

# Dukka B. KC

## List of Publications by Year in descending order

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Version: 2024-02-01

26  
papers

497  
citations

687363

13  
h-index

713466

21  
g-index

29  
all docs

29  
docs citations

29  
times ranked

577  
citing authors

#	ARTICLE	IF	CITATIONS
1	GPU-I-TASSER: a GPU accelerated I-TASSER protein structure prediction tool. <i>Bioinformatics</i> , 2022, 38, 1754-1755.	4.1	6
2	Einsteinâ€“Roscoe regression for the slag viscosity prediction problem in steelmaking. <i>Scientific Reports</i> , 2022, 12, 6541.	3.3	7
3	FEPS: A Tool for Feature Extraction from Protein Sequence. <i>Methods in Molecular Biology</i> , 2022, , 65-104.	0.9	3
4	Deep Learningâ€“Based Advances In Protein Posttranslational Modification Site and Protein Cleavage Prediction. <i>Methods in Molecular Biology</i> , 2022, , 285-322.	0.9	8
5	Deep Learning-Based Advances in Protein Structure Prediction. <i>International Journal of Molecular Sciences</i> , 2021, 22, 5553.	4.1	57
6	DTL-DephosSite: Deep Transfer Learning Based Approach to Predict Dephosphorylation Sites. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 662983.	3.7	12
7	A deep learning based approach for prediction of <i>Chlamydomonas reinhardtii</i> phosphorylation sites. <i>Scientific Reports</i> , 2021, 11, 12550.	3.3	10
8	DeepNGlyPred: A Deep Neural Network-Based Approach for Human N-Linked Glycosylation Site Prediction. <i>Molecules</i> , 2021, 26, 7314.	3.8	13
9	Comparison of Machine Learning and Deep Learning Models for Network Intrusion Detection Systems. <i>Future Internet</i> , 2020, 12, 167.	3.8	47
10	DeepRMethylSite: a deep learning based approach for prediction of arginine methylation sites in proteins. <i>Molecular Omics</i> , 2020, 16, 448-454.	2.8	18
11	RF-MaloSite and DL-Malosite: Methods based on random forest and deep learning to identify malonylation sites. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 852-860.	4.1	14
12	DeepSuccinylSite: a deep learning based approach for protein succinylation site prediction. <i>BMC Bioinformatics</i> , 2020, 21, 63.	2.6	45
13	RF-GlutarySite: a random forest based predictor for glutarylation sites. <i>Molecular Omics</i> , 2019, 15, 189-204.	2.8	30
14	Advances in Protein Super-Secondary Structure Prediction and Application to Protein Structure Prediction. <i>Methods in Molecular Biology</i> , 2019, 1958, 15-45.	0.9	8
15	SVM-SulfoSite: A support vector machine based predictor for sulfenylation sites. <i>Scientific Reports</i> , 2018, 8, 11288.	3.3	14
16	RF-NR: Random Forest Based Approach for Improved Classification of Nuclear Receptors. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018, 15, 1844-1852.	3.0	8
17	Recent advances in sequence-based protein structure prediction: Table 1. <i>Briefings in Bioinformatics</i> , 2017, 18, bbw070.	6.5	26
18	CNN-BLPred: a Convolutional neural network based predictor for $\hat{1}^2$ -Lactamases (BL) and their classes. <i>BMC Bioinformatics</i> , 2017, 18, 577.	2.6	19

#	ARTICLE	IF	CITATIONS
19	The evolution of logic circuits for the purpose of protein contact map prediction. PeerJ, 2017, 5, e3139.	2.0	5
20	Parallel-SymD: A Parallel Approach to Detect Internal Symmetry in Protein Domains. BioMed Research International, 2016, 2016, 1-9.	1.9	1
21	RF-Phos: A Novel General Phosphorylation Site Prediction Tool Based on Random Forest. BioMed Research International, 2016, 2016, 1-12.	1.9	34
22	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
23	RF-Hydroxysite: a random forest based predictor for hydroxylation sites. Molecular BioSystems, 2016, 12, 2427-2435.	2.9	24
24	The PFP and ESC protein function prediction methods in 2014: effect of database updates and ensemble approaches. GigaScience, 2015, 4, 43.	6.4	16
25	SymD webserver: a platform for detecting internally symmetric protein structures. Nucleic Acids Research, 2014, 42, W296-W300.	14.5	19
26	STRUCTURE-BASED METHODS FOR COMPUTATIONAL PROTEIN FUNCTIONAL SITE PREDICTION. Computational and Structural Biotechnology Journal, 2013, 8, e201308005.	4.1	30