Dukka B. KC

List of Publications by Year
in descending order

26	497	687363 13	713466 21
papers	citations	h-index	g-index

29	29	29	577
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Deep Learning-Based Advances in Protein Structure Prediction. International Journal of Molecular Sciences, 2021, 22, 5553.	4.1	57
2	Comparison of Machine Learning and Deep Learning Models for Network Intrusion Detection Systems. Future Internet, 2020, 12, 167.	3.8	47
3	DeepSuccinylSite: a deep learning based approach for protein succinylation site prediction. BMC Bioinformatics, 2020, 21, 63.	2.6	45
4	RF-Phos: A Novel General Phosphorylation Site Prediction Tool Based on Random Forest. BioMed Research International, 2016, 2016, 1-12.	1.9	34
5	STRUCTURE-BASED METHODS FOR COMPUTATIONAL PROTEIN FUNCTIONAL SITE PREDICTION. Computational and Structural Biotechnology Journal, 2013, 8, e201308005.	4.1	30
6	RF-GlutarySite: a random forest based predictor for glutarylation sites. Molecular Omics, 2019, 15, 189-204.	2.8	30
7	Recent advances in sequence-based protein structure prediction: Table 1. Briefings in Bioinformatics, 2017, 18, bbw070.	6.5	26
8	RF-Hydroxysite: a random forest based predictor for hydroxylation sites. Molecular BioSystems, 2016, 12, 2427-2435.	2.9	24
9	Numerical and experimental investigation of hydrodynamics and light transfer in open raceway ponds at various algal cell concentrations and medium depths. Chemical Engineering Science, 2016, 156, 11-23.	3.8	23
10	SymD webserver: a platform for detecting internally symmetric protein structures. Nucleic Acids Research, 2014, 42, W296-W300.	14.5	19
11	CNN-BLPred: a Convolutional neural network based predictor for Î²-Lactamases (BL) and their classes. BMC Bioinformatics, 2017, 18, 577.	2.6	19
12	DeepRMethylSite: a deep learning based approach for prediction of arginine methylation sites in proteins. Molecular Omics, 2020, 16, 448-454.	2.8	18
13	The PFP and ESG protein function prediction methods in 2014: effect of database updates and ensemble approaches. GigaScience, 2015, 4, 43.	6.4	16
14	SVM-SulfoSite: A support vector machine based predictor for sulfenylation sites. Scientific Reports, 2018, 8, 11288.	3.3	14
15	RF-MaloSite and DL-Malosite: Methods based on random forest and deep learning to identify malonylation sites. Computational and Structural Biotechnology Journal, 2020, 18, 852-860.	4.1	14
16	DeepNGlyPred: A Deep Neural Network-Based Approach for Human N-Linked Glycosylation Site Prediction. Molecules, 2021, 26, 7314.	3.8	13
17	DTL-DephosSite: Deep Transfer Learning Based Approach to Predict Dephosphorylation Sites. Frontiers in Cell and Developmental Biology, 2021, 9, 662983.	3.7	12
18	A deep learning based approach for prediction of Chlamydomonas reinhardtii phosphorylation sites. Scientific Reports, 2021, 11, 12550.	3.3	10

#	Article	IF	Citations
19	RF-NR: Random Forest Based Approach for Improved Classification of Nuclear Receptors. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 1844-1852.	3.0	8
20	Advances in Protein Super-Secondary Structure Prediction and Application to Protein Structure Prediction. Methods in Molecular Biology, 2019, 1958, 15-45.	0.9	8
21	Deep Learningâ€“Based Advances In Protein Posttranslational Modification Site and Protein Cleavage Prediction. Methods in Molecular Biology, 2022, , 285-322.	0.9	8
22	Einsteinâ€“Roscoe regression for the slag viscosity prediction problem in steelmaking. Scientific Reports, 2022, 12, 6541.	3.3	7
23	GPU-I-TASSER: a GPU accelerated I-TASSER protein structure prediction tool. Bioinformatics, 2022, 38, 1754-1755.	4.1	6
24	The evolution of logic circuits for the purpose of protein contact map prediction. PeerJ, 2017, 5, e3139.	2.0	5
25	FEPS: A Tool for Feature Extraction from Protein Sequence. Methods in Molecular Biology, 2022, , 65-104.	0.9	3
26	Parallel-SymD: A Parallel Approach to Detect Internal Symmetry in Protein Domains. BioMed Research International, 2016, 2016, 1-9.	1.9	1