

Oruganty Krishnadev

List of Publications by Year in descending order

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Version: 2024-02-01

19
papers

779
citations

687220

13
h-index

794469

19
g-index

20
all docs

20
docs citations

20
times ranked

1157
citing authors

#	ARTICLE	IF	CITATIONS
1	Identification and classification of small molecule kinases: insights into substrate recognition and specificity. <i>BMC Evolutionary Biology</i> , 2016, 16, 7.	3.2	16
2	Hydrophobic Core Variations Provide a Structural Framework for Tyrosine Kinase Evolution and Functional Specialization. <i>PLoS Genetics</i> , 2016, 12, e1005885.	1.5	35
3	Inhibiting EGFR Dimerization Using Triazolyl-Bridged Dimerization Arm Mimics. <i>PLoS ONE</i> , 2015, 10, e0118796.	1.1	31
4	The Tribbles 2 (TRB2) pseudokinase binds to ATP and autophosphorylates in a metal-independent manner. <i>Biochemical Journal</i> , 2015, 467, 47-62.	1.7	70
5	Mitochondrial ADCK3 Employs an Atypical Protein Kinase-like Fold to Enable Coenzyme Q Biosynthesis. <i>Molecular Cell</i> , 2015, 57, 83-94.	4.5	104
6	Co-Conserved MAPK Features Couple D-Domain Docking Groove to Distal Allosteric Sites via the C-Terminal Flanking Tail. <i>PLoS ONE</i> , 2015, 10, e0119636.	1.1	19
7	X-ray structure of the human mitochondrial kinase ADCK3 elucidates the kinase fold of the ancient UbiB family (LB173). <i>FASEB Journal</i> , 2014, 28, LB173.	0.2	0
8	Identification of a hidden strain switch provides clues to an ancient structural mechanism in protein kinases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 924-929.	3.3	41
9	Evolutionary variation and adaptation in a conserved protein kinase allosteric network: Implications for inhibitor design. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2013, 1834, 1322-1329.	1.1	9
10	Deciphering the Structural Basis of Eukaryotic Protein Kinase Regulation. <i>PLoS Biology</i> , 2013, 11, e1001680.	2.6	172
11	Design principles underpinning the regulatory diversity of protein kinases. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2012, 367, 2529-2539.	1.8	33
12	Prediction of protein-protein interactions between human host and a pathogen and its application to three pathogenic bacteria. <i>International Journal of Biological Macromolecules</i> , 2011, 48, 613-619.	3.6	49
13	AlignHUSH: Alignment of HMMs using structure and hydrophobicity information. <i>BMC Bioinformatics</i> , 2011, 12, 275.	1.2	11
14	Prediction of protein-protein interactions between <i>Helicobacter pylori</i> and a human host. <i>Molecular BioSystems</i> , 2009, 5, 1630.	2.9	31
15	A data integration approach to predict host-pathogen protein-protein interactions: application to recognize protein interactions between human and a malarial parasite. <i>In Silico Biology</i> , 2008, 8, 235-50.	0.4	29
16	Strategies for the effective identification of remotely related sequences in multiple PSSM search approach. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 67, 789-794.	1.5	12
17	Interaction preferences across protein-protein interfaces of obligatory and non-obligatory components are different. <i>BMC Structural Biology</i> , 2005, 5, 15.	2.3	84
18	A graph spectral analysis of the structural similarity network of protein chains. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 61, 152-163.	1.5	21

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19	PRODOC: a resource for the comparison of tethered protein domain architectures with in-built information on remotely related domain families. <i>Nucleic Acids Research</i> , 2005, 33, W126-W129.	6.5	9