

# 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	Structural complexity and functional diversity of plant NADPH oxidases. <i>Amino Acids</i> , 2018, 50, 79-94.	2.7	31
2	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. <i>BMC Structural Biology</i> , 2018, 18, 5.	2.3	6
3	Comparative analyses of the proteins from Mycobacterium tuberculosis and human genomes: Identification of potential tuberculosis drug targets. <i>Gene</i> , 2016, 579, 69-74.	2.2	11
4	Serotype 1 and 8 Pneumococci Evade Sensing by Inflammasomes in Human Lung Tissue. <i>PLoS ONE</i> , 2015, 10, e0137108.	2.5	31
5	Analyses of the Sequence and Structural Properties Corresponding to Pentapeptide and Large Palindromes in Proteins. <i>PLoS ONE</i> , 2015, 10, e0139568.	2.5	3
6	Versatile roles of plant NADPH oxidases and emerging concepts. <i>Biotechnology Advances</i> , 2014, 32, 551-563.	11.7	103
7	Can Natural Proteins Designed with "Inverted" Peptide Sequences Adopt Native-Like Protein Folds?. <i>PLoS ONE</i> , 2014, 9, e107647.	2.5	8
8	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
9	Analysis of the Conformations Corresponding to Hexapeptide and Large Sequences Characterized by Continuous Single Amino Acid Repeats in Proteins. <i>Protein and Peptide Letters</i> , 2010, 17, 1459-1465.	0.9	3
10	Conformational Analysis Corresponding to Intra-Chain Disulfide Bridged Peptides in Proteins of Known Three-Dimensional Structure. <i>Protein and Peptide Letters</i> , 2008, 15, 160-187.	0.9	0
11	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. <i>International Journal of Biological Macromolecules</i> , 2007, 41, 109-113.	7.5	3
12	Analysis of disulphide bond connectivity patterns in protein tertiary structure. <i>International Journal of Biological Macromolecules</i> , 2006, 38, 174-179.	7.5	11
13	Juxtaposed Half-Cystines as Disulphide Bridged Partners in Protein Tertiary Structure. <i>Protein and Peptide Letters</i> , 2006, 13, 577-579.	0.9	0
14	The automatic detection of known $\hat{\Gamma}^2$ -propeller structural motifs from protein tertiary structure. <i>International Journal of Biological Macromolecules</i> , 2005, 36, 176-183.	7.5	1
15	PSSARD: Protein sequence-structure analysis relational database. <i>International Journal of Biological Macromolecules</i> , 2005, 36, 259-262.	7.5	5
16	Structural plasticity associated with the $\hat{\Gamma}^2$ -propeller architecture. <i>International Journal of Biological Macromolecules</i> , 2004, 34, 55-61.	7.5	14
17	Three-dimensional models corresponding to the C-terminal domain of human $\hat{\Gamma}^2$ A- and $\hat{\Gamma}^2$ B-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
18	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. <i>Biochemistry</i> , 1998, 37, 2768-2777.	2.5	23

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19	The Aspartic Proteinases. <i>Advances in Experimental Medicine and Biology</i> , 1998, , 1-13.	1.6	17
20	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
21	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
22	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
23	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
24	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
25	Snail and spider toxins share a similar tertiary structure and a cystine motif™. <i>Nature Structural and Molecular Biology</i> , 1994, 1, 850-852.	8.2	94
26	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