

Priyabrata R Panigrahi

List of Publications by Year in descending order

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Version: 2024-02-01

14
papers

336
citations

1040056

9
h-index

1058476

14
g-index

14
all docs

14
docs citations

14
times ranked

681
citing authors

#	ARTICLE	IF	CITATIONS
1	Structure and function of a highly active Bile Salt Hydrolase (BSH) from <i>Enterococcus faecalis</i> and post-translational processing of BSH enzymes. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2018, 1866, 507-518.	2.3	45
2	Elucidation of molecular mechanism of stability of the heme-regulated eIF2 α kinase upon binding of its ligand, hemin in its catalytic kinase domain. <i>Journal of Biomolecular Structure and Dynamics</i> , 2018, 36, 2845-2861.	3.5	4
3	FusionHub: A unified web platform for annotation and visualization of gene fusion events in human cancer. <i>PLoS ONE</i> , 2018, 13, e0196588.	2.5	41
4	<i>Fusarium oxysporum</i> mediates systems metabolic reprogramming of chickpea roots as revealed by a combination of proteomics and metabolomics. <i>Plant Biotechnology Journal</i> , 2016, 14, 1589-1603.	8.3	63
5	Structural analysis of a penicillin V acylase from <i>Pectobacterium atrosepticum</i> confirms the importance of two Trp residues for activity and specificity. <i>Journal of Structural Biology</i> , 2016, 193, 85-94.	2.8	9
6	Structure mediation in substrate binding and post-translational processing of penicillin acylases: Information from mutant structures of <i>Kluyvera citrophila</i> penicillin G acylase. <i>Protein Science</i> , 2015, 24, 1660-1670.	7.6	10
7	Metabolic profiling of chickpea- <i>Fusarium</i> interaction identifies differential modulation of disease resistance pathways. <i>Phytochemistry</i> , 2015, 116, 120-129.	2.9	34
8	Sequence and structure-based comparative analysis to assess, identify and improve the thermostability of penicillin G acylases. <i>Journal of Industrial Microbiology and Biotechnology</i> , 2015, 42, 1493-1506.	3.0	5
9	Engineering Proteins for Thermostability with iRDP Web Server. <i>PLoS ONE</i> , 2015, 10, e0139486.	2.5	20
10	In-Silico Analysis of Binding Site Features and Substrate Selectivity in Plant Flavonoid-3-O Glycosyltransferases (F3GT) through Molecular Modeling, Docking and Dynamics Simulation Studies. <i>PLoS ONE</i> , 2014, 9, e92636.	2.5	13
11	A new role for penicillin acylases: Degradation of acyl homoserine lactone quorum sensing signals by <i>Kluyvera citrophila</i> penicillin G acylase. <i>Enzyme and Microbial Technology</i> , 2014, 56, 1-7.	3.2	56
12	An improved method for specificity annotation shows a distinct evolutionary divergence among the microbial enzymes of the cholyglycine hydrolase family. <i>Microbiology (United Kingdom)</i> , 2014, 160, 1162-1174.	1.8	22
13	Structural modelling of substrate binding and inhibition in penicillin V acylase from <i>Pectobacterium atrosepticum</i> . <i>Biochemical and Biophysical Research Communications</i> , 2013, 437, 538-543.	2.1	12
14	Dimensionality reduction in computational demarcation of protein tertiary structures. <i>Journal of Molecular Modeling</i> , 2012, 18, 2741-2754.	1.8	2