</i> . <i>International Journal of Biological Macromolecules</i> , 2016, 88, 36-43.	3.6	8
20	Active site gate of M32 carboxypeptidases illuminated by crystal structure and molecular dynamics simulations. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2017, 1865, 1406-1415.	1.1	8
21	Structures and activities of widely conserved small prokaryotic aminopeptidases clarify classification of M24B peptidases. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019, 87, 212-225.	1.5	8
22	Two-domain aminopeptidase of M1 family: Structural features for substrate binding and gating in absence of C-terminal domain. <i>Journal of Structural Biology</i> , 2019, 208, 51-60.	1.3	8
23	Structure of Asp-bound peptidase E from <i>Salmonella enterica</i> : Active site at dimer interface illuminates Asp recognition. <i>FEBS Letters</i> , 2018, 592, 3346-3354.	1.3	7
24	An overview of the fatty acid biosynthesis in the protozoan parasite <i>Leishmania</i> and its relevance as a drug target against leishmaniasis. <i>Molecular and Biochemical Parasitology</i> , 2021, 246, 111416.	0.5	7
25	A conformational switch from a closed apo- to an open holo-form equips the acyl carrier protein for acyl chain accommodation. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2019, 1867, 163-174.	1.1	6
26	The members of M20D peptidase subfamily from <i>Burkholderia cepacia</i> , <i>Deinococcus radiodurans</i> and <i>Staphylococcus aureus</i> (HmrA) are carboxydipeptidases, primarily specific for Met-X dipeptides. <i>Archives of Biochemistry and Biophysics</i> , 2015, 587, 18-30.	1.4	5
27	Catalytic triad heterogeneity in S51 peptidase family: Structural basis for functional variability. <i>Proteins: Structure, Function and Bioinformatics</i> , 2019, 87, 679-692.	1.5	5
28	Crystal structures of pyrrolidone-carboxylate peptidase I from <i>Deinococcus radiodurans</i> reveal the mechanism of L-pyroglutamate recognition. <i>Acta Crystallographica Section D: Structural Biology</i> , 2019, 75, 308-316.	1.1	5
29	Biophysical characterization of the homodimers of HomA and HomB, outer membrane proteins of <i>Helicobacter pylori</i> . <i>Scientific Reports</i> , 2021, 11, 24471.	1.6	5
30	Assembly of <i>Bacillus subtilis</i> FtsA: Effects of pH, ionic strength and nucleotides on FtsA assembly. <i>International Journal of Biological Macromolecules</i> , 2013, 52, 170-176.	3.6	4
31	Structural and mutational analyses reveal the functional role of active-site Lys-154 and Asp-173 of <i>Salmonella typhimurium</i> AphA protein. <i>Archives of Biochemistry and Biophysics</i> , 2007, 464, 70-79.	1.4	3
32	Expression, purification, crystallization and preliminary X-ray diffraction analysis of acylpeptide hydrolase from <i>Deinococcus radiodurans</i> . <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 1292-1295.	0.4	3
33	Crystal structure of a novel prolidase from <i>Deinococcus radiodurans</i> identifies new subfamily of bacterial prolidases. <i>Proteins: Structure, Function and Bioinformatics</i> , 2017, 85, 2239-2251.	1.5	3
34	Crystal structures and biochemical analyses of intermediate cleavage peptidase: role of dynamics in enzymatic function. <i>FEBS Letters</i> , 2019, 593, 443-454.	1.3	3
35	Machine learning classifiers aid virtual screening for efficient design of mini-protein therapeutics. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2021, 38, 127852.	1.0	3
36	Autoproteolysis of Procerain and Procerain B mediated by structural changes. <i>Phytochemistry</i> , 2022, 196, 113086.	1.4	3

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37	Isolation and characterization of a recombinant class C acid phosphatase from <i>Sphingobium</i> sp. RSMS strain. <i>Biotechnology Reports</i> (Amsterdam, Netherlands), 2022, 33, e00709.	2.1	3
38	Evolutionary conservation of protein dynamics: insights from all-atom molecular dynamics simulations of α -peptidase domain of Spt16. <i>Journal of Biomolecular Structure and Dynamics</i> , 2023, 41, 1445-1457.	2.0	3
39	Crystallization and preliminary X-ray crystallographic analysis of an artificial molten-globular-like triosephosphate isomerase protein of mixed phylogenetic origin. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 1521-1525.	0.4	2
40	Structural basis for the unusual substrate specificity of unique two-domain M1 metallopeptidase. <i>International Journal of Biological Macromolecules</i> , 2020, 147, 304-313.	3.6	2
41	Crystal structure of aspartyl dipeptidase from <i>Xenopus laevis</i> revealed ligand binding induced loop ordering and catalytic triad assembly. <i>Proteins: Structure, Function and Bioinformatics</i> , 2022, 90, 299-308.	1.5	0
42	Crystal structure of XCC3289 from <i>Xanthomonas campestris</i> : homology with the N-terminal substrate-binding domain of Lon peptidase. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2020, 76, 488-494.	0.4	0