

Abdollah Dehzangi

List of Publications by Year in descending order

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Version: 2024-02-01

52
papers

2,463
citations

218677

26
h-index

206112

48
g-index

54
all docs

54
docs citations

54
times ranked

1938
citing authors

#	ARTICLE	IF	CITATIONS
1	Improving prediction of secondary structure, local backbone angles and solvent accessible surface area of proteins by iterative deep learning. <i>Scientific Reports</i> , 2015, 5, 11476.	3.3	290
2	Gram-positive and Gram-negative protein subcellular localization by incorporating evolutionary-based descriptors into Chou's general PseAAC. <i>Journal of Theoretical Biology</i> , 2015, 364, 284-294.	1.7	232
3	A feature extraction technique using bi-gram probabilities of position specific scoring matrix for protein fold recognition. <i>Journal of Theoretical Biology</i> , 2013, 320, 41-46.	1.7	139
4	SPIDER2: A Package to Predict Secondary Structure, Accessible Surface Area, and Main-Chain Torsional Angles by Deep Neural Networks. <i>Methods in Molecular Biology</i> , 2017, 1484, 55-63.	0.9	137
5	Predicting backbone ϕ angles and dihedrals from protein sequences by stacked sparse auto-encoder deep neural network. <i>Journal of Computational Chemistry</i> , 2014, 35, 2040-2046.	3.3	133
6	A review on deep learning approaches in healthcare systems: Taxonomies, challenges, and open issues. <i>Journal of Biomedical Informatics</i> , 2021, 113, 103627.	4.3	133
7	iDTI-ESBoost: Identification of Drug Target Interaction Using Evolutionary and Structural Features with Boosting. <i>Scientific Reports</i> , 2017, 7, 17731.	3.3	99
8	PyFeat: a Python-based effective feature generation tool for DNA, RNA and protein sequences. <i>Bioinformatics</i> , 2019, 35, 3831-3833.	4.1	80
9	Highly accurate sequence-based prediction of half-sphere exposures of amino acid residues in proteins. <i>Bioinformatics</i> , 2016, 32, 843-849.	4.1	79
10	iDNAProt-ES: Identification of DNA-binding Proteins Using Evolutionary and Structural Features. <i>Scientific Reports</i> , 2017, 7, 14938.	3.3	73
11	Predict Gram-Positive and Gram-Negative Subcellular Localization via Incorporating Evolutionary Information and Physicochemical Features Into Chou's General PseAAC. <i>IEEE Transactions on Nanobioscience</i> , 2015, 14, 915-926.	3.3	72
12	PSSM-Suc: Accurately predicting succinylation using position specific scoring matrix into bigram for feature extraction. <i>Journal of Theoretical Biology</i> , 2017, 425, 97-102.	1.7	65
13	A Tri-Gram Based Feature Extraction Technique Using Linear Probabilities of Position Specific Scoring Matrix for Protein Fold Recognition. <i>IEEE Transactions on Nanobioscience</i> , 2014, 13, 44-50.	3.3	64
14	SucStruct: Prediction of succinylated lysine residues by using structural properties of amino acids. <i>Analytical Biochemistry</i> , 2017, 527, 24-32.	2.4	55
15	A Combination of Feature Extraction Methods with an Ensemble of Different Classifiers for Protein Structural Class Prediction Problem. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2013, 10, 564-575.	3.0	53
16	Improving succinylation prediction accuracy by incorporating the secondary structure via helix, strand and coil, and evolutionary information from profile bigrams. <i>PLoS ONE</i> , 2018, 13, e0191900.	2.5	51
17	Success: evolutionary and structural properties of amino acids prove effective for succinylation site prediction. <i>BMC Genomics</i> , 2018, 19, 923.	2.8	50
18	SPRINT-Gly: predicting N- and O-linked glycosylation sites of human and mouse proteins by using sequence and predicted structural properties. <i>Bioinformatics</i> , 2019, 35, 4140-4146.	4.1	48

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19	HMMBinder: DNA-Binding Protein Prediction Using HMM Profile Based Features. <i>BioMed Research International</i> , 2017, 2017, 1-10.	1.9	41
20	A strategy to select suitable physicochemical attributes of amino acids for protein fold recognition. <i>BMC Bioinformatics</i> , 2013, 14, 233.	2.6	40
21	iProtGly€SS: Identifying protein glycation sites using sequence and structure based features. <i>Proteins: Structure, Function and Bioinformatics</i> , 2018, 86, 777-789.	2.6	32
22	EvoStruct-Sub: An accurate Gram-positive protein subcellular localization predictor using evolutionary and structural features. <i>Journal of Theoretical Biology</i> , 2018, 443, 138-146.	1.7	31
23	PhoglyStruct: Prediction of phosphoglycerylated lysine residues using structural properties of amino acids. <i>Scientific Reports</i> , 2018, 8, 17923.	3.3	31
24	GlyStruct: glycation prediction using structural properties of amino acid residues. <i>BMC Bioinformatics</i> , 2019, 19, 547.	2.6	31
25	ACP-MHCNN: an accurate multi-headed deep-convolutional neural network to predict anticancer peptides. <i>Scientific Reports</i> , 2021, 11, 23676.	3.3	31
26	iPHLoc-ES: Identification of bacteriophage protein locations using evolutionary and structural features. <i>Journal of Theoretical Biology</i> , 2017, 435, 229-237.	1.7	29
27	Gram-positive and gram-negative subcellular localization using rotation forest and physicochemical-based features. <i>BMC Bioinformatics</i> , 2015, 16, S1.	2.6	26
28	Predicting protein-peptide binding sites with a deep convolutional neural network. <i>Journal of Theoretical Biology</i> , 2020, 496, 110278.	1.7	25
29	CNN-KCL: Automatic myocarditis diagnosis using convolutional neural network combined with k-means clustering. <i>Mathematical Biosciences and Engineering</i> , 2022, 19, 2381-2402.	1.9	23
30	CFSBoost: Cumulative feature subspace boosting for drug-target interaction prediction. <i>Journal of Theoretical Biology</i> , 2019, 464, 1-8.	1.7	20
31	Enhancing protein backbone angle prediction by using simpler models of deep neural networks. <i>Scientific Reports</i> , 2020, 10, 19430.	3.3	18
32	Using Rotation Forest for Protein Fold Prediction Problem: An Empirical Study. <i>Lecture Notes in Computer Science</i> , 2010, , 217-227.	1.3	18
33	EvolStruct-Phogly: incorporating structural properties and evolutionary information from profile bigrams for the phosphoglycerylation prediction. <i>BMC Genomics</i> , 2019, 19, 984.	2.8	17
34	Accurately Predicting Glutarylation Sites Using Sequential Bi-Peptide-Based Evolutionary Features. <i>Genes</i> , 2020, 11, 1023.	2.4	17
35	VIRMOTIF: A User-Friendly Tool for Viral Sequence Analysis. <i>Genes</i> , 2021, 12, 186.	2.4	17
36	A novel one-class classification approach to accurately predict disease-gene association in acute myeloid leukemia cancer. <i>PLoS ONE</i> , 2019, 14, e0226115.	2.5	16

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37	SumSec: Accurate Prediction of Sumoylation Sites Using Predicted Secondary Structure. <i>Molecules</i> , 2018, 23, 3260.	3.8	13
38	HseSUMO: Sumoylation site prediction using half-sphere exposures of amino acids residues. <i>BMC Genomics</i> , 2019, 19, 982.	2.8	12
39	Mal-Light: Enhancing Lysine Malonylation Sites Prediction Problem Using Evolutionary-based Features. <i>IEEE Access</i> , 2020, 8, 77888-77902.	4.2	12
40	C-iSUMO: A sumoylation site predictor that incorporates intrinsic characteristics of amino acid sequences. <i>Computational Biology and Chemistry</i> , 2020, 87, 107235.	2.3	12
41	Enhancing the Performance of a Model to Predict Driving Distraction with the Random Forest Classifier. <i>Transportation Research Record</i> , 2021, 2675, 612-622.	1.9	12
42	Proposing a novel community detection approach to identify cointeracting genomic regions. <i>Mathematical Biosciences and Engineering</i> , 2020, 17, 2193-2217.	1.9	12
43	Bigram-PGK: phosphoglycerylation prediction using the technique of bigram probabilities of position specific scoring matrix. <i>BMC Molecular and Cell Biology</i> , 2019, 20, 57.	2.0	11
44	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.	4.1	11
45	SEMal: Accurate protein malonylation site predictor using structural and evolutionary information. <i>Computers in Biology and Medicine</i> , 2020, 125, 104022.	7.0	10
46	Whole-Genome Analysis of De Novo Somatic Point Mutations Reveals Novel Mutational Biomarkers in Pancreatic Cancer. <i>Cancers</i> , 2021, 13, 4376.	3.7	9
47	CluSem: Accurate clustering-based ensemble method to predict motor imagery tasks from multi-channel EEG data. <i>Journal of Neuroscience Methods</i> , 2021, 364, 109373.	2.5	9
48	A Machine Learning Distracted Driving Prediction Model. , 2019, , .		7
49	PupStruct: Prediction of Pupylated Lysine Residues Using Structural Properties of Amino Acids. <i>Genes</i> , 2020, 11, 1431.	2.4	6
50	RAM-PGK: Prediction of Lysine Phosphoglycerylation Based on Residue Adjacency Matrix. <i>Genes</i> , 2020, 11, 1524.	2.4	5
51	Importance of dimensionality reduction in protein fold recognition. , 2015, , .		1
52	Computational Prediction of Lysine Pupylation Sites in Prokaryotic Proteins Using Position Specific Scoring Matrix into Bigram for Feature Extraction. <i>Lecture Notes in Computer Science</i> , 2019, , 488-500.	1.3	1