

Kunchur Guruprasad

List of Publications by Year in descending order

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Version: 2024-02-01

26
papers

697
citations

759233

12
h-index

610901

24
g-index

26
all docs

26
docs citations

26
times ranked

864
citing authors

#	ARTICLE	IF	CITATIONS
1	Versatile roles of plant NADPH oxidases and emerging concepts. <i>Biotechnology Advances</i> , 2014, 32, 551-563.	11.7	103
2	Snail and spider toxins share a similar tertiary structure and α -cystine motif TM . <i>Nature Structural and Molecular Biology</i> , 1994, 1, 850-852.	8.2	94
3	Exploration of subsite binding specificity of human cathepsin D through kinetics and rule-based molecular modeling. <i>Protein Science</i> , 1993, 2, 264-276.	7.6	91
4	Comparative modelling of barley-grain aspartic proteinase: A structural rationale for observed hydrolytic specificity. <i>FEBS Letters</i> , 1994, 352, 131-136.	2.8	80
5	Comparative modelling and analysis of amino acid substitutions suggests that the family of pregnancy-associated glycoproteins includes both active and inactive aspartic proteinases. <i>Protein Engineering, Design and Selection</i> , 1996, 9, 849-856.	2.1	72
6	Exploring the binding preferences/specificity in the active site of human cathepsin E. <i>Proteins: Structure, Function and Bioinformatics</i> , 1995, 22, 168-181.	2.6	32
7	Structural complexity and functional diversity of plant NADPH oxidases. <i>Amino Acids</i> , 2018, 50, 79-94.	2.7	31
8	Serotype 1 and 8 Pneumococci Evade Sensing by Inflammasomes in Human Lung Tissue. <i>PLoS ONE</i> , 2015, 10, e0137108.	2.5	31
9	Cleavage Efficiency of the Novel Aspartic Protease Yapsin 1 (Yap3p) Enhanced for Substrates with Arginine Residues Flanking the P1 Site: A Correlation with Electronegative Active-Site Pockets Predicted by Molecular Modeling TM . <i>Biochemistry</i> , 1998, 37, 2768-2777.	2.5	23
10	Structure and Possible Function of Aspartic Proteinases in Barley and other Plants. <i>Advances in Experimental Medicine and Biology</i> , 1995, 362, 241-254.	1.6	23
11	Three-dimensional models corresponding to the C-terminal domain of human α - and β -crystallins based on the crystal structure of the small heat-shock protein HSP16.9 from wheat. <i>International Journal of Biological Macromolecules</i> , 2003, 33, 107-112.	7.5	20
12	The Aspartic Proteinases. <i>Advances in Experimental Medicine and Biology</i> , 1998, , 1-13.	1.6	17
13	Structural plasticity associated with the β -propeller architecture. <i>International Journal of Biological Macromolecules</i> , 2004, 34, 55-61.	7.5	14
14	Analysis of disulphide bond connectivity patterns in protein tertiary structure. <i>International Journal of Biological Macromolecules</i> , 2006, 38, 174-179.	7.5	11
15	Comparative analyses of the proteins from <i>Mycobacterium tuberculosis</i> and human genomes: Identification of potential tuberculosis drug targets. <i>Gene</i> , 2016, 579, 69-74.	2.2	11
16	Certain heptapeptide and large sequences representing an entire helix, strand or coil conformation in proteins are associated as chameleon sequences. <i>International Journal of Biological Macromolecules</i> , 2011, 49, 218-222.	7.5	9
17	Can Natural Proteins Designed with α -Inverted TM Peptide Sequences Adopt Native-Like Protein Folds?. <i>PLoS ONE</i> , 2014, 9, e107647.	2.5	8
18	Aspartic proteinases: The structures and functions of a versatile superfamily of enzymes. <i>Journal of Computer - Aided Molecular Design</i> , 1995, 2, 329-341.	1.0	6

#	ARTICLE	IF	CITATIONS
19	Three-dimensional models of Mycobacterium tuberculosis proteins Rv1555, Rv1554 and their docking analyses with sildenafil, tadalafil, vardenafil drugs, suggest interference with quinol binding likely to affect protein's function. BMC Structural Biology, 2018, 18, 5.	2.3	6
20	PSSARD: Protein sequence-structure analysis relational database. International Journal of Biological Macromolecules, 2005, 36, 259-262.	7.5	5
21	PSSARD (2.0): A database server for making flexible queries relating amino acid sequences to main-chain secondary structure conformations for proteins of known three-dimensional structure and certain useful applications. International Journal of Biological Macromolecules, 2007, 41, 109-113.	7.5	3
22	Analyses of the Sequence and Structural Properties Corresponding to Pentapeptide and Large Palindromes in Proteins. PLoS ONE, 2015, 10, e0139568.	2.5	3
23	Analysis of the Conformations Corresponding to Hexapeptide and Large Sequences Characterized by Continuous Single Amino Acid Repeats in Proteins. Protein and Peptide Letters, 2010, 17, 1459-1465.	0.9	3
24	The automatic detection of known β^2 -propeller structural motifs from protein tertiary structure. International Journal of Biological Macromolecules, 2005, 36, 176-183.	7.5	1
25	Juxtaposed Half-Cystines as Disulphide Bridged Partners in Protein Tertiary Structure. Protein and Peptide Letters, 2006, 13, 577-579.	0.9	0
26	Conformational Analysis Corresponding to Intra-Chain Disulfide Bridged Peptides in Proteins of Known Three-Dimensional Structure. Protein and Peptide Letters, 2008, 15, 160-187.	0.9	0