Swakkhar Shatabda

List of Publications by Year
in descending order

82 papers	1,371 citations	393982 19 h-index	433756 31 g-index
89 all docs	89 docs citations	89 times ranked	845 citing authors

#	Article	IF	Citations
1	PanClassif: Improving pan cancer classification of single cell RNA-seq gene expression data using machine learning. Genomics, 2022, 114, 110264.	1.3	9
2	BanglaSER: A speech emotion recognition dataset for the Bangla language. Data in Brief, 2022, 42, 108091.	0.5	8
3	Predicting Academic Performance: Analysis of Students' Mental Health Condition from Social Media Interactions. Behavioral Sciences (Basel, Switzerland), 2022, 12, 87.	1.0	5
4	iProtGly-SS: A Tool to Accurately Predict Protein Glycation Site Using Structural-Based Features. Methods in Molecular Biology, 2022, , 125-134.	0.4	1
5	Figbird: a probabilistic method for filling gaps in genome assemblies. Bioinformatics, 2022, 38, 3717-3724.	1.8	0
6	A convolution based computational approach towards DNA N6-methyladenine site identification and motif extraction in rice genome. Scientific Reports, 2021, 11, 10357.	1.6	10
7	SubFeat: Feature subspacing ensemble classifier for function prediction of DNA, RNA and protein sequences. Computational Biology and Chemistry, 2021, 92, 107489.	1.1	6
8	Convolutional neural networks with image representation of amino acid sequences for protein function prediction. Computational Biology and Chemistry, 2021, 92, 107494.	1.1	8
9	OriC-ENS: A sequence-based ensemble classifier for predicting origin of replication in S. cerevisiae. Computational Biology and Chemistry, 2021, 92, 107502.	1.1	3
10	OriFeat: Origin of Replication Identification Using DNA Sequence Based Features. , 2021, , .		0
11	Application of Internet of Things for Early Detection of COVID-19 using Wearables. , 2021, , .		1
12	Towards development of IoT-ML driven healthcare systems: A survey. Journal of Network and Computer Applications, 2021, 196, 103244.	5.8	35
13	ACP-MHCNN: an accurate multi-headed deep-convolutional neural network to predict anticancer peptides. Scientific Reports, 2021, 11, 23676.	1.6	31
14	SEMal: Accurate protein malonylation site predictor using structural and evolutionary information. Computers in Biology and Medicine, 2020, 125, 104022.	3.9	10
15	Accurately Predicting Glutarylation Sites Using Sequential Bi-Peptide-Based Evolutionary Features. Genes, 2020, 11, 1023.	1.0	17
16	Accurate prediction of RNA 5-hydroxymethylcytosine modification by utilizing novel position-specific gapped k-mer descriptors. Computational and Structural Biotechnology Journal, 2020, 18, 3528-3538.	1.9	11
17	Poribohon-BD: Bangladeshi local vehicle image dataset with annotation for classification. Data in Brief, 2020, 33, 106465.	0.5	12
18	FRnet-DTI: Deep convolutional neural network for drug-target interaction prediction. Heliyon, 2020, 6, e03444.	1.4	35

#	Article	IF	Citations
19	DeepDBP: Deep neural networks for identification of DNA-binding proteins. Informatics in Medicine Unlocked, 2020, 19, 100318.	1.9	20
20	iPromoter-BnCNN: a novel branched CNN-based predictor for identifying and classifying sigma promoters. Bioinformatics, 2020, 36, 4869-4875.	1.8	37
21	Mal-Light: Enhancing Lysine Malonylation Sites Prediction Problem Using Evolutionary-based Features. IEEE Access, 2020, 8, 77888-77902.	2.6	12
22	Locate-R: Subcellular localization of long non-coding RNAs using nucleotide compositions. Genomics, 2020, 112, 2583-2589.	1.3	29
23	Recent Development of Machine Learning Methods in Microbial Phosphorylation Sites. Current Genomics, 2020, 21, 194-203.	0.7	8
24	Image-based effective feature generation for protein structural class and ligand binding prediction. PeerJ Computer Science, 2020, 6, e253.	2.7	1
25	Native Vehicles Classification on Bangladeshi Roads Using CNN with Transfer Learning. , 2020, , .		11
26	A Data Selection Methodology to Train Linear Regression Model to Predict Bitcoin Price. , 2020, , .		13
27	iPromoter-FSEn: Identification of bacterial Ïƒ70 promoter sequences using feature subspace based ensemble classifier. Genomics, 2019, 111, 1160-1166.	1.3	36
28	iRSpot-SF: Prediction of recombination hotspots by incorporating sequence based features into Chou's Pseudo components. Genomics, 2019, 111, 966-972.	1.3	30
29	EPAI-NC: Enhanced prediction of adenosine to inosine RNA editing sites using nucleotide compositions. Analytical Biochemistry, 2019, 569, 16-21.	1.1	11
30	Protein structure prediction from inaccurate and sparse NMR data using an enhanced genetic algorithm. Computational Biology and Chemistry, 2019, 79, 6-15.	1.1	8
31	PyFeat: a Python-based effective feature generation tool for DNA, RNA and protein sequences. Bioinformatics, 2019, 35, 3831-3833.	1.8	80
32	Real-Time EEG Classification of Voluntary Hand Movement Directions using Brain Machine Interface. , 2019, , .		4
33	Big Data with Decision Tree Induction. , 2019, , .		7
34	Improving Detection Accuracy for Imbalanced Network Intrusion Classification using Cluster-based Under-sampling with Random Forests. , 2019, , .		28
35	Big Data Mining in the Presence of Concept Drifting. , 2019, , .		2
36	iPro70-FMWin: identifying Sigma70 promoters using multiple windowing and minimal features. Molecular Genetics and Genomics, 2019, 294, 69-84.	1.0	43

#	Article	IF	Citations
37	Wavelet and Pyramid Histogram Features for Image-Based Leaf Detection. Advances in Intelligent Systems and Computing, 2019, , 269-278.	0.5	3
38	Prediction of Bacteriophage Protein Locations Using Deep Neural Networks. Advances in Intelligent Systems and Computing, 2019, , 29-38.	0.5	1
39	CFSBoost: Cumulative feature subspace boosting for drug-target interaction prediction. Journal of Theoretical Biology, 2019, 464, 1-8.	0.8	20
40	Effective DNA binding protein prediction by using key features via Chou's general PseAAC. Journal of Theoretical Biology, 2019, 460, 64-78.	0.8	49
41	iProtGly-SS: Identifying protein glycation sites using sequence and structure based features. Proteins: Structure, Function and Bioinformatics, 2018, 86, 777-789.	1.5	32
42	EvoStruct-Sub: An accurate Gram-positive protein subcellular localization predictor using evolutionary and structural features. Journal of Theoretical Biology, 2018, 443, 138-146.	0.8	31
43	Prediction of Origin of Replication in Genome Using DNA Sequence Based Features. , 2018, , .		1
44	Active Learning for Mining Big Data. , 2018, , .		2
45	Bangla Sentence Correction Using Deep Neural Network Based Sequence to Sequence Learning. , 2018, , .		14
46	IEEE WIECON-ECE 2018 Novel Class Detection in Concept Drifting Data Streams Using Decision Tree Leaves. , 2018, , .		1
47	Bangla Content Categorization Using Text Based Supervised Learning Methods. , 2018, , .		8
48	iRecSpot-EF: Effective sequence based features for recombination hotspot prediction. Computers in Biology and Medicine, 2018, 103, 17-23.	3.9	19
49	DPP-PseAAC: A DNA-binding protein prediction model using Chou's general PseAAC. Journal of Theoretical Biology, 2018, 452, 22-34.	0.8	126
50	iPHLoc-ES: Identification of bacteriophage protein locations using evolutionary and structural features. Journal of Theoretical Biology, 2017, 435, 229-237.	0.8	29
51	iDNAProt-ES: Identification of DNA-binding Proteins Using Evolutionary and Structural Features. Scientific Reports, 2017, 7, 14938.	1.6	73
52	CycloAnt. , 2017, , .		2
53	iDTI-ESBoost: Identification of Drug Target Interaction Using Evolutionary and Structural Features with Boosting. Scientific Reports, 2017, 7, 17731.	1.6	99
54	EGAGP: An enhanced genetic algorithm for producing efficient graph partitions. , 2017, , .		3

#	Article	IF	Citations
55	Impact of learning analytics on product marketing with serious games in Bangladesh. , 2017, , .		4
56	HMMBinder: DNA-Binding Protein Prediction Using HMM Profile Based Features. BioMed Research International, 2017, 2017, 1-10.	0.9	41
57	MEBoost: Mixing estimators with boosting for imbalanced data classification. , 2017, , .		11
58	Hybrid Methods for Class Imbalance Learning Employing Bagging with Sampling Techniques. , 2017, , .		24
59	CUSBoost: Cluster-Based Under-Sampling with Boosting for Imbalanced Classification. , 2017, , .		39
60	Guiding Artificial Neural Networks Using Discriminatory Information In Hidden Layers. , 2017, , .		0
61	An ant colony optimization algorithm for load shedding minimization in smart grids. , 2016, , .		8
62	CoMOGrad and PHOG: From Computer Vision to Fast and Accurate Protein Tertiary Structure Retrieval. Scientific Reports, 2015, 5, 13275.	1.6	6
63	A new effective algorithm for protein chain lattice fit problem. , 2015, , .		0
64	A tabu-based heuristic optimization algorithm for load shedding minimization. , 2015, , .		2
65	An efficient genetic algorithm for discovering diverse-frequent patterns. , 2015, , .		4
66	FGPGA: An efficient genetic approach for producing feasible graph partitions. , 2015, , .		2
67	Efficient conformational space exploration in ab initio protein folding simulation. Royal Society Open Science, 2015, 2, 150238.	1.1	3
68	Gene Transfer: A Novel Genetic Operator for Discovering Diverse-Frequent Patterns. Lecture Notes in Computer Science, 2015, , 309-316.	1.0	1
69	How Good Are Simplified Models for Protein Structure Prediction?. Advances in Bioinformatics, 2014, 2014, 1-9.	5.7	12
70	A Parallel Framework for Multipoint Spiral Search in <i>ab Initio</i> Protein Structure Prediction. Advances in Bioinformatics, 2014, 2014, 1-17.	5.7	2
71	Stochastic local search for pattern set mining. , 2014, , .		3
72	GraATP: A graph theoretic approach for Automated Theorem Proving in plane geometry. , 2014, , .		0

#	Article	IF	Citations
73	GreMuTRRR: A novel genetic algorithm to solve distance geometry problem for protein structures. , 2014, , .		0
74	GreMuTRRR: A novel genetic algorithm to solve distance geometry problem for protein structures. , 2014, , .		0
75	Constraint-Based Evolutionary Local Search for Protein Structures with Secondary Motifs. Lecture Notes in Computer Science, 2014, , 333-344.	1.0	2
76	The road not taken: retreat and diverge in local search for simplified protein structure prediction. BMC Bioinformatics, 2013, 14, S19.	1.2	13
77	Spiral search: a hydrophobic-core directed local search for simplified PSP on 3D FCC lattice. BMC Bioinformatics, 2013, 14, S16.	1.2	13
78	An efficient encoding for simplified protein structure prediction using genetic algorithms. , 2013, , .		8
79	Random-walk. , 2012, , .		9
80	Memory-based local search for simplified protein structure prediction. , 2012, , .		13
81	An approximation algorithm for sorting by reversals and transpositions. Journal of Discrete Algorithms, 2008, 6, 449-457.	0.7	43
82	PRESa2i: incremental decision trees for prediction of Adenosine to Inosine RNA editing sites. F1000Research, 0, 9, 262.	0.8	6