Mahesh Chandra Patra

List of Publications by Year
in descending order

31 papers	539 citations	623734 14 h-index	677142 22 g-index
31 all docs	31 docs citations	31 times ranked	846 citing authors

#	Article	IF	Citations
1	Toll-like receptor-induced cytokines as immunotherapeutic targets in cancers and autoimmune diseases. Seminars in Cancer Biology, 2020, 64, 61-82.	9.6	59
2	A Novel Small-Molecule Inhibitor of Endosomal TLRs Reduces Inflammation and Alleviates Autoimmune Disease Symptoms in Murine Models. Cells, 2020, 9, 1648.	4.1	8
3	A peptide derived from the core β²-sheet region of TIRAP decoys TLR4 and reduces inflammatory and autoimmune symptoms in murine models. EBioMedicine, 2020, 52, 102645.	6.1	13
4	A Computational Probe into the Structure and Dynamics of the Full-Length Toll-Like Receptor 3 in a Phospholipid Bilayer. International Journal of Molecular Sciences, 2020, 21, 2857.	4.1	8
5	A cell-penetrating peptide blocks Toll-like receptor-mediated downstream signaling and ameliorates autoimmune and inflammatory diseases in mice. Experimental and Molecular Medicine, 2019, 51, 1-19.	7.7	20
6	Insight into Phosphatidylinositol-Dependent Membrane Localization of the Innate Immune Adaptor Protein Toll/Interleukin 1 Receptor Domain-Containing Adaptor Protein. Frontiers in Immunology, 2018, 9, 75.	4.8	10
7	Computational Insight Into the Structural Organization of Full-Length Toll-Like Receptor 4 Dimer in a Model Phospholipid Bilayer. Frontiers in Immunology, 2018, 9, 489.	4.8	20
8	Structural insights into the Middle East respiratory syndrome coronavirus 4a protein and its dsRNA binding mechanism. Scientific Reports, 2017, 7, 11362.	3.3	23
9	Recent Progress in the Molecular Recognition and Therapeutic Importance of Interleukin-1 Receptor-Associated Kinase 4. Molecules, 2016, 21, 1529.	3.8	25
10	Recent progress in the development of Toll-like receptor (TLR) antagonists. Expert Opinion on Therapeutic Patents, 2016, 26, 719-730.	5.0	67
11	Comparison of Copy Number of HSF Genes in Two Buffalo Genomes. Animal Biotechnology, 2016, 27, 141-147.	1.5	1
12	Computational studies on receptor–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
13	Comparative Genomic Analysis of Buffalo (Bubalus bubalis) NOD1 and NOD2 Receptors and Their Functional Role in In-Vitro Cellular Immune Response. PLoS ONE, 2015, 10, e0119178.	2.5	6
14	Diversity, Antimicrobial Action and Structure-Activity Relationship of Buffalo Cathelicidins. PLoS ONE, 2015, 10, e0144741.	2.5	26
15	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
16	Noninvasive Method of DNA Isolation From Fecal Epithelial Tissue of Dairy Animals. Animal Biotechnology, 2015, 26, 211-216.	1.5	6
17	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
18	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

#	Article	IF	Citations
19	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
20	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
21	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
22	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
23	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
24	Computational insights into the binding mechanism of antagonists with neuropeptide B/W receptor 1. Molecular BioSystems, 2014, 10, 2236.	2.9	2
25	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
26	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
27	Insights into Molecular Assembly of ACCase Heteromeric Complex in Chlorella variabilisâ€"A Homology Modelling, Docking and Molecular Dynamic Simulation Study. Applied Biochemistry and Biotechnology, 2013, 170, 1437-1457.	2.9	6
28	Insights into the structureâ€"function relationship of disease resistance protein HCTR in maize (Zea) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5 2013, 45, 50-64.	2.4	9
29	Homology modeling and docking studies of FabH (Î²-ketoacyl-ACP synthase III) enzyme involved in type II fatty acid biosynthesis ofChlorella variabilis: a potential algal feedstock for biofuel production. Journal of Biomolecular Structure and Dynamics, 2013, 31, 241-257.	3.5	11
30	Structural Analysis of Respirasomes in Electron Transfer Pathway of *Acidithiobacillus ferrooxidans*: A Computer-Aided Molecular Designing Study. , 2013, 2013, 1-14.		4
31	Comparative modeling of human kappa opioid receptor and docking analysis with the peptide YFa. Journal of Molecular Graphics and Modelling, 2012, 33, 44-51.	2.4	3