Abdollah Dehzangi

List of Publications by Year
in descending order

52	2,463	218677 26	206112 48
papers	citations	h-index	g-index

54	54	54	1938
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	CNN-KCL: Automatic myocarditis diagnosis using convolutional neural network combined with k-means clustering. Mathematical Biosciences and Engineering, 2022, 19, 2381-2402.	1.9	23
2	A review on deep learning approaches in healthcare systems: Taxonomies, challenges, and open issues. Journal of Biomedical Informatics, 2021, 113, 103627.	4.3	133
3	VIRMOTIF: A User-Friendly Tool for Viral Sequence Analysis. Genes, 2021, 12, 186.	2.4	17
4	Whole-Genome Analysis of De Novo Somatic Point Mutations Reveals Novel Mutational Biomarkers in Pancreatic Cancer. Cancers, 2021, 13, 4376.	3.7	9
5	Enhancing the Performance of a Model to Predict Driving Distraction with the Random Forest Classifier. Transportation Research Record, 2021, 2675, 612-622.	1.9	12
6	CluSem: Accurate clustering-based ensemble method to predict motor imagery tasks from multi-channel EEG data. Journal of Neuroscience Methods, 2021, 364, 109373.	2.5	9
7	ACP-MHCNN: an accurate multi-headed deep-convolutional neural network to predict anticancer peptides. Scientific Reports, 2021, 11, 23676.	3.3	31
8	PupStruct: Prediction of Pupylated Lysine Residues Using Structural Properties of Amino Acids. Genes, 2020, 11, 1431.	2.4	6
9	SEMal: Accurate protein malonylation site predictor using structural and evolutionary information. Computers in Biology and Medicine, 2020, 125, 104022.	7.0	10
10	Accurately Predicting Glutarylation Sites Using Sequential Bi-Peptide-Based Evolutionary Features. Genes, 2020, 11, 1023.	2.4	17
11	Enhancing protein backbone angle prediction by using simpler models of deep neural networks. Scientific Reports, 2020, 10, 19430.	3.3	18
12	RAM-PGK: Prediction of Lysine Phosphoglycerylation Based on Residue Adjacency Matrix. Genes, 2020, 11, 1524.	2.4	5
13	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.	4.1	11
14	Mal-Light: Enhancing Lysine Malonylation Sites Prediction Problem Using Evolutionary-based Features. IEEE Access, 2020, 8, 77888-77902.	4.2	12
15	C-iSUMO: A sumoylation site predictor that incorporates intrinsic characteristics of amino acid sequences. Computational Biology and Chemistry, 2020, 87, 107235.	2.3	12
16	Predicting protein-peptide binding sites with a deep convolutional neural network. Journal of Theoretical Biology, 2020, 496, 110278.	1.7	25
17	Proposing a novel community detection approach to identify cointeracting genomic regions. Mathematical Biosciences and Engineering, 2020, 17, 2193-2217.	1.9	12
18	EvolStruct-Phogly: incorporating structural properties and evolutionary information from profile bigrams for the phosphoglycerylation prediction. BMC Genomics, 2019, 19, 984.	2.8	17

#	Article	IF	Citations
19	HseSUMO: Sumoylation site prediction using half-sphere exposures of amino acids residues. BMC Genomics, 2019, 19, 982.	2.8	12
20	SPRINT-Gly: predictingN-andO-linked glycosylation sites of human and mouse proteins by using sequence and predicted structural properties. Bioinformatics, 2019, 35, 4140-4146.	4.1	48
21	PyFeat: a Python-based effective feature generation tool for DNA, RNA and protein sequences. Bioinformatics, 2019, 35, 3831-3833.	4.1	80
22	GlyStruct: glycation prediction using structural properties of amino acid residues. BMC Bioinformatics, 2019, 19, 547.	2.6	31
23	Bigram-PGK: phosphoglycerylation prediction using the technique of bigram probabilities of position specific scoring matrix. BMC Molecular and Cell Biology, 2019, 20, 57.	2.0	11
24	A novel one-class classification approach to accurately predict disease-gene association in acute myeloid leukemia cancer. PLoS ONE, 2019, 14, e0226115.	2.5	16
25	CFSBoost: Cumulative feature subspace boosting for drug-target interaction prediction. Journal of Theoretical Biology, 2019, 464, 1-8.	1.7	20
26	Computational Prediction of Lysine Pupylation Sites in Prokaryotic Proteins Using Position Specific Scoring Matrix into Bigram for Feature Extraction. Lecture Notes in Computer Science, 2019, , 488-500.	1.3	1
27	A Machine Learning Distracted Driving Prediction Model. , 2019, , .		7
28	iProtGlyâ€SS: Identifying protein glycation sites using sequence and structure based features. Proteins: Structure, Function and Bioinformatics, 2018, 86, 777-789.	2.6	32
29	EvoStruct-Sub: An accurate Gram-positive protein subcellular localization predictor using evolutionary and structural features. Journal of Theoretical Biology, 2018, 443, 138-146.	1.7	31
30	PhoglyStruct: Prediction of phosphoglycerylated lysine residues using structural properties of amino acids. Scientific Reports, 2018, 8, 17923.	3.3	31
31	SumSec: Accurate Prediction of Sumoylation Sites Using Predicted Secondary Structure. Molecules, 2018, 23, 3260.	3.8	13
32	Success: evolutionary and structural properties of amino acids prove effective for succinylation site prediction. BMC Genomics, 2018, 19, 923.	2.8	50
33	Improving succinylation prediction accuracy by incorporating the secondary structure via helix, strand and coil, and evolutionary information from profile bigrams. PLoS ONE, 2018, 13, e0191900.	2.5	51
34	PSSM-Suc: Accurately predicting succinylation using position specific scoring matrix into bigram for feature extraction. Journal of Theoretical Biology, 2017, 425, 97-102.	1.7	65
35	SucStruct: Prediction of succinylated lysine residues by using structural properties of amino acids. Analytical Biochemistry, 2017, 527, 24-32.	2.4	55
36	iPHLoc-ES: Identification of bacteriophage protein locations using evolutionary and structural features. Journal of Theoretical Biology, 2017, 435, 229-237.	1.7	29

#	Article	IF	Citations
37	iDNAProt-ES: Identification of DNA-binding Proteins Using Evolutionary and Structural Features. Scientific Reports, 2017, 7, 14938.	3.3	73
38	SPIDER2: A Package to Predict Secondary Structure, Accessible Surface Area, and Main-Chain Torsional Angles by Deep Neural Networks. Methods in Molecular Biology, 2017, 1484, 55-63.	0.9	137
39	iDTI-ESBoost: Identification of Drug Target Interaction Using Evolutionary and Structural Features with Boosting. Scientific Reports, 2017, 7, 17731.	3.3	99
40	HMMBinder: DNA-Binding Protein Prediction Using HMM Profile Based Features. BioMed Research International, 2017, 2017, 1-10.	1.9	41
41	Highly accurate sequence-based prediction of half-sphere exposures of amino acid residues in proteins. Bioinformatics, 2016, 32, 843-849.	4.1	79
42	Importance of dimensionality reduction in protein fold recognition. , 2015, , .		1
43	Gram-positive and gram-negative subcellular localization using rotation forest and physicochemical-based features. BMC Bioinformatics, 2015, 16, S1.	2.6	26
44	Predict Gram-Positive and Gram-Negative Subcellular Localization via Incorporating Evolutionary Information and Physicochemical Features Into Chou's General PseAAC. IEEE Transactions on Nanobioscience, 2015, 14, 915-926.	3.3	72
45	Improving prediction of secondary structure, local backbone angles and solvent accessible surface area of proteins by iterative deep learning. Scientific Reports, 2015, 5, 11476.	3.3	290
46	Gram-positive and Gram-negative protein subcellular localization by incorporating evolutionary-based descriptors into Chou×³s general PseAAC. Journal of Theoretical Biology, 2015, 364, 284-294.	1.7	232
47	Predicting backbone CÎ± angles and dihedrals from protein sequences by stacked sparse autoâ€encoder deep neural network. Journal of Computational Chemistry, 2014, 35, 2040-2046.	3.3	133
48	A Tri-Gram Based Feature Extraction Technique Using Linear Probabilities of Position Specific Scoring Matrix for Protein Fold Recognition. IEEE Transactions on Nanobioscience, 2014, 13, 44-50.	3.3	64
49	A strategy to select suitable physicochemical attributes of amino acids for protein fold recognition. BMC Bioinformatics, 2013, 14, 233.	2.6	40
50	A feature extraction technique using bi-gram probabilities of position specific scoring matrix for protein fold recognition. Journal of Theoretical Biology, 2013, 320, 41-46.	1.7	139
51	A Combination of Feature Extraction Methods with an Ensemble of Different Classifiers for Protein Structural Class Prediction Problem. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2013, 10, 564-575.	3.0	53
52	Using Rotation Forest for Protein Fold Prediction Problem: An Empirical Study. Lecture Notes in Computer Science, 2010, , 217-227.	1.3	18