Maqsood Hayat

List of Publications by Year
in descending order

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59 papers	2,963 citations	126708 33 h-index	168136 53 g-index
61 all docs	61 docs citations	61 times ranked	1103 citing authors

#	Article	IF	Citations
1	Predicting membrane protein types by fusing composite protein sequence features into pseudo amino acid composition. Journal of Theoretical Biology, 2011, 271, 10-17.	0.8	148
2	Discriminating Outer Membrane Proteins with Fuzzy K-Nearest Neighbor Algorithms Based on the General Form of Chouâ€™s PseAAC. Protein and Peptide Letters, 2012, 19, 411-421.	0.4	145
3	Discrimination of acidic and alkaline enzyme using Chouâ€™s pseudo amino acid composition in conjunction with probabilistic neural network model. Journal of Theoretical Biology, 2015, 365, 197-203.	0.8	140
4	Classification of membrane protein types using Voting Feature Interval in combination with Choux3s Pseudo Amino Acid Composition. Journal of Theoretical Biology, 2015, 384, 78-83.	0.8	137
5	iMethyl-STTNC: Identification of N6-methyladenosine sites by extending the idea of SAAC into Chou's PseAAC to formulate RNA sequences. Journal of Theoretical Biology, 2018, 455, 205-211.	0.8	121
6	iRSpot-GAEnsC: identifing recombination spots via ensemble classifier and extending the concept of Chouâ€™s PseAAC to formulate DNA samples. Molecular Genetics and Genomics, 2016, 291, 285-296.	1.0	120
7	iACP-GAEnsC: Evolutionary genetic algorithm based ensemble classification of anticancer peptides by utilizing hybrid feature space. Artificial Intelligence in Medicine, 2017, 79, 62-70.	3.8	106
8	Unb-DPC: Identify mycobacterial membrane protein types by incorporating un-biased dipeptide composition into Chou's general PseAAC. Journal of Theoretical Biology, 2017, 415, 13-19.	0.8	98
9	Identification of Heat Shock Protein families and J-protein types by incorporating Dipeptide Composition into Chou's general PseAAC. Computer Methods and Programs in Biomedicine, 2015, 122, 165-174.	2.6	96
10	iMem-2LSAAC: A two-level model for discrimination of membrane proteins and their types by extending the notion of SAAC into chou's pseudo amino acid composition. Journal of Theoretical Biology, 2018, 442, 11-21.	0.8	96
11	iNuc-STNC: a sequence-based predictor for identification of nucleosome positioning in genomes by extending the concept of SAAC and Chou's PseAAC. Molecular BioSystems, 2016, 12, 2587-2593.	2.9	94
12	MemHyb: Predicting membrane protein types by hybridizing SAAC and PSSM. Journal of Theoretical Biology, 2012, 292, 93-102.	0.8	82
13	Prediction of Protein Submitochondrial Locations by Incorporating Dipeptide Composition into Chouâ€™s General Pseudo Amino Acid Composition. Journal of Membrane Biology, 2016, 249, 293-304.	1.0	81
14	Early and accurate detection and diagnosis of heart disease using intelligent computational model. Scientific Reports, 2020, 10, 19747.	1.6	73
15	Prediction of membrane proteins using split amino acid and ensemble classification. Amino Acids, 2012, 42, 2447-2460.	1.2	68
16	Discriminating protein structure classes by incorporating Pseudo Average Chemical Shift to Chou's general PseAAC and Support Vector Machine. Computer Methods and Programs in Biomedicine, 2014, 116, 184-192.	2.6	66
17	Identification of DNA binding proteins using evolutionary profiles position specific scoring matrix. Neurocomputing, 2016, 199, 154-162.	3.5	66
18	Predicting subcellular localization of multi-label proteins by incorporating the sequence features into Chou's PseAAC. Genomics, 2019, 111, 1325-1332.	1.3	64

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19	iHBP-DeepPSSM: Identifying hormone binding proteins using PsePSSM based evolutionary features and deep learning approach. Chemometrics and Intelligent Laboratory Systems, 2020, 204, 104103.	1.8	64
20	Deep-AntiFP: Prediction of antifungal peptides using distanct multi-informative features incorporating with deep neural networks. Chemometrics and Intelligent Laboratory Systems, 2021, 208, 104214.	1.8	58
21	iNR-2L: A two-level sequence-based predictor developed via Chou's 5-steps rule and general PseAAC for identifying nuclear receptors and their families. Genomics, 2020, 112, 276-285.	1.3	54
22	iAtbP-Hyb-EnC: Prediction of antitubercular peptides via heterogeneous feature representation and genetic algorithm based ensemble learning model. Computers in Biology and Medicine, 2021, 137, 104778.	3.9	54
23	iNuc-ext-PseTNC: an efficient ensemble model for identification of nucleosome positioning by extending the concept of Chouâ€™s PseAAC to pseudo-tri-nucleotide composition. Molecular Genetics and Genomics, 2019, 294, 199-210.	1.0	52
24	cACP: Classifying anticancer peptides using discriminative intelligent model via Chouâ€™s 5-step rules and general pseudo components. Chemometrics and Intelligent Laboratory Systems, 2020, 196, 103912.	1.8	50
25	Sequence based predictor for discrimination of enhancer and their types by applying general form of Chou's trinucleotide composition. Computer Methods and Programs in Biomedicine, 2017, 146, 69-75.	2.6	47
26	MFSC: Multi-voting based feature selection for classification of Golgi proteins by adopting the general form of Chou's PseAAC components. Journal of Theoretical Biology, 2019, 463, 99-109.	0.8	46
27	Pred-BVP-Unb: Fast prediction of bacteriophage Virion proteins using un-biased multi-perspective properties with recursive feature elimination. Genomics, 2020, 112, 1565-1574.	1.3	44
28	Machine learning approaches for discrimination of Extracellular Matrix proteins using hybrid feature space. Journal of Theoretical Biology, 2016, 403, 30-37.	0.8	40
29	cACP-DeepGram: Classification of anticancer peptides via deep neural network and skip-gram-based word embedding model. Artificial Intelligence in Medicine, 2022, 131, 102349.	3.8	40
30	Mem-PHybrid: Hybrid features-based prediction system for classifying membrane protein types. Analytical Biochemistry, 2012, 424, 35-44.	1.1	39
31	iAFPs-EnC-GA: Identifying antifungal peptides using sequential and evolutionary descriptors based multi-information fusion and ensemble learning approach. Chemometrics and Intelligent Laboratory Systems, 2022, 222, 104516.	1.8	37
32	Prediction of protein structure classes using hybrid space of multi-profile Bayes and bi-gram probability feature spaces. Journal of Theoretical Biology, 2014, 346, 8-15.	0.8	35
33	Machine learning based identification of proteinâ€“protein interactions using derived features of physiochemical properties and evolutionary profiles. Artificial Intelligence in Medicine, 2017, 78, 61-71.	3.8	35
34	Application of machine learning and data mining in predicting the performance of intermediate and secondary education level student. Education and Information Technologies, 2020, 25, 4677-4697.	3.5	35
35	CE-PLoc: An ensemble classifier for predicting protein subcellular locations by fusing different modes of pseudo amino acid composition. Computational Biology and Chemistry, 2011, 35, 218-229.	1.1	34
36	iTIS-PseKNC: Identification of Translation Initiation Site in human genes using pseudo k-tuple nucleotides composition. Computers in Biology and Medicine, 2015, 66, 252-257.	3.9	32

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37	iRNA-PseTNC: identification of RNA 5-methylcytosine sites using hybrid vector space of pseudo nucleotide composition. Frontiers of Computer Science, 2020, 14, 451-460.	1.6	29
38	cACP-2LFS: Classification of Anticancer Peptides Using Sequential Discriminative Model of KSAAP and Two-Level Feature Selection Approach. IEEE Access, 2020, 8, 131939-131948.	2.6	29
39	Intelligent computational model for classification of sub-Golgi protein using oversampling and fisher feature selection methods. Artificial Intelligence in Medicine, 2017, 78, 14-22.	3.8	28
40	PSOFuzzySVM-TMH: identification of transmembrane helix segments using ensemble feature space by incorporated fuzzy support vector machine. Molecular BioSystems, 2015, 11, 2255-2262.	2.9	27
41	iPredCNC: Computational prediction model for cancerlectins and non-cancerlectins using novel cascade features subset selection. Chemometrics and Intelligent Laboratory Systems, 2019, 195, 103876.	1.8	27
42	Prediction of N6-methyladenosine sites using convolution neural network model based on distributed feature representations. Neural Networks, 2020, 129, 385-391.	3.3	27
43	â€œiSS-Hyb-mRMRâ€ Identification of splicing sites using hybrid space of pseudo trinucleotide and pseudo tetranucleotide composition. Computer Methods and Programs in Biomedicine, 2016, 128, 1-11.	2.6	25
44	WRF-TMH: predicting transmembrane helix by fusing composition index and physicochemical properties of amino acids. Amino Acids, 2013, 44, 1317-1328.	1.2	24
45	iAFP-gap-SMOTE: An Efficient Feature Extraction Scheme Gapped Dipeptide Composition is Coupled with an Oversampling Technique for Identification of Antifreeze Proteins. Letters in Organic Chemistry, 2019, 16, 294-302.	0.2	23
46	A Two-Layer Computational Model for Discrimination of Enhancer and Their Types Using Hybrid Features Pace of Pseudo K-Tuple Nucleotide Composition. Arabian Journal for Science and Engineering, 2018, 43, 6719-6727.	1.7	18
47	Identification of antioxidant proteins using a discriminative intelligent model of k-space amino acid pairs based descriptors incorporating with ensemble feature selection. Biocybernetics and Biomedical Engineering, 2022, 42, 727-735.	3.3	18
48	Bi-PSSM: Position specific scoring matrix based intelligent computational model for identification of mycobacterial membrane proteins. Journal of Theoretical Biology, 2017, 435, 116-124.	0.8	16
49	kDeepBind: Prediction of RNA-Proteins binding sites using convolution neural network and k-gram features. Chemometrics and Intelligent Laboratory Systems, 2021, 208, 104217.	1.8	16
50	An intelligent computational model for prediction of promoters and their strength via natural language processing. Chemometrics and Intelligent Laboratory Systems, 2020, 202, 104034.	1.8	11
51	Efficient computational model for classification of protein localization images using Extended Threshold Adjacency Statistics and Support Vector Machines. Computer Methods and Programs in Biomedicine, 2018, 157, 205-215.	2.6	10
52	A convolution neural network-based computational model to identify the occurrence sites of various RNA modifications by fusing varied features. Chemometrics and Intelligent Laboratory Systems, 2021, 211, 104233.	1.8	10
53	A deep learning-based computational approach for discrimination of DNA N6-methyladenosine sites by fusing heterogeneous features. Chemometrics and Intelligent Laboratory Systems, 2020, 206, 104151.	1.8	9
54	Intelligent and robust computational prediction model for DNA N4-methylcytosine sites via natural language processing. Chemometrics and Intelligent Laboratory Systems, 2021, 217, 104391.	1.8	6

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55	Prediction of Membrane Protein Types Using Pseudo-Amino Acid Composition and Ensemble Classification. International Journal of Computer and Electrical Engineering, 2013, , 456-459.	0.2	6
56	ML-RBF: Predict protein subcellular locations in a multi-label system using evolutionary features. Chemometrics and Intelligent Laboratory Systems, 2020, 203, 104055.	1.8	2
57	Prediction of Piwi-Interacting RNAs and Their Functions via Convolutional Neural Network. IEEE Access, 2021, 9, 54233-54240.	2.6	2
58	An effective machine learning-based model for the prediction of proteinâ€“protein interaction sites in health systems. Neural Computing and Applications, 2024, 36, 65-75.	3.2	2
59	An Effective Deep Learning-Based Architecture for Prediction of N7-Methylguanosine Sites in Health Systems. Electronics (Switzerland), 2022, 11, 1917.	1.8	1