Jitendra Maharana

List of Publications by Year
in descending order

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39 papers	518 citations	623734 14 h-index	713466 21 g-index
40 all docs	40 docs citations	40 times ranked	572 citing authors

#	Article	IF	Citations
1	Structural insights into the MDP binding and CARD-CARD interaction in zebrafish (Danio rerio) NOD2: a molecular dynamics approach. Journal of Molecular Recognition, 2014, 27, 260-275.	2.1	38
2	Structural insights of rohu TLR3, its binding site analysis with fish reovirus dsRNA, poly I:C and zebrafish TRIF. International Journal of Biological Macromolecules, 2012, 51, 531-543.	7.5	35
3	Structural Models of Zebrafish (Danio rerio) NOD1 and NOD2 NACHT Domains Suggest Differential ATP Binding Orientations: Insights from Computational Modeling, Docking and Molecular Dynamics Simulations. PLoS ONE, 2015, 10, e0121415.	2.5	31
4	Deciphering the ATP-binding mechanism(s) in NLRP-NACHT 3D models using structural bioinformatics approaches. PLoS ONE, 2018, 13, e0209420.	2.5	28
5	Structure-Based Computational Study of Two Disease Resistance Gene Homologues (Hm1 and Hm2) in Maize (Zea mays L.) with Implications in Plant-Pathogen Interactions. PLoS ONE, 2014, 9, e97852.	2.5	28
6	A conformational analysis of mouse Nalp3 domain structures by molecular dynamics simulations, and binding site analysis. Molecular BioSystems, 2014, 10, 1104-1116.	2.9	27
7	Understanding the distinguishable structural and functional features in zebrafish TLR3 and TLR22, and their binding modes with fish dsRNA viruses: an exploratory structural model analysis. Amino Acids, 2015, 47, 381-400.	2.7	27
8	Structural and functional investigation of zebrafish (Danio rerio) NOD1 leucine rich repeat domain and its interaction with iE-DAP. Molecular BioSystems, 2014, 10, 2942-2953.	2.9	23
9	Structural and functional insights into CARDs of zebrafish (Danio rerio) NOD1 and NOD2, and their interaction with adaptor protein RIP2. Molecular BioSystems, 2015, 11, 2324-2336.	2.9	23
10	Identification of MDP (muramyl dipeptide)-binding key domains in NOD2 (nucleotide-binding and) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 1007-1023.	2.3	20
11	Deep insights into the mode of ATP-binding mechanism in Zebrafish cyclin-dependent protein kinase-like 1 (zCDKL1): A molecular dynamics approach. Journal of Molecular Graphics and Modelling, 2018, 81, 175-183.	2.4	19
12	NOD1CARD Might Be Using Multiple Interfaces for RIP2-Mediated CARD-CARD Interaction: Insights from Molecular Dynamics Simulation. PLoS ONE, 2017, 12, e0170232.	2.5	18
13	Structural and dynamic investigation of bovine folate receptor alpha (FOLR1), and role of ultra-high temperature processing on conformational and thermodynamic characteristics of FOLR1â€“folate complex. Colloids and Surfaces B: Biointerfaces, 2014, 121, 307-318.	5.0	17
14	Microwave-assisted Î²-cyclodextrin/chrysin inclusion complexation: An economical and green strategy for enhanced hemocompatibility and chemosensitivity in vitro. Journal of Molecular Liquids, 2020, 310, 113257.	4.9	17
15	Molecular dynamics simulation of human serum paraoxonase 1 in DPPC bilayer reveals a critical role of transmembrane helix H1 for HDL association. European Biophysics Journal, 2014, 43, 35-51.	2.2	12
16	POP1 might be recruiting its typeâ€Ia interface for NLRP3â€mediated PYDâ€PYD interaction: Insights from MD simulation. Journal of Molecular Recognition, 2017, 30, e2632.	2.1	12
17	Structural bioinformatics insights into ATP binding mechanism in zebrafish (Danio rerio) cyclinâ€dependent kinaseâ€like 5 (zCDKL5) protein. Journal of Cellular Biochemistry, 2019, 120, 9437-9447.	2.6	12
18	Molecular characterization, constitutive expression and GTP binding mechanism of Cirrhinus mrigala (Hamilton, 1822) Myxovirus resistance (Mx) protein. International Journal of Biological Macromolecules, 2019, 136, 1258-1272.	7.5	11

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19	Further Insights on Structural Modifications of Muramyl Dipeptides to Study the Human NOD2 Stimulating Activity. Chemistry - an Asian Journal, 2020, 15, 3836-3844.	3.3	11
20	Harnessing tissue-specific genome editing in plants through CRISPR/Cas system: current state and future prospects. Planta, 2022, 255, 28.	3.2	10
21	Elucidating the interfaces involved in CARD-CARD interactions mediated by NLRP1 and Caspase-1 using molecular dynamics simulation. Journal of Molecular Graphics and Modelling, 2018, 80, 7-14.	2.4	9
22	Exploration of the binding modes of buffalo PGRP1 receptor complexed with meso-diaminopimelic acid and lysine-type peptidoglycans by molecular dynamics simulation and free energy calculation. Chemico-Biological Interactions, 2014, 220, 255-268.	4.0	8
23	Molecular recognition of avirulence protein (avrxa5) by eukaryotic transcription factor xa5 of rice (Oryza sativa L.): Insights from molecular dynamics simulations. Journal of Molecular Graphics and Modelling, 2015, 57, 49-61.	2.4	8
24	Spectroscopic and computational insights into theophylline/Î²-cyclodextrin complexation: inclusion accomplished by diverse methods. Journal of Microencapsulation, 2018, 35, 667-679.	2.8	8
25	Mechanism Underlying Heat Stability of the Rice Endosperm Cytosolic ADP-Glucose Pyrophosphorylase. Frontiers in Plant Science, 2019, 10, 70.	3.6	8
26	Poly I:C stimulation in-vitro as a marker for an antiviral response in different cell types generated from Buffalo (Bubalus bubalis). Molecular Immunology, 2020, 121, 136-143.	2.2	8
27	Understanding the thermal response of rice eukaryotic transcription factor eIF4A1 towards dynamic temperature stress: insights from expression profiling and molecular dynamics simulation. Journal of Biomolecular Structure and Dynamics, 2021, 39, 2575-2584.	3.5	8
28	Molecular dynamics simulation of neuropeptide B and neuropeptide W in the dipalmitoylphosphatidylcholine membrane bilayer. Journal of Biomolecular Structure and Dynamics, 2014, 32, 1118-1131.	3.5	6
29	Functional Screening and Molecular Characterization of Halophilic and Halotolerant Bacteria by 16S rRNA Gene Sequence Analysis. Proceedings of the National Academy of Sciences India Section B - Biological Sciences, 2015, 85, 957-964.	1.0	6
30	Insight into Buffalo (Bubalus bubalis) RIG1 and MDA5 Receptors: A Comparative Study on dsRNA Recognition and In-Vitro Antiviral Response. PLoS ONE, 2014, 9, e89788.	2.5	6
31	Structural Analysis of Respirasomes in Electron Transfer Pathway of Acidithiobacillus ferrooxidans: A Computer-Aided Molecular Designing Study. , 2013, 2013, 1-14.		4
32	SlHyPRP1 and DEA1, the multiple stress responsive eight-cysteine motif family genes of tomato (Solanum lycopersicum L.) are expressed tissue specifically, localize and interact at cytoplasm and plasma membrane in vivo. Physiology and Molecular Biology of Plants, 2020, 26, 2553-2568.	3.1	4
33	Structural Elucidation of Inter-CARD Interfaces involved in NOD2 Tandem CARD Association and RIP2 Recognition. Journal of Physical Chemistry B, 2021, 125, 13349-13365.	2.6	4
34	Transcriptome-wide analysis of North-East Indian rice cultivars in response to Bipolaris oryzae infection revealed the importance of early response to the pathogen in suppressing the disease progression. Gene, 2022, 809, 146049.	2.2	3
35	Genetic Diversity of Asian Sea Bass, Lates calcarifer (Bloch) Populations in India Revealed by Randomly Amplified Polymorphic DNA. Proceedings of the National Academy of Sciences India Section B - Biological Sciences, 2014, 84, 1013-1019.	1.0	2
36	Computational insights into the binding mechanism of antagonists with neuropeptide B/W receptor 1. Molecular BioSystems, 2014, 10, 2236.	2.9	2

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37	Draft Genome Sequence of the Extremely Halophilic Bacterium Halomonas salina Strain CIFRI1, Isolated from the East Coast of India. Genome Announcements, 2015, 3, .	0.8	2
38	XSP10 and SlSAMT, Fusarium wilt disease responsive genes of tomato (Solanum lycopersicum L.) express tissue specifically and interact with each other at cytoplasm in vivo. Physiology and Molecular Biology of Plants, 2021, 27, 1559-1575.	3.1	2
39	Computational studies on receptorâ€“ligand interactions between novel buffalo (Bubalus bubalis) nucleotide-binding oligomerization domain-containing protein 2 (NOD2) variants and muramyl dipeptide (MDP). Journal of Molecular Graphics and Modelling, 2016, 65, 15-26.	2.4	1