

# Jitendra Maharana

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9397234/publications.pdf>

Version: 2024-02-01

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	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.	2.2	3
2	Harnessing tissue-specific genome editing in plants through CRISPR/Cas system: current state and future prospects. <i>Planta</i> , 2022, 255, 28.	3.2	10
3	Understanding the thermal response of rice eukaryotic transcription factor eIF4A1 towards dynamic temperature stress: insights from expression profiling and molecular dynamics simulation. <i>Journal of Biomolecular Structure and Dynamics</i> , 2021, 39, 2575-2584.	3.5	8
4	XSP10 and SISAMT, Fusarium wilt disease responsive genes of tomato ( <i>Solanum lycopersicum</i> L.) express tissue specifically and interact with each other at cytoplasm in vivo. <i>Physiology and Molecular Biology of Plants</i> , 2021, 27, 1559-1575.	3.1	2
5	Structural Elucidation of Inter-CARD Interfaces involved in NOD2 Tandem CARD Association and RIP2 Recognition. <i>Journal of Physical Chemistry B</i> , 2021, 125, 13349-13365.	2.6	4
6	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.	3.3	11
7	SlHyPRP1 and DEA1, the multiple stress responsive eight-cysteine motif family genes of tomato ( <i>Solanum lycopersicum</i> L.) 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.	3.1	4
8	Microwave-assisted $\beta$ -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.	4.9	17
9	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.	2.2	8
10	Mechanism Underlying Heat Stability of the Rice Endosperm Cytosolic ADP-Glucose Pyrophosphorylase. <i>Frontiers in Plant Science</i> , 2019, 10, 70.	3.6	8
11	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.	7.5	11
12	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.	2.6	12
13	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.	2.4	19
14	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.	2.4	9
15	Spectroscopic and computational insights into theophylline/ $\beta$ -cyclodextrin complexation: inclusion accomplished by diverse methods. <i>Journal of Microencapsulation</i> , 2018, 35, 667-679.	2.8	8
16	Deciphering the ATP-binding mechanism(s) in NLRP-NACHT 3D models using structural bioinformatics approaches. <i>PLoS ONE</i> , 2018, 13, e0209420.	2.5	28
17	POP1 might be recruiting its type-I interface for NLRP3-mediated PYD-PYD interaction: Insights from MD simulation. <i>Journal of Molecular Recognition</i> , 2017, 30, e2632.	2.1	12
18	NOD1CARD Might Be Using Multiple Interfaces for RIP2-Mediated CARD-CARD Interaction: Insights from Molecular Dynamics Simulation. <i>PLoS ONE</i> , 2017, 12, e0170232.	2.5	18

#	ARTICLE	IF	CITATIONS
19	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.	2.4	1
20	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.	2.4	8
21	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.	1.0	6
22	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, .	0.8	2
23	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, 2324-2336.	2.9	23
24	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.	2.7	27
25	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.	2.5	31
26	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.	1.0	2
27	Molecular dynamics simulation of neuropeptide B and neuropeptide W in the dipalmitoylphosphatidylcholine membrane bilayer. <i>Journal of Biomolecular Structure and Dynamics</i> , 2014, 32, 1118-1131.	3.5	6
28	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.	2.2	12
29	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, 260-275.	2.1	38
30	A conformational analysis of mouse Nalp3 domain structures by molecular dynamics simulations, and binding site analysis. <i>Molecular BioSystems</i> , 2014, 10, 1104-1116.	2.9	27
31	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, 307-318.	5.0	17
32	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, 2942-2953.	2.9	23
33	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, 255-268.	4.0	8
34	Computational insights into the binding mechanism of antagonists with neuropeptide B/W receptor 1. <i>Molecular BioSystems</i> , 2014, 10, 2236.	2.9	2
35	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.	2.5	6
36	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.	2.5	28

#	ARTICLE	IF	CITATIONS
37	Identification of MDP (muramyl dipeptide)-binding key domains in NOD2 (nucleotide-binding and) Tj ETQq1 1 0.784314 rgBT /Overlook 1007-1023.	2.3	20
38	Structural Analysis of Respirasomes in Electron Transfer Pathway of <i>Acidithiobacillus ferrooxidans</i> : A Computer-Aided Molecular Designing Study. , 2013, 2013, 1-14.		4
39	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