Hammad Naveed

List of Publications by Year
in descending order

54 papers	746 citations	623734 14 h-index	580821 25 g-index
56 all docs	56 docs citations	56 times ranked	1064 citing authors

#	Article	IF	Citations
1	Structure-based Analysis of VDAC1 Protein. Journal of Biological Chemistry, 2012, 287, 2179-2190.	3.4	73
2	Lipid-binding surfaces of membrane proteins: Evidence from evolutionary and structural analysis. Biochimica Et Biophysica Acta - Biomembranes, 2011, 1808, 1092-1102.	2.6	68
3	Predicting weakly stable regions, oligomerization state, and protein–protein interfaces in transmembrane domains of outer membrane proteins. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 12735-12740.	7.1	62
4	Identification of potential inhibitors of three key enzymes of SARS-CoV2 using computational approach. Computers in Biology and Medicine, 2020, 122, 103848.	7.0	44
5	Predicting Three-Dimensional Structures of Transmembrane Domains of β-Barrel Membrane Proteins. Journal of the American Chemical Society, 2012, 134, 1775-1781.	13.7	41
6	Computational studies of membrane proteins: Models and predictions for biological understanding. Biochimica Et Biophysica Acta - Biomembranes, 2012, 1818, 927-941.	2.6	36
7	CoCiter: An Efficient Tool to Infer Gene Function by Assessing the Significance of Literature Co-Citation. PLoS ONE, 2013, 8, e74074.	2.5	36
8	ModuleAlign: module-based global alignment of protein–protein interaction networks. Bioinformatics, 2016, 32, i658-i664.	4.1	34
9	High-resolution structure prediction of β -barrel membrane proteins. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 1511-1516.	7.1	32
10	Engineered Oligomerization State of OmpF Protein through Computational Design Decouples Oligomer Dissociation from Unfolding. Journal of Molecular Biology, 2012, 419, 89-101.	4.2	28
11	Mechanisms of Regulating Cell Topology in Proliferating Epithelia: Impact of Division Plane, Mechanical Forces, and Cell Memory. PLoS ONE, 2012, 7, e43108.	2.5	27
12	Outer Membrane Protein Folding and Topology from a Computational Transfer Free Energy Scale. Journal of the American Chemical Society, 2016, 138, 2592-2601.	13.7	23
13	Improving the Resistance of a Eukaryotic β-Barrel Protein to Thermal and Chemical Perturbations. Journal of Molecular Biology, 2011, 413, 150-161.	4.2	21
14	HECNet: a hierarchical approach to enzyme function classification using a Siamese Triplet Network. Bioinformatics, 2020, 36, 4583-4589.	4.1	19
15	Geometric order in proliferating epithelia: Impact of rearrangements and cleavage plane orientation. , 2010, 2010, 3808-11.		16
16	Mechanisms of Regulating Tissue Elongation in Drosophila Wing: Impact of Oriented Cell Divisions, Oriented Mechanical Forces, and Reduced Cell Size. PLoS ONE, 2014, 9, e86725.	2.5	16
17	Finding optimal interaction interface alignments between biological complexes. Bioinformatics, 2015, 31, i133-i141.	4.1	16
18	An integrated structure- and system-based framework to identify new targets of metabolites and known drugs. Bioinformatics, 2015, 31, btv477.	4.1	15

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19	The structure of the TOM core complex in the mitochondrial outer membrane. Biological Chemistry, 2020, 401, 687-697.	2.5	15
20	Mechanical Model of Geometric Cell and Topological Algorithm for Cell Dynamics from Single-Cell to Formation of Monolayered Tissues with Pattern. PLoS ONE, 2015, 10, e0126484.	2.5	13
21	Weakly Stable Regions and Protein-Protein Interactions in Beta-Barrel Membrane Proteins. Current Pharmaceutical Design, 2014, 20, 1268-1273.	1.9	13
22	Identification of destabilizing SNPs in SARS-CoV2-ACE2 protein and spike glycoprotein: implications for virus entry mechanisms. Journal of Biomolecular Structure and Dynamics, 2022, 40, 1205-1215.	3.5	12
23	SAlignâ€"a structure aware method for global PPI network alignment. BMC Bioinformatics, 2020, 21, 500.	2.6	9
24	Modeling spatial population dynamics of stem cell lineage in tissue growth. , 2012, 2012, 5502-5.		8
25	A hierarchical deep learning based approach for multiâ€functional enzyme classification. Protein Science, 2021, 30, 1935-1945.	7.6	8
26	Structureâ€based proteinâ€protein interaction networks and drug design. Quantitative Biology, 2013, 1, 183-191.	0.5	7
27	Dynamic mechanical finite element model of biological cells for studying cellular pattern formation. , 2013, 2013, 4517-20.		7
28	Mechanical forces mediate localized topological change in epithelia. , 2011, 2011, 178-81.		5
29	GeTFEP: A general transfer free energy profile of transmembrane proteins. Protein Science, 2020, 29, 469-479.	7.6	5
30	GOntoSim: a semantic similarity measure based on LCA and common descendants. Scientific Reports, 2022, 12, 3818.	3.3	5
31	Modeling spatial population dynamics of stem cell lineage in wound healing and cancerogenesis. , 2013, 2013, 5550-3.		4
32	Multiscale Modeling of Cellular Epigenetic States: Stochasticity in Molecular Networks, Chromatin Folding in Cell Nuclei, and Tissue Pattern Formation of Cells. Critical Reviews in Biomedical Engineering, 2015, 43, 323-346.	0.9	4
33	TMBB-Explorer: A Webserver to Predict the Structure, Oligomerization State, Ppi Interface, and Thermodynamic Properties of the Transmembrane Domains of Outer Membrane Proteins. Biophysical Journal, 2012, 102, 469a.	0.5	3
34	Effects of mechanical properties on tumor invasion: Insights from a cellular model. , 2014, 2014, 6818-21.		3
35	Efficient computation of transfer free energies of amino acids in beta-barrel membrane proteins. Bioinformatics, 2017, 33, 1664-1671.	4.1	3
36	PMNet: A probability map based scaled network for breast cancer diagnosis. Computerized Medical Imaging and Graphics, 2021, 89, 101863.	5.8	3

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37	Predicting the pathogenicity of protein coding mutations using Natural Language Processing. , 2020, 2020, 5842-5846.		2
38	PRRAT_AMâ€"An advanced ant-miner to extract accurate and comprehensible classification rules. Applied Soft Computing Journal, 2020, 92, 106326.	7.2	2
39	Engineering Biological Nanopores with Enhanced Properties. Biophysical Journal, 2012, 102, 188a-189a.	0.5	1
40	GPADRlex: Grouped Phrasal Adverse Drug Reaction lexicon. , 2019, , .		1
41	Enzyme Function Prediction using Deep Learning. Biophysical Journal, 2020, 118, 533a.	0.5	1
42	Identifying Novel Drug Targets by iDTPnd: A Case Study of Kinase Inhibitors. Genomics, Proteomics and Bioinformatics, 2021, 19, 986-997.	6.9	1
43	Leveraging digital media data for pharmacovigilance. AMIA ... Annual Symposium proceedings, 2020, 2020, 442-451.	0.2	1
44	Cell fate determination is influenced by Notch heterogeneity. , 2021, 2021, 4143-4146.		1
45	On Mechanisms of Regulation of Tissue Elongation in Drosophila Wing. Biophysical Journal, 2012, 102, 593a.	0.5	0
46	Computational Free Energy Scale of Amino Acid Residues in Membrane Protein from Statistical Mechanics. Biophysical Journal, 2012, 102, 59a.	0.5	0
47	Statistical Mechanical Model for the Transfer Free Energy of Amino Acids in the Context of Membrane Protein OmpLA. Biophysical Journal, 2013, 104, 401a.	0.5	0
48	Pairwise structure alignment specifically tuned for surface pockets and interaction interfaces. , 2015, , .		0
49	Improved 3D Structure Prediction of Beta-Barrel Membrane Proteins by using Evolutionary Coupling Constraints, Reduced State Space and an Empirical Potential Function. Biophysical Journal, 2016, 110, 56a.	0.5	0
50	Improving 3D Structure Prediction of Beta-Barrel Membrane Proteins. Biophysical Journal, 2017, 112, 55a.	0.5	0
51	A Structure Based Framework to Identify Novel Targets of FDA Approved Kinase Inhibitors. Biophysical Journal, 2017, 112, 349a.	0.5	0
52	Understanding the Toxicity and Repurposing Potential of Kinase Inhibitors. Biophysical Journal, 2018, 114, 225a.	0.5	0
53	Genetic Mutation Classification using Machine Learning. Biophysical Journal, 2019, 116, 292a.	0.5	0
54	Role of Cell Morphology in Classical Delta-Notch Pattern Formation. , 2021, 2021, 4139-4142.		0