

Hammad Naveed

List of Publications by Year in descending order

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Version: 2024-02-01

54
papers

746
citations

623188

14
h-index

580395

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. <i>Journal of Biological Chemistry</i> , 2012, 287, 2179-2190.	1.6	73
2	Lipid-binding surfaces of membrane proteins: Evidence from evolutionary and structural analysis. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2011, 1808, 1092-1102.	1.4	68
3	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, 12735-12740.	3.3	62
4	Identification of potential inhibitors of three key enzymes of SARS-CoV2 using computational approach. <i>Computers in Biology and Medicine</i> , 2020, 122, 103848.	3.9	44
5	Predicting Three-Dimensional Structures of Transmembrane Domains of β -Barrel Membrane Proteins. <i>Journal of the American Chemical Society</i> , 2012, 134, 1775-1781.	6.6	41
6	Computational studies of membrane proteins: Models and predictions for biological understanding. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2012, 1818, 927-941.	1.4	36
7	CoCiter: An Efficient Tool to Infer Gene Function by Assessing the Significance of Literature Co-Citation. <i>PLoS ONE</i> , 2013, 8, e74074.	1.1	36
8	ModuleAlign: module-based global alignment of protein-protein interaction networks. <i>Bioinformatics</i> , 2016, 32, i658-i664.	1.8	34
9	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.	3.3	32
10	Engineered Oligomerization State of OmpF Protein through Computational Design Decouples Oligomer Dissociation from Unfolding. <i>Journal of Molecular Biology</i> , 2012, 419, 89-101.	2.0	28
11	Mechanisms of Regulating Cell Topology in Proliferating Epithelia: Impact of Division Plane, Mechanical Forces, and Cell Memory. <i>PLoS ONE</i> , 2012, 7, e43108.	1.1	27
12	Outer Membrane Protein Folding and Topology from a Computational Transfer Free Energy Scale. <i>Journal of the American Chemical Society</i> , 2016, 138, 2592-2601.	6.6	23
13	Improving the Resistance of a Eukaryotic β -Barrel Protein to Thermal and Chemical Perturbations. <i>Journal of Molecular Biology</i> , 2011, 413, 150-161.	2.0	21
14	HECNet: a hierarchical approach to enzyme function classification using a Siamese Triplet Network. <i>Bioinformatics</i> , 2020, 36, 4583-4589.	1.8	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. <i>PLoS ONE</i> , 2014, 9, e86725.	1.1	16
17	Finding optimal interaction interface alignments between biological complexes. <i>Bioinformatics</i> , 2015, 31, i133-i141.	1.8	16
18	An integrated structure- and system-based framework to identify new targets of metabolites and known drugs. <i>Bioinformatics</i> , 2015, 31, btv477.	1.8	15

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19	The structure of the TOM core complex in the mitochondrial outer membrane. <i>Biological Chemistry</i> , 2020, 401, 687-697.	1.2	15
20	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.	1.1	13
21	Weakly Stable Regions and Protein-Protein Interactions in Beta-Barrel Membrane Proteins. <i>Current Pharmaceutical Design</i> , 2014, 20, 1268-1273.	0.9	13
22	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> , 2022, 40, 1205-1215.	2.0	12
23	SAlign—a structure aware method for global PPI network alignment. <i>BMC Bioinformatics</i> , 2020, 21, 500.	1.2	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 multi-functional enzyme classification. <i>Protein Science</i> , 2021, 30, 1935-1945.	3.1	8
26	Structure-based protein-protein interaction networks and drug design. <i>Quantitative Biology</i> , 2013, 1, 183-191.	0.3	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. <i>Protein Science</i> , 2020, 29, 469-479.	3.1	5
30	GOntoSim: a semantic similarity measure based on LCA and common descendants. <i>Scientific Reports</i> , 2022, 12, 3818.	1.6	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. <i>Critical Reviews in Biomedical Engineering</i> , 2015, 43, 323-346.	0.5	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. <i>Biophysical Journal</i> , 2012, 102, 469a.	0.2	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. <i>Bioinformatics</i> , 2017, 33, 1664-1671.	1.8	3
36	PMNet: A probability map based scaled network for breast cancer diagnosis. <i>Computerized Medical Imaging and Graphics</i> , 2021, 89, 101863.	3.5	3

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37	Predicting the pathogenicity of protein coding mutations using Natural Language Processing. , 2020, 2020, 5842-5846.		2
38	PRRAT_AMê”An advanced ant-miner to extract accurate and comprehensible classification rules. Applied Soft Computing Journal, 2020, 92, 106326.	4.1	2
39	Engineering Biological Nanopores with Enhanced Properties. Biophysical Journal, 2012, 102, 188a-189a.	0.2	1
40	GPADRLex: Grouped Phrasal Adverse Drug Reaction lexicon. , 2019, , .		1
41	Enzyme Function Prediction using Deep Learning. Biophysical Journal, 2020, 118, 533a.	0.2	1
42	Identifying Novel Drug Targets by iDTPnd: A Case Study of Kinase Inhibitors. Genomics, Proteomics and Bioinformatics, 2021, 19, 986-997.	3.0	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.	0.2	0
46	Computational Free Energy Scale of Amino Acid Residues in Membrane Protein from Statistical Mechanics. Biophysical Journal, 2012, 102, 59a.	0.2	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.	0.2	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.	0.2	0
50	Improving 3D Structure Prediction of Beta-Barrel Membrane Proteins. Biophysical Journal, 2017, 112, 55a.	0.2	0
51	A Structure Based Framework to Identify Novel Targets of FDA Approved Kinase Inhibitors. Biophysical Journal, 2017, 112, 349a.	0.2	0
52	Understanding the Toxicity and Repurposing Potential of Kinase Inhibitors. Biophysical Journal, 2018, 114, 225a.	0.2	0
53	Genetic Mutation Classification using Machine Learning. Biophysical Journal, 2019, 116, 292a.	0.2	0
54	Role of Cell Morphology in Classical Delta-Notch Pattern Formation. , 2021, 2021, 4139-4142.		0