Zhu-Hong You

List of Publications by Year
in descending order

61	3,076	257450	161849
papers	citations	24 h-index	54 g-index

63	63	63	1914
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Predicting miRNAâ€“disease associations based on graph random propagation network and attention network. Briefings in Bioinformatics, 2022, 23, .	6.5	25
2	Predicting Protein-Protein Interactions via Random Ferns with Evolutionary Matrix Representation. Computational and Mathematical Methods in Medicine, 2022, 2022, 1-11.	1.3	1
3	Multi-view heterogeneous molecular network representation learning for proteinâ€“protein interaction prediction. BMC Bioinformatics, 2022, 23, .	2.6	8
4	MISSIM: An Incremental Learning-Based Model With Applications to the Prediction of miRNA-Disease Association. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 1733-1742.	3.0	10
5	Computational Prediction of Protein-Protein Interactions in Plants Using Only Sequence Information. Lecture Notes in Computer Science, 2021, , 115-125.	1.3	1
6	Protein-Protein Interaction Prediction by Integrating Sequence Information and Heterogeneous Network Representation. Lecture Notes in Computer Science, 2021, , 617-626.	1.3	1
7	An Efficient Computational Model for Large-Scale Prediction of Proteinâ€“Protein Interactions Based on Accurate and Scalable Graph Embedding. Frontiers in Genetics, 2021, 12, 635451.	2.3	7
8	In silico drug repositioning using deep learning and comprehensive similarity measures. BMC Bioinformatics, 2021, 22, 293.	2.6	6
9	A survey of current trends in computational predictions of protein-protein interactions. Frontiers of Computer Science, 2020, 14, 1.	2.4	19
10	A learning based framework for diverse biomolecule relationship prediction in molecular association network. Communications Biology, 2020, 3, 118.	4.4	19
11	A deep learning-based method for drug-target interaction prediction based on long short-term memory neural network. BMC Medical Informatics and Decision Making, 2020, 20, 49.	3.0	64
12	Bioentity2vec: Attribute- and behavior-driven representation for predicting multi-type relationships between bioentities. GigaScience, 2020, 9, .	6.4	10
13	A MapReduce-Based Parallel Random Forest Approach for Predicting Large-Scale Protein-Protein Interactions. Lecture Notes in Computer Science, 2020, , 400-407.	1.3	2
14	Inferring Drug-miRNA Associations by Integrating Drug SMILES and MiRNA Sequence Information. Lecture Notes in Computer Science, 2020, , 279-289.	1.3	2
15	Predicting LncRNA-miRNA Interactions via Network Embedding with Integrated Structure and Attribute Information. Lecture Notes in Computer Science, 2020, , 493-501.	1.3	2
16	Predicting Human Disease-Associated piRNAs Based on Multi-source Information and Random Forest. Lecture Notes in Computer Science, 2020, , 227-238.	1.3	3
17	Inferring Disease-Associated Piwi-Interacting RNAs via Graph Attention Networks. Lecture Notes in Computer Science, 2020, , 239-250.	1.3	5
18	Predicting Protein-Protein Interactions from Protein Sequence Information Using Dual-Tree Complex Wavelet Transform. Lecture Notes in Computer Science, 2020, , 132-142.	1.3	0

#	Article	IF	Citations
19	GCNSP: A Novel Prediction Method of Self-Interacting Proteins Based on Graph Convolutional Networks. Lecture Notes in Computer Science, 2020, , 109-120.	1.3	1
20	Combining LSTM Network Model and Wavelet Transform for Predicting Self-interacting Proteins. Lecture Notes in Computer Science, 2019, , 166-174.	1.3	2
21	Combining Evolutionary Information and Sparse Bayesian Probability Model to Accurately Predict Self-interacting Proteins. Lecture Notes in Computer Science, 2019, , 460-467.	1.3	1
22	Combining High Speed ELM with a CNN Feature Encoding to Predict LncRNA-Disease Associations. Lecture Notes in Computer Science, 2019, , 406-417.	1.3	3
23	MISSIM: Improved miRNA-Disease Association Prediction Model Based on Chaos Game Representation and Broad Learning System. Lecture Notes in Computer Science, 2019, , 392-398.	1.3	13
24	An Ensemble Classifier to Predict Proteinâ€“Protein Interactions by Combining PSSM-based Evolutionary Information with Local Binary Pattern Model. International Journal of Molecular Sciences, 2019, 20, 3511.	4.1	17
25	In Silico Identification of Anticancer Peptides with Stacking Heterogeneous Ensemble Learning Model and Sequence Information. Lecture Notes in Computer Science, 2019, , 313-323.	1.3	1
26	Prediction of Self-Interacting Proteins from Protein Sequence Information Based on Random Projection Model and Fast Fourier Transform. International Journal of Molecular Sciences, 2019, 20, 930.	4.1	30
27	A High Efficient Biological Language Model for Predicting Proteinâ€“Protein Interactions. Cells, 2019, 8, 122.	4.1	56
28	Identification of self-interacting proteins by integrating random projection classifier and finite impulse response filter. BMC Genomics, 2019, 20, 928.	2.8	4
29	A Gated Recurrent Unit Model for Drug Repositioning by Combining Comprehensive Similarity Measures and Gaussian Interaction Profile Kernel. Lecture Notes in Computer Science, 2019, , 344-353.	1.3	2
30	An Efficient LightGBM Model to Predict Protein Self-interacting Using Chebyshev Moments and Bi-gram. Lecture Notes in Computer Science, 2019, , 453-459.	1.3	2
31	A Deep Learning Framework for Robust and Accurate Prediction of ncRNA-Protein Interactions Using Evolutionary Information. Molecular Therapy - Nucleic Acids, 2018, 11, 337-344.	5.1	116
32	Predicting Protein Interactions Using a Deep Learning Method-Stacked Sparse Autoencoder Combined with a Probabilistic Classification Vector Machine. Complexity, 2018, 2018, 1-12.	1.6	17
33	A heterogeneous label propagation approach to explore the potential associations between miRNA and disease. Journal of Translational Medicine, 2018, 16, 348.	4.4	41
34	Improving Prediction of Self-interacting Proteins Using Stacked Sparse Auto-Encoder with PSSM profiles. International Journal of Biological Sciences, 2018, 14, 983-991.	6.4	19
35	An Ensemble Classifier with Random Projection for Predicting Proteinâ€“Protein Interactions Using Sequence and Evolutionary Information. Applied Sciences (Switzerland), 2018, 8, 89.	2.5	24
36	PCLPred: A Bioinformatics Method for Predicting Proteinâ€“Protein Interactions by Combining Relevance Vector Machine Model with Low-Rank Matrix Approximation. International Journal of Molecular Sciences, 2018, 19, 1029.	4.1	27

#	Article	IF	Citations
37	RP-FIRF: Prediction of Self-interacting Proteins Using Random Projection Classifier Combining with Finite Impulse Response Filter. Lecture Notes in Computer Science, 2018, , 232-240.	1.3	10
38	Efficient Framework for Predicting ncRNA-Protein Interactions Based on Sequence Information by Deep Learning. Lecture Notes in Computer Science, 2018, , 337-344.	1.3	3
39	Long non-coding RNAs and complex diseases: from experimental results to computational models. Briefings in Bioinformatics, 2017, 18, bbw060.	6.5	477
40	An improved sequence-based prediction protocol for protein-protein interactions using amino acids substitution matrix and rotation forest ensemble classifiers. Neurocomputing, 2017, 228, 277-282.	5.9	54
41	A novel computational model based on super-disease and miRNA for potential miRNAâ€“disease association prediction. Molecular BioSystems, 2017, 13, 1202-1212.	2.9	47
42	Predicting proteinâ€“protein interactions from protein sequences by a stacked sparse autoencoder deep neural network. Molecular BioSystems, 2017, 13, 1336-1344.	2.9	114
43	Detection of Interactions between Proteins by Using Legendre Moments Descriptor to Extract Discriminatory Information Embedded in PSSM. Molecules, 2017, 22, 1366.	3.8	28
44	PCVMZM: Using the Probabilistic Classification Vector Machines Model Combined with a Zernike Moments Descriptor to Predict Proteinâ€“Protein Interactions from Protein Sequences. International Journal of Molecular Sciences, 2017, 18, 1029.	4.1	61
45	Using the Relevance Vector Machine Model Combined with Local Phase Quantization to Predict Protein-Protein Interactions from Protein Sequences. BioMed Research International, 2016, 2016, 1-9.	1.9	20
46	FMLNCSIM: fuzzy measure-based lncRNA functional similarity calculation model. Oncotarget, 2016, 7, 45948-45958.	1.8	103
47	HGIMDA: Heterogeneous graph inference for miRNA-disease association prediction. Oncotarget, 2016, 7, 65257-65269.	1.8	219
48	IRWRLDA: improved random walk with restart for lncRNA-disease association prediction. Oncotarget, 2016, 7, 57919-57931.	1.8	200
49	RVMAB: Using the Relevance Vector Machine Model Combined with Average Blocks to Predict the Interactions of Proteins from Protein Sequences. International Journal of Molecular Sciences, 2016, 17, 757.	4.1	14
50	WBSMDA: Within and Between Score for MiRNA-Disease Association prediction. Scientific Reports, 2016, 6, 21106.	3.3	314
51	Improving proteinâ€“protein interactions prediction accuracy using protein evolutionary information and relevance vector machine model. Protein Science, 2016, 25, 1825-1833.	7.6	31
52	ILNCSIM: improved lncRNA functional similarity calculation model. Oncotarget, 2016, 7, 25902-25914.	1.8	122
53	Predicting Protein-Protein Interactions from Primary Protein Sequences Using a Novel Multi-Scale Local Feature Representation Scheme and the Random Forest. PLoS ONE, 2015, 10, e0125811.	2.5	136
54	Detecting Protein-Protein Interactions with a Novel Matrix-Based Protein Sequence Representation and Support Vector Machines. BioMed Research International, 2015, 2015, 1-9.	1.9	45

#	Article	IF	Citations
55	Using Weighted Sparse Representation Model Combined with Discrete Cosine Transformation to Predict Protein-Protein Interactions from Protein Sequence. BioMed Research International, 2015, 2015, 1-10.	1.9	94
56	Large-Scale Protein-Protein Interactions Detection by Integrating Big Biosensing Data with Computational Model. BioMed Research International, 2014, 2014, 1-9.	1.9	51
57	Using Chou's amphiphilic Pseudo-Amino Acid Composition and Extreme Learning Machine for prediction of Protein-protein interactions. , 2014, , .		5
58	Prediction of protein-protein interactions from amino acid sequences using a novel multi-scale continuous and discontinuous feature set. BMC Bioinformatics, 2014, 15, S9.	2.6	119
59	Prediction of protein-protein interactions from amino acid sequences with ensemble extreme learning machines and principal component analysis. BMC Bioinformatics, 2013, 14, S10.	2.6	232
60	Prediction of protein-protein interactions from amino acid sequences using extreme learning machine combined with auto covariance descriptor. , 2013, , .		6
61	A novel method to predict protein-protein interactions based on the information of protein sequence. , 2012, , .		7