

Hammad Naveed

List of Publications by Citations

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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.

43
papers

576
citations

14
h-index

23
g-index

56
ext. papers

661
ext. citations

3.9
avg, IF

4.1
L-index

#	Paper	IF	Citations
43	Lipid-binding surfaces of membrane proteins: evidence from evolutionary and structural analysis. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2011 , 1808, 1092-102	3.8	63
42	Structure-based analysis of VDAC1 protein: defining oligomer contact sites. <i>Journal of Biological Chemistry</i> , 2012 , 287, 2179-90	5.4	57
41	Predicting weakly stable regions, oligomerization state, and protein-protein interfaces in transmembrane domains of outer membrane proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 12735-40	11.5	55
40	Identification of potential inhibitors of three key enzymes of SARS-CoV2 using computational approach. <i>Computers in Biology and Medicine</i> , 2020 , 122, 103848	7	33
39	Predicting three-dimensional structures of transmembrane domains of β barrel membrane proteins. <i>Journal of the American Chemical Society</i> , 2012 , 134, 1775-81	16.4	32
38	Computational studies of membrane proteins: models and predictions for biological understanding. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2012 , 1818, 927-41	3.8	32
37	CoCiter: an efficient tool to infer gene function by assessing the significance of literature co-citation. <i>PLoS ONE</i> , 2013 , 8, e74074	3.7	31
36	ModuleAlign: module-based global alignment of protein-protein interaction networks. <i>Bioinformatics</i> , 2016 , 32, i658-i664	7.2	27
35	Engineered oligomerization state of OmpF protein through computational design decouples oligomer dissociation from unfolding. <i>Journal of Molecular Biology</i> , 2012 , 419, 89-101	6.5	26
34	Mechanisms of regulating cell topology in proliferating epithelia: impact of division plane, mechanical forces, and cell memory. <i>PLoS ONE</i> , 2012 , 7, e43108	3.7	22
33	Outer Membrane Protein Folding and Topology from a Computational Transfer Free Energy Scale. <i>Journal of the American Chemical Society</i> , 2016 , 138, 2592-601	16.4	20
32	Improving the resistance of a eukaryotic β barrel protein to thermal and chemical perturbations. <i>Journal of Molecular Biology</i> , 2011 , 413, 150-61	6.5	19
31	Mechanisms of regulating tissue elongation in Drosophila wing: impact of oriented cell divisions, oriented mechanical forces, and reduced cell size. <i>PLoS ONE</i> , 2014 , 9, e86725	3.7	15
30	Geometric order in proliferating epithelia: impact of rearrangements and cleavage plane orientation. <i>Annual International Conference of the IEEE Engineering in Medicine and Biology Society IEEE Engineering in Medicine and Biology Society Annual International Conference</i> , 2010 , 2010, 3808-11	0.9	15
29	High-resolution structure prediction of β -barrel membrane proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, 1511-1516	11.5	12
28	Weakly stable regions and protein-protein interactions in beta-barrel membrane proteins. <i>Current Pharmaceutical Design</i> , 2014 , 20, 1268-73	3.3	12
27	Finding optimal interaction interface alignments between biological complexes. <i>Bioinformatics</i> , 2015 , 31, i133-41	7.2	11

26	Mechanical model of geometric cell and topological algorithm for cell dynamics from single-cell to formation of monolayered tissues with pattern. <i>PLoS ONE</i> , 2015 , 10, e0126484	3.7	9
25	Modeling spatial population dynamics of stem cell lineage in tissue growth. <i>Annual International Conference of the IEEE Engineering in Medicine and Biology Society IEEE Engineering in Medicine and Biology Society Annual International Conference</i> , 2012 , 2012, 5502-5	0.9	8
24	Identification of destabilizing SNPs in SARS-CoV2-ACE2 protein and spike glycoprotein: implications for virus entry mechanisms. <i>Journal of Biomolecular Structure and Dynamics</i> , 2020 , 1-11	3.6	8
23	Structure-based protein-protein interaction networks and drug design. <i>Quantitative Biology</i> , 2013 , 1, 183-191	3.9	7
22	An integrated structure- and system-based framework to identify new targets of metabolites and known drugs. <i>Bioinformatics</i> , 2015 , 31, 3922-9	7.2	6
21	The structure of the TOM core complex in the mitochondrial outer membrane. <i>Biological Chemistry</i> , 2020 , 401, 687-697	4.5	6
20	Dynamic mechanical finite element model of biological cells for studying cellular pattern formation. <i>Annual International Conference of the IEEE Engineering in Medicine and Biology Society IEEE Engineering in Medicine and Biology Society Annual International Conference</i> , 2013 , 2013, 4517-20	0.9	6
19	SAlign-a structure aware method for global PPI network alignment. <i>BMC Bioinformatics</i> , 2020 , 21, 500	3.6	5
18	Mechanical forces mediate localized topological change in epithelia. <i>Annual International Conference of the IEEE Engineering in Medicine and Biology Society IEEE Engineering in Medicine and Biology Society Annual International Conference</i> , 2011 , 2011, 178-81	0.9	5
17	HECNet: a hierarchical approach to enzyme function classification using a Siamese Triplet Network. <i>Bioinformatics</i> , 2020 , 36, 4583-4589	7.2	5
16	Modeling spatial population dynamics of stem cell lineage in wound healing and cancerogenesis. <i>Annual International Conference of the IEEE Engineering in Medicine and Biology Society IEEE Engineering in Medicine and Biology Society Annual International Conference</i> , 2013 , 2013, 5550-3	0.9	4
15	Efficient computation of transfer free energies of amino acids in beta-barrel membrane proteins. <i>Bioinformatics</i> , 2017 , 33, 1664-1671	7.2	3
14	Multiscale Modeling of Cellular Epigenetic States: Stochasticity in Molecular Networks, Chromatin Folding in Cell Nuclei, and Tissue Pattern Formation of Cells. <i>Critical Reviews in Biomedical Engineering</i> , 2015 , 43, 323-46	1.1	3
13	Effects of mechanical properties on tumor invasion: insights from a cellular model. <i>Annual International Conference of the IEEE Engineering in Medicine and Biology Society IEEE Engineering in Medicine and Biology Society Annual International Conference</i> , 2014 , 2014, 6818-21	0.9	3
12	TMBB-Explorer: A Webserver to Predict the Structure, Oligomerization State, Ppi Interface, and Thermodynamic Properties of the Transmembrane Domains of Outer Membrane Proteins. <i>Biophysical Journal</i> , 2012 , 102, 469a	2.9	3
11	A hierarchical deep learning based approach for multi-functional enzyme classification. <i>Protein Science</i> , 2021 , 30, 1935-1945	6.3	3
10	PRRAT_AMAn advanced ant-miner to extract accurate and comprehensible classification rules. <i>Applied Soft Computing Journal</i> , 2020 , 92, 106326	7.5	2
9	GeTFEP: A general transfer free energy profile of transmembrane proteins		2

8	Cell fate determination is influenced by Notch heterogeneity. <i>Annual International Conference of the IEEE Engineering in Medicine and Biology Society IEEE Engineering in Medicine and Biology Society Annual International Conference, 2021</i> , 2021, 4143-4146	0.9	1
7	GeTFEP: A general transfer free energy profile of transmembrane proteins. <i>Protein Science, 2020</i> , 29, 469-479	6.3	1
6	Predicting the pathogenicity of protein coding mutations using Natural Language Processing. <i>Annual International Conference of the IEEE Engineering in Medicine and Biology Society IEEE Engineering in Medicine and Biology Society Annual International Conference, 2020</i> , 2020, 5842-5846	0.9	1
5	Identifying Novel Drug Targets by iDTPnd: A Case Study of Kinase Inhibitors. <i>Genomics, Proteomics and Bioinformatics, 2021</i> ,	6.5	1
4	PMNet: A probability map based scaled network for breast cancer diagnosis. <i>Computerized Medical Imaging and Graphics, 2021</i> , 89, 101863	7.6	0
3	GOntoSim: a semantic similarity measure based on LCA and common descendants.. <i>Scientific Reports, 2022</i> , 12, 3818	4.9	0
2	Leveraging digital media data for pharmacovigilance 2020 , 2020, 442-451	0.7	
1	Role of Cell Morphology in Classical Delta-Notch Pattern Formation. <i>Annual International Conference of the IEEE Engineering in Medicine and Biology Society IEEE Engineering in Medicine and Biology Society Annual International Conference, 2021</i> , 2021, 4139-4142	0.9	