Hammad Naveed

List of Publications by Year
in descending order

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54	746	623734	580821
papers	citations	14 h-index	25 g-index

56	56	56	1064
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	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
2	GOntoSim: a semantic similarity measure based on LCA and common descendants. Scientific Reports, 2022, 12, 3818.	3.3	5
3	Identifying Novel Drug Targets by iDTPnd: A Case Study of Kinase Inhibitors. Genomics, Proteomics and Bioinformatics, 2021, 19, 986-997.	6.9	1
4	PMNet: A probability map based scaled network for breast cancer diagnosis. Computerized Medical Imaging and Graphics, 2021, 89, 101863.	5.8	3
5	A hierarchical deep learning based approach for multiâ€functional enzyme classification. Protein Science, 2021, 30, 1935-1945.	7.6	8
6	Cell fate determination is influenced by Notch heterogeneity. , 2021, 2021, 4143-4146.		1
7	Role of Cell Morphology in Classical Delta-Notch Pattern Formation. , 2021, 2021, 4139-4142.		0
8	GeTFEP: A general transfer free energy profile of transmembrane proteins. Protein Science, 2020, 29, 469-479.	7.6	5
9	Predicting the pathogenicity of protein coding mutations using Natural Language Processing. , 2020, 2020, 5842-5846.		2
10	SAlignâ€“a structure aware method for global PPI network alignment. BMC Bioinformatics, 2020, 21, 500.	2.6	9
11	The structure of the TOM core complex in the mitochondrial outer membrane. Biological Chemistry, 2020, 401, 687-697.	2.5	15
12	Enzyme Function Prediction using Deep Learning. Biophysical Journal, 2020, 118, 533a.	0.5	1
13	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
14	PRRAT_AMâ€”An advanced ant-miner to extract accurate and comprehensible classification rules. Applied Soft Computing Journal, 2020, 92, 106326.	7.2	2
15	HECNet: a hierarchical approach to enzyme function classification using a Siamese Triplet Network. Bioinformatics, 2020, 36, 4583-4589.	4.1	19
16	Leveraging digital media data for pharmacovigilance. AMIA ... Annual Symposium proceedings, 2020, 2020, 442-451.	0.2	1
17	Genetic Mutation Classification using Machine Learning. Biophysical Journal, 2019, 116, 292a.	0.5	0
18	GPADRlex: Grouped Phrasal Adverse Drug Reaction lexicon. , 2019, , .		1

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19	High-resolution structure prediction of Î² -barrel membrane proteins. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 1511-1516.	7.1	32
20	Understanding the Toxicity and Repurposing Potential of Kinase Inhibitors. Biophysical Journal, 2018, 114, 225a.	0.5	0
21	Improving 3D Structure Prediction of Beta-Barrel Membrane Proteins. Biophysical Journal, 2017, 112, 55a.	0.5	0
22	A Structure Based Framework to Identify Novel Targets of FDA Approved Kinase Inhibitors. Biophysical Journal, 2017, 112, 349a.	0.5	0
23	Efficient computation of transfer free energies of amino acids in beta-barrel membrane proteins. Bioinformatics, 2017, 33, 1664-1671.	4.1	3
24	ModuleAlign: module-based global alignment of proteinâ€“protein interaction networks. Bioinformatics, 2016, 32, i658-i664.	4.1	34
25	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
26	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
27	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
28	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
29	Pairwise structure alignment specifically tuned for surface pockets and interaction interfaces. , 2015, , .		0
30	Finding optimal interaction interface alignments between biological complexes. Bioinformatics, 2015, 31, i133-i141.	4.1	16
31	An integrated structure- and system-based framework to identify new targets of metabolites and known drugs. Bioinformatics, 2015, 31, btv477.	4.1	15
32	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
33	Effects of mechanical properties on tumor invasion: Insights from a cellular model. , 2014, 2014, 6818-21.		3
34	Weakly Stable Regions and Protein-Protein Interactions in Beta-Barrel Membrane Proteins. Current Pharmaceutical Design, 2014, 20, 1268-1273.	1.9	13
35	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
36	Structureâ€based proteinâ€protein interaction networks and drug design. Quantitative Biology, 2013, 1, 183-191.	0.5	7

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37	Dynamic mechanical finite element model of biological cells for studying cellular pattern formation. , 2013, 2013, 4517-20.		7
38	Modeling spatial population dynamics of stem cell lineage in wound healing and cancerogenesis. , 2013, 2013, 5550-3.		4
39	CoCiter: An Efficient Tool to Infer Gene Function by Assessing the Significance of Literature Co-Citation. PLoS ONE, 2013, 8, e74074.	2.5	36
40	Structure-based Analysis of VDAC1 Protein. Journal of Biological Chemistry, 2012, 287, 2179-2190.	3.4	73
41	On Mechanisms of Regulation of Tissue Elongation in Drosophila Wing. Biophysical Journal, 2012, 102, 593a.	0.5	0
42	Predicting Three-Dimensional Structures of Transmembrane Domains of Î²-Barrel Membrane Proteins. Journal of the American Chemical Society, 2012, 134, 1775-1781.	13.7	41
43	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
44	Computational studies of membrane proteins: Models and predictions for biological understanding. Biochimica Et Biophysica Acta - Biomembranes, 2012, 1818, 927-941.	2.6	36
45	Modeling spatial population dynamics of stem cell lineage in tissue growth. , 2012, 2012, 5502-5.		8
46	Engineering Biological Nanopores with Enhanced Properties. Biophysical Journal, 2012, 102, 188a-189a.	0.5	1
47	Computational Free Energy Scale of Amino Acid Residues in Membrane Protein from Statistical Mechanics. Biophysical Journal, 2012, 102, 59a.	0.5	0
48	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
49	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
50	Lipid-binding surfaces of membrane proteins: Evidence from evolutionary and structural analysis. Biochimica Et Biophysica Acta - Biomembranes, 2011, 1808, 1092-1102.	2.6	68
51	Improving the Resistance of a Eukaryotic Î²-Barrel Protein to Thermal and Chemical Perturbations. Journal of Molecular Biology, 2011, 413, 150-161.	4.2	21
52	Mechanical forces mediate localized topological change in epithelia. , 2011, 2011, 178-81.		5
53	Geometric order in proliferating epithelia: Impact of rearrangements and cleavage plane orientation. , 2010, 2010, 3808-11.		16
54	Predicting weakly stable regions, oligomerization state, and proteinâ€“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