

Jitendra Maharana

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

38

papers

381

citations

13

h-index

17

g-index

40

ext. papers

448

ext. citations

3.7

avg, IF

3.43

L-index

#	Paper	IF	Citations
38	Structural insights into the MDP binding and CARD-CARD interaction in zebrafish (<i>Danio rerio</i>) NOD2: a molecular dynamics approach. <i>Journal of Molecular Recognition</i> , 2014 , 27, 260-75	2.6	35
37	Structural insights of rohu TLR3, its binding site analysis with fish reovirus dsRNA, poly I:C and zebrafish TRIF. <i>International Journal of Biological Macromolecules</i> , 2012 , 51, 531-43	7.9	27
36	Structural models of zebrafish (<i>Danio rerio</i>) NOD1 and NOD2 NACHT domains suggest differential ATP binding orientations: insights from computational modeling, docking and molecular dynamics simulations. <i>PLoS ONE</i> , 2015 , 10, e0121415	3.7	25
35	A conformational analysis of mouse Nalp3 domain structures by molecular dynamics simulations, and binding site analysis. <i>Molecular BioSystems</i> , 2014 , 10, 1104-16		22
34	Structural and functional investigation of zebrafish (<i>Danio rerio</i>) NOD1 leucine rich repeat domain and its interaction with iE-DAP. <i>Molecular BioSystems</i> , 2014 , 10, 2942-53		22
33	Structural and functional insights into CARDs of zebrafish (<i>Danio rerio</i>) NOD1 and NOD2, and their interaction with adaptor protein RIP2. <i>Molecular BioSystems</i> , 2015 , 11, 2324-36		21
32	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. <i>Amino Acids</i> , 2015 , 47, 381-400	3.5	21
31	Structure-based computational study of two disease resistance gene homologues (Hm1 and Hm2) in maize (<i>Zea mays</i> L.) with implications in plant-pathogen interactions. <i>PLoS ONE</i> , 2014 , 9, e97852	3.7	21
30	Identification of MDP (muramyl dipeptide)-binding key domains in NOD2 (nucleotide-binding and oligomerization domain-2) receptor of <i>Labeo rohita</i> . <i>Fish Physiology and Biochemistry</i> , 2013 , 39, 1007-23	2.7	19
29	Deep insights into the mode of ATP-binding mechanism in Zebrafish cyclin-dependent protein kinase-like 1 (zCDKL1): A molecular dynamics approach. <i>Journal of Molecular Graphics and Modelling</i> , 2018 , 81, 175-183	2.8	16
28	Deciphering the ATP-binding mechanism(s) in NLRP-NACHT 3D models using structural bioinformatics approaches. <i>PLoS ONE</i> , 2018 , 13, e0209420	3.7	15
27	Structural and dynamic investigation of bovine folate receptor alpha (FOLR1), and role of ultra-high temperature processing on conformational and thermodynamic characteristics of FOLR1-folate complex. <i>Colloids and Surfaces B: Biointerfaces</i> , 2014 , 121, 307-18	6	14
26	NOD1CARD Might Be Using Multiple Interfaces for RIP2-Mediated CARD-CARD Interaction: Insights from Molecular Dynamics Simulation. <i>PLoS ONE</i> , 2017 , 12, e0170232	3.7	13
25	Molecular dynamics simulation of human serum paraoxonase 1 in DPPC bilayer reveals a critical role of transmembrane helix H1 for HDL association. <i>European Biophysics Journal</i> , 2014 , 43, 35-51	1.9	12
24	Structural bioinformatics insights into ATP binding mechanism in zebrafish (<i>Danio rerio</i>) cyclin-dependent kinase-like 5 (zCDKL5) protein. <i>Journal of Cellular Biochemistry</i> , 2019 , 120, 9437-9447	4.7	10
23	POP1 might be recruiting its type-Ia interface for NLRP3-mediated PYD-PYD interaction: Insights from MD simulation. <i>Journal of Molecular Recognition</i> , 2017 , 30, e2632	2.6	8
22	Molecular recognition of avirulence protein (<i>avrxa5</i>) by eukaryotic transcription factor <i>xa5</i> of rice (<i>Oryza sativa</i> L.): insights from molecular dynamics simulations. <i>Journal of Molecular Graphics and Modelling</i> , 2015 , 57, 49-61	2.8	8

21	Microwave-assisted β -cyclodextrin/chrysin inclusion complexation: An economical and green strategy for enhanced hemocompatibility and chemosensitivity in vitro. <i>Journal of Molecular Liquids</i> , 2020 , 310, 113257	6	7
20	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. <i>Chemico-Biological Interactions</i> , 2014 , 220, 255-68	5	7
19	Functional Screening and Molecular Characterization of Halophilic and Halotolerant Bacteria by 16S rRNA Gene Sequence Analysis. <i>Proceedings of the National Academy of Sciences India Section B - Biological Sciences</i> , 2015 , 85, 957-964	1.4	6
18	Elucidating the interfaces involved in CARD-CARD interactions mediated by NLRP1 and Caspase-1 using molecular dynamics simulation. <i>Journal of Molecular Graphics and Modelling</i> , 2018 , 80, 7-14	2.8	6
17	Further Insights on Structural Modifications of Muramyl Dipeptides to Study the Human NOD2 Stimulating Activity. <i>Chemistry - an Asian Journal</i> , 2020 , 15, 3836-3844	4.5	6
16	Mechanism Underlying Heat Stability of the Rice Endosperm Cytosolic ADP-Glucose Pyrophosphorylase. <i>Frontiers in Plant Science</i> , 2019 , 10, 70	6.2	5
15	Molecular characterization, constitutive expression and GTP binding mechanism of <i>Cirrhinus mrigala</i> (Hamilton, 1822) Myxovirus resistance (Mx) protein. <i>International Journal of Biological Macromolecules</i> , 2019 , 136, 1258-1272	7.9	5
14	Molecular dynamics simulation of neuropeptide B and neuropeptide W in the dipalmitoylphosphatidylcholine membrane bilayer. <i>Journal of Biomolecular Structure and Dynamics</i> , 2014 , 32, 1118-31	3.6	5
13	Spectroscopic and computational insights into theophylline/ β -cyclodextrin complexation: inclusion accomplished by diverse methods. <i>Journal of Microencapsulation</i> , 2018 , 35, 667-679	3.4	5
12	Structural Analysis of Respirasomes in Electron Transfer Pathway of <i>Acidithiobacillus ferrooxidans</i> : A Computer-Aided Molecular Designing Study 2013 , 2013, 1-14		4
11	Insight into buffalo (<i>Bubalus bubalis</i>) RIG1 and MDA5 receptors: a comparative study on dsRNA recognition and in-vitro antiviral response. <i>PLoS ONE</i> , 2014 , 9, e89788	3.7	4
10	Understanding the thermal response of rice eukaryotic transcription factor towards dynamic temperature stress: insights from expression profiling and molecular dynamics simulation. <i>Journal of Biomolecular Structure and Dynamics</i> , 2021 , 39, 2575-2584	3.6	3
9	Draft Genome Sequence of the Extremely Halophilic Bacterium <i>Halomonas salina</i> Strain CIFRI1, Isolated from the East Coast of India. <i>Genome Announcements</i> , 2015 , 3,		2
8	and , the multiple stress responsive eight-cysteine motif family genes of tomato (<i>L.</i>) are expressed tissue specifically, localize and interact at cytoplasm and plasma membrane in vivo. <i>Physiology and Molecular Biology of Plants</i> , 2020 , 26, 2553-2568	2.8	2
7	Poly I:C stimulation in-vitro as a marker for an antiviral response in different cell types generated from Buffalo (<i>Bubalus bubalis</i>). <i>Molecular Immunology</i> , 2020 , 121, 136-143	4.3	2
6	Computational insights into the binding mechanism of antagonists with neuropeptide B/W receptor 1. <i>Molecular BioSystems</i> , 2014 , 10, 2236-46		1
5	and , Fusarium wilt disease responsive genes of tomato (<i>L.</i>) express tissue specifically and interact with each other at cytoplasm in vivo. <i>Physiology and Molecular Biology of Plants</i> , 2021 , 27, 1559-1575	2.8	1
4	Harnessing tissue-specific genome editing in plants through CRISPR/Cas system: current state and future prospects.. <i>Planta</i> , 2021 , 255, 28	4.7	1

3	Computational studies on receptor-ligand interactions between novel buffalo (<i>Bubalus bubalis</i>) nucleotide-binding oligomerization domain-containing protein 2 (NOD2) variants and muramyl dipeptide (MDP). <i>Journal of Molecular Graphics and Modelling</i> , 2016 , 65, 15-26	2.8	o
2	Transcriptome-wide analysis of North-East Indian rice cultivars in response to <i>Bipolaris oryzae</i> infection revealed the importance of early response to the pathogen in suppressing the disease progression. <i>Gene</i> , 2022 , 809, 146049	3.8	o
1	Genetic Diversity of Asian Sea Bass, <i>Lates calcarifer</i> (Bloch) Populations in India Revealed by Randomly Amplified Polymorphic DNA. <i>Proceedings of the National Academy of Sciences India Section B - Biological Sciences</i> , 2014 , 84, 1013-1019	1.4	