## Narayanan Manoj

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Protein tyrosine phosphatase-PEST mediates hypoxia-induced endothelial autophagy and angiogenesis via AMPK activation. Journal of Cell Science, 2021, 134, .	2.0	10
2	A conserved π-helix plays a key role in thermoadaptation of catalysis in the glycoside hydrolase family 4. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2021, 1869, 140523.	2.3	3
3	Evolutionary history of histamine receptors: Early vertebrate origin and expansion of the H3-H4 subtypes. Molecular Phylogenetics and Evolution, 2021, 154, 106989.	2.7	6
4	Structural basis of catalysis and substrate recognition by the NAD(H)-dependent α-d-glucuronidase from the glycoside hydrolase family 4. Biochemical Journal, 2021, 478, 943-959.	3.7	2
5	Crystallographic Snapshots of the Dunathan and Quinonoid Intermediates provide Insights into the Reaction Mechanism of Group II Decarboxylases. Journal of Molecular Biology, 2020, 432, 166692.	4.2	2
6	Structure of an α-glucuronidase in complex with Co2+ and citrate provides insights into the mechanism and substrate recognition in the family 4 glycosyl hydrolases. Biochemical and Biophysical Research Communications, 2019, 518, 197-203.	2.1	4
7	Structural insights into the mechanism of internal aldimine formation and catalytic loop dynamics in an archaeal Group II decarboxylase. Journal of Structural Biology, 2019, 208, 137-151.	2.8	5
8	Amarogentin, a secoiridoid glycoside, activates AMP- activated protein kinase (AMPK) to exert beneficial vasculo-metabolic effects. Biochimica Et Biophysica Acta - General Subjects, 2019, 1863, 1270-1282.	2.4	18
9	Molecular evolution of proteins mediating mitochondrial fission–fusion dynamics. FEBS Letters, 2019, 593, 703-718.	2.8	15
10	Crystal structure of yeast xylose reductase in complex with a novel <scp>NADP</scp> â€ <scp>DTT</scp> adduct provides insights into substrate recognition and catalysis. FEBS Journal, 2018, 285, 4445-4464.	4.7	9
11	Structural role of a conserved active site <i>cis</i> proline in the <scp><i>T</i></scp> <i>hermotoga maritima</i> acetyl esterase from the carbohydrate esterase family 7. Proteins: Structure, Function and Bioinformatics, 2017, 85, 694-708.	2.6	9
12	A temperature-responsive gene in sorghum encodes a glycine-rich protein that interacts with calmodulin. Biochimie, 2017, 137, 115-123.	2.6	7
13	Role of an N-terminal extension in stability and catalytic activity of a hyperthermostable α/β hydrolase fold esterase. Protein Engineering, Design and Selection, 2017, 30, 559-570.	2.1	13
14	An extended loop in CE7 carbohydrate esterase family is dispensable for oligomerization but required for activity and thermostability. Journal of Structural Biology, 2016, 194, 434-445.	2.8	12
15	Phenotypic Variations in the 22q11 Deletion Syndrome — Study in a South Indian Population. Indian Journal of Pediatrics, 2016, 83, 746-747.	0.8	Ο
16	Crystal structure of Thermotoga maritima acetyl esterase complex with a substrate analog: Insights into the distinctive substrate specificity in the CE7 carbohydrate esterase family. Biochemical and Biophysical Research Communications, 2016, 476, 63-68.	2.1	7
17	Phosphatidylserine and Phosphatidylethanolamine Bind to Protein Z Cooperatively and with Equal Affinity. PLoS ONE, 2016, 11, e0161896.	2.5	10
18	The GPCR repertoire in the demosponge Amphimedon queenslandica: insights into the GPCR system at the early divergence of animals. BMC Evolutionary Biology, 2014, 14, 270.	3.2	42

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19	Evolutionary history of the neuropeptide S receptor/neuropeptide S system. General and Comparative Endocrinology, 2014, 209, 11-20.	1.8	11
20	Molecular Evolution of the Neuropeptide S Receptor. PLoS ONE, 2012, 7, e34046.	2.5	20
21	Molecular evolution of the EGF–CFC protein family. Gene, 2011, 482, 43-50.	2.2	12
22	Molecular evolution of theN-acetylglucosamine-6-phosphate deacetylase gene. , 2010, , .		1
23	The Repertoire of Heterotrimeric G Proteins and RGS Proteins in Ciona intestinalis. PLoS ONE, 2009, 4, e7349.	2.5	3
24	Biochemical characterization of Alr1529, a novel SCNH hydrolase variant from Anabaena sp. PCC 7120. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2009, 1794, 324-334.	2.3	9
25	The repertoire of G protein-coupled receptors in the sea squirt Ciona intestinalis. BMC Evolutionary Biology, 2008, 8, 129.	3.2	95
26	Phospholipid scramblases: An overview. Archives of Biochemistry and Biophysics, 2007, 462, 103-114.	3.0	203
27	Structural and Biochemical Properties of Pectinases. , 2007, , 99-115.		24
28	Structure of Human Phosphopantothenoylcysteine Synthetase at 2.3 Ã Resolution. Structure, 2003, 11, 927-936.	3.3	30
29	Unusual space-group pseudosymmetry in crystals of human phosphopantothenoylcysteine decarboxylase. Acta Crystallographica Section D: Biological Crystallography, 2003, 59, 1762-1766.	2.5	15
30	X-ray studies on crystalline complexes involving amino acids and peptides. XXXVII. Novel aggregation patterns and effect of chirality in the complexes of DL- and L-lysine with glutaric acid. Acta Crystallographica Section B: Structural Science, 2001, 57, 366-371.	1.8	15
31	Crystallization and preliminary X-ray studies of snake gourd lectin: homology with type II ribosome-inactivating proteins. Acta Crystallographica Section D: Biological Crystallography, 2001, 57, 912-914.	2.5	7
32	X-ray studies on crystalline complexes involving amino acids and peptides. XXXVI. Crystal structures of hydrated glycyl-l -histidine andl -histidyl-l -alanine complexes with oxalic acid. Chemical Biology and Drug Design, 2000, 56, 210-217.	1.1	5
33	Carbohydrate specificity and salt-bridge mediated conformational change in acidic winged bean agglutinin 1 1Edited by A. Klug. Journal of Molecular Biology, 2000, 302, 1129-1137.	4.2	38
34	Crystallization and preliminary crystallographic analysis of winged bean acidic lectin. Acta Crystallographica Section D: Biological Crystallography, 1999, 55, 564-565.	2.5	2
35	Structure of basic winged-bean lectin and a comparison with its saccharide-bound form. Acta Crystallographica Section D: Biological Crystallography, 1999, 55, 794-800.	2.5	7