Dong-Jun Yu

List of Publications by Year
in descending order

82	2,691	172207	205818
papers	citations	29 h-index	48 g-index

83	83	83	1837
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	MAResNet: predicting transcription factor binding sites by combining multi-scale bottom-up and top-down attention and residual network. Briefings in Bioinformatics, 2022, 23, .	3.2	7
2	ATPdock: a template-based method for ATP-specific proteinâ€“ligand docking. Bioinformatics, 2022, 38, 556-558.	1.8	5
3	Short-term traffic flow prediction based on a hybrid optimization algorithm. Applied Mathematical Modelling, 2022, 102, 385-404.	2.2	16
4	StackACPred: Prediction of anticancer peptides by integrating optimized multiple feature descriptors with stacked ensemble approach. Chemometrics and Intelligent Laboratory Systems, 2022, 220, 104458.	1.8	26
5	Robust Least Squares Twin Support Vector Regression With Adaptive FOA and PSO for Short-Term Traffic Flow Prediction. IEEE Transactions on Intelligent Transportation Systems, 2022, 23, 14542-14556.	4.7	6
6	Enhancing Characteristic Gene Selection and Tumor Classification by the Robust Laplacian Supervised Discriminative Sparse PCA. Journal of Chemical Information and Modeling, 2022, , .	2.5	2
7	Robust ensemble method for short-term traffic flow prediction. Future Generation Computer Systems, 2022, 133, 395-410.	4.9	8
8	Prediction of disease-associated nsSNPs by integrating multi-scale ResNet models with deep feature fusion. Briefings in Bioinformatics, 2022, 23, .	3.2	13
9	Performing protein fold recognition by exploiting a stack convolutional neural network with the attention mechanism. Analytical Biochemistry, 2022, 651, 114695.	1.1	1
10	TripletGO: Integrating Transcript Expression Profiles with Protein Homology Inferences for Gene Function Prediction. Genomics, Proteomics and Bioinformatics, 2022, 20, 1013-1027.	3.0	4
11	Robust distance metric optimization driven GEPSVM classifier for pattern classification. Pattern Recognition, 2022, 129, 108779.	5.1	3
12	Deep learning geometrical potential for high-accuracy ab initio protein structure prediction. IScience, 2022, 25, 104425.	1.9	7
13	PScL-DDCFPred: an ensemble deep learning-based approach for characterizing multiclass subcellular localization of human proteins from bioimage data. Bioinformatics, 2022, 38, 4019-4026.	1.8	6
14	Predicting RNA solvent accessibility from multi-scale context feature via multi-shot neural network. Analytical Biochemistry, 2022, 654, 114802.	1.1	3
15	SP-GAN: Self-Growing and Pruning Generative Adversarial Networks. IEEE Transactions on Neural Networks and Learning Systems, 2021, 32, 2458-2469.	7.2	14
16	DeepPPSite: A deep learning-based model for analysis and prediction of phosphorylation sites using efficient sequence information. Analytical Biochemistry, 2021, 612, 113955.	1.1	24
17	TargetDBP+: Enhancing the Performance of Identifying DNA-Binding Proteins via Weighted Convolutional Features. Journal of Chemical Information and Modeling, 2021, 61, 505-515.	2.5	11
18	Why can deep convolutional neural networks improve protein fold recognition? A visual explanation by interpretation. Briefings in Bioinformatics, 2021, 22, .	3.2	10

#	Article	IF	Citations
19	Comprehensive assessment of machine learning-based methods for predicting antimicrobial peptides. Briefings in Bioinformatics, 2021, 22, .	3.2	55
20	Deducing high-accuracy protein contact-maps from a triplet of coevolutionary matrices through deep residual convolutional networks. PLoS Computational Biology, 2021, 17, e1008865.	1.5	70
21	SAResNet: self-attention residual network for predicting DNA-protein binding. Briefings in Bioinformatics, 2021, 22, .	3.2	22
22	Improving protein fold recognition using triplet network and ensemble deep learning. Briefings in Bioinformatics, 2021, 22, .	3.2	12
23	PScL-HDeep: image-based prediction of protein subcellular location in human tissue using ensemble learning of handcrafted and deep learned features with two-layer feature selection. Briefings in Bioinformatics, 2021, 22, .	3.2	27
24	Leveraging the attention mechanism to improve the identification of DNA N6-methyladenine sites. Briefings in Bioinformatics, 2021, 22, .	3.2	29
25	DeepnsSNPs: Accurate prediction of non-synonymous single-nucleotide polymorphisms by combining multi-scale convolutional neural network and residue environment information. Chemometrics and Intelligent Laboratory Systems, 2021, 215, 104326.	1.8	10
26	Accurate prediction of protein-ATP binding residues using position-specific frequency matrix. Analytical Biochemistry, 2021, 626, 114241.	1.1	6
27	Protein interâ€residue contact and distance prediction by coupling complementary coevolution features with deep residual networks in <scp>CASP14</scp>. Proteins: Structure, Function and Bioinformatics, 2021, 89, 1911-1921.	1.5	23
28	Improved protein relative solvent accessibility prediction using deep multi-view feature learning framework. Analytical Biochemistry, 2021, 631, 114358.	1.1	1
29	Accurate multistage prediction of protein crystallization propensity using deep-cascade forest with sequence-based features. Briefings in Bioinformatics, 2021, 22, .	3.2	11
30	TargetMM: Accurate Missense Mutation Prediction by Utilizing Local and Global Sequence Information with Classifier Ensemble. Combinatorial Chemistry and High Throughput Screening, 2021, 25, 38-52.	0.6	5
31	MutTMPredictor: Robust and accurate cascade XGBoost classifier for prediction of mutations in transmembrane proteins. Computational and Structural Biotechnology Journal, 2021, 19, 6400-6416.	1.9	16
32	ASCENT: Active Supervision for Semi-Supervised Learning. IEEE Transactions on Knowledge and Data Engineering, 2020, 32, 868-882.	4.0	13
33	SDBP-Pred: Prediction of single-stranded and double-stranded DNA-binding proteins by extending consensus sequence and K-segmentation strategies into PSSM. Analytical Biochemistry, 2020, 589, 113494.	1.1	28
34	TargetCPP: accurate prediction of cell-penetrating peptides from optimized multi-scale features using gradient boost decision tree. Journal of Computer-Aided Molecular Design, 2020, 34, 841-856.	1.3	46
35	Sequenceâ€based Detection of DNAâ€binding Proteins using Multipleâ€view Features Allied with Feature Selection. Molecular Informatics, 2020, 39, e2000006.	1.4	8
36	SSCpred: Single-Sequence-Based Protein Contact Prediction Using Deep Fully Convolutional Network. Journal of Chemical Information and Modeling, 2020, 60, 3295-3303.	2.5	8

#	Article	IF	Citations
37	Ensembling multiple raw coevolutionary features with deep residual neural networks for contactâ€map prediction in CASP13. Proteins: Structure, Function and Bioinformatics, 2019, 87, 1082-1091.	1.5	96
38	ResPRE: high-accuracy protein contact prediction by coupling precision matrix with deep residual neural networks. Bioinformatics, 2019, 35, 4647-4655.	1.8	142
39	Fast SRC using quadratic optimisation in downsized coefficient solution subspace. Signal Processing, 2019, 161, 101-110.	2.1	5
40	DNAPred: Accurate Identification of DNA-Binding Sites from Protein Sequence by Ensembled Hyperplane-Distance-Based Support Vector Machines. Journal of Chemical Information and Modeling, 2019, 59, 3057-3071.	2.5	53
41	An Integrated Feature Selection Algorithm for Cancer Classification using Gene Expression Data. Combinatorial Chemistry and High Throughput Screening, 2019, 21, 631-645.	0.6	19
42	Efficient and robust TWSVM classification via a minimum L1-norm distance metric criterion. Machine Learning, 2019, 108, 993-1018.	3.4	22
43	TargetDBP: Accurate DNA-Binding Protein Prediction via Sequence-based Multi-View Feature Learning. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 17, 1-1.	1.9	28
44	Prediction of membrane protein types by exploring local discriminative information from evolutionary profiles. Analytical Biochemistry, 2019, 564-565, 123-132.	1.1	21
45	Neighborhood attribute reduction: a multi-criterion approach. International Journal of Machine Learning and Cybernetics, 2019, 10, 731-742.	2.3	52
46	DeepTF: Accurate Prediction of Transcription Factor Binding Sites by Combining Multi-scale Convolution and Long Short-Term Memory Neural Network. Lecture Notes in Computer Science, 2019, , 126-138.	1.0	6
47	Boosting Granular Support Vector Machines for the Accurate Prediction of Protein-Nucleotide Binding Sites. Combinatorial Chemistry and High Throughput Screening, 2019, 22, 455-469.	0.6	2
48	LS-align: an atom-level, flexible ligand structural alignment algorithm for high-throughput virtual screening. Bioinformatics, 2018, 34, 2209-2218.	1.8	62
49	Accurate RNA 5-methylcytosine site prediction based on heuristic physical-chemical properties reduction and classifier ensemble. Analytical Biochemistry, 2018, 550, 41-48.	1.1	43
50	ATPbind: Accurate Proteinâ€“ATP Binding Site Prediction by Combining Sequence-Profiling and Structure-Based Comparisons. Journal of Chemical Information and Modeling, 2018, 58, 501-510.	2.5	57
51	Improving prediction of extracellular matrix proteins using evolutionary information via a grey system model and asymmetric under-sampling technique. Chemometrics and Intelligent Laboratory Systems, 2018, 174, 22-32.	1.8	25
52	A Self-Training Subspace Clustering Algorithm under Low-Rank Representation for Cancer Classification on Gene Expression Data. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 1315-1324.	1.9	45
53	Least squares twin bounded support vector machines based on L1-norm distance metric for classification. Pattern Recognition, 2018, 74, 434-447.	5.1	80
54	L1-Norm GEPSVM Classifier Based on an Effective Iterative Algorithm for Classification. Neural Processing Letters, 2018, 48, 273-298.	2.0	23

#	Article	IF	Citations
55	Predicting DNase I hypersensitive sites via un-biased pseudo trinucleotide composition. Chemometrics and Intelligent Laboratory Systems, 2017, 167, 78-84.	1.8	31
56	Predicting Protein-DNA Binding Residues by Weightedly Combining Sequence-Based Features and Boosting Multiple SVMs. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2017, 14, 1389-1398.	1.9	64
57	Short-Term traffic condition prediction of urban road network based on improved SVM. , 2017, , .		14
58	Efficient and Robust TWSVM Classifier Based on L1-Norm Distance Metric for Pattern Classification. , 2017, , .		1
59	Multi-label learning with label-specific feature reduction. Knowledge-Based Systems, 2016, 104, 52-61.	4.0	120
60	TargetM6A: Identifying N⁶-Methyladenosine Sites From RNA Sequences via Position-Specific Nucleotide Propensities and a Support Vector Machine. IEEE Transactions on Nanobioscience, 2016, 15, 674-682.	2.2	73
61	TargetCrys: protein crystallization prediction by fusing multi-view features with two-layered SVM. Amino Acids, 2016, 48, 2533-2547.	1.2	39
62	Improving N6-methyladenosine site prediction with heuristic selection of nucleotide physicalâ€“chemical properties. Analytical Biochemistry, 2016, 508, 104-113.	1.1	43
63	Prediction of Proteinâ€“Protein Interaction Sites with Machine-Learning-Based Data-Cleaning and Post-Filtering Procedures. Journal of Membrane Biology, 2016, 249, 141-153.	1.0	34
64	GPCRâ€“drug interactions prediction using random forest with drug-association-matrix-based post-processing procedure. Computational Biology and Chemistry, 2016, 60, 59-71.	1.1	29
65	Proteinâ€“protein interaction sites prediction by ensembling SVM and sample-weighted random forests. Neurocomputing, 2016, 193, 201-212.	3.5	99
66	KNN-based dynamic query-driven sample rescaling strategy for class imbalance learning. Neurocomputing, 2016, 191, 363-373.	3.5	20
67	pRNAm-PC: Predicting N6-methyladenosine sites in RNA sequences via physicalâ€“chemical properties. Analytical Biochemistry, 2016, 497, 60-67.	1.1	247
68	Disulfide Connectivity Prediction Based on Modelled Protein 3D Structural Information and Random Forest Regression. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2015, 12, 611-621.	1.9	18
69	TargetFreeze: Identifying Antifreeze Proteins via a Combination of Weights using Sequence Evolutionary Information and Pseudo Amino Acid Composition. Journal of Membrane Biology, 2015, 248, 1005-1014.	1.0	36
70	Constructing Query-Driven Dynamic Machine Learning Model With Application to Protein-Ligand Binding Sites Prediction. IEEE Transactions on Nanobioscience, 2015, 14, 45-58.	2.2	29
71	A Cascade Random Forests Algorithm for Predicting Protein-Protein Interaction Sites. IEEE Transactions on Nanobioscience, 2015, 14, 746-760.	2.2	48
72	Enhancing protein-vitamin binding residues prediction by multiple heterogeneous subspace SVMs ensemble. BMC Bioinformatics, 2014, 15, 297.	1.2	35

#	Article	IF	Citations
73	A New Supervised Over-Sampling Algorithm with Application to Protein-Nucleotide Binding Residue Prediction. PLoS ONE, 2014, 9, e107676.	1.1	37
74	Designing Template-Free Predictor for Targeting Protein-Ligand Binding Sites with Classifier Ensemble and Spatial Clustering. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2013, 10, 994-1008.	1.9	106
75	TargetATPsite: A templateâ€free method for ATPâ€binding sites prediction with residue evolution image sparse representation and classifier ensemble. Journal of Computational Chemistry, 2013, 34, 974-985.	1.5	64
76	Improving protein-ATP binding residues prediction by boosting SVMs with random under-sampling. Neurocomputing, 2013, 104, 180-190.	3.5	62
77	Learning protein multi-view features in complex space. Amino Acids, 2013, 44, 1365-1379.	1.2	19
78	SOMPNN: an efficient non-parametric model for predicting transmembrane helices. Amino Acids, 2012, 42, 2195-2205.	1.2	16
79	A Complete and Rapid Feature Extraction Method for Face Recognition. , 2006, , .		2
80	An efficient renovation on kernel Fisher discriminant analysis and face recognition experiments. Pattern Recognition, 2004, 37, 2091-2094.	5.1	64
81	Integrating rough set theory and fuzzy neural network to discover fuzzy rules. Intelligent Data Analysis, 2003, 7, 59-73.	0.4	3
82	Kernel-SOM Based Visualization of Financial Time Series Forecasting. , 0, , .		1