

# Swakkhar Shatabda

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7501062/publications.pdf>

Version: 2024-02-01

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  | DPP-PseAAC: A DNA-binding protein prediction model using Chou's general PseAAC. Journal of Theoretical Biology, 2018, 452, 22-34.   | 0.8 | 126       |
| 2  | iDTI-ESBoost: Identification of Drug Target Interaction Using Evolutionary and Structural Features with Boosting. Scientific Reports, 2017, 7, 17731.                               | 1.6 | 99        |
| 3  | PyFeat: a Python-based effective feature generation tool for DNA, RNA and protein sequences. Bioinformatics, 2019, 35, 3831-3833.   | 1.8 | 80        |
| 4  | iDNAProt-ES: Identification of DNA-binding Proteins Using Evolutionary and Structural Features. Scientific Reports, 2017, 7, 14938.   | 1.6 | 73        |
| 5  | 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        |
| 6  | An approximation algorithm for sorting by reversals and transpositions. Journal of Discrete Algorithms, 2008, 6, 449-457.   | 0.7 | 43        |
| 7  | iPro70-FMWin: identifying Sigma70 promoters using multiple windowing and minimal features. Molecular Genetics and Genomics, 2019, 294, 69-84.                                       | 1.0 | 43        |
| 8  | HMMBinder: DNA-Binding Protein Prediction Using HMM Profile Based Features. BioMed Research International, 2017, 2017, 1-10.  | 0.9 | 41        |
| 9  | CUSBoost: Cluster-Based Under-Sampling with Boosting for Imbalanced Classification. , 2017, , .   |     | 39        |
| 10 | iPromoter-BnCNN: a novel branched CNN-based predictor for identifying and classifying sigma promoters. Bioinformatics, 2020, 36, 4869-4875.   | 1.8 | 37        |
| 11 | iPromoter-FSEn: Identification of bacterial $\sigma$ 70 promoter sequences using feature subspace based ensemble classifier. Genomics, 2019, 111, 1160-1166.                        | 1.3 | 36        |
| 12 | FRnet-DTI: Deep convolutional neural network for drug-target interaction prediction. Heliyon, 2020, 6, e03444.  | 1.4 | 35        |
| 13 | Towards development of IoT-ML driven healthcare systems: A survey. Journal of Network and Computer Applications, 2021, 196, 103244.   | 5.8 | 35        |
| 14 | iProtGlycSS: Identifying protein glycation sites using sequence and structure based features. Proteins: Structure, Function and Bioinformatics, 2018, 86, 777-789.                  | 1.5 | 32        |
| 15 | 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        |
| 16 | ACP-MHCNN: an accurate multi-headed deep-convolutional neural network to predict anticancer peptides. Scientific Reports, 2021, 11, 23676.  | 1.6 | 31        |
| 17 | iRSpot-SF: Prediction of recombination hotspots by incorporating sequence based features into Chou's Pseudo components. Genomics, 2019, 111, 966-972.                               | 1.3 | 30        |
| 18 | iPHLoc-ES: Identification of bacteriophage protein locations using evolutionary and structural features. Journal of Theoretical Biology, 2017, 435, 229-237.                        | 0.8 | 29        |

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|----|---|-----|-----------|
| 19 | Locate-R: Subcellular localization of long non-coding RNAs using nucleotide compositions. <i>Genomics</i> , 2020, 112, 2583-2589.   | 1.3 | 29        |
| 20 | Improving Detection Accuracy for Imbalanced Network Intrusion Classification using Cluster-based Under-sampling with Random Forests. , 2019, , .  |     | 28        |
| 21 | Hybrid Methods for Class Imbalance Learning Employing Bagging with Sampling Techniques. , 2017, , .   |     | 24        |
| 22 | CFSBoost: Cumulative feature subspace boosting for drug-target interaction prediction. <i>Journal of Theoretical Biology</i> , 2019, 464, 1-8.  | 0.8 | 20        |
| 23 | DeepDBP: Deep neural networks for identification of DNA-binding proteins. <i>Informatics in Medicine Unlocked</i> , 2020, 19, 100318.   | 1.9 | 20        |
| 24 | iRecSpot-EF: Effective sequence based features for recombination hotspot prediction. <i>Computers in Biology and Medicine</i> , 2018, 103, 17-23.   | 3.9 | 19        |
| 25 | Accurately Predicting Glutarylation Sites Using Sequential Bi-Peptide-Based Evolutionary Features. <i>Genes</i> , 2020, 11, 1023.   | 1.0 | 17        |
| 26 | Bangla Sentence Correction Using Deep Neural Network Based Sequence to Sequence Learning. , 2018, , .   |     | 14        |
| 27 | Memory-based local search for simplified protein structure prediction. , 2012, , .  |     | 13        |
| 28 | The road not taken: retreat and diverge in local search for simplified protein structure prediction. <i>BMC Bioinformatics</i> , 2013, 14, S19.   | 1.2 | 13        |
| 29 | Spiral search: a hydrophobic-core directed local search for simplified PSP on 3D FCC lattice. <i>BMC Bioinformatics</i> , 2013, 14, S16.  | 1.2 | 13        |
| 30 | A Data Selection Methodology to Train Linear Regression Model to Predict Bitcoin Price. , 2020, , .   |     | 13        |
| 31 | How Good Are Simplified Models for Protein Structure Prediction?. <i>Advances in Bioinformatics</i> , 2014, 2014, 1-9.  | 5.7 | 12        |
| 32 | Poribohon-BD: Bangladeshi local vehicle image dataset with annotation for classification. <i>Data in Brief</i> , 2020, 33, 106465.  | 0.5 | 12        |
| 33 | Mal-Light: Enhancing Lysine Malonylation Sites Prediction Problem Using Evolutionary-based Features. <i>IEEE Access</i> , 2020, 8, 77888-77902.   | 2.6 | 12        |
| 34 | MEBoost: Mixing estimators with boosting for imbalanced data classification. , 2017, , .  |     | 11        |
| 35 | EPAl-NC: Enhanced prediction of adenosine to inosine RNA editing sites using nucleotide compositions. <i>Analytical Biochemistry</i> , 2019, 569, 16-21.  | 1.1 | 11        |
| 36 | Accurate prediction of RNA 5-hydroxymethylcytosine modification by utilizing novel position-specific gapped k-mer descriptors. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 3528-3538. | 1.9 | 11        |

| #  | ARTICLE  | IF  | CITATIONS |
|----|--|-----|-----------|
| 37 | Native Vehicles Classification on Bangladeshi Roads Using CNN with Transfer Learning. , 2020, , .  |     | 11        |
| 38 | SEMaI: Accurate protein malonylation site predictor using structural and evolutionary information. Computers in Biology and Medicine, 2020, 125, 104022.                 | 3.9 | 10        |
| 39 | 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        |
| 40 | Random-walk. , 2012, , .   |     | 9         |
| 41 | PanClassif: Improving pan cancer classification of single cell RNA-seq gene expression data using machine learning. Genomics, 2022, 114, 110264.                         | 1.3 | 9         |
| 42 | An efficient encoding for simplified protein structure prediction using genetic algorithms. , 2013, , .  |     | 8         |
| 43 | An ant colony optimization algorithm for load shedding minimization in smart grids. , 2016, , .  |     | 8         |
| 44 | Bangla Content Categorization Using Text Based Supervised Learning Methods. , 2018, , .  |     | 8         |
| 45 | 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         |
| 46 | Convolutional neural networks with image representation of amino acid sequences for protein function prediction. Computational Biology and Chemistry, 2021, 92, 107494.  | 1.1 | 8         |
| 47 | Recent Development of Machine Learning Methods in Microbial Phosphorylation Sites. Current Genomics, 2020, 21, 194-203.  | 0.7 | 8         |
| 48 | BanglaSER: A speech emotion recognition dataset for the Bangla language. Data in Brief, 2022, 42, 108091.  | 0.5 | 8         |
| 49 | Big Data with Decision Tree Induction. , 2019, , .   |     | 7         |
| 50 | CoMOGrad and PHOG: From Computer Vision to Fast and Accurate Protein Tertiary Structure Retrieval. Scientific Reports, 2015, 5, 13275.                                   | 1.6 | 6         |
| 51 | SubFeat: Feature subsampling ensemble classifier for function prediction of DNA, RNA and protein sequences. Computational Biology and Chemistry, 2021, 92, 107489.       | 1.1 | 6         |
| 52 | PRESa2i: incremental decision trees for prediction of Adenosine to Inosine RNA editing sites. F1000Research, 0, 9, 262.  | 0.8 | 6         |
| 53 | Predicting Academic Performance: Analysis of Studentsâ€™ Mental Health Condition from Social Media Interactions. Behavioral Sciences (Basel, Switzerland), 2022, 12, 87. | 1.0 | 5         |
| 54 | An efficient genetic algorithm for discovering diverse-frequent patterns. , 2015, , .  |     | 4         |

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|----|--|-----|-----------|
| 55 | Impact of learning analytics on product marketing with serious games in Bangladesh. , 2017, , .  |     | 4         |
| 56 | Real-Time EEG Classification of Voluntary Hand Movement Directions using Brain Machine Interface. , 2019, , .  |     | 4         |
| 57 | Stochastic local search for pattern set mining. , 2014, , .  |     | 3         |
| 58 | Efficient conformational space exploration in ab initio protein folding simulation. Royal Society Open Science, 2015, 2, 150238.                                     | 1.1 | 3         |
| 59 | EGAGP: An enhanced genetic algorithm for producing efficient graph partitions. , 2017, , .   |     | 3         |
| 60 | Wavelet and Pyramid Histogram Features for Image-Based Leaf Detection. Advances in Intelligent Systems and Computing, 2019, , 269-278.                               | 0.5 | 3         |
| 61 | OriC-ENS: A sequence-based ensemble classifier for predicting origin of replication in <i>S. cerevisiae</i> . Computational Biology and Chemistry, 2021, 92, 107502. | 1.1 | 3         |
| 62 | 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         |
| 63 | A tabu-based heuristic optimization algorithm for load shedding minimization. , 2015, , .  |     | 2         |
| 64 | FGPGA: An efficient genetic approach for producing feasible graph partitions. , 2015, , .  |     | 2         |
| 65 | CycloAnt. , 2017, , .  |     | 2         |
| 66 | Active Learning for Mining Big Data. , 2018, , .   |     | 2         |
| 67 | Big Data Mining in the Presence of Concept Drifting. , 2019, , .   |     | 2         |
| 68 | Constraint-Based Evolutionary Local Search for Protein Structures with Secondary Motifs. Lecture Notes in Computer Science, 2014, , 333-344.                         | 1.0 | 2         |
| 69 | Gene Transfer: A Novel Genetic Operator for Discovering Diverse-Frequent Patterns. Lecture Notes in Computer Science, 2015, , 309-316.                               | 1.0 | 1         |
| 70 | Prediction of Origin of Replication in Genome Using DNA Sequence Based Features. , 2018, , .   |     | 1         |
| 71 | IEEE WIECON-ECE 2018 Novel Class Detection in Concept Drifting Data Streams Using Decision Tree Leaves. , 2018, , .  |     | 1         |
| 72 | Prediction of Bacteriophage Protein Locations Using Deep Neural Networks. Advances in Intelligent Systems and Computing, 2019, , 29-38.                              | 0.5 | 1         |

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|----|--|-----|-----------|
| 73 | Application of Internet of Things for Early Detection of COVID-19 using Wearables. , 2021, , .   |     | 1         |
| 74 | Image-based effective feature generation for protein structural class and ligand binding prediction. PeerJ Computer Science, 2020, 6, e253.      | 2.7 | 1         |
| 75 | iProtGly-SS: A Tool to Accurately Predict Protein Glycation Site Using Structural-Based Features. Methods in Molecular Biology, 2022, , 125-134. | 0.4 | 1         |
| 76 | GraATP: A graph theoretic approach for Automated Theorem Proving in plane geometry. , 2014, , .  |     | 0         |
| 77 | GreMuTRRR: A novel genetic algorithm to solve distance geometry problem for protein structures. , 2014, , .                                      |     | 0         |
| 78 | GreMuTRRR: A novel genetic algorithm to solve distance geometry problem for protein structures. , 2014, , .                                      |     | 0         |
| 79 | A new effective algorithm for protein chain lattice fit problem. , 2015, , .   |     | 0         |
| 80 | Guiding Artificial Neural Networks Using Discriminatory Information In Hidden Layers. , 2017, , .  |     | 0         |
| 81 | OriFeat: Origin of Replication Identification Using DNA Sequence Based Features. , 2021, , .   |     | 0         |
| 82 | Figbird: a probabilistic method for filling gaps in genome assemblies. Bioinformatics, 2022, 38, 3717-3724.                                      | 1.8 | 0         |